



International Meeting on Emerging Diseases and Surveillance

Vienna, Austria • February 4–7, 2011

Co-sponsored by

ProMED-mail, the Program for Monitoring Emerging Diseases

EcoHealth Alliance

European Centre for Disease Prevention and Control (ECDC)

European Commission (EC)

European Society of Clinical Microbiology and Infectious Diseases (ESCMID)

HealthMap

Wildlife Conservation Society (WCS)

World Organisation for Animal Health (OIE)



Organized by International Society for Infectious Diseases

FINAL PROGRAM

<http://ntd.isid.org/>

2011

ISID-NTD

Neglected Tropical
Diseases Meeting

JULY 8–10, 2011
Boston, Massachusetts • USA

Over 1 billion of the world's poorest people suffer from one or more NTDs that profoundly affect their lives. These diseases are termed "neglected" because, in spite of the great suffering they cause, only limited resources have been available to prevent and treat them even though some of the most common NTDs can be treated effectively at very low cost.

Awareness about the problem of NTDs has grown over recent years. Governments, foundations and nonprofit organizations are increasingly taking notice and taking action. ISID aims to bring this community of providers and investigators together by organizing the first ISID-NTD meeting to encourage cross-discipline sharing of information related to combating NTDs as well as provide an opportunity to raise public awareness of the importance of NTDs around the world.

Abstract Submission Deadline: April 15, 2011

Partial List of NTDs:

- Schistosomiasis
- Lymphatic Filariasis
- African Trypanosomiasis
- Chagas Disease
- Soil Transmitted Helminthiasis
- Trachoma
- Onchocerciasis
- Leishmaniasis

Planned Topics Include:

- Documenting the global NTD burden
- Development of diagnostics and drugs for NTDs
- Current NTD treatment and control programs: Successes and challenges
- Program integration: Sharing of infrastructure and operations
- Achieving sustained control and elimination of NTDs
- Improving access to clean water and sanitation to prevent NTDs
- The role of human and animal health integration in the control of NTDs

ISID-NTD Program Committee

Uche Amazigo, African Programme for Onchocerciasis Control

Alan Fenwick, Imperial College

Eduardo Gotuzzo, Instituto de Medicina Tropical

Alexander von Humboldt

Peter Hotez, Sabin Vaccine Institute

Adrian Hopkins, Task Force for Global Health

Julie Jacobson, Bill and Melinda Gates Foundation

Seung Lee, Save the Children

Daniel Lew, Geneva University Hospital and

International Society for Infectious Diseases

Pascal Lutumba, Institut National de Recherche

Bio-Médicale Kinshasa

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Adel Mahmoud, Princeton University

David Molyneux, Liverpool School of Tropical Medicine

Mary Moran, George Institute

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2011

IMED

International Meeting

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and Surveillance

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FINAL PROGRAM



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Welcome to the International Meeting on Emerging Diseases and Surveillance, IMED 2011. Now in its third iteration, IMED has established itself as a key forum for the exchange of ideas and the presentation of new data in the realm of emerging infectious diseases and new pathogens. As early proponents of the “One Health” model, IMED and its co-sponsors each approach novel pathogens and the expansion of known ones, from an ecological perspective. This recognition of the interactions between humans and other species, wild and domesticated, is fundamental to our understanding of infectious diseases. Human and animal migration, changes in climate and culture, evolution and biodiversity all have an impact on the emergence of infectious agents on our planet.

One of the speakers at IMED 2007 warned us against looking for pandemic threats through a metaphorical telescope, while real threats loomed elsewhere on the horizon. Indeed, when the first influenza pandemic in forty years arrived, it was not a direct “jump” from birds, nor was it first detected in Asia. The pandemic H1N1 story continues to unfold, but at this meeting we will begin to understand its lessons. How can we better prepare for the next one? Can we identify viral strains in pigs and birds (or other species) that are likely to cause disease in humans? Can we develop vaccines fast enough, in enough quantity, and distribute them widely enough to prevent widespread morbidity, social disruption and death?

Other outbreaks have also focused our attention in the years since the last IMED—the epidemics of cholera in Haiti, in Zimbabwe, and in Papua New Guinea; the yellow fever outbreak in Uganda; the ongoing geographic expansion of dengue; the observation that rabies became China’s most commonly reported lethal infectious disease. Outbreaks of vaccine-preventable diseases in both animals and man—Foot and Mouth disease, measles, mumps, polio—flared in several areas of the world. Antimicrobial resistant microbes continued their march across continents, across species boundaries, in and out of healthcare settings.

IMED 2011 will highlight these and other events, our progress toward understanding and reducing the threats of emerging infectious diseases, and the many challenges that remain. We thank our co-sponsors, speakers, co-operating organizations, participants and staff, and the beautiful City of Vienna for making this meeting possible.

Larry MADOFF
Chair, Scientific Program Committee
Editor, ProMED-mail



Scientific Program Committee

- Jacques ACAR, Paris, France
- Yin Myo AYE, Bangkok, Thailand
- Karim BEN JEBARA, Paris, France
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Co-Sponsors



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- ProMED-mail, the Program for Monitoring Emerging Diseases
- EcoHealth Alliance
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- HealthMap
- Wildlife Conservation Society (WCS)
- World Organisation for Animal Health (OIE)



Co-operating Organizations

Austrian Agency for Health and Food Safety (AGES)
Austrian Federal Ministry of Health
Austrian Society for Antimicrobial Chemotherapy (ÖGACH)
Austrian Society for Infectious Diseases (OEGI)
Austrian Society of Hygiene, Microbiology and Preventive Medicine (ÖGHMP)
Austrian Society of Tropical Medicine and Parasitology (ÖGTP)
Ecole des Hautes Etudes en Santé Publique (EHESP)
Federation of Veterinarians of Europe (FVE)
International Society for Chemotherapy (ISC)
University of Veterinary Medicine Vienna

Contributors

Austrian Airlines
City of Vienna
Vienna Hilton Am Stadtpark
Vienna Convention Bureau

Exhibitors

Elsevier, England
European Centre for Disease Prevention and Control (ECDC)
HealthMap, USA
ISID, International Society for Infectious Diseases, USA
Mikrogen, Germany
OIE, Paris
John Wiley and Sons, England
Quidel, USA

**We invite you to visit the Exhibits in the
Pre-Function Area on the Ground Level.**



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Conference Office

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Opening Hours of the Registration and Information Desk

Friday, February 4, 2011 11:00 – 19:00hrs
Saturday, February 5, 2011 08:00 – 18:00hrs
Sunday, February 6, 2011 08:00 – 18:00hrs
Monday, February 7, 2011 08:00 – 12:00hrs

Congress Venue

Hilton Vienna • Am Stadtpark • 1030 Vienna
Tel: +43 1 717 000 • <http://www.hilton.com>

Registration Fees

Participants: EUR 495.00
Students: EUR 275.00

Social Program

The Welcome Reception will be held on Friday, February 4 from 17.30 to 19.00hrs at the Hilton Hotel Vienna on the Gallery (Upper Level).

The conference dinner at a typical Viennese wine tavern ('Heuriger') is partly supported by the Mayor of Vienna and will take place on Saturday, February 5. Buses will leave from the Hilton Am Stadtpark at 19.00hrs and return at approximately 22.30hrs. An invitation card is needed to gain access to this dinner and is subject to availability. The price is EUR 20,00 per person.

For both functions smart casual attire is appropriate.

Badges

Please wear your name badge at all times during the conference in order to gain access to the scientific program and all conference functions.

Internet Access

Three internet terminals will be available to conference participants in the registration area free of charge. WiFi access is also available for a fee through the Hotel. Tickets can be purchased from the Business Center on Mezzanine Level (EUR 27 for 24 hours).

CME

The International Meeting on Emerging Diseases and Surveillance 2011 (IMED 2011) is designated for a maximum of, or up to 18 European CME credits (ECMEC's). Each medical specialist should claim only those hours of credit that he/she actually spent in the educational activity. EACCME credits are recognized by the American Medical Association towards the Physician's Recognition Award (PRA). To convert EACCME credit to AMA PRA category 1 credit, contact the AMA.

This program has been submitted (but not yet approved) for 14 hours of continuing education credit in jurisdictions which recognize AAVSB RACE approval; however participants should be aware that some boards have limitations on the number of hours accepted in certain categories and/or restrictions on certain methods of delivery of continuing education. Call Norman Stein at +1-617-277-0551 for further information.

The CME form is included in the congress bag. Please complete and return it to the ISID after the conference is over as indicated on the form.



Poster Presentations

Poster Presentations will be held on Saturday, February 5 and Sunday, February 6 from 11.45 to 14.00hrs. During this period all presenters must be available for discussion at their posters.

Set-up for Poster Presentations I (Saturday):

Saturday, February 5 from 07.30 to 10.30hrs

Removal: Saturday, February 5 from 16.30 to 18.00hrs

Set-up for Poster Presentations II (Sunday):

Sunday, February 6 from 07.30 to 10.30hrs

Removal: Sunday, February 6, from 16.30 to 18.00hrs

Poster Areas (Upper Level)

Saturday, February 5, 2011 / Poster Presentations I 11:45–14:00

Room Bruckner/Mahler/Brahms / Upper Level:

<i>Abstract Number</i>	<i>Topic</i>
12.001 – 12.038	Antimicrobial resistance
12.039 – 12.048	Bioterrorism and biological warfare
12.049 – 12.052	Climate change and ecological factors in disease emergence
12.053 – 12.085	Diseases at the interface of humans, wildlife and other animals
12.086 – 12.116	Foodborne and waterborne diseases
12.117 – 12..126	Infections related to travel and migration

Klimt Ballroom I / Upper Level:

<i>Abstract Number</i>	<i>Topic</i>
12.127 – 12.166	Influenza and other respiratory infections
12.167 – 12.174	New pathogen discovery
12.175 – 12.176	Outbreak modeling
12.177 – 12.182	Sociopolitical factors in disease emergence

Sunday, February 6, 2011 / Poster Presentations II 11:45–14:00

Room Bruckner/Mahler/Brahms / Upper Level:

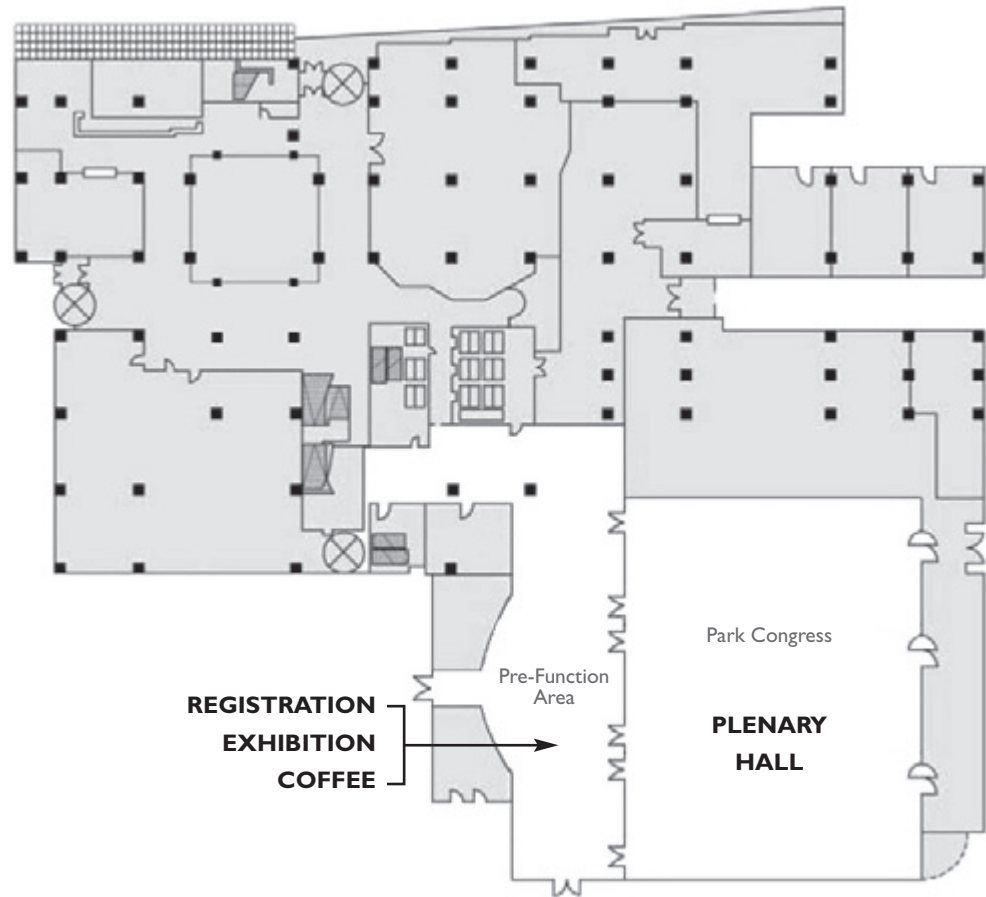
<i>Abstract Number</i>	<i>Topic</i>
21.001 – 21.053	Infections of public health significance
21.054 – 21.066	Innovations in diagnostic tests for emerging diseases
21.067 – 21.096	New approaches to outbreak surveillance and monitoring
21.097 – 21.113	Outbreak response and control
21.114 – 21.126	Public communication of outbreaks and emerging diseases

Klimt Ballroom I / Upper Level:

<i>Abstract Number</i>	<i>Topic</i>
21.127 – 21.139	Vaccines and emergence of vaccine preventable diseases
21.140 – 21.187	Vectorborne diseases

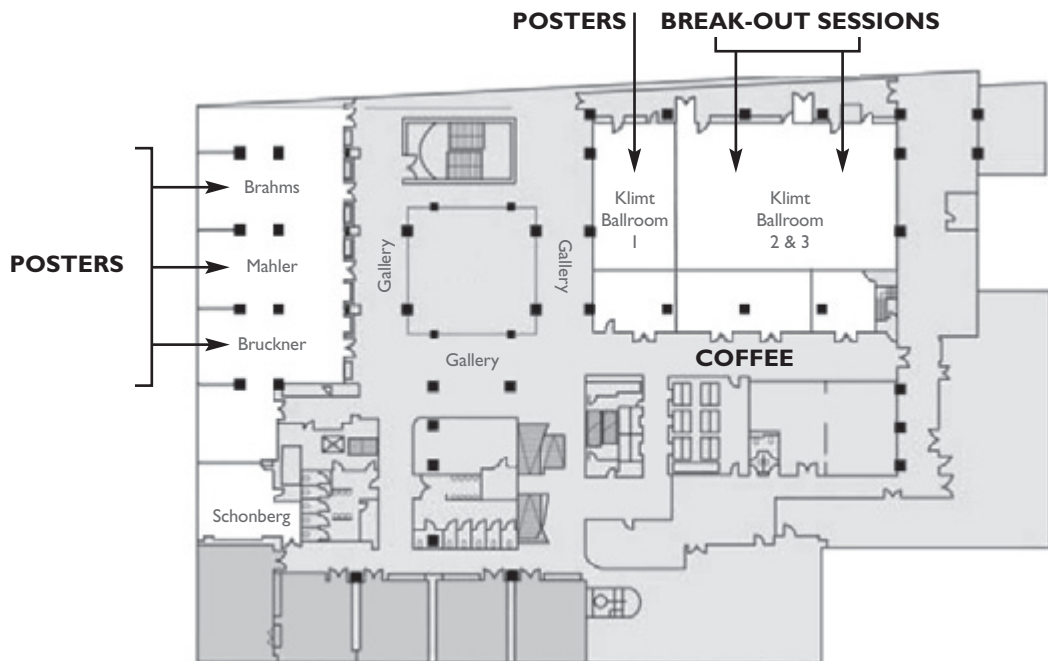


GROUND LEVEL



FIRST LEVEL

ProMED-mail Meeting (Mon.)





PROGRAM-AT-A-GLANCE

International Meeting on Emerging Diseases and Surveillance 2011

Time	Friday, February 4, 2011	Room
11:00–19:00	Registration and Information Desk	Foyer/Park Congress/Ground Level
14:00–14:20	Welcome & Opening	Park Congress/Ground Level
14:20–15:00	Session 1: Plenary Lecture: Monitoring Emerging Disease Threats in Europe	Park Congress/Ground Level
15:00–16:30	Session 2: Diseases at the Wildlife-Human Frontier	Park Congress/Ground Level
16:30–17:15	Session 3: Plenary Lecture: Wildlife and Emerging Diseases: Drivers, Maps and the Road Ahead	Park Congress/Ground Level
17:30–19:00	Welcome: Cocktail Reception	Gallery/Upper Level
Time	Saturday, February 5, 2011	Room
07:00–08:00	Session 4: Early Morning Session: GIDEON	Klimt Ballroom 2&3/Upper Level
08:30–10:30	2 Parallel Sessions: Session 5: H1N1 Pandemic Session 6: Oral Presentations: Vectorborne Diseases	Park Congress/Ground Level Klimt Ballroom 2&3/Upper Level
10:30–11:00	Coffee Break	Ground Level and Upper Level
11:00–11:45	Session 7: Plenary Lecture: Emerging Arenaviruses	Park Congress/Ground Level
11:45–14:00	Poster Presentations I (Session 12)	Bruckner/Mahler/Brahms/Upper Level and Klimt Ballroom 1/Upper Level
14:30–16:00	2 Parallel Sessions: Session 8: Emerging Diseases and Public Communication Session 9: Biosecurity and One Health	Park Congress/Ground Level Klimt Ballroom 2&3/Upper Level
16:00–16:30	Coffee Break	Ground Level and Upper Level
16:30–18:00	2 Parallel Sessions: Session 10: New Vaccines and Old Foes Session 11: Antibiotic Resistance	Park Congress/Ground Level Klimt Ballroom 2&3/Upper Level
19:00–22:30	Dinner at the wine tavern ('Heuriger')	Fuhrgassl Huber (bus transportation)
Time	Sunday, February 6, 2011	Room
07:00–08:00	Session 13: Early Morning Session: Surveillance of Stewardship	Klimt Ballroom 2&3/Upper Level
08:30–10:30	2 Parallel Sessions: Session 14: New Surveillance Strategies Session 15: Oral Presentations: Surveillance & Public Health	Park Congress/Ground Level Klimt Ballroom 2&3/Upper Level
10:30–11:00	Coffee Break	Ground Level and Upper Level
11:00–11:45	Session 16: Plenary Lecture: The Spread of Emerging Diseases by Global Air Travel	Park Congress/Ground Level
11:45–14:00	Poster Presentations II (Session 21)	Bruckner/Mahler/Brahms/Upper Level and Klimt Ballroom 1/Upper Level
14:30–16:00	2 Parallel Sessions: Session 17: Q Fever in the Netherlands Session 18: Climate Change and Infectious Diseases	Park Congress/Ground Level Klimt Ballroom 2&3/Upper Level
16:00–16:30	Coffee Break	Ground Level and Upper Level
16:30–18:00	2 Parallel Sessions: Session 19: Emerging Infection Prevention in the Healthcare Setting Session 20: Oral Presentations: Current Approaches to New Threats	Park Congress/Ground Level Klimt Ballroom 2&3/Upper Level
Time	Monday, February 7, 2011	Room
07:00–08:00	Session 22: Early Morning Session: ED in Public Health Education	Klimt Ballroom 2&3/Upper Level
08:30–10:30	2 Parallel Sessions: Session 23: Farm to Table: Foodborne Infections Session 24: Oral Presentations: Emerging Infectious Pathogens of Animals & Man	Park Congress/Ground Level Klimt Ballroom 2&3/Upper Level
10:30–11:00	Coffee Break	Ground Level and Upper Level
11:00–11:45	Session 25: Plenary Lecture: Identifying New and Emerging Viruses of Bat Origin	Park Congress/Ground Level



OPENING SESSION

International Meeting on Emerging Diseases and Surveillance 2011

Room: Park Congress • Ground Level

Friday, February 4, 2011

14:00–14:20

Opening Session

Welcome to IMED 2011

Larry Madoff

Boston, MA (USA)

Welcome to Vienna

Norbert Nowotny

Vienna (Austria)

Official Opening of the Conference jointly by

Sonja Hammerschmid, Rector of the University of Veterinary Medicine Vienna
and

Wolfgang Schütz, Rector of the Medical University of Vienna
Vienna (Austria)

Welcome by the President of the International Society for Infectious Diseases (ISID)

Daniel Lew

Geneva (Switzerland)



PLENARY LECTURE • SESSION 1

International Meeting on Emerging Diseases and Surveillance 2011

Room: Park Congress • Ground Level

Friday, February 4, 2011

14:20–15:00

Monitoring Emerging Disease Threats in Europe

Chair: Johan Giesecke, Sweden

1.001 Monitoring emerging disease threats in Europe
M. Sprenger
Stockholm (Sweden)



SYMPOSIUM • SESSION 2

International Meeting on Emerging Diseases and Surveillance 2011

Room: Park Congress • Ground Level

Friday, February 4, 2011

15:00–16:30

Diseases at the Wildlife-Human Frontier

Co-Chairs: William Karesh, USA
Nina Marano, USA

2.001 Public health and conservation: Collision or collaboration
J. Childs
New Haven, CT (USA)

2.002 Looking at bats for emerging infectious agents
S.Y. Zhang
Shanghai (China)

2.003 Rabies threats to people and endangered wildlife: If everybody benefits, who pays?
R. Woodroffe
London (United Kingdom)



PLENARY LECTURE • SESSION 3

International Meeting on Emerging Diseases and Surveillance 2011

Room: Park Congress • Ground Level

Friday, February 4, 2011

16:30–17:15

Wildlife and Emerging Diseases: Drivers, Maps and the Road Ahead

Chair: Daniel Lew, Switzerland

3.001 Wildlife and emerging diseases: Drivers, maps and the road ahead
P. Daszak¹, T. Bogich¹, P. Hosseini¹, K. Olival¹, C. Zambrana-Torrel¹, W. Karesh¹,
J. Mazet², S. Morse¹
¹New York, NY (USA), ²Davis, CA (USA)

17:30–19:00 **Welcome Reception**
Gallery/Upper Level



EARLY MORNING SESSION • SESSION 4

International Meeting on Emerging Diseases and Surveillance 2011

Room: Klimt Ballroom 2&3 • Upper Level

Saturday, February 5, 2011

07:00–08:00

GIDEON

Chair: Daniel Lucey, USA

4.001 GIDEON: A global web-based system for disease simulation and informatics in the field of geographic medicine

S. Berger
Tel Aviv (Israel)



PARALLEL SESSION • SESSION 5

International Meeting on Emerging Diseases and Surveillance 2011

Room: Park Congress • Ground Level

Saturday, February 5, 2011

08:30–10:30

H1N1 Pandemic

Co-Chairs: Ilaria Capua, Italy
Howard Markel, USA

5.001 The 2009 A/H1N1 influenza pandemic and the “Blame Game”: A brief history

H. Markel
Ann Arbor, MI (USA)

5.002 Influenza transmission: Pigs to people and back

K. Van Reeth
Ghent (Belgium)

5.003 Pandemic influenza: The early days in New York City

A. Fine
New York, NY (USA)

5.004 One health, one flu?

I. Capua¹, C. Giovanni²
¹Padua (Italy), ²Legnaro (Italy)

10:30–11:00 **Coffee Break** (Ground Level AND Upper Level)



PARALLEL SESSION • SESSION 6

International Meeting on Emerging Diseases and Surveillance 2011

Room: Klimt Ballroom 2&3 • Upper Level

Saturday, February 5, 2011

08:30–10:30

Vectorborne Diseases (Oral Presentations)

Co-Chairs: Jack Woodall, Brazil
Natalia Pshenichnaya, Russia

6.001 Transgenic mosquitoes to control dengue and chikungunya in Malaysia

S. Vasan, N.W. Ahmad, H. L. Lee
Kuala Lumpur (Malaysia)



Room: Klimt Ballroom 2&3 • Upper Level

Saturday, February 5, 2011

08:30–10:30

- 6.002 First report of concomitant leptospirosis and hantavirus nephropathy, and of an as yet unknown hantavirus in Sri-Lanka
J. Clement¹, N. Sunil-Chandra², M. Van Esbroeck³, P. Maes¹, M. Van Ranst¹
¹Louvain (Belgium), ²Kelaniya (Sri Lanka), ³Antwerp (Belgium)
- 6.003 West Nile Outbreak in the Mediterranean region, August–November 2010
P. Barboza¹, S. Ios¹, **F. Ait- El-Belghiti**¹, V. Gauthier¹, G. La Ruche¹, I. Capek¹, M. Dente², R. Vorou³, M. Gastellu¹
¹St Maurice (France), ²Italy (Italy), ³Athens (Greece)
- 6.004 Mosquito flavivirus survey in Portugal, 2006–2009
L. Zé-Zé¹, H. C. Osório¹, F. Amaro¹, I. M. Chelo², REVIVE Workgroup¹, M.-J. Alves¹
¹Águas de Moura (Portugal), ²Oeiras (Portugal)
- 6.005 Characterization of Chikungunya infection in an in vitro primary human skeletal muscle model
K. Mohamed Hussain, M. L. Ng, J. J. H. Chu
Singapore (Singapore)
- 6.006 Detection of rickettsia and anaplasma in lizards ticks, Algeria
H. Soualah-Alila, A. Belabed, Z. Bouslama
Annaba (Algeria)
- 6.007 First autochthonous dengue virus infections in south-east France in a context of a sharp increase in imported dengue cases in 2010
S. Ios¹, G. La Ruche¹, Y. Souares¹, A. Armangaud¹, P. Despres², I. Leparç Goffart³, M. Debryne⁴, G. Denoyel⁵, S. Brichler⁶, S. Plumet³, D. Dejour Salamanca¹, M. Grandadam², M. Gastellu¹
¹St Maurice (France), ²Paris (France), ³Marseilles (France), ⁴St Ouen l'Aumone (France), ⁵Lyons (France), ⁶Bobigny (France)
- 6.008 Laboratory based surveillance of dengue viral infection in a tertiary care hospital of Pakistan
cancelled **T. Ijaz**¹, Z. Salahuddin¹, S. Aslam², B. M. Ahmad³, S. Ijaz¹, M. K. Shahzad³, S. A. Raja¹
¹Lahore (Pakistan), ²Lahore (Pakistan), ³Lahore, Punjab (Pakistan)
- 6.009 Re-emerging mosquito-borne diseases in Europe
W. Van Bortel, E. Warns-Petit, K. Leitmeyer, T. Mollet, H. Zeller
Stockholm (Sweden)
- 6.010 West Nile: An emerging viral disease in North East India
S. Khan, P. Dutta, P. Chowdhury, J. Borah, J. Mahanta
Dibrugarh, Assam (India)
- 6.011 Emergence and explosive spread of West Nile virus infections in Europe—
A matter of both public health and veterinary concern
N. Nowotny¹, T. Bakonyi²
¹Vienna (Austria), ²Budapest (Hungary)
- 10:30–11:00 **Coffee Break** (Ground Level AND Upper Level)



PLENARY LECTURE • SESSION 7

International Meeting on Emerging Diseases and Surveillance 2011

Room: Park Congress • Ground Level

Saturday, February 5, 2011

11:00–11:45

Emerging Arenaviruses

Chair: Marjorie Pollack, USA

7.001 Emerging arenaviruses
R. Swanepoel
Johannesburg (South Africa)



POSTER PRESENTATIONS I • SEE PAGES 14–30

International Meeting on Emerging Diseases and Surveillance 2011

Room: Bruckner/Mahler/Brahms • Upper Level and Klimt Ballroom I • Upper Level

Saturday, February 5, 2011

11:45–14:00



PARALLEL SESSION • SESSION 8

International Meeting on Emerging Diseases and Surveillance 2011

Room: Park Congress • Ground Level

Saturday, February 5, 2011

14:30–16:00

Emerging Diseases and Public Communication

Co-Chairs: Germain Thinus, Luxembourg
Daniel Lew, Switzerland

8.001 Health security communicators network of the EC and lessons learned from H1N1
G. Thinus
Luxembourg (Luxembourg)

8.002 Using data from social networking sites to predict the spread of pandemic influenza
J. Östh¹, T. Niedomysl², B. Malmberg²
¹Uppsala (Sweden), ²Stockholm (Sweden)

8.003 'OMG, are we all gonna die?'—Covering the 2009 flu pandemic, from confusion to terror to indifference, with stops at journalistic poverty, White House intimidation, Google-worship, summer camp and the video game formerly known as sneeze
D. G. McNeil Jr.
New York, NY (USA)

16:00–16:30 **Coffee Break** (Ground Level AND Upper Level)



PARALLEL SESSION • SESSION 9

International Meeting on Emerging Diseases and Surveillance 2011

Room: Klimt Ballroom 2&3 • Upper Level

Saturday, February 5, 2011

14:30–16:00

Biosecurity and One Health — Session co-sponsored by OIE

Co-Chairs: Bernard Vallat, France
Dagmar Hanold, Australia

- 9.001 Animals as detectors of bio-events
B. Vallat
Paris, (France)
- 9.002 Biosecurity and plant pathogens
I. Sache
Paris (France)
- 9.003 Twinning between laboratories will improve disease security worldwide
K. Hamilton
Paris (France)
- 9.004 Bees, agricultural health and food security
M.-P. Chauzat
Sophia Antipolis (France)

16:00–16:30 **Coffee Break** (Ground Level AND Upper Level)



PARALLEL SESSION • SESSION 10

International Meeting on Emerging Diseases and Surveillance 2011

Room: Park Congress • Ground Level

Saturday, February 5, 2011

16:30–18:00

New Vaccines and Old Foes: Emerging Issues in Vaccine Preventable Diseases

Co-Chairs: Marjorie Pollack, USA
Norbert Nowotny, Austria

- 10.001 Polio—Vaccine end game strategy
R. Sutter
Geneva (Switzerland)
- 10.002 Vaccination towards the global control and eradication of foot-and-mouth disease
L. Rodriguez, E. Rieder
¹Orient Pt., NY (USA)
- 10.003 Measles—Is eradication feasible?
C.A. de Quadros
Washington, DC (USA)



PARALLEL SESSION • SESSION II

International Meeting on Emerging Diseases and Surveillance 2011

Room: Klimt Ballroom 2&3 • Upper Level

Saturday, February 5, 2011

16:30–18:00

Antibiotic Resistance — Session co-sponsored by ESCMID

Co-Chairs: Giuseppe Cornaglia, Italy
Larry Lutwick, USA

11.001 Emergence of resistance in the clinic

G. Cornaglia
Siena (Italy)

11.002 Surveillance of antimicrobial resistance and antibiotic use
in humans and animals

O. Heuer¹, K. Grave², P.A. Beloeil³, H. Goossens⁴, H. C. Wegener⁵
¹Stockholm (Sweden), ²London (United Kingdom), ³Parma (Italy),
⁴Antwerp (Belgium), ⁵Copenhagen (Denmark)

11.003 Shared resistance determinants in humans and animals

speaker to be confirmed

11.004 Common epidemiological cutoffs (ECOFFs) for surveillance
of resistance: Is it feasible?

G. Kahlmeter
Växjö (Sweden)

19:00–22:30 **Dinner at the wine tavern ('Heuriger')**
Fuhrgassl Huber, Neustift am Walde

Buses will leave at 19.00hrs from the Hilton Hotel
(side entrance) and will return to the Hilton at
approximately 22.30hrs



POSTER PRESENTATIONS • SESSION 12

International Meeting on Emerging Diseases and Surveillance 2011

Saturday, February 5, 2011 • Poster Presentations I • 11:45–14:00

Room Bruckner/Mahler/Brahms • Upper Level:

Abstract Number	Topic
12.001 – 12.038	Antimicrobial resistance
12.039 – 12.048	Bioterrorism and biological warfare
12.049 – 12.052	Climate change and ecological factors in disease emergence
12.053 – 12.085	Diseases at the interface of humans, wildlife and other animals
12.086 – 12.116	Foodborne and waterborne diseases
12.117 – 12.126	Infections related to travel and migration

Klimt Ballroom I • Upper Level:

Abstract Number	Topic
12.127 – 12.166	Influenza and other respiratory infections
12.167 – 12.174	New pathogen discovery
12.175 – 12.176	Outbreak modeling
12.177 – 12.182	Sociopolitical factors in disease emergence



Room: Bruckner/Mahler/Brahms • Upper Level

Saturday, February 5, 2011

11:45–14:00

- 12.001
cancelled In vitro evaluation of the effect of hops (*Humulus lupulus*) alcoholic extract on sensitive and resistant strains of *Mycobacterium tuberculosis*
B. Nasr Esfahani¹, K. Kermanshahi², J. Esmi³, G. Asghari¹
¹Isfahan (Iran), ²Tehran (Iran), ³Gom (Iran)
- 12.002 Antibacterial susceptibility patterns and contributing factors to nosocomial and ventilator associated pneumonia in ICUs, Shiraz, Iran
A. Japoni, A. Vazin, M. A. Davarpanah, M. Afkhami Ardakani, A. Alborzi¹, S. Japoni, N. Rafaatpour
Shiraz (Iran)
- 12.003 Periodontitis and antibacterial susceptibility patterns of *Porphyromonas gingivalis* isolated from adult patients
A. Japoni, A. Vasin, S. Noushadi¹, F. Kiany, S. Japoni, A. Alborzi
Shiraz (Iran)
- 12.004 Frequency and antibiotic susceptibility of Gram-positive bacteria in Makkah hospitals—Saudi Arabia
A. Asghar
Makkah (Saudi Arabia)
- 12.005 Recovery of a Tn402-like class I integron with a novel cassette array and flanking miniature inverted-repeat transposable element-like structures
M. R. Gillings, M. Labbate, **A. Sajjad**, M. Holley, H. Stokes
Sydney, NSW (Australia)
- 12.006 Presence of multidrug-resistant vibrio species isolated from molluscan shellfish in the coastal environments of Canada
S. Banerjee, L. Bakouche, J. M. Farber
Ottawa, ON (Canada)
- 12.007 Infection/colonisation with methicillin resistant *Staphylococcus aureus* (MRSA), penicillin-resistant *Streptococcus pneumoniae* (PRP) and vancomycin resistant enterococci (VRE), Oppland and Hedmark Counties, Norway — 1995–2009
V. Hasseltvedt
Lillehammer (Norway)
- 12.008 Changing trends in antimicrobial resistance in *Salmonella* serovar typhi: An epidemiological study
S. Kumar, M. Rizvi, S. R. Saigal
New Delhi (India)
- 12.009 Assessing the rising cases of methicillin-resistant *Staphylococcus aureus*: Hospital and community-associated cases
C. Oraka
Nnewi (Nigeria)
- 12.010 Antibiotic sensitivity and resistance patterns of *S.typhi* isolated from Khairpur, Sindh Pakistan
cancelled **Y. Kazi**
Khairpur (Pakistan)



Room: Bruckner/Mahler/Brahms • Upper Level

Saturday, February 5, 2011

11:45–14:00

- 12.011 Characterization of extended-spectrum β -lactamases in the isolates of *Enterobacter cloacae* from Split, Croatia
B. Bedenic¹, I. Franolic-Kukina², S. Sardelic³, M. Ajman⁴, J. Vranes¹
¹Zagreb (Croatia), ²Gospic (Croatia), ³Split (Croatia), ⁴Rijeka (Croatia)
- 12.012 Detection of plasmid-mediated AmpC beta-lactamase producing *Klebsiella pneumoniae* in blood culture
S. Luk, W. K. Wong, T. K. Ng, W. K. To, S. Lo
Hong Kong (China)
- 12.013 Antimicrobial susceptibility acinetobacter species
I. Zurak
Zagreb (Croatia)
- 12.014 Multidrug-resistant organisms in a military medical facility in Masar-e-Sharif
F. Herrmann
Munich (Germany)
- 12.015 Surveillance of antiretroviral resistance among HIV patients receiving ART in Georgia
N. Chkhartishvili, N. Dvali, **L. Sharvadze**, M. Karchava, T. Tsertsvadze
Tbilisi (Georgia)
- 12.016 Tuberculous Meningitis: Novel ways to evade antimicrobial resistance
R. Bhandari, I. P. Kaur
Chandigarh (India)
- 12.017 Rates of methicillin resistant *S. aureus* bloodstream infections and infection control policies in California hospitals
M. Pogorzelska, E. Larson, P. Stone
New York, NY (USA)
- 12.018 Risk factors for multidrug-resistant invasive pneumococcal disease in South Africa, 2003–2008
P. Crowther-Gibson¹, C. Cohen¹, K. Klugman², L. de Gouveia¹, A. von Gottberg¹
¹Johannesburg (South Africa), ²Atlanta, GA (USA)
- 12.019 Antibiotic resistance in wild greater flamingos (*Phoenicopterus roseus*): Results from a network of Mediterranean sites provide evidence of spatial variability
E. Diskin, D. Coleman, D. Taylor, A. Donnelly
Dublin (Ireland)
- 12.020 Effectiveness of porcine lysozyme as a candidate antibacterial agent to supersede antibiotics
Y. Tsuchiya¹, S. Inumaru²
¹Kodaira, Tokyo (Japan), ²Tsukuba, Ibaraki (Japan)
- 12.021 Antimicrobial susceptibility in children with urinary tract infection in a pediatric hospital of Western Venezuela
A. Herrera-Martinez¹, M. Limper², J. Cotua¹, Y. Herrera-Martinez¹, E. van Gorp³, I. Arias¹
¹Barquisimeto (Venezuela), ²Amsterdam (Netherlands), ³Rotterdam (Netherlands)
- 12.022 WHO Global Foodborne Infections Network external quality assurance system (EQAS) for antimicrobial susceptibility testing of *Salmonella* isolates
S. Karlslose¹, R. S. Hendriksen¹, M. Mikoleit², A. B. Jensen¹, A. Aidara-Kane³, D. M. Lo Fo Wong³, F. M. Aarestrup¹
¹Kgs. Lyngby (Denmark), ²Atlanta, GA (USA), ³Geneva (Switzerland)



Room: Bruckner/Mahler/Brahms • Upper Level

Saturday, February 5, 2011

11:45–14:00

- 12.023 Clinical mastitis in cows and their response to in vitro sensitivity
A. Agha, O. N. Ermithi, M. A. Abujila
Tripoli (Libya)
- 12.024 Shiga toxin-producing *Escherichia coli* (STEC) isolates from different origins showed high antimicrobial susceptibilities
R. Bonke¹, N. Drees¹, E. Stüber¹, M. Eggert¹, C. Bumann¹, M. Fredriksson-Ahomaa², E. Märtilbauer¹
¹Oberschleißheim (Germany), ²Helsinki (Finland)
- 12.025 Trends in pediatric bacterial meningitis in Sudan 2005–2006
M. Mahmoud, S. M. A. Bakhiet, A. H. A. Mohammed, M. E. M. ElKarsani
Khartoum (Sudan)
- 12.026 Role of limited access dressing in eliminating multi-drug resistant organisms capable of forming biofilms in wound infections
cancelled **P. Kumar**¹, I. Bairy², K. Chawla², S. Sarkar², A. Sarkar²
¹Karnataka (India), ²Manipal (India)
- 12.027 Isolation resistant *Enterococci* from hospitalised patients in two years
F. Fallah, G. Eslami, H. Goudarzi
Tehran, (Iran),
- 12.028 Phage nanobiotechnology, applications for defense against emerging pathogens
D. Trudil
Reisterstown, MD (USA)
- 12.029 Multidrug-resistant bacteria in urban surface waters
E. B. M. Denner, L. Strebinger, I. Gerstl, S. Hagemann, B. Velimirov
Vienna (Austria)
- 12.030 Antimicrobial susceptibility of *Pseudomonas aeruginosa* invasive isolates in Clinical Center of Serbia: 2007–2010
T. Tosic, M. Jovanovic, B. Stosovic, I. Milosevic, L. Lavadinovic, O. Dulovic, M. Svabic-Vlahovic
Belgrade (Serbia)
- 12.031 Evaluation of antimicrobial Resistance of *Vibrio cholera* obtained from patients and contaminated water of Kashan city 1998–2009
A. Hasan, A. Khorshidi
Kashan, Isfahan (Iran)
- 12.032 Antibiotic-resistant cholera strains isolated in Kazakhstan
R. Mussagaliyeva¹, Z. Zhumadilova², B. Atshabar¹, U. Sagymbek¹, Z. Sagiyev¹, G. Omarova³
¹Almaty (Kazakhstan), ²Astana (Kazakhstan), ³Atyrau (Kazakhstan)
- 12.033 Detection of Integron elements and gene groups encoding ESBLs and their prevalence in *E. coli* and *Klebsiella* isolated from urine and stool samples of patients who referred to Mofeed children hospital in Tehran by PCR method
F. Fallah, **M. Malekan**, A. Karimi, E. Mirsamadi, S. Jahani Sharafat
Tehran, (Iran)



Room: Bruckner/Mahler/Brahms • Upper Level

Saturday, February 5, 2011

11:45–14:00

- 12.034 Ambiguity in the diagnosis of pneumococcal infections and emerging of optochin resistance in clinical isolates of *Streptococcus pneumoniae* in Iran
M. Oskoui, S. Nobari, F. Rahmati Ghezalgeh
Tehran (Iran)
- 12.035 Emerging of *Streptococcus pneumoniae* isolates with high-level resistance to penicillin in Iran
M. Oskoui, F. Rahmati Ghezalgeh, S. Nobari
Tehran (Iran)
- 12.036 Clinical outcomes of patients with *Klebsiella pneumoniae* carbapenemase (KPC) in a Mexico general hospital
P. Rodriguez Zulueta, **J. Reyes Mar**, F. Velez Perez, C. Amabile Cuevas, L. Ochoa Carrera, R. Rodriguez Badillo, D. Moncada Baron, S. Arroyo Escalante, C. Espinoza Lopez, R. Hernandez Castro, R. Valdez Vazquez
Mexico City (Mexico)
- 12.037 Nasal carriage of multidrug resistant *Staphylococcus aureus* in medical personnel of tertiary care hospital in Nepal
K. Sapkota¹, S. Raj Basnyat², K. Sapkota³, C. Devi Shrestha², J. Shrestha²
¹Las Cruces, NM (USA), ²Kathmandu (Nepal), ³Myagdi (Nepal)
- 12.038 National survey on MRSA in pigs in Finland in 2009–2010
S. Raulo, A.-L. Myllyniemi, S. Salmenlinna, T. Laine, H. Helin-Soilevaara
Helsinki (Finland)
- 12.039 Knowledge, attitude and practice (KAP) regarding anthrax among health care workers in some hospitals in Tehran, 2010
A. Ghalyanchi Langeroudi¹, **K. Majidzadeh**¹, M. Soleimani², M. M. Kian¹, S. Shams¹, A. H. Mohseni¹
¹Tehran (Iran), ²Qom (Iran)
- 12.040 Simultaneous and rapid detection of *Bacillus anthracis*, *Salmonella typhi* and *Yersinia pestis* by multiplex PCR
A. Karami
Tehran (Iran)
- 12.041 Rapid detection of *Bacillus anthracis* by multiplex PCR
A. Karami
Tehran (Iran)
- 12.042 Challenges to administrative and management facilitation to a research laboratory handling Ebola and Marburg viruses at a virus research institution without BSL3 and BSL 4 facilities in an African country
cancelled **M. Musagara**
Entebbe (Uganda)
- 12.043 Early diagnostics for the biothreat agent *Burkholderia pseudomallei*
H. Rose, T. Parsons, A. Essex-Lopresti, G. Hartley, B. Walker, R. Lukaszewski
Salisbury (United Kingdom)
- 12.044 Comparison of real time PCR and ELISA tests for clinical diagnostics
T. Parsons¹, H. Rose², A. Essex-Lopresti², G. Hartley², B. Walker², R. Lukaszewski²
Salisbury (United Kingdom)



Room: Bruckner/Mahler/Brahms • Upper Level

Saturday, February 5, 2011

11:45–14:00

- 12.045 Electrostatic detection and characterization of bio-nanoparticles and intact viruses
G. Allmaier, G. Bacher, P. Kallinger, **W.W. Szymanski**
Vienna (Austria)
- 12.046 The rise and fall of the bioterrorism 'myth'
P. Washer
London (United Kingdom)
- 12.047 Biological threat prevention—Approaches for increased international co-operation
W. Crocker
Moscow (Russia)
- 12.048 United States Department of Agriculture (USDA): Application for permit to import or transport controlled material or organisms or vectors
T. Letonja
Riverdale, MD (USA)
- 12.049 Teschen disease emergence and environment pollutions
A. Buzun
Kharkiv (Ukraine)
- 12.050 Impact of agricultural development on the emergence of visceral leishmaniasis in Central Tunisia
K. Aoun¹, F. Jeddi¹, B. Zouari¹, F. Amri², A. Bouratbine¹
¹Tunis (Tunisia), ²Kairouan (Tunisia)
- 12.051 Trendy of leptospirosis in Albania
E. Puca, A. Pilaca, P. Pipero, **G. Stroni**, S. Kurti, E. Tomini, E. Abazaj, T. Myrseli, E. Puca
Tirana (Albania)
- 12.052 *cancelled* Soil-helminthiasis and schistosomiasis prevalence before and after rainy season
H. Niangaly
Bamako (Mali)
- 12.053 A search for the rodent hosts of *Leishmania major* in Southern Iran: Demonstration of the parasite in *Tatera indica* and *Gerbillus* sp., by microscopy, culture and PCR
D. Mehrabani, M. H. Motazedian, A. Oryan, Q. Asgari, G. R. Hatam, M. Karamian
Shiraz (Iran)
- 12.054 *Tatera indica* as reservoir host of *Leishmania major* in Estahban, Southern Iran
D. Mehrabani, M. H. Motazedian, Q. Asgari, G. R. Hatam, S. M. Owji, A. Oryan
Shiraz (Iran)
- 12.055 *Rattus norvegicus* as reservoir host of *Leishmania major* in Fars Province, Southern Iran
M. H. Motazedian, M. Parhizkari, **D. Mehrabani**, G. R. Hatam, Q. Asgari
Shiraz (Iran)
- 12.056 *Tatera indica* as reservoir host of *L. major* in Shiraz, Southern Iran
Q. Asgari¹, M. H. Motazedian¹, **D. Mehrabani**¹, A. Oryan¹, G. R. Hatam¹, H. Paykari²
¹Shiraz (Iran), ²Tehran (Iran)
- 12.057 *cancelled* The survey of drug resistance and prevalence of Urinary Tract Infections amongst hospitalized infants and neonates in the west of Iran (Ilam) during 2008–2010
A. Feizi, **H. Peyman**, M. Mohammad Hassan Nahal, F. Soheili, S. Soroush,
M. Taherikalani
Ilam (Iran)



Room: Bruckner/Mahler/Brahms • Upper Level

Saturday, February 5, 2011

11:45–14:00

- 12.058 *Yersinia pseudotuberculosis*, iron and disease
S. Cork
Calgary, AB (Canada)
- 12.059 Pathogenic leptospira in rodents in the Canary Islands
P. Foronda¹, A. Martin-Alonso¹, C. Feliu², M. Lopez¹, N. Abreu-Acosta¹,
A. Fernandez-Alvarez¹, H. Gil Gil³, B. Valladares¹
¹La Laguna (Spain), ²Barcelona (Spain), ³Madrid (Spain)
- 12.060 Digestive tract disorders in leptospirosis
G. Stroni, D. Kraja, B. Byku, G. Sulcebeg
Tirana (Albania)
- 12.061 Serological confirmation is decisive for the diagnoses of
Dobrava virus infection. Case report
E. Puca, A. Pilaca, A. Ndreu, K. Shkurti, **G. Stroni**, M. Kote, E. Rogozi,
E. Puca, S. Bino, P. Pipero, D. Kraja
Tirane (Albania)
- 12.062 Current status of Q fever in Ukraine and needs for expand surveillance
of *Coxiella burnetii*
I. Kurhanova¹, Z. Kushnir¹, A. Tarasyuk¹, N. Bek¹, T. Lutsyk¹, I. Vsyaka¹,
W. Nicholson², A. Richards³
¹Lviv, UA (Ukraine), ²Atlanta, GA (USA), ³Silver Spring, MD (USA)
- 12.063 Equine herpesvirus-5 associated with equine multinodular pulmonary fibrosis
in four Horses
A. Gruber, B. Schwarz, V. Benetka, K. Fragner, B. Rütgen, H. Weissenboeck
Vienna (Austria)
- 12.064 Diagnosis of a human parapoxvirus infection in Austria, in 2010
S. Richter¹, S. Revilla-Fernández¹, H. Plicka¹, B. Kranzelbinder², W. Aberer², F. Allerberger¹
¹Vienna (Austria), ²Graz (Austria)
- 12.065 Emergence and re-emergence of smallpox
S. Shchelkunov
Koltsovo (Russia)
- 12.066 Campylobacter and Salmonella occurrence in young greater flamingos
(*Phoenicopterus ruber roseus*) in northeastern Spain
N. Antilles, **M. Cerdà-Cuellar**
Bellaterra (Spain)
- 12.067 Prevalence of canine visceral leishmaniasis in dogs (*Canis lupus familiaris*)
in Palestine
S. Damaj¹, **A. Al-Jawabreh**², O. Hamarsheh¹, A. Nasereddin¹, S. Sawalha¹,
H. Al-Jawabreh³, K. Azmi¹, A. Amro¹, S. Arekat¹, S. Qaddomi¹, Z. Abdeen¹
¹Jerusalem, ²Jericho



POSTER PRESENTATIONS • SESSION 12

International Meeting on Emerging Diseases and Surveillance 2011

Room: Bruckner/Mahler/Brahms • Upper Level

Saturday, February 5, 2011

11:45–14:00

- 12.068 Hepatitis E in Belgium: an imported disease or a viral zoonosis?
V. Hutse, B. Brochier
Brussels (Belgium)
- 12.069 Emerging infectious diseases: a long term multidisciplinary study in the Camargue
M. Vittecoq¹, F. Thomas², M. Gauthier-Clerc¹
¹Arles (France), ²Montpellier (France)
- 12.070 Detection of Chikungunya virus from domestic animal samples collected from epidemic and non-epidemic areas in Thailand
S. Thongyuan, W. Uamcharoen, P. Kittayapong
Nakhon Pathom, TH (Thailand)
- 12.071 Domestic and wild mammals as possible reservoirs hosts of Leishmania spp. in Darién region of Colombia
J. E. Pérez Jaramillo, L. M. Carrillo Bonilla, H. Cadena Peña, C. D. Agudelo Rivera, K. Mondragon Shem, L. A. Acosta Cardona, A. F. Vélez Mira, I. D. Vélez Bernal
Medellin, Antioquia (Colombia)
- 12.072 Potential economic impact of poultry restructuring in Vietnam using an ecohealth approach
D. Hall, Q. L. Ba
Calgary, (Canada)
- 12.074 Current epidemiologic situation with dangerous bacterial and viral diseases in Azerbaijan
S. Gurbanov, **R. M. Abdullayev**, R. I. Ismaylova
Baku (Azerbaijan)
- 12.075 Cowpoxvirus infection in farmed llamas in Italy
G. Cardeti¹, A. Brozzi², C. Eleni¹, N. Polici², G. D'Alterio², F. Carletti¹, M. T. Scicluna¹, C. Castilletti¹, A. Di Caro¹, G. L. Autorino¹, D. Amaddeo¹
¹Rome (Italy), ²Viterbo (Italy)
- 12.076 Blood variation in brucellosis
L. Klodiana
Tirana, Albania (Albania)
- 12.077 Junin, Machupo, and Guanarito: Patterns of New World arenaviruses
L. Moore
Arlington, VA (USA)
- 12.078 Human hantavirus outbreak in Bavaria, Germany in 2010: An emerging problem?
C. Klinc¹, M.-S. Ludwig², K. Schönberger², W. Hautmann², M. Wildner²
¹Oberschleissheim (Germany), ²Oberschleißheim (Germany)
- 12.079 Orthopoxviruses seroprevalence among cats from different areas of Friuli Venezia Giulia, Italy
cancelled **C. Castilletti**¹, D. Lapa¹, A. Troi², F. Bragantini², E. Ndip Nganyuo², A. Arzese², A. Di Caro¹, M. Capobianchi¹, A. Beltrame²
¹Rome (Italy), ²Udine (Italy)



Room: Bruckner/Mahler/Brahms • Upper Level

Saturday, February 5, 2011

11:45–14:00

- 12.080 Ten years of fox variant rabies epidemiology in Nunavik, Québec, 1999–2009
C. Aenishaenslin¹, T. Forde², C. Fehlner-Gardiner³, I. Picard⁴, D. Bélanger⁵
¹Saint-Hyacinthe, QC (Canada), ²Calgary, AL (Canada), ³Ottawa, ON (Canada),
⁴Québec, Qc (Canada), ⁵Saint-Hyacinthe, QU (Canada)
- 12.081 The U.S. Armed Forces Health Surveillance Center: Efforts in disease surveillance at the human-animal interface
K. Vest, R. L. Burke
Silver Spring, MD (USA)
- 12.082 Cowpox virus outbreak in pet rats
D. Thaller¹, P. Wohlsein², J. Kolodziejek¹, H. Lussy¹, H. Weissenboeck¹, N. Nowotny¹
¹Vienna (Austria), ²Hanover (Germany)
- 12.083 Farmed wildlife surveillance: The missing link in understanding the ecology and diversity of pathogens posing risks to people, free-ranging wildlife, and livestock
S. Newman, T. McCracken
Rome (Italy)
- 12.084 Isolation, identification, serotyping and evaluation of diagnostic test on leptospira from urine of slaughtered cattle
T. T. Myiang, H. H. Win, L. L. Htun, S. S. Wai, S. Bawn, K. S. Linn, M. T. Hnin Oo
Nay Pyi Taw (Myanmar)
- 12.085 Pathogen Spillover, Zoonotic Disease, and the Use of Modeling Tools to Address Public Health Needs
K. A. Alexander, B. Lewis, M. Marathe, S. Eubank
Blacksburg, VA (USA)
- 12.086 The antimicrobial properties of silver nano particle on food-borne pathogens
Y. Abdolvand, S. Mehrabian, N. Amirmozafari
Tehran (Iran)
- 12.087 Effect of pasteurization on microbial characteristics of liquid eggs in Iran: The first comprehensive study
A. Ghalyanchi Langeroudi¹, **M. R. Rafeie**¹, K. Majidzadeh¹, M. Soleimani², A. Dashtbani¹
¹Tehran (Iran), ²Qom (Iran)
- 12.088 Campylobacteriosis in Oppland and Hedmark Counties, Norway, 1981–2009
V. Hasseltvedt
Lillehammer (Norway)
- 12.089 Globalisation and the food supply
S. Cork
Calgary (Canada)
- 12.090 Outbreak of gastroenteritis in Tibetan transit school, Dharamshala, Himachal Pradesh, India, 2006
S. Gupta¹, N. Gupta¹, N. Mehta²
¹Kangra, Himachal Pradesh (India), ²Kangra, Himachal Pradesh (India)
- 12.091 Yersiniosis in Oppland and Hedmark counties, Norway, 1990–2009
V. Hasseltvedt
Lillehammer (Norway)



Room: Bruckner/Mahler/Brahms • Upper Level

Saturday, February 5, 2011

11:45–14:00

- 12.092 A study of allergic sensitization to *Anisakis* species in experimental mice
R. G. Diab, M. M. El-Temahy, E. D. El-Kerdany, **M. R. Gaafar**
Alexandria (Egypt)
- 12.093 Evaluation of the co-agglutination test in diagnosis of experimental microsporidiosis
M. R. Gaafar
Alexandria (Egypt)
- 12.094 Seroepidemiology of *Cryptosporidium* and variation over time associated with changes in the treatment of drinking water
K. Pollock, C. N. Ramsay
Glasgow (United Kingdom)
- 12.095 Molecular epidemiological analysis of *Campylobacter* infection in Fukuoka, Japan
S. Fujimoto¹, F. Kojima¹, Y. Harada¹, S. Higashida¹, M. Shigematsu²
¹Fukuoka (Japan), ²Tokyo (Japan)
- 12.096 Non-typhoidal salmonellosis in Oppland and Hedmark counties, Norway, 1990–November 20, 2010
V. Hasseltvedt
Lillehammer (Norway)
- 12.097 Toxoplasma seroprevalence and genotypes in cats and ground feeders of Israel
H. Salant, D. T. Spira, J. Hamburger
Jerusalem (Israel)
- 12.098 Seroprevalence of antibodies against HEV in slaughter pigs in Southern Bavaria, Germany
S. Wacheck¹, C. Werres¹, U. Mohn², S. Dorn², M. Fredriksson-Ahomaa³, E. Märklbauer¹
¹Oberschleißheim (Germany), ²Neuried (Germany), ³Helsinki (Finland)
- 12.099 Localization of proteases in amoeba of the genus *Acanthamoeba*
M. Santana-Morales, R. Afonso-Lehmann, D. Deniz-Garcia, M. Arredondo, P. Foronda, B. Valladares, E. Martinez-Carretero
La Laguna (Spain)
- 12.100 Occurrence of potentially pathogenic bacteria in Kuwait fish market
S. Al-Mouqatea, **A. Akbar**, H. Bahbahani, D. Al-Baijan, A. Bin Haji
Kuwait (Kuwait)
- 12.101 Evolution of RepFIB putative virulence plasmids of *Cronobacter* spp.
C. Grim, A. Franco, L. Hu, G. Gopinath, V. Sathyamoorthy, M. Kotewicz, M. Kothary, K. Jarvis, C. Lee, J. Sadowski, B. Tall
Laurel, MD (USA)
- 12.102 Microbiological quality of different snack foods in an urban city of Pakistan
M. Ahmad, M. Muhammad Hassan
Lahore (Pakistan)
- 12.103 Application of enzyme linked immune-sorbent assay in diagnosis of neurocysticercosis in endemic region of Nepal
K. Sapkota¹, K. Sapkota², S. Singh³, K. Malla⁴
¹Myagdi (Nepal), ²New Mexico, NM (USA), ³Kathmandu (Nepal), ⁴Pokhara (Nepal)
- 12.104 WHO Global Foodborne Infections Network (GFN): Over 10 years of strengthening national capacities to detect and control foodborne and other enteric infections globally
M. Ayele¹, S. DeLong¹, D. Wong², J. Wagenaar³, S. Karlsmose⁴, N. Maxwell⁵, K. Knope¹, T. Chiller⁴
¹Atlanta, GA (USA), ²Geneva (Switzerland), ³Netherlands (Netherlands), ⁴Copenhagen (Denmark), ⁵Canberra (Australia)



Room: Bruckner/Mahler/Brahms • Upper Level

Saturday, February 5, 2011

11:45–14:00

- 12.105 Prevalence and antimicrobial resistance of *Listeria* spp Isolated from foods in Behshahr; Iran
cancelled **B. Asghari**, A. Ebrahimzadehnamvar
Tehran (Iran)
- 12.106 Cpa, the outer membrane protease of *Cronobacter sakazakii* activates plasminogen and mediates resistance to serum bactericidal activity
A. Franco-Mora, M. Kothary, G. Gopinath, K. Jarvis, C. Grim, L. Hu, A. R. Datta, B. A. McCardell, B. Tall
Laurel, MD (USA)
- 12.107 A case of autochthonous hepatitis E in Austria
W. Hoepler, **H. Laferl**, K. Kandel, M. Redlberger-Fritz, T. Popow-Kraupp, C. Wenisch
Vienna (Austria)
- 12.108 Epidemiological study of intestinal parasitic infestation in rural village of Nepal
K. Sapkota¹, K. Sapkota², I. Subedi¹
¹Myagdi (Nepal), ²New Mexico, NM (USA)
- 12.109 Statistical modeling of risk factors of *Escherichia coli* O157:H7 contamination in a beef processing plant
cancelled J. E. B. Moore¹, **D. Rice**², D. Morrow², A. Hill¹
¹Fort Collins, CO (USA), ²Elizabeth, CO (USA)
- 12.110 Detection of indicator bacteria from multiple drinking water sources—West Amhara, Ethiopia, 2005–2009
B. Beyene¹, R. Luce², B. Abera Beyene¹, F. Demeke¹
¹Bahir Dar (Ethiopia), ²Addis Ababa (Ethiopia)
- 12.111 Etiological investigation of diarrheal diseases in the suburbs of Nairobi, Kenya
Y. Ichinose¹, M. Bundi¹, A. Makumi¹, G. Miringu¹, M. Karama¹, S. Suka¹, M. Abubakar¹, V. Ager¹, S. Ochi², T. Tsuji², S. Inoue¹, M. Shimada¹
¹Nairobi (Kenya), ²Toyoake (Japan)
- 12.112 The enemy of good is perfect; *Saccharomyces fungemia* in a patient taking probiotic
U. Kelly, E. C. Oldfield
Norfolk, VA (USA)
- 12.113 Ethiological spectrum of foodborne infections in Timis Country, Romania
I. Marincu, L. Negrutiu, I. Iacobiciu, A. M. Neghina, L. Tirnea, T. R. Olariu, R. Neghina
Timisoara (Romania)
- 12.114 Multiple outbreaks of norovirus gastroenteritis linked to an infected post-symptomatic food handler
C. Thornley¹, L. Perumal¹, J. Wong¹, G. Greening²
¹Auckland (New Zealand), ²Porirua (New Zealand)
- 12.115 Food-borne *Listeria monocytogenes* outbreak associated with a traditional herring product, Germany 2010
E. Aichinger¹, E. Göhring-Zwacka¹, D. Lohr¹, K.-H. Janke¹, G. Klittich¹, A. Milde-Busch², K. Stark², R. Prager³, A. Flieger³, S. Huhulescu⁴, M. Contzen¹, W. Hautmann⁵, G. Pfaff¹
¹Stuttgart (Germany), ²Berlin (Germany), ³Wernigerode (Germany), ⁴Vienna (Austria), ⁵Oberschleißheim (Germany)



POSTER PRESENTATIONS • SESSION 12

International Meeting on Emerging Diseases and Surveillance 2011

Room: Bruckner/Mahler/Brahms • Upper Level

Saturday, February 5, 2011

11:45–14:00

- 12.116 A field laboratory method for the recovery of *Vibrio cholerae* isolates from food and environmental samples suitable for epidemiological investigations in developing countries
S. Baron, J. Lesne
Rennes (France)
- 12.117 The incidence rate of travel-associated infectious diseases among Japanese travelers by destination country
F. Odaira, T. Shimada, Y. Tada, N. Okabe
Tokyo (Japan)
- 12.118 Imported Cases of Chikungunya Fever in the Czech Republic
F. Stejskal¹, **M. Trojanek**¹, D. Tomickova¹, H. Zelena², N. Sojkova¹, J. Maixner¹, V. Maresova¹
¹Prague (Czech Republic), ²Ostrava (Czech Republic)
- 12.119 A case of severe typhus in a man returning from Africa
M. Eder¹, A. Abbara¹, L. S. Baxter¹, G. Thomson², L. M. John¹, R. N. Davidson¹
¹London (United Kingdom), ²Salisbury (United Kingdom)
- 12.120 Dengue infections in travellers to Thailand: Risk estimates
E. Massad¹, J. Rocklov², **A. Wilder-Smith**³
¹Sao Paulo (Brazil), ²Umea (Sweden), ³Heidelberg (Germany)
- 12.121 Imported malaria: Experience of a referral center in Tokyo
Y. Kato, Y. Mizuno, T. Kobayashi, M. Ujiie, N. Takeshita, S. Kanagawa, S. Kano, K. Kudo
Tokyo (Japan)
- 12.122 Concept of operation for emergency response plans at United States Airport point of entry
O. Grady-Erickson¹, A. Black², J. Yonkman¹
¹Cadillac, MI (USA), ²DFW Airport, TX (USA)
- 12.123 Migration and the globalization of disease: The reemergence of cholera in the Americas
L. Moore¹, J. Malaty²
¹Arlington, VA (USA), ²Washington, DC (USA)
- 12.124 *cancelled* Chagas disease in Murcia (Spain): A major emergent infection
B. Carrilero, L. Murcia, M. Segovia
Murcia (Spain)
- 12.125 Use of malaria imported cases in non endemic countries to assess the return of chloroquine susceptibility of *P. falciparum* strains from Senegal
M. Gharbi¹, B. Pradines², E. Kendjo¹, V. Hubert¹, P. Guérin³, J. Le Bras¹
¹Paris (France), ²Marseilles (France), ³Oxford (United Kingdom)
- 12.126 Increasing Trends in Hospitalizations for Dengue in the United States
J. Streit, M. Yang, J. E. Cavanaugh, P. Polgreen
Iowa City, IA (USA)



Room: Klimt Ballroom I • Upper Level

Saturday, February 5, 2011

11:45–14:00

- 12.127 Evaluation of the rapid influenza diagnostic tests and bioinformation analysis for 2009 A (H1N1) strain in Taiwan
Y.-M. Li, C.-W. Chang, W. Chia
Tao-Yuan (Taiwan, R.O.C.)
- 12.128 Pandemic 2009 influenza A H1N1 infection among Iranian Hajj pilgrims 2009: A real-time RT-PCR and serological based study
M. Ziyaeyan, A. Alborzi, M. Jamalidoust, M. Moieni, G. R. Pouladfr, B. Pourabbas
Shiraz (Iran)
- 12.129 Comparison of five genotypic techniques for identification of Optochin-resistant pneumococcus
Y. Abdolvand¹, **S. Anvari**², S. Koohestani³, P. Zeirani⁴
¹Gilan (Iran), ²Rasht (Iran), ³Karaj (Iran), ⁴Iahijan (Iran)
- 12.130 Survey of influenza-like illness among returning Hajj Pilgrims at Lagos Airport, Nigeria, December, 2009
M. Aworh, S. Badaru, L. Davis, G. Poggensee, H. Akpan, P. Nguku
Abuja (Nigeria)
- 12.131 A decade of influenza: Trends in WHO collaborating laboratory surveillance data
A. Bishop
Atlanta, GA (USA)
- 12.132 Social contacts and mixing patterns for influenza illness in Thailand
W. Putthasri
Nonthaburi (Thailand)
- 12.133 Extracorporeal membrane oxygenation for (2009) H1N1 influenza in a Belgian University teaching hospital
N. Ausselet, B. Delaere, M. Bourgeois, I. Michaux, **C. Dangoisse**
Yvoir (Belgium)
- 12.134 Designing specific real-time RT-PCR assays for Spanish Avian Influenza Virus subtyping
M. Elizalde, M. Agüero, D. Buitrago, M. Arias, M. J. Muñoz, **J. Fernandez-Pinero**
Madrid (Spain)
- 12.135 Modeling the health impact and cost-effectiveness of an adjuvanted influenza vaccine with enhanced effectiveness in the Canadian population
A. Tuite, D. Fisman
Toronto (Canada)
- 12.136 Mycoplasma bovis—An emerging pathogen in Czech cattle herds
J. Pospíchalová, D. Zendulkova, K. Rosenbergova, A. Sperlova, A. Hekrlova
Brno (Czech Republic)
- 12.137 The A(H1N1)2009 influenza pandemic: Lessons learned in Latvia
B. Rozentale, J. Storozenko, V. Sondore, J. Keiss
Riga (Latvia)
- 12.138 Epidemiology of PCR confirmed H1N1 Influenza in South-East Austria
K. Tovilo, H. Flick, H. J. Salzer, I. Zollner-Schwetz, T. Valentin, R. Raggam, A. J. Grisold, H. Olschewski, R. Krause, M. Hoenigl
Graz (Austria)



POSTER PRESENTATIONS • SESSION 12

International Meeting on Emerging Diseases and Surveillance 2011

Room: Klimt Ballroom I • Upper Level

Saturday, February 5, 2011

11:45–14:00

- 12.139 The role of interaction between influenza viruses in the substitution of epidemic strains
L. Ju, **L. Jiang**, Y. Gao, X. Lv, Q. Jiang
Shanghai (China)
- 12.140 Indirect impact of the 2009–2010 influenza pandemic on pertussis and gastro-enteritis epidemics
P. Crépey¹, M. Pivette¹, M. Desvarieux²
¹Paris (France), ²New York City, NY (USA)
- 12.141 Determination of an ICU triage protocol in a context of pandemic influenza planning for acute care settings in Belgium
N. Ausselet, M. Bourgeois, I. Michaux, B. Delaere, **C. Dangoisse**
Yvoir (Belgium)
- 12.142 Rapid differentiation of influenza A/H1N1 pandemic and seasonal strain infections and the analysis of co-infection by multitemperature single-strand conformational polymorphism (MSSCP) technique
B. Pajak¹, **K. Leppek**², M. Szeliga¹, B. Szewczyk², K. Kucharczyk¹
¹Warsaw (Poland), ²Gdansk (Poland)
- 12.143 Seroprevalence and molecular identification of swine influenza virus: Epidemiological implications
L. F. Caron, V. Thomaz-Soccol, M. E. Joineau
Curitiba (Brazil)
- 12.144 Four years of non-sentinel surveillance of respiratory syncytial virus through the Spanish Influenza Sentinel Surveillance System
S. Jiménez-Jorge, M. C. Delgado-Sanz, S. de Mateo, A. Larrauri
Madrid (Spain)
- 12.145 Clinical and epidemiological characteristics of deaths attributed to pandemic influenza A (H1N1), 2009–2010, East Ukraine
T. Chumachenko, G. Gradil, G. Gubina-Vakulik, V. Kozko
Kharkiv (Ukraine)
- 12.146 H5N1 avian influenza A – Emergence, trends and pandemic threats in Egypt and Indonesia
J. Malaty
Washington, DC (USA)
- 12.147 H9N2 avian influenza reassortants in live bird retail shops in Pakistan contain signatures of public health concern
cancelled **M. Chaudhry**¹, H. B. Rashid¹, A. Angot², G. Trovò², A. Drago², V. Valastro², M. Thrusfield¹, M. Hussain³, M. Eisler⁴, S. Welburn¹, G. Cattoli², I. Capua²
¹Edinburgh (United Kingdom), ²Legnaro (Italy), ³Rawalpindi (Pakistan), ⁴Bristol, (United Kingdom)
- 12.148 Application of the real-time PCR method for the detection of human influenza A (H1N1) of pandemic potential in Albania
D. Ulqinaku, I. Hatibi, S. Bino
Tirana (Albania)



Room: Klimt Ballroom I • Upper Level

Saturday, February 5, 2011

11:45–14:00

- 12.149 Actual issues regarding influenza infection in Romania; the last two seasons analysis before pandemic AH1N1
C. P. Popescu, S. A. Florescu, A. G. Kosa, I. Apostol, C. Sbarcea, G. Necula, M. Mihai, E. Ceausu, P. I. Calistru, V. Alexandrescu
Bucharest (Romania)
- 12.150 Years of life lost associated with influenza seasons in Spain, 1980–2008
L. Simon, T. Lopez-Cuadrado, N. Lopez, A. Larrauri, S. de Mateo
Madrid (Spain)
- 12.151 Rapid sequencing and genetic analysis of the pandemic (H1N1)V influenza virus circulating in pigs in Italy
G. Vaccari¹, A. M. Moreno Martin², L. Di Trani¹, S. Faccini², L. Alborali², D. Nigrelli², M. B. Boniotti², E. Falcone¹, A. Boni¹, D. Lelli², A. Guercio³, G. Purpari³, P. Cordioli²
¹Rome (Italy), ²Brescia (Italy), ³Palermo (Italy)
- 12.152 Genetic diversity of H1, H2 and H3 subtypes of Influenza A circulating in wild birds in Italy, 2005–2010
I. Monne, **A. Fusaro**, V. Valastro, A. Schivo, A. Burattin, C. Terregino, I. Capua, G. Cattoli
Legnaro (PD) (Italy)
- 12.153 The controversial role of *Chlamydia pneumoniae* in chronic infection and vascular disease
K. Mitsakos
Sydney (Australia)
- 12.154 Estimated impact of global antiviral prophylaxis in containing an outbreak of pandemic influenza H1N1 in an isolated first nations community
Y. Xiao¹, **D. Fisman**²
¹London (Canada), ²Toronto (Canada)
- 12.155 Reverse line blot typing and genome evolution of *Bordetella pertussis*
C. Lam, S. Octavia, V. Sintchenko, G. Gilbert, P. Reeves, R. Lan
Sydney (Australia)
- 12.156 Emergence of novel H1N1: India
A. Choudhry
New Delhi (India)
- 12.157 An outbreak of influenza b in a prison in West Midlands UK, 2008
M. Afza¹, R. Robinson², A. Beaumont³, H. Duggal⁴
¹Staffordshire (United Kingdom), ²Warwick (United Kingdom), ³Walsall (United Kingdom), ⁴Stafford (United Kingdom)
- 12.158 Outbreak of human adenovirus in patients with acute respiratory infection in Korea at 2010
H. M. Cheong, Y.-J. Kim, H. Y. Lee, H. Kim, W. J. Lee, H.-B. Oh, K. Kim
Cheungcheongbuk-do (Korea)
- 12.159 Evidence and genetic analysis of swine A (H1N1) influenza viruses circulating in Austrian pigs within the last ten years
J. Kolodziejek¹, A. Schachner¹, H. Homola¹, R. Duerrwald², L. Fischer¹, H. Lussy¹, N. Nowotny¹
¹Vienna (Austria), ²Rodleben (Germany)



Room: Klimt Ballroom I • Upper Level

Saturday, February 5, 2011

11:45–14:00

- 12.160 Descriptive and comparative epidemiology of influenza type A and B viruses: Towards a tetravalent seasonal vaccine?
T. Seyler¹, M. Saadatian-Elahi², A. Moren¹
¹Paris (France), ²Lyon (France)
- 12.161 Evaluation of rapid antigen tests for detection of pandemic influenza H1N1 2009
B. M. Mohamed
Tunis (Tunisia)
- 12.162 Exposure assessment using a novel influenza protein micro-array to detect antibodies against human and animal influenza viruses
M. Koopmans¹, **E. D. Bruin**², J. Reimerink², M. Boni³, G.-J. Godeke², S. de Wit⁴, R. van Doorn³, M. de Jong⁵
¹Rotterdam (Netherlands), ²Bilthoven (Netherlands), ³Ho Chi Minh City (Viet Nam), ⁴Deventer (Netherlands), ⁵Amsterdam (Netherlands)
- 12.163 Pandemic Influenza on the territory of Skopje, R.Macedonia
L. Lazarevska, G. Skakiri, M. Manev
Skopje (Macedonia)
- 12.164 Awareness of H1N1 among Hajj returning pilgrims, Gombe State, Nigeria 2009
R. Dankoli, L. Maina, P. Ngukup
Abuja (Nigeria)
- 12.165 Pediatric Influenza A (H1N1)v infection: Insights from virologic surveillance
P. Affanni, F. Paganuzzi, M. E. Colucci, L. Veronesi, E. Capobianco, C. Cesari, R. Giordano,
M. Riccò, P. Manotti, C. Boccuni, C. Signorelli, M. L. Tanzi
Parma (Italy)
- 12.166 Vaccine Effectiveness of Pandemic Influenza A(H1N1) in Korea
M. Ki¹, B. Choi², J. Lim¹, S. Hong², J. Kim³, J. Park⁴, J. Kim⁵, C. Kim⁶, H. Yoon¹
¹Daejeon (Korea), ²Seoul (Korea), ³Gangneung (Korea), ⁴Cheonan (Korea), ⁵Junju (Korea), ⁶Bucheon (Korea)
- 12.167 Wound infection/abscess formation caused by *Eggerthella lenta*
V. Hasseltvedt¹, I. Nordøy²
¹Lillehammer (Norway), ²Oslo (Norway)
- 12.168 Bacteraemia caused by *Varibaculum* species
V. Hasseltvedt¹, D. Caugant², E. A. Høiby²
¹Lillehammer (Norway), ²Oslo (Norway)
- 12.169 Infectious pancreatic necrosis (IPN), a new threat of cultured rainbow trout in Iran
M. Ghasemi¹, N. J. Olesen², H. F. Skall², S. Haghighi Karsidani¹, S. P. Jonstrup²,
S. J. Zorriehzahra³, I. Sharifpour⁴, M. Soltani⁴, M. Sharifrohani⁴
¹Bandar Anzali (Iran), ²Arhus (Denmark), ³Tonekabon Mazandaran Province (Iran, Islamic Republic of), ⁴Tehran (Iran)
- 12.170 Clinical manifestations and outcome in *Bacillus cereus* bacteremia
“underestimated complications”
G. Ohji¹, W. Igarashi¹, B. Hayama¹, Y. Oba¹, R. Suganaga¹, D. Uchida¹, H. Kagawa¹,
K. Takimoto¹, H. Oka¹, H. Yoshida², K. Iwata¹
¹Hyogo (Japan), ²Kobe (Japan)



Room: Klimt Ballroom I • Upper Level

Saturday, February 5, 2011

11:45–14:00

- 12.171 Insectivore-borne human hantavirus infections: first report of two (retrospective) cases
J. Clement, P. Maes, M. Van Ranst
Louvain (Belgium)
- 12.172 The first isolation of Mycobacterium elephantis from tuberculin-reactive cattle
A. Skrypnyk¹, I. Moser², H. Hotzel², K. Sachse², O. Deryabin¹, V. Skrypnyk¹
¹Kiev (Ukraine), ²Jena (Germany)
- 12.173 Novel avian orthoreovirus strain associated with runting-stunting syndrome in broilers
K. Bányai¹, **E. Dandár**¹, K. Moore Dorsey², T. Mató¹, V. Palya¹
¹Budapest (Hungary), ²Lenexa, KS (USA)
- 12.174 Emergence of new variants of Shigella and their characterization
K. Ali Talukder¹, I. J. Azmi¹, M. S. Iqbal¹, I. S. Ud-Din¹, D. K. Dutta¹, M. A. Islam¹,
Z. Islam¹, M. Akter¹, M. A. Hossain¹, A. Faruque¹, M. Ansaruzzaman¹, I. Filliol²,
T. Cheasty³, H. P. Endtz¹, A. Cravioto¹
¹Dhaka (Bangladesh), ²Paris (France), ³London (United Kingdom)
- 12.175 Impact of Isoniazid for preventing tuberculosis among non-HIV population in Malaysia: an age-structured model
N. Ismail¹, A. B. Awang Mahmud¹, N. J. Nagelkerke², O. Awang¹
¹Kuala Lumpur (Malaysia), ²Al-Ain (United Arab Emirates)
- 12.176 Analyzing the impact of superspreading using hospital contact networks
D. Naylor, T. Hornbeck, A. Segre, P. Polgreen
Iowa City, IA (USA)
- 12.177 State capacity influences on the epidemiology of neglected tropical and vector-borne diseases in Africa
E. Filauri
Rockville, MD (USA)
- 12.178 Help seeking behavior of mothers of children with and without measles in Shahpur block of district Kangra, Himachal Pradesh, India, 2008
S. Gupta, N. Gupta
Kangra, Himachal Pradesh (India)
- 12.179 Social and behavioural research on Avian Influenza in Solok, Indonesia
S. Kosen¹, R. Prasodjo¹, **T. Respati**²
¹Jakarta (Indonesia), ²Bandung (Indonesia)
- 12.180 Cross-sectoral dengue fever prevention initiatives in Brazil and the participation of waste pickers in the informal trash economy
C. Alley
Brooklyn, NY (USA)
- 12.181 Knowledge and attitude of persons living with HIV+/AIDS (PLWAs) towards HIV/AIDS in Iran
A. Madani¹, M. Jamshidi Makiani², P. Davoodian¹
¹Bandarabbas (Iran), ²Tehran (Iran)
- 12.182 Cultural practices and spread of cholera in Bauchi North Eastern Nigeria— Does it matter?
Y. Jibrin, A. Mohammed
Bauchi, Bauchi (Nigeria)



EARLY MORNING SESSION • SESSION 13

International Meeting on Emerging Diseases and Surveillance 2011

Room: Klimt Ballroom 2&3 • Upper Level

Sunday, February 6, 2011

07:00–08:00

Surveillance of Antibiotic Stewardship

Chair: Matt Levison, USA

13.001 Surveillance of antibiotic stewardship
J. Hutchinson
St. John's (Canada)



PARALLEL SESSION • SESSION 14

International Meeting on Emerging Diseases and Surveillance 2011

Room: Park Congress • Ground Level

Sunday, February 6, 2011

08:30–10:30

New Surveillance Strategies

Co-Chairs: Benson Estambale, Kenya
Tim Brewer, Canada

14.001 Innovative technologies for emerging disease surveillance
C. Freifeld
Boston, MA (USA)

14.002 Regional disease surveillance networks, the ProMED experience in East Africa
B. Estambale
Nairobi (Kenya)

14.003 Travel-related illnesses in Europe, EuroTravNet 2009
S. Odolini¹, P. Parola², **F. Castelli**¹
¹Brescia (Italy), ²Marseille (France)

14.004 New approaches to public health surveillance: MUsings from US CDC
T. Kass-Hout
Washington, DC (USA)

10:30–11:00 **Coffee Break** (Ground Level AND Upper Level)



Room: Klimt Ballroom 2&3 • Upper Level

Sunday, February 6, 2011

08:30–10:30

Surveillance & Public Health (Oral Presentations)

Co-Chairs: Jacques Acar, France
Louise Boily, Canada

- 15.001 Information management in PREDICT: Digital and field surveillance to detect emerging infectious diseases of wildlife origin and protect human and animal health
D. Joly¹, T. O'Rourke¹, J. Palmer², J. Brownstein³, A. Sonricker³, L. Madoff⁴, P. Rabinowitz⁵, J. Wilson⁶, L. Gunasekara⁷, T. Goldstein⁸, C. Kreuder Johnson⁸, N. Wolfe⁷, P. Daszak⁹, W. Karesh⁹, J. Fair⁷, S. Morse⁹, J. Mazet⁸
¹Nanaimo, BC (Canada), ²Moshi (Tanzania, United Republic of), ³Boston, MA (USA), ⁴Brookline, MA (USA), ⁵New Haven, CT (USA), ⁶Seattle, WA (USA), ⁷San Francisco, CA (USA), ⁸Davis, CA (USA), ⁹New York, NY (USA)
- 15.002 Electronic health market used to predict the spread of dengue
C. Franco¹, T. K. Sell¹, A. T. Y. Ho², P. Polgreen²
¹Baltimore, MD (USA), ²Iowa City, IA (USA)
- 15.003 EpiSouth Plus Project: the new challenge of the EpiSouth Network for enhancing the control of public health threats and other risks in the Mediterranean region and Balkans
M. Dente¹, M. Bejaoui², **M. Fabiani**¹, V. Alfonsi¹, D. Lausevic³, G. Salamina⁴, K. Victoir⁵, H. Kalaycioglu⁶, F. Simon Soria⁷, C. Martin de Pando⁷, D. Hannoun⁸, P. Barboza⁹, F. Belghiti¹⁰, A. Leventhal¹¹, F. Riccardo¹, P. Nabeth¹², S. Declich¹
¹Rome (Italy), ²Tunis (Tunisia), ³Podgorica (Montenegro), ⁴Turin (Italy), ⁵Paris (France), ⁶Ankara (Turkey), ⁷Madrid (Spain), ⁸Algiers (Algeria), ⁹St Maurice (France), ¹⁰Saint Maurice Cedex (France), ¹¹Jerusalem (Israel), ¹²Lyon (France)
- 15.004 Comprehensive analysis of OIE world animal health data as a means to identify global disease trends
U. Sperling¹, U. Kihm¹, J. W. Smith²
¹Berne (Switzerland), ²Washington, DC (USA)
- 15.005 Cholera outbreak in Haiti, 2010 – Using a gravity model to explain spatial dynamics
A. Tuite¹, J. Tien², D. J. Earn³, M. Eisenberg², **D. Fisman**¹
¹Toronto (Canada), ²Columbus, OH (USA), ³Hamilton (Canada)
- 15.006 A method for quantifying transmission of Stage III zoonoses
J. Pulliam¹, S. Blumberg², J. O. Lloyd-Smith²
¹Bethesda, MD (USA), ²Los Angeles, CA (USA)
- 15.007 Laboratory-acquired human cowpox infection in the US: Case investigation
A. McCollum, C. Austin, J. Nawrocki, J. Howland, J. Pryde, A. Vaid, D. Holmes, R. Weil, Y. Li, K. Wilkins, H. Zhao, S. Smith, K. Karem, M. Reynolds, I. Damon
Atlanta, GA (USA)
- 15.009 Recurring transmission of norovirus on a passenger aircraft
C. Thornley¹, J. Rapana¹, G. Greening²
¹Auckland (New Zealand), ²Porirua (New Zealand)



PARALLEL SESSION • SESSION 15

International Meeting on Emerging Diseases and Surveillance 2011

Room: Klimt Ballroom 2&3 • Upper Level

Sunday, February 6, 2011

08:30–10:30

- 15.010 Deomography, migration and health: mosaics of a globalized world
D. Tomianovic, K. Liske, V. Lee, M. Cetron
Atlanta, GA (USA)
- 15.011 Understanding the multidimensional socio-economic impacts of animal diseases:
a case study of PPR and HPAI
cancelled **N. de Haan**¹, T. Kimani², E. Geerlings³
¹Rome (Italy), ²Nairobi (Kenya), ³Reading (United Kingdom)
- 15.012 ProMED-mail early warnings in Africa: Descriptive summaries of 5 years of information
dissemination and the development of the African regional networks
P. Cowen¹, **F. N. Ekue**², A. Sonricker³, N. Mtui-Malamsha⁴, O. O. Babalobi⁵, G. Anacle⁶,
B. Estambale⁷, S. Coulibaly⁸, J. Brownstein³, E. Chan³, T. Garland⁹, M. Hugh-Jones¹⁰,
A. Shimshony¹¹, A. Bodenheimer³, L. Madoff¹², M. Pollack¹³
¹North Carolina 27606, NC (USA), ²Buea (Cameroon), ³Boston, MA (USA),
⁴Dar es Saalam (Tanzania, United Republic of), ⁵Ibadan (Nigeria), ⁶N'Djaména (Chad),
⁷Nairobi (Kenya), ⁸Ouagadougou (Burkina Faso), ⁹College Station, Tx (USA), ¹⁰Baton
Rouge, LA (USA), ¹¹Jerusalem (Israel), ¹²Brookline, MA (USA), ¹³New York, NY (USA)
- 15.013 Impact of a video-based intervention on knowledge and attitudes of Ebola prevention
and care in the rural Republic of Congo, 2007–2010
A. Roess¹, C. Moses¹, S. Gallagher¹, E. Kinzonzi²
¹Washington, DC (USA), ²Brazzaville (Congo)
- 10:30–11:00 **Coffee Break** (Ground Level AND Upper Level)



PLENARY LECTURE • SESSION 16

International Meeting on Emerging Diseases and Surveillance 2011

Room: Park Congress • Ground Level

Sunday, February 6, 2011

11:00–11:45

The Spread of Emerging Diseases by Global Air Travel

Chair: David Fisman, Canada

- 16.001 The spread of emerging diseases by global air travel
K. Khan
Toronto (Canada)



POSTER PRESENTATIONS II • SEE PAGES 36–54

International Meeting on Emerging Diseases and Surveillance 2011

Room: Bruckner/Mahler/Brahms • Upper Level
and Klimt Ballroom I • Upper Level

Sunday, February 6, 2011

11:45–14:00



PARALLEL SESSION • SESSION 17

International Meeting on Emerging Diseases and Surveillance 2011

Room: Park Congress • Ground Level

Sunday, February 6, 2011

14:30–16:00

Q Fever in the Netherlands

Co-Chairs: Amon Shimshony, Israel
Jim Van Steenbergen, Netherlands

17.001 Q fever in the Netherlands: The animal health aspects
C. Bruschke
The Hague (Netherlands)

17.002 Q fever in the Netherlands: The public health aspects
J. Van Steenbergen¹, W.V. D. Hoek¹, D. Notermans¹, C. Wijkmans², T. Oomen¹
¹Bilthoven (Netherlands), ²s-Hertogenbosch (Netherlands)

17.003 Q fever in the Netherlands: *Coxiella burnetii*, laboratory aspects
H.-J. Roest
Lelystad (Netherlands)

16:00–16:30 **Coffee Break** (Ground Level AND Upper Level)



PARALLEL SESSION • SESSION 18

International Meeting on Emerging Diseases and Surveillance 2011

Room: Klimt Ballroom 2&3 • Upper Level

Sunday, February 6, 2011

14:30–16:00

Climate Change and Infectious Diseases

Co-Chairs: David Fisman, Canada
Martin Hugh-Jones, USA

18.001 Plague and climate change
N. Chr. Stenseth
Oslo (Norway)

18.002 Malaria, climate change and policy
D. Campbell-Lendrum
Geneva (Switzerland)

18.003 The emergence of Lyme disease in Canada: Is there evidence?
for an effect of climate change?
N. Ogden
Ottawa (Canada)

16:00–16:30 **Coffee Break** (Ground Level AND Upper Level)



PARALLEL SESSION • SESSION 19

International Meeting on Emerging Diseases and Surveillance 2011

Room: Park Congress • Ground Level

Sunday, February 6, 2011

16:30–18:00

Emerging Infection Prevention in the Healthcare Setting

Co-Chairs: Phil Polgreen, USA
Stuart Handsides, United Kingdom

- 19.001 Infection prevention and control challenges experienced in the Lujo Arenavirus outbreak in South Africa, 2008
A. Duse
Johannesburg (South Africa)
- 19.002 The changing epidemiology of *Clostridium difficile* infection
P. Polgreen
Iowa, IA (USA)
- 19.003 Controlling transmission of glanders—The veterinary health setting
U. Wernery
Dubai (United Arab Emirates)



PARALLEL SESSION • SESSION 20

International Meeting on Emerging Diseases and Surveillance 2011

Room: Klimt Ballroom 2&3 • Upper Level

Sunday, February 6, 2011

16:30–18:00

Current Approaches to New Threats (Oral Presentations)

Co-Chairs: Sidi Coulibaly, Burkina Faso
Tom Yuill, USA

- 20.001 Polio in Europe: Strategies to prevent further resurgence
D. Jankovic, E. Gavrillin, A. Goel, S. Deshevoi, S. Huseynov, R. Martin
Copenhagen (Denmark)
- 20.002 The epidemiology of hospitalised adults from a 22 year whole-population study on bacteraemic streptococcal pneumoniae community acquired pneumonia (CAP)—Darwin, Northern Territory, Australia
S. Jacups, S. Moberley, A. Cheng
Darwin (Australia)
- 20.003 Cost-effectiveness of alternative case finding strategies for prisons with high prevalence of multidrug-resistant tuberculosis
D. Winetsky¹, D. Negoescu¹, E. DeMarchis¹, O. Almukhamedova², D. Pulatov², N. Vezhnina³, B. Zhussupov³, A. Dooronbekova³, J. Goldhaber-Fiebert¹
¹Stanford, CA (USA), ²Dushanbe (Tajikistan), ³Almaty (Kazakhstan)
- 20.004 Emergence of multidrug resistant NDM-1-producing superbugs in Bangladesh
M. Islam¹, P. Talukdar¹, A. Hoque¹, M. Huq¹, A. Nabi¹, I. Azmi¹, D. Ahmed¹, K. Talukder¹, J. Hays², A. Cravioto¹, H. Endtz¹
¹Dhaka (Bangladesh), ²Rotterdam (Netherlands)



PARALLEL SESSION • SESSION 20

International Meeting on Emerging Diseases and Surveillance 2011

Room: Klimt Ballroom 2&3 • Upper Level

Sunday, February 6, 2011

16:30–18:00

Current Approaches to New Threats (Oral Presentations) *continued*

- 20.005 Novel multiplex polymerase chain reaction primer and probe design tools applied to rapid diagnosis and characterization of viruses and bacteria
P. Naraghi-Arani, S. Gardner, D. Hysom, M. El-Sheikh, A. C. Carrillo, J. Olivas
Livermore, CA (USA)
- 20.006 Impact of vaccination on the genetic evolution of H5N1 viruses in Egypt
A. Fusaro¹, I. Monne¹, A. Salviato¹, F. Coven², A. Dakman³, I. Capua¹, G. Cattoli¹
¹Padua (Italy), ²Izmir (Turkey), ³Ankara (Turkey)
- 20.007 Using surveillance data to estimate influenza vaccine effectiveness in Spain during seven seasons (2002–2009)
C. Savulescu, S. Jiménez-Jorge, S. de Mateo, A. Larrauri, and The Spanish Influenza Sentinel Surveillance System
Madrid (Spain)
- 20.008 Timing, progression and community impact of 2009 Influenza Pandemic: A comparison with historical seasons in countries of WHO/European Region
L. Martirosyan¹, J. W. Paget¹, P. Jorgensen², C. S. Brown², D. Pereyaslov², T. Meerhoff³, J. Mott²
¹Utrecht (Netherlands), ²Copenhagen (Denmark), ³Nijmegen (Netherlands)
- 20.009 A strategy on antimicrobial resistance for WHO regional office for Europe
B. Ganter
Copenhagen (Denmark)
- 20.010 Evaluation of the 2009–2010 Oral Fox Vaccination (OFV) campaigns in North-Eastern Italy
P. Mulatti¹, L. Gagliazzo¹, M. Lorenzetto¹, T. Patregnani¹, P. De Benedictis¹, F. Mutinelli¹, V. Guberti², L. Bonfanti¹, S. Marangon¹
¹Legnaro (Italy), ²Bologna (Italy)



POSTER PRESENTATIONS • SESSION 21

International Meeting on Emerging Diseases and Surveillance 2011

Sunday, February 6, 2011 • Poster Presentations II • 11:45–14:00

Room Bruckner/Mahler/Brahms • Upper Level:

Abstract Number	Topic
21.001 – 21.053	Infections of public health significance
21.054 – 21.066	Innovations in diagnostic tests for emerging diseases
21.067 – 21.096	New approaches to outbreak surveillance and monitoring
21.097 – 21.113	Outbreak response and control
21.114 – 21.126	Public communication of outbreaks and emerging diseases

Klimt Ballroom I • Upper Level:

Abstract Number	Topic
21.127 – 21.139	Vaccines and emergence of vaccine preventable diseases
21.140 – 21.187	Vectorborne diseases



POSTER PRESENTATIONS • SESSION 21

International Meeting on Emerging Diseases and Surveillance 2011

Room: Bruckner/Mahler/Brahms • Upper Level

Sunday, February 6, 2011

11:45–14:00

- 21.001 Clinical profile of tuberculosis in chronic kidney disease
T. John, K. Jayakumar, V. Chandran, J. Vinu, **A. G. Jacob**, C. N. Jacob
Kottaya, Kerala (India)
- 21.002 Design and evaluation of Taq Man Real Time PCR for molecular diagnosis of typhoid fever
K. Majidzadeh¹, **M. Soleimani**², N. Amini², A. Ghalyanchi Langeroudi¹
¹Tehran (Iran), ²Qom (Iran)
- 21.003 Demographic trends among *Mycobacterium tuberculosis* cases in an aging population with medium disease burden in Taiwan
M.-M. Kuan, T. Lin, F.-Y. Chang
Taipei (Taiwan, R.O.C.)
- 21.004 Monitoring of cytomegalovirus quantity and antigenemia following stem cell transplantation with a focus on plasma and PMN results
M. Ziyaeyan, A. Alborzi, A. Japoni, M. Jamalidoust, B. Pourabbas
Shiraz (Iran)
- 21.005 Uncommon syndrome secondary to sepsis with an uncommon pathogen
T. John¹, C. Ittycheria¹, P. Jabbar¹, S. Subramaniam¹, C. N. Jacob¹, A. G. Jacob², A. M. George²
¹Kottayam, Kerala (India), ²Trivandrum (India)
- 21.006 *cancelled* Dog bite, recognized as a public health concern in Addis Ababa, Ethiopia
F. Deribe, K. H. Hamza, A. A. Mohamed, G. G. Ayana, D. S. Fujaga
Addis Ababa (Ethiopia)
- 21.007 Neurobrucellosis in children, a report of 2 cases and a review of the literature
M. AlAyed
Najran (Saudi Arabia)
- 21.008 Two sequential measles outbreak investigations in highly immunized hilly areas of district Kangra, Himachal Pradesh, India, 2007
S. Gupta¹, V. Ramachandran², N. Gupta¹, N. Mehta¹
¹Kangra, Himachal Pradesh (India), ²Chennai (India)
- 21.009 Inhibition performed by a synthetic microbicidal peptide on the replication of Influenza virus
G. Conti, V. Magliani, S. Conti, L. Polonelli
Parma (Italy)
- 21.010 Leprosy presenting as Immune Reconstitution Inflammatory Syndrome (IRIS) in patients on Highly Active Anti-Retroviral Treatment (HAART)—A case series study from a tertiary care centre in Kerala, South India
T. John¹, C. N. Jacob¹, K. Shobhanakumary¹, S. M.S.¹, A. G. Jacob¹, A. M. George²
¹Kottayam, Kerala (India) ²Trivandrum, Kerala (India)
- 21.011 *cancelled* A case control study for the identification of risk factors associated with HCV infection in a tertiary care hospital of Pakistan
B. M. Ahmad¹, **T. Ijaz**¹, J. K. Khan¹, M. K. Shahzad¹, K. Siddique¹, M. S. Hussain², Z. Salahuddin¹
¹Lahore, Punjab (Pakistan), ²Faisalabad (Pakistan)



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11:45–14:00

- 21.012 A triple approach of an outbreak of conjunctivitis in a nursing home for psycho geriatric patients in the Rotterdam-Rijnmond area in the Netherlands
M.-C. Trompenaars¹, P. Borsje², M. de Winkel¹, I. van der Meer¹, G. van Nielen³
¹Rotterdam (Netherlands), ²Spijkensisse (Netherlands), ³Schiedam (Netherlands)
- 21.013 Small molecule inhibitors of dengue virus replication are active in vivo
cancelled
A. Kosaraju
New York, NY (USA)
- 21.014 Wetland drainage (habitat modification) for mosquito control in the Ilparpa Swamp, Northern Territory, Australia
S. Jacups
Darwin (Australia)
- 21.015 Prognostication of thrombocytopenia development in patients with chronic hepatitis C
N. Pshenichnaya, G. Kuznetsova
Rostov-on-Don (Russia)
- 21.016 Herpes simplex virus 1 & 2 are common causes of viral meningoencephalitis in Peru
C. Nelson¹, N. Mori¹, V. Celis², A. Romero³, I. Reyes³, G. Ramirez³, M. Sihuinchu⁴, E. Halsey³, S. Montano³, J. Zunt⁵
¹Bethesda, MD (USA), ²Trujillo (Peru), ³Lima (Peru), ⁴Iquitos (Peru), ⁵Seattle, WA (USA)
- 21.017 An outbreak of pulmonary leptospirosis in Honduras
E. Bu
Tegucigalpa, (Honduras)
- 21.018 Aerial dissemination of *Clostridium difficile* spores inside and outside a pig farm
E. Keessen¹, C. Donswijk¹, C. Harmanus², E. Kuijper², L. Lipman¹
¹Utrecht (Netherlands), ²Leiden (Netherlands)
- 21.019 Excess early mortality in patients starting antiretroviral therapy in Georgia
N. Chkhartishvili, L. Sharvadze, N. Dvali, N. Badridze, L. Gatsereia, T. Tsertsvadze
Tbilisi (Georgia)
- 21.020 Emerging West Nile Fever Infection in Mesopotomia region of Turkey
Z. C. Karakoc¹, M. B. Tuzuner¹, O. Ergonul², A. Pierro³, E. Di Fonzo³, V. Sambri³
¹Istanbul (Turkey), ²Kadikoy (Turkey), ³Bologna (Italy)
- 21.021 Detection of *Clostridium difficile* toxins in stools of patients reporting in a tertiary care hospital of North India
C. Vaishnavi, M. Singh, K. Singh
Chandigarh (India)
- 21.022 Prevalence of hepatitis B and C among HIV positive patients in Georgia and it's associated risk factors
N. Badridze, T. Tsertsvadze, L. Sharvadze
Tbilisi (Georgia)



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- 21.023 High seroprevalence, norms, social network and HIV related behaviours among injection drug users (IDUs) in Faisalabad, Pakistan
cancelled B. M. Ahmad¹, M. S. Hussain², K. Rahman², **T. Ijaz**¹, J. K. Khan¹, M. A. Khan¹, M. S. Ashraf¹, Z. Salahuddin¹
¹Lahore, Punjab (Pakistan), ²Faisalabad (Pakistan)
- 21.024 Prevalence and risk factors for human hydatidosis and canine echinococcosis in rural areas of the Limari province, Chile
G. Acosta¹, T. Weitzel², C. Adones³, I. Reiter-Owona⁴
¹Valdivia (Chile), ²Berlin (Germany), ³La Serena (Chile), ⁴Bonn (Germany)
- 21.025 Molecular epidemiological tracing of HIV-1 cases in Georgia
N. Dvali, N. Chkhartishvili, **L. Sharvadze**, M. Karchava, T. Tsertsvadze
Tbilisi (Georgia)
- 21.026 Influence of mother HIV and/or syphilis infection on the outcome of newborns
A. Herrera-Martinez¹, Y. Herrera-Martinez¹, M. Limper²
¹Barquisimeto (Venezuela), ²Amsterdam (Netherlands)
- 21.027 Super early viral response and IL 28 B genotype as the strong predictor for SVR for HCV Genotype 1 patients
M. Karchava, L. Sharvadze, E. Dolmazashvili, M. Zhamutashvili, T. Iobashvili, N. Chkhartishvili, L. Gatsrelia, N. Dvali, L. Dzigua, T. Tsertsvadze
Tbilisi (Georgia),
- 21.028 Is there a need to do West Nile surveillance in Asia?
G. Yap
Singapore (Singapore)
- 21.029 Retrospective analysis of suspected rabies cases reported in Dodoma Region, Tanzania
F. Vairo¹, B. Nguhuni², E. Nicastrì¹, Z. Chaula², G. J. Mtey², N. Bevilacqua¹, G. Ippolito¹
¹Rome (Italy), ²Dodoma (Tanzania)
- 21.030 Pathogen inactivation of blood components for prevention of transfusion-transmitted emerging infectious diseases: The INTERCEPT blood system
L. Corten, L. Sawyer, W. Liu, L. Lin
Concord, CA (USA)
- 21.031 Assessment of liver fibrosis/cirrhosis using Fibroscan and FibroTest/FibroMax in patients with chronic HBV and HCV infection in Georgia
E. Dolmazashvili, L. Sharvadze, M. Karchava, F. Gabunia, M. Zhamutashvili, M. Svanidze, A. Abutidze, T. Tsertsvadze
Tbilisi (Georgia)
- 21.032 Performance of four rapid diagnostic tests for the diagnosis of falciparum and non-falciparum malaria in endemic areas of Gondar region, Northern Ethiopia
K. Aysheshm
Addis Ababa (Ethiopia)
- 21.033 Prognostic value of IL28B for spontaneous clearance from HCV infection
L. Sharvadze, M. Karchava, L. Gatsrelia, N. Chkhartishvili, E. Dolmazashvili, N. Dvali, N. Badridze, T. Tsertsvadze
Tbilisi (Georgia)



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- 21.034 Correlation between the result of leishmanin skin test and clinical forms of cutaneous leishmaniasis and species of parasite
A. Fata, F. Maaleki, E. Shirangi, M. Meshkat, S. Fata, M. Gaffarian, M. Afzal-Aghaee
Mashhad (Iran)
- 21.035 Unexpectedly high incidence of HTLV1 infection and atypical HPV genotypes detected in cervical smears from HIV positive and negative Kenyan women
I. Maranga¹, L. Hampson¹, A. Oliver¹, X. He¹, P. Gichangi², F. Rana², I. Hampson¹
¹Manchester, GMC (United Kingdom), ²Nairobi (Kenya)
- 21.036 Prevalence of tuberculosis in slaughter camels (*Camelus dromedaries*) based on lateral-flow technology (Camelid TB-STAT PAK™)
U. Bello Abubakar, C. Ayuba Kudi, I. Alhaji Abdulkadir, O. Olu Solomon
Zaria, Kaduna (Nigeria)
- 21.037 Haiti in the time of cholera
J. Malaty¹, L. Moore²
¹Washington, DC (USA), ²Arlington, VA (USA)
- 21.038 HBV, HCV in the street children
cancelled
S. Siabani
Tehran (Iran)
- 21.039 Risk of complications and progression to death from diarrhea due to *C. difficile* infection compared with non-*C. difficile* diarrhea
H.-W. Kuo, D. Schmid, C. Wensch, F. Allerberger
Vienna (Austria)
- 21.040 Evaluation of neonatal tetanus surveillance system in Baluchistan—Pakistan, 2009
A. Akbar Mengal¹, M. A. Ali²
¹Balochistan, Balochistan (Pakistan), ²Quetta, Balochistan (Pakistan)
- 21.041 Incidence of cerebral edema in CNS infections among adults in Tirana population in Albania
A. Ndreu, E. Puca, E. Mingomataj, **G. Stroni**, D. Kraja, I. Akshia
Tirana (Albania)
- 21.042 Persistence of the influenza A(H1N1) pandemic virus in water and on non-porous surface
A. Dublineau¹, C. Batéjat¹, A. Pinon², A.-M. Burguière¹, I. Leclercq¹, J.-C. Manuguerra¹
¹Paris (France), ²Lille (France)
- 21.043 Diversity of Rotavirus Strains in Diarrhea Children in Lagos, Nigeria
C. Ayolabi¹, D. Ojo², I. Akpan³, G. Armah⁴
¹Lagos State, LOS (Nigeria), ²Abeokuta (Nigeria), ³Abeokuta (Nigeria),
⁴Accra (Ghana)
- 21.044 Association of Neonatal Sepsis with Maternal Premature Rupture of the Membranes (PROM) in Our Area Since 2010
H. Babaei, A. Hormati, M. Affian, S. Kavandi
Zanjan (Iran)



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- 21.045 Relationships of 7th pandemic *Vibrio cholerae* using genome wide single nucleotide polymorphisms and multilocus variable number tandem repeat analysis
C. Lam¹, S. Octavia¹, R. Lan¹, P. Reeves¹, L. Wang²
¹Sydney (Australia), ²Tianjin (China)
- 21.046 Impact and incidence of sputum smear positive tuberculosis on children in the era of ART attending Kanombe Military Hospital between January 2009–June 2010
J. Orikiiriza, I. A. Izimukwiye, C. Muhinda, J. Lule, C. Murego
Kigali (Rwanda)
- 21.047 *cancelled* Molecular epidemiology hepatitis C in Belarus, prevalens of 1 b and 3a genotypes
V. Eremin, **E. L. Gasich**, S. V. Sosinovich, M. G. Pinchuk
Minsk (Belarus)
- 21.048 *cancelled* Prevalance of syphilis (STD) in healthy blood donors of Lahore, Pakistan
B. M. Ahmad¹, R. Munim², J. K. Khan¹, T. Malik², S. Qamar², **T. Ijaz**¹, M. K. Shahzad², M. S. Hussain¹
¹Lahore, Punjab (Pakistan), ²Faisalabad (Pakistan)
- 21.049 *cancelled* Prevalance of HBV, HCV and HIV in healthy volunteer blood donors of Lahore, Pakistan
B. M. Ahmad, R. Munim, J. K. Khan, M. S. Ashraf, M. K. Shahzad, M. A. Khan, K. Siddique, B. Ahsan, **T. Ijaz**
Lahore, Punjab (Pakistan)
- 21.050 Amyotrophic lateral sclerosis: A case control study on infectious agents as etiologic factors
M. Riccò¹, T. Halperin Ben Ami¹, V. Pietrini¹, P. Manotti¹, A. Odone¹, M. Vinceti², C. Signorelli¹
¹Parma (Italy), ²Reggio Emilia-Modena (Italy)
- 21.051 Risk factors in patients with chronic hepatitis C from Timis Country, Romania
I. Marincu, L. Negrutiu, I. Iacobiciu, A. M. Neghina, L. Tirnea, T. R. Olariu, M. Cornianu, R. Neghina
Timisoara (Romania)
- 21.052 *cancelled* *Mycobacterium tuberculosis* infection and associated risk factors including HIV co-infection among the prison inmates in a jail of Pakistan
T. Ijaz, B. M. Ahmad, S. Ijaz, M. K. Shahzad, A. M. Akhtar, S. Aslam
Lahore, Punjab (Pakistan)
- 21.053 Zoonotic aspects of *Coxiella burnetii* antibody positivity between dairy cattle herds and their farmers
J. F. Agger¹, O. F. Miazzi¹, A.-B. Christoffersen², J. S. Agerholm¹, S. Villumsen², B. Kantsoe², E. Bosnjak³, H. Nielsen³
¹Frederiksberg (Denmark), ²Copenhagen (Denmark), ³Aalborg (Denmark)
- 21.054 Development of simple, rapid and very sensitive molecular detection method for laboratories and filed applications
A. Karami
Tehran (Iran)



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- 21.055 A specific serum IgA antibody discriminates pneumonia from colonization state in patients with *Pseudomonas aeruginosa* in sputum culture
M. Yamashita, Y. Hida, H. Sugimoto, N. Takahashi, H. Kimura, H. Yoshida, T. Ishizaki Fukui (Japan)
- 21.056 Newly sensitive competitive ELISA using monoclonal antibody against NS1 of West Nile Virus NY99 strain
J. Hirota¹, K. Morita², S. Shimizu¹
¹Tsukuba (Japan), ²Nagasaki (Japan)
- 21.057 Simultaneous detection and differentiation of influenza A virus and Newcastle Disease Virus by real-time PCR
D. Nidzworski¹, E. Wasilewska¹, B. Gromadzka¹, K. Smietanka², Z. Minta², B. Szewczyk¹
¹Gdansk (Poland), ²Pulawy (Poland)
- 21.058 Searching online books of infectious diseases: A new way to load decision-support software with the most up-to-date information
J. Brown
Tacoma, WA (USA)
- 21.059 Detection and quantification of avian hepatitis E virus from clinical samples by a new TaqMan real-time RT-PCR including an internal control
S. Troxler, A. Marek, I. Prokofieva, I. Bilic, M. Hess
Vienna (Austria)
- 21.060 Continuous improvement of a novel real-time PCR for detection and quantification of DNA from pathogenic leptospires
A. Steinrigl¹, M. Müller¹, Z. Bagó¹, L. Fischer², S. Revilla-Fernández¹, F. Schmoll³, P. Winter²
¹Mödling (Austria), ²Vienna (Austria), ³Leipzig (Germany)
- 21.061 Diagnosis of Mediterranean visceral leishmaniasis by detection of Leishmania antibodies and Leishmania DNA in oral fluid samples
A. Bouratbine¹, Y. Galai¹, N. Chabchoub¹, M. Benabid¹, S. Lakhal¹, I. Ben-abda¹, M. Chibani², F. Amri³, K. Aoun¹
¹Tunis (Tunisia), ²Zaghouan (Tunisia), ³Kairouan (Tunisia)
- 21.062 Proventricular dilatation disease in psittacines may be caused by mixed infections with different genotypes of avian bornaviruses
N. Nedorost, A. Maderner, J. Kolodziejek, N. Nowotny, H. Weissenboeck
Vienna (Austria)
- 21.063 Chromogenic in situ hybridization as a tool for identification of emerging protist species in tissue samples
M. Mostegl¹, N. Dinhopl¹, B. Richter¹, D. Binanti², S. Chvala-Mannsberger¹, N. Nedorost¹, A. Maderner¹, B. Habenbacher¹, V. Janauschek¹, M. Ondrovics¹, A. Wetscher¹, P. Schießl¹, P. Prouzova¹, S. Gurtner¹, Z. Karakas¹, D. Liebhart¹, H. Weissenboeck¹
¹Vienna (Austria), ²Milan (Italy)
- 21.064 Non-invasive dengue diagnosis: Can saliva substitute blood?
G. Yap, L.-C. Ng
Singapore (Singapore)



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- 21.065 Role of the protein microarray technology in the development of a rapid immunoassay for the influenza virus
L. d'Episcopo¹, M. Di Cristina², L. Nunziangeli², M. A. Giubilei², B. Capuccini², G. Mazzoleni¹, F. Baldracchini¹, M. Maccari¹, R. Spaccapelo², A. Crisanti²
¹London (United Kingdom), ²Perugia (Italy)
- 21.066 Descriptive study of iron biomarkers in Ethiopian Visceral leishmaniasis patients
T. Ambaye
Gondar (Ethiopia)
- 21.067 Did advances in global surveillance and notification systems make a difference in the 2009 H1N1 pandemic?
M. Stoto
Washington, DC (USA)
- 21.068 Origin and diffusion of tuberculosis breakdowns by *Mycobacterium caprae* in cattle herds in an officially tuberculosis free Province of Italy
G. Zanardi¹, M. B. Boniotti¹, C. Costanzi², F. Chin², A. Moresco², M. L. Pacciarini¹
¹Brescia (Italy), ²Trent (Italy)
- 21.069 Are we ready for new challenges in epidemic intelligence?
K. Denecke, A. Stewart
Hanover (Germany)
- 21.070 Pattern detection for social media-based epidemic intelligence: A user study
A. Stewart, K. Denecke
Hanover (Germany)
- 21.071 Risk map of highly pathogenic avian influenza spreading areas in poultry based on risk factors
I. Iglesias, J. M. Sanchez-Vizcaino, M. J. Muñoz, M. Martínez, J. Fernandez-Pinero, A. de la Torre
Madrid (Spain)
- 21.072 Serological monitoring of Newcastle disease virus in poultry, synanthropic, zoo, and wild birds in Ukraine in 2006–2009
A. Skrypnyk, Y. Krasnobayev, Z. Trotsenko, V. Skrypnyk
Kiev (Ukraine)
- 21.073 Strengthening links in disease surveillance in the international setting
L. Wilson
Orkney (United Kingdom)
- 21.074 Development of influenza epidemiology and virology surveillance in Indonesia, 2009
S. Farida
Jakarta (Indonesia)
- 21.075 Essential requirements for surveillance systems for emerging diseases
J. Richardson¹, A. Afonso¹, P.-A. Beloeil¹, P. Hendrikx², R. Thiery³, D. Verloo¹
¹Parma (Italy), ²Lyons (France), ³Sophia Antipolis (France)



POSTER PRESENTATIONS • SESSION 2I

International Meeting on Emerging Diseases and Surveillance 2011

Room: Bruckner/Mahler/Brahms • Upper Level

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11:45–14:00

- 21.076 Surveillance of arbovirus infections in the French forces: Being less specific to be more efficient
C. Marimoutou¹, A. Dia¹, V. Pommier de Santi¹, F. Delaval¹, C. Decam¹, G. Texier¹, C. Verret², R. Haus-Cheymol², X. DeParis¹
¹Marseille (France), ²Paris (France)
- 21.077 VSD: A database for virus nucleotide sequence including epidemiological information
M. G. Han¹, H. Hong¹, S. H. Kang¹, Y. E. Jeong¹, J. S. Ryou¹, B. Kang¹, S. Y. Paik², K. J. Song², Y. S. Jeong², S. Kim², Y. B. Kim², Y. R. Ju¹, J. S. Lee¹
¹Cheongwon-gun (Korea), ²Seoul (Korea)
- 21.078 GEMMA and ENPS—New tools for the analysis of functional protein complexes, lipoparticles and viruses
W. W. Szymanski, M. Havlik, C. Laschober, **G. Allmaier**
Vienna (Austria)
- 21.079 Mobile technology for syndromic surveillance of livestock diseases in Kenya
J. Walker¹, E. Ogola², D. Knobel²
¹Redwood City, CA (USA), ²Kisumu (Kenya)
- 21.080 Social media and epidemiology: Tweets indicate Norovirus outbreak at a university
E. Velasco¹, M. Kriek², L. Otrusina³, F. Bazoche⁴, J. Linge⁵, T. Eckmanns¹, J. Dreesman²
¹Berlin (Germany), ²Hanover (Germany), ³Brno (Czech Republic), ⁴Oldenburg (Germany), ⁵Ispra (Italy)
- 21.081 Horizon scanning—Helping predict the next emerging infection
K. Hansford, E. Bennett, O. Snowden, M. Pietzsch, J. Medlock
Porton Down (United Kingdom)
- 21.082 Surveillance and monitoring of an influenza pandemic: A network of web-based platform
D. Paolotti, V. Colizza, C. Gioannini, A. Vespignani
Turin (Italy)
- 21.083 Identification of dynamic and consequences of an epidemic of highly pathogenic avian influenza in poultry farms using spread modelling
I. Iglesias¹, A. Torre¹, M. J. Muñoz¹, M. Martínez¹, J. Fernandez-Pinero¹, J. M. Sanchez-Vizcaino²
¹Valdeolmos Madrid (Spain), ²Madrid (Spain)
- 21.084 Integrated disease surveillance program (IDSP): A long overdue initiative for Pakistan
M. S. Cheema, **S. M. Mursalin**, S. M. Mubashar
Islamabad (Pakistan)
- 21.085 Global Food Safety Portal: A visualisation tool to promote new research into data relations and assess trends, patterns and risk factors for foodborne pathogens
A. R. Domingues¹, A. Vieira¹, R. S. Hendriksen¹, **S. Karlslose**¹, D. M. Lo Fo Wong², F. M. Aarestrup¹
¹Kgs. Lyngby (Denmark), ²Geneva (Switzerland)
- 21.086 An interdisciplinary approach to Chagas surveillance: How the New Mexico Geo-Epidemiology Network addresses the challenges of a neglected disease
M. McConnell¹, J. Fair², J. Franke¹
¹Albuquerque, NM (USA), ²Los Alamos, NM (USA)



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- 21.087 SAGES: A suite of freely-available software tools for electronic disease surveillance in resource-limited settings
B. Feighner¹, S. Lewis¹, W. Loschen¹, R. Wojcik¹, J. Skora¹, J. Coberly¹, D. Blazes²
¹Laurel, MD (USA), ²Silver Spring, MD (USA)
- 21.088 Ecology, genetic clustering, and virulence of medically important bacterial and viral pathogens in Georgia
L. Bakanidze¹, N. Tsertsvadze¹, S. Tsanova¹, P. Imnadze¹, I. Sikharulidze¹, J. Lee², R. Obiso³, S. Francesconi⁴
¹Tbilisi (Georgia), ²Frederick, MD (USA), ³Christiansburg, VA (USA), ⁴Silver Spring, MD (USA)
- 21.089 Personalized event-based surveillance and alerting support for the assessment of risk
A. Stewart¹, **R. G. Lage**², E. Diaz-Aviles¹, P. Dolog²
¹Hanover (Germany), ²Aalborg (Denmark)
- 21.090 Assessment of IDSR implementation at the local government level in Nigeria 2009
I. Dalhatu¹, E. E. Ekanem², A. Olupelumi³, O. Ojo¹, E. Ilori¹, A. Adebayo¹, **H. Akpan**¹
¹Abuja, FCT (Nigeria), ²Lagos, (Nigeria), ³Ibadan (Nigeria)
- 21.091 Using spatio-temporal modeling to predict exposure to ticks at a fine-scale and recommendations on the prevention and monitoring of Lyme borreliosis
C. Meha
Paris (France)
- 21.092 A Global, Web-based Food-borne Pathogen Annotated Tracking Resource Network (PATRN) System
R. Jain¹, K. L. Hari¹, G. Gopinathrao¹, M. Kothary², A. R. Datta², K. Jarvis², A. Franco², L. Hu², V. Sathyamoorthy², C. Grim², M. K. Mammel², I. Patel², S. Jackson², M. Kotewicz², J. E. LeClerc², B. A. McCardell², B. Tall²
¹Fremont, CA (USA), ²Laurel, MA (USA)
- 21.093 The medical ecosystem [M-Eco] project: Personalized event-based surveillance
K. Denecke¹, E. Diaz-Aviles¹, P. Dolog², T. Eckmanns³, M. Fischella¹, R. G. Lage², J. Linge⁴, P. Smrz⁵, A. Stewart¹
¹Hanover (Germany), ²Aalborg (Denmark), ³Berlin (Germany), ⁴Ispra (Italy), ⁵Brno (Czech Republic)
- 21.094 Using an ecohealth approach to livestock production: community surveillance of newly emerging infectious diseases (nEIDs)
Q. Le Ba, D. Hall
Calgary, (Canada)
- 21.095 Using Craigslist messages for syphilis surveillance
J. Fries, A. T.Y. Ho, A. Segre, P. Polgreen
Iowa City, IA (USA)
- 21.096 Samos: A community-driven open-access prediction market system
J. Paton, P. Polgreen, F. Nelson, A. Segre
Iowa City, IA (USA)



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- 21.097 Methodological supplies of African swine fever monitoring and preparedness in Ukraine by NSC 'IECVM'
B. T. Stegnyy, A. Buzun, A. Gerilovych
Kharkiv (Ukraine)
- 21.098 Appropriate time-interval dosage of alcohol hand gel on reducing influenza-like illnesses among preschool children: A randomized, controlled trial
D. Pandejpong¹, N. Vanprapa¹, T. Pandejpong¹, E. F. Cook², S. Danchaiwijitr¹
¹Bangkok (Thailand), ²Boston, MA (USA)
- 21.099 A rubella outbreak appears in unvaccinated border hilly districts of Chamba-Kangra, Himachal Pradesh, India, 2007
S. Gupta¹, V. Ramachandran¹, N. Gupta², N. Mehta¹
¹Kangra, Himachal Pradesh (India), ²Chennai (India)
- 21.100 Utility of phosphorodiamidate morpholino oligimer (PMOplus™) technology in rapid response to RNA virus pandemics and epidemics
A. Heald, P. Iversen, P. Sazani, S. Shrewsbury
Bothell, WA (USA)
- 21.101 Effective planning for outbreaks by emerging infections: Pathogen traffic and activities of daily life
R. Lee
Orchard Park, NY (USA)
- 21.102 Diffuse outbreak of hepatitis A suspected by national case based surveillance in Japan, 2010
N. Nakamura, T. Shimada, Y. Tada, T. Kiyohara, K. Ishii, M. Noda
Tokyo (Japan)
- 21.103 Epidemiological features of Crimean-Congo hemorrhagic fever and description of control measures, South Kazakhstan oblast, Kazakhstan, 2009–2010
K. Kyraubayev¹, B. Baiserkin¹, Z. Medetov², **Y. Bumburidi**¹
¹Almaty (Kazakhstan), ²Shymkent (Kazakhstan)
- 21.104 Investigation of a multi-prefectural outbreak of Enterohemorrhagic Escherichia coli O157 infection—Japan, 2009
F. Odaira, N. Nakamura, Y. Yahata, K. Nakashima, N. Okabe
Tokyo (Japan)
- 21.105 Causes of death as reflected by hospital records in Pakistan
M. S. Cheema, **S. M. Mursalin**, S. M. Mubashar
Islamabad (Pakistan)
- 21.106 Cluster of cutaneous mycobacteriosis in a school in Rome, school year 2009–2010
E. Kanitz¹, J. L. Sinagra¹, C. Cerochi¹, G. Prignano¹, L. Bonadonna¹, R. Briancesco¹, R. Paradiso¹, E. Tortoli², B. Capitanio¹, F. D'Ancona¹
¹Rome (Italy), ²Florence (Italy)
- 21.107 Evaluation of preparedness status of provincial laboratories in Kenya to respond to public health emergencies, 2010
Y. Ronoh
Kapsabet, Rift-Valley (Kenya)



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- 21.108 Highland malaria outbreak in Homeyo District, Papua Province, Indonesia: An entomological investigation
A. Oktavian¹, H. Kawulur¹, M. Widiyanti¹, M. Raharjo¹, D. Triboewono²
¹Jayapura (Indonesia), ²salatiga (Indonesia)
- 21.109 Epidemiology, clinical and paraclinical features of definite cases of influenza A (H1N1) in Kashan, Iran 2009
A. Hasan, M. Momen Heravi, Z. Soleimani, A. Sharif
Kashan, Isfahan (Iran)
- 21.110 Inactivation of several BSL3 viral pathogens by disinfectants and nucleic acid lysis buffers
F. X. Abad, D. Solanes, M. Domingo
Bellaterra, Barcelona (Spain)
- 21.111 Control measures and response on West Nile Virus during the outbreak in Northern and Central Greece
G. Dellis¹, F. Goma², S. Chalkidou², G. Ferentinos¹, P. Smeti¹, A. Chrisostomou¹, R.-M. Sillantavou¹, C. Kefaloudi¹, T. Mamali¹, F. Koukouritakis¹, L. Kostopoulos¹, A. Bakali¹, I. Ignatiadi¹, G. Saroglou¹, A. Pavli¹, K. Syrros¹, A. Economopoulou¹
¹Athens (Greece), ²Thessaloniki (Greece)
- 21.112 Characterization of *Cronobacter sakazakii* strains from two recent neonatal meningitis cases and comparison of historical archival strains using PATRN, a novel global web-based pathogen tracking system
G. Gopinathrao¹, B. Tall¹, M. Kothary¹, R. Jain², K. L. Hari², A. Franco¹, L. Hu¹, V. Sathyamoorthy¹, C. Grim¹, C. Lee¹, J. Sadowski¹, M. K. Mammel¹, I. Patel¹, S. Jackson¹, M. Kotewicz¹, J. E. LeClerc¹, B. A. McCardell¹, M. Wekell¹
¹Laurel, MD (USA), ²Fremont, CA (USA)
- 21.113 *C. difficile* in a hospital in Vienna before and after implementation of CDI control measures, Austria, 2009–2010
S. Kasper, D. Schmid, A. Indra, W. Ulrich, H. Masoud, S. Eberl, S. Huhulesco, F. Allerberger
Vienna (Austria)
- 21.114 Sero prevalence of Dengue 2 virus infections in patients presenting with febrile illness in selected health facilities in Trans Nzoia Region, Kenya
S. Nzou
Nairobi (Kenya)
cancelled
- 21.115 New flavivirus in Europe: Bagaza virus outbreak in partridges and pheasants in Southern Spain, 2010
M. Agüero¹, J. Fernandez-Pinero², D. Buitrago¹, A. Sanchez¹, M. Elizalde², E. San Miguel¹, R. Villalba¹, F. Llorente², **M. A. Jimenez-Clavero**²
¹Algete, Madrid (Spain), ²Valdeolmos, Madrid (Spain)
- 21.116 Invasive *Klebsiella pneumoniae* liver abscess syndrome broadens its horizons
D. O'Shea, **R. Moore**, G. Sheehan, T. Geoghegan
Dublin (Ireland)
- 21.117 Dengue in East Africa
F. Vairo¹, E. Nicastrì¹, N. Bevilacqua¹, S. Meschi¹, B. Nguhuni², M. Sane Schepisi¹, A. Di Caro¹, G. Ippolito¹
¹Rome (Italy), ²Dodoma (Tanzania)



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- 21.118 Sporadic circulation of dengue in febrile outpatients in Tanzania mainland and in Pemba Island, Zanzibar
F. Vairo¹, E. Nicastrì¹, S. Meschi¹, M. Sane Schepisi¹, M. Paglia¹, N. Bevilacqua¹, S. Mangi², M. Jape³, V. Racialbuto¹, M. Capobianchi¹, A. Di Caro¹, G. Ippolito¹
¹Rome (Italy), ²Iringa (Tanzania), ³Pemba (Tanzania)
- 21.119 Does source matter? Comparing the timeliness of outbreak reports from governmental and non-governmental sources
L. Mondor¹, J. Brownstein², E. Chan², A. Sonricker², L. Madoff³, M. Pollack⁴, T. Brewer⁵
¹Montreal, QC (Canada), ²Boston, MA (USA), ³Brookline, MA (USA),
⁴New York, NY (USA), ⁵Montreal (Canada)
- 21.120 Is *Vibrio fluvialis* emerging as a predominant pathogen causing epidemics of diarrhea in coastal regions of Eastern India?
R. Pal, K. Sarkar
Kolkata (India)
- 21.121 Outbreak of West Nile Virus in Cádiz (Andalusia, Spain)
E. Figueroa Murillo, M. Prieto Uceda, A. Pérez Alonso, M. Polo Montes, M. L. Martin Vicente, M. Conde Lama
Puerto Real (Spain)
- 21.122 The Confirmation of *psaA* by PCR in the different serotypes of *Streptococcus pneumoniae* isolated from nasopharynx of healthy children
F. Fallah, **A. Karimi**, M. Navidinia, F. Shiva, M. Hadipour Jahromi
Tehran, (Iran)
- 21.123 The study of Phospholipase C genes in Beijing strains of *Mycobacterium tuberculosis*
H. Goudarzi, E. Mirsamadi, S. Jahani sharafat, P. Farnia
Tehran (Iran)
- 21.124 Emergence and spread of *Vibrio cholerae* O1 El Tor with classical *ctxB* genotype 1 and tetracycline resistant strains in Assam, northeast India
B. Borkakoty, D. Biswas, U. Devi, J. Mahanta
Dibrugarh, Assam (India),
- 21.125 How to introduce the subject of conservation medicine into veterinary studies? First experiences at JLU Giessen, Germany
C. Riedel¹, S. Knauf²
¹Giessen (Germany), ²Kronberg (Germany)
- 21.126 Evaluation of the effectiveness of animal diseases reporting system in Oyo State, Nigeria (1995–2005): The relevance of ProMED-mail
T. Babalobi
Ibadan (Nigeria)



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- 21.127 Active immunization using exotoxin A confers protection against *Pseudomonas aeruginosa* infection in a mouse burn model
A. Manafi¹, J. Kohanteb², **D. Mehrabani**², A. Japoni², M. Amini², M. Naghmachi³, A. Hosseinzadeh Zaghi¹, N. Khalili²
¹Tehran (Iran), ²Shiraz (Iran), ³Yasuj (Iran)
- 21.128 Pertussis outbreaks and associated factors, Taiwan, January 2006–June 2010
C.-M. Liu¹, S.-E. Huang¹, **H.-W. Kuo**²
¹Taipei (Taiwan, R.O.C.), ²Vienna (Austria)
- 21.129 Vaccination coverage against influenza, pandemic and seasonal in the Canary Islands. 2009–2010 Season
A. J. García Rojas¹, P. Garcia Castellano¹, D. Nuñez Gallo², J. Solis Romero¹, D. Trujillo Herrera²
¹Las Palmas de Gran Canaria (Spain), ²Santa Cruz de Tenerife (Spain)
- 21.130 Genetic profile of new porcine parvovirus isolates and high rate of viral evolution in the capsid protein gene
A. F. Streck¹, S. L. Bonatto², T. Homeier¹, N. Leinecker¹, C. K. Souza², D. Gava², C. W. Canal², U. Truyen¹
¹Leipzig (Germany), ²Porto Alegre (Brazil)
- 21.131 Changes in the circulating rotaviruses genotypes detected during the surveillance and its implications for the rotavirus vaccination in Colombia, South America
C. Ramirez, D. Pelaez
Bogota (Colombia)
- 21.132 Characterization of candidate vaccines by a new bioanalytical approach—Gas-phase electrophoretic mobility macromolecular analysis with an electrostatic nanoparticle sampler
M. Havlik¹, M. Marchetti-Deschmann¹, G. Friedbacher¹, W. Winkler¹, G. Fuhrmann², L. Pérez-Burgos², C. Dworak², P. Messner¹, W. W. Szymanski¹, C. Tauer², G. Allmaier¹
¹Vienna (Austria), ²Orth/Donau (Austria)
- 21.133 A measles and rubella laboratory based surveillance report in Tanzania, 2008
D. Kadigi, F. Mosha, M. Mashulano, M. Matee
Dar es Salaam (Tanzania)
- 21.134 Vaccine-derived poliovirus infection in an Colombian infant with congenital agammaglobulinemia
J. C. Orrego Arango¹, J. J. Silvestre², V. R. Torres², J. L. Franco², L. M. Arboleda²
¹Medellín (Colombia), ²Manizales (Colombia),
- 21.135 Lyophilization of *Brucella abortus* S19 vaccine using two different preservatives in the Sudan
M. F. E. M. Alawad, M. T. Musa
Khartoum (Sudan)
- 21.136 Measles outbreak in South of Iran
P. Davoodian, A. Daryanavard, T. Eqbal Eftekhaari, R. Safari², K. Soleimani, S. Fekri
Bandar Abbas (Iran)



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- 21.137 Emerging human rotavirus strains, 2006–2010, Hungary
B. Laszlo¹, **H. Papp**², E. Dandár², J. Deák³, J. Gray⁴, M. Iturriza-Gomara⁴, F. Jakab⁵, Á. Juhász¹, J. Kovács⁶, J. Kónya¹, G. Lengyel², V. Martella⁷, J. Mészáros¹, Z. Mészner², I. Mihály², P. Molnár², Z. Nyúl⁸, L. Pátri⁸, E. Puskás⁹, F. Schneider¹⁰, A. Tóth², E. Tóth¹¹, G. Sz. cs¹², K. Bányai²
¹Debrecen (Hungary), ²Budapest (Hungary), ³Szeged (Hungary), ⁴London (United Kingdom), ⁵Pécs, (Hungary), ⁶Bordány (Hungary), ⁷Bari (Italy), ⁸Pécs (Hungary), ⁹Miskolc (Hungary), ¹⁰Szombathely (Hungary), ¹¹Nyíregyháza (Hungary), ¹²Kuwait (Kuwait)
- 21.138 Batch release of veterinary vaccines in Finland
L. Kaartinen, M. Jakava-Viljanen, K. Alm-Packalen
Helsinki (Finland)
- 21.139 Outbreaks of hepatitis A among children in orphanages
L. Lazarevska, G. Shakiri, L. Koceva
Skopje (Macedonia)
- 21.140 Tularemia in Oppland and Hedmark counties, Norway, 2003–August 25, 2010
V. Hasseltvedt
Lillehammer (Norway)
- 21.141 Haemorrhagic fever with renal syndrome (HFRS) in Oppland and Hedmark Counties, Norway, 1981–2009
V. Hasseltvedt
Lillehammer (Norway)
- 21.142 High incidence of rickettsiosis correlated with the prevalence of *Rickettsia japonica* among *Haemaphysalis longicornis* tick associated with Japanese deer density in Shimane Peninsula, Shimane Prefecture, Japan
T. Kenji¹, K. Hiroki², I. Asao¹, Y. Takeo³, F. Hiromi⁴, T. Nobuhiro⁵
¹Matsue (Japan), ²Tokyo, Tokyo (Japan), ³Imizu, Toyama (Japan), ⁴Fukushima, Fukushima (Japan), ⁵Fukui (Japan)
- 21.143 Temporal trends of malaria cases and deaths-Nigeria, 2003–2009
O. Ajumobi¹, J. Onyeneke¹, O. Olanpeleke¹, P. Nguku¹, G. Poggensee¹, K. Sabitu², E. Ilori¹, B. Coker¹, B. Audu¹, O. Oresanya¹, G. Ntadom¹, H. Akpan¹
¹Abuja (Nigeria), ²Zaria (Nigeria)
- 21.144 Ten years experience of Crimean-Congo Haemorrhagic Fever as a vector borne disease in Iran
S. Chinikar, R. Mirahmadi, M. Moradi, S. M. Ghiasi, A. Sadeh, S. Khakifirouz, F. S. Varaeae, M. Asl Solaimani
Tehran (Iran)
- 21.145 Using Ross River virus outbreak models to deliver practical management tools for mosquito control efforts in the Northern Territory, Australia
S. Jacups
Darwin (Australia)
- 21.146 Effectiveness of alpha-cypermethrin (Cyperthor) and lambda-cyhalothrin (Demand) in the reduction or prevention of *Aedes* mosquito breeding in tyres under tropical conditions
S. Jacups
Darwin (Australia)



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- 21.147 Current status of Q fever in Ukraine and needs for expanded surveillance of *Coxiella burnetii*
Z. Kushnir, I. Kurhanova, A. Tarasyuk
Lviv (Ukraine)
- 21.148 Visceral leishmaniasis (V-L) in pregnancy: Case report
A. Pilaca, Z. Delia, G. Stroni, A. Pepa, E. Puca, S. Kurti, D. Kraja
Tirana (Albania)
- 21.149 WNV monitoring activities implemented in Veneto region from 2008 to 2010
M. Cecchinato¹, **P. Mulatti**¹, T. Patregnani¹, F. Montarsi¹, C. Terregino¹, G. Frison²,
L. Bonfanti¹, S. Marangon¹, M. Bricchese²
¹Legnaro (Italy), ²Venice (Italy)
- 21.150 Comparative analysis of the genomic sequences of dengue type 2 viruses associated
with different genotypes/sampling times/epidemics/disease severity in Thailand from
1964 to 2001
cancelled J. Li¹, P. Chinnawirotpisan², A. Zhang¹, A. Nisalak², R. Putnak¹, **C. Zhang**¹
¹Silver Spring, MD (USA), ²Bangkok (Thailand)
- 21.151 Visceral leishmaniasis in Kairouan, Tunisia: Clinical and epidemiological characteristics
and factors of bad prognosis
K. Aoun¹, O. Rkhami², Z. Habboul², S. Lakhel¹, A. Bouratbine¹, F. Amri²
¹Tunis (Tunisia), ²Kairouan (Tunisia)
- 21.152 A metapopulation model to simulate West Nile virus circulation in southern Europe
and the Mediterranean basin
cancelled **V. Chevalier**¹, G. Balanca², T. Baldet³, B. Durand⁴
¹Montpellier (France), ²34398 (France), ³Cotonou (Benin), ⁴Maisons-lfort (France)
- 21.153 Bluetongue disease in wild ruminants in the Czech Republic
A. Sperlova, D. Zendulkova, K. Rosenbergova, Z. Pospisil
Brno (Czech Republic)
- 21.154 Four years of mosquito-based arbovirus surveys in Emilia-Romagna Region
(Northern Italy)
M. Calzolari¹, P. Bonilauri¹, R. Bellini², A. Albieri², F. DeFilippo¹, G. Maioli¹, M. Tamba¹,
P. Angelini³, M. Dottori¹
¹Brescia (Italy), ²Crevalcore (Italy), ³Bologna (Italy)
- 21.155 Acaricide use and the control of *Theileria parva* infection at the wildlife-livestock
disease interface in Kenya
J. Walker, E. Klein
Princeton, NJ (USA)
- 21.156 Dengue surveillance in Kerala, South-India, from 2007–2010:
A laboratory-based analysis
A. Manakkadan
Trivandrum, Kerala (India)
- 21.157 A clinical, immunological and neuroimaging study in Lyme neuroborreliosis
B. Tilea, I. Tilea, K. Branzaniuc, I. A. Tilea
Tirgu Mures, Mures (Romania)



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- 21.158 Experimental Tacaribe virus infection of Jamaican fruit bats
T. Schountz¹, A. Hawkinson¹, R. Bowen², C. H. Calisher²
¹Greeley, CO (USA), ²Fort Collins, CO (USA)
- 21.159 Abundance of *Culicoides sonorensis* (Diptera: Ceratopogonidae) in Southern Alberta (Canada) and Montana (USA)
A. Zuliani¹, T. J. Lysyk², G. Johnson³, A. Massolo¹, R. Waeckerlin¹, S. Cork¹
¹Calgary, AB (Canada), ²Lethbridge, AB (Canada), ³Bozeman, MT (USA)
- 21.160 Diagnosis of tick-borne encephalitis (TBE) based on the detection of NS5 gene sequences by the qRT-PCR in canine samples
A. Hekrlova, K. Rosenbergova, P. Lany
Brno (Czech Republic)
- 21.161 Seasonal abundance and prevalence of *Culicoides* biting midges in Sicily, Italy
A. Torina, S. Scimeca, R. Longo
Palermo (Italy)
- 21.162 Molecular characterization of *B. bovis* Merozoite surface antigen 2c (Msa2c) from Italian strains
A. Torina¹, A. Agnone¹, V. Blanda¹, A. Alongi¹, R. D'Agostino¹, E. De Carlo², F. Cusumano¹, G. Sireci¹, M. Florin-Christensen³
¹Palermo (Italy), ²Naples (Italy), ³Buenos Aires (Argentina)
- 21.163 Characterization of *Rickettsia* infections in Sicily, Italy
A. Torina, A. Alongi, V. Blanda, R. D'Agostino, S. Scimeca, G. M. Giammanco, P. Ammatuna
Palermo (Italy)
- 21.164 Serologic and genetic evidence of Dobrava-Belgrade and Saaremaa hantaviruses among Apodemus mice in Hungary and Northern Croatia
V. Németh¹, M. Madai¹, A. Maráczsi¹, B. Bérczi¹, G. Horváth¹, M. Oldal¹, T. Kovács¹, K. Bányai², F. Jakab¹
¹Pécs, Baranya (Hungary), ²Budapest, PEST (Hungary)
- 21.165 *Dirofilaria repens*—Occurrence and emergence in Austria
G. Duscher, A. Joachim
Vienna (Austria)
- 21.166 Association between *Anaplasma phagocytophilum* in ticks and anaplasmosis in dogs in Latvia
I. Berzina¹, A. Bormane², I. Matise¹
¹Jelgava (Latvia), ²Riga (Latvia)
- 21.167 Malaria in rural Zimbabwe: Are WHO's goals for disease control being achieved?
J. Pires, J. Duarte
Lisbon (Portugal)
- 21.168 Humoral immune response to rickettsial pathogens in dogs regularly infested by ticks in Eastern Austria
M. Leschnik, R. Peschke, **N. Affenzeller**, G. Duscher, A. Feiler
Vienna (Austria)



Room: Klimt Ballroom I • Upper Level

Sunday, February 6, 2011

11:45–14:00

- 21.169 Serological evidence of Toscana virus in Portugal
F. Amaro¹, T. Luz¹, P. Parreira¹, A. Marchi², M. G. Ciufolini², **L. Zé-Zé**¹, M.-J. Alves¹
¹Águas de Moura (Portugal), ²Rome (Italy)
- 21.170 Abundance and distribution of potential West Nile Virus mosquito vectors in North Western Canada
R. Waeckerlin¹, A. Mukherjee-Wilske¹, J. Swann¹, K. Karunakaran¹, B. Elkin², A. Massolo¹, S. Cork¹
¹Calgary, AB (Canada), ²Yellowknife, NT (Canada)
- 21.171 Evaluation of CCHF patients: Laboratory findings of the first two days
M. Yesilyurt¹, S. Gul¹, **B. Ozturk**², B. C. Kayhan¹, M. Celik¹, C. Uyar¹, F. Erdogan¹
¹Yozgat (Turkey), ²Ankara (Turkey)
- 21.172 Detection of pathogenic arboviral zoonoses in Central Asia
B. Atkinson¹, C. Logue¹, L. Bakanidze², N. Barnabishvili², A. Junushov³, F. Tishkova⁴, I. Hay⁵, B. Briggs⁵, P. Larsen⁶, C. Phillips⁶, R. Baker⁶, R. Hewson¹
¹Salisbury (United Kingdom), ²Tbilisi (Georgia), ³Bishkek (Kyrgyzstan), ⁴Dushanbe (Tajikistan), ⁵Buffalo, NY (USA), ⁶Lubbock, TX (USA)
- 21.173 Identification of an inhibitor of flavivirus protease with antiviral activity
V. Monteil¹, D. Rolland², I. Leparç-Goffart¹, F. Berree⁴, S. Plumet³, B. Carboni³, H. Tolou¹
¹Marseille (France), ²Marcy l'Etoile (France), ³Rennes (France)
- 21.174 Viral features associated to Chikungunya virus emergence in metropolitan France
I. Leparç-Goffart¹, V. Caro², S. Plumet¹, Y. Souares³, P. Despres², H. Tolou¹, M. Grandadam²
¹Marseille (France), ²Paris (France), ³St. Maurice (France)
- 21.175 The role of South American camelids in bluetongue virus serotype 8 epidemiology
C. Schulz¹, M. Eschbaumer², M. Gauly³, D. Werner⁴, P. König², M. Rudolf², R. Wäckerlin⁵, M. Beer², C. G. Grevelding¹, B. Hoffmann², C. Bauer¹
¹Giessen (Germany), ²Greifswald-Insel Riems (Germany), ³Goettingen (Germany), ⁴Muencheberg (Germany), ⁵Calgary (Canada)
- 21.176 Effect of transportation on the efficacy of a formalin inactivated Rift Valley Fever vaccine
N. Lagerqvist¹, B. Moiane¹, L. Neves², J. Paweska³, C. Ahlm⁴, Å. Lundkvist¹, K. Falk¹
¹Solna (Sweden), ²Maputo (Mozambique), ³Sandringham (South Africa), ⁴Umeå (Sweden)
- 21.177 Do they meet often?—Genetic similarity between European populations of a potent disease vector *Culex pipiens*
M. Löhmus, M. Björklund, A. Lindström
Uppsala (Sweden)
- 21.178 A model to predict areas of potential BTV outbreaks
M. C. Radaelli¹, L. Chiavacci¹, A. Barbaro¹, S. Travaglio¹, W. Mignone², L. Masoero¹, M. Goria¹, G. Savini³, N. Vitale¹
¹Turin (Italy), ²Imperia (Italy), ³Teramo (Italy)



Room: Klimt Ballroom I • Upper Level

Sunday, February 6, 2011

11:45–14:00

- 21.179 Studies on the pathogenicity of the 2009 West Nile Italian strain (Italy/2009)
F. Monaco, F. Lopes, A. Polci, P. Migliaccio, G. Savini, R. Lelli
Teramo (Italy)
- 21.180 Age- and sex-specific mortality patterns in hemorrhagic fever with renal syndrome caused by Puumala virus
M. Hjertqvist¹, S. L. Klein², C. Ahlm³, **J. Klingström**¹
¹Solna (Sweden), ²Baltimore, MD (USA), ³Umeå (Sweden)
- 21.181 Wild mammal diversity and animal keeping relationships: The link for a better comprehension of sleeping sickness re-emergence in Fontem (Cameroon) old focus
J. A. Massussi¹, Z. Tadu¹, C. Djiéto Lordon¹, F. Njiokou¹, C. Laveissière², J. D. van der Ploeg³
¹Yaoundé (Cameroon), ²Mont Pellier (France), ³Wageningen (Netherlands)
- 21.182 Serosurvey of Crimean-Congo Hemorrhagic Fever in human populations in Kenya
A. Ismail, L. Musila, A. Makio, S. Limbaso, E. Chekorir, A. Abade, S. Amwayi, J. Omollo, J. Oundo, R. Sang
Nairobi (Kenya)
- 21.183 Risk maps for mosquito-borne diseases (Diptera, Culicidae): Distribution and abundance of mosquitoes in the Canaries Archipelago (Spain)
M. C. Pou Barreto¹, R. Melero Alcibar², R. Morchon Garcia³, C. Gonzalez Martin¹, A. del Castillo Remiro¹, R. Molina², B. Valladares¹
¹La Laguna (Spain), ²Madrid (Spain), ³Salamanca (Spain)
- 21.184 Surveillance of dengue in France: Different modalities for different situations and results for 2010
cancelled **D. Dejour-Salamanca**¹, J. De valk¹, S. Larrieu², T. Lernout³, G. La Ruche¹, J. Rosine⁴, Y. Souares⁵, A. Tarantola¹, V. Vaillant¹
¹Saint-Maurice (France), ²Saint Denis de La Reunion (France), ³Mamoudzou (France), ⁴Fort de France (France), ⁵Marseilles (France)
- 21.185 First laboratory confirmed case of tick-borne fever in dairy cattle in Germany
C. Silaghi¹, D. Hamel¹, M. Nieder², K. Pfister¹, R. Schmäscke², **M. Pfeffer**²
¹Munich (Germany), ²Leipzig (Germany)
- 21.186 Ecological surveillance of West Nile virus in Catalonia 2007–2010: Continuously evolving
A. Alba¹, A. Allepuz², J. Casal², **F. X. Abad**¹, E. Serrano¹, C. Aranda³, R. Escosa⁴, E. Marques⁵, N. Busquets¹
¹Bellaterra, Barcelona (Spain), ²Bellaterra (Spain), ³Sant Feliu de Llobregat (Spain), ⁴Amposta (Spain), ⁵Castelló d'Empúries (Spain)
- 21.187 Health related quality of life and the prevalence of post traumatic stress disorder among CHF survivors 12 months after disease
S. Gul¹, E. Uz Gul¹, M. Yesilyurt¹, **B. Ozturk**², F. Kusu², O. Ergonul³
¹Yozgat (Turkey), ²Ankara (Turkey), ³Kadikoy (Turkey)



EARLY MORNING SESSION • SESSION 22

International Meeting on Emerging Diseases and Surveillance 2011

Room: Klimt Ballroom 2&3 • Upper Level

Monday, February 7, 2011

07:00–08:00

Emerging Diseases in Public Health Education

Chair: Jaime Torres, Venezuela

- 22.001 Emerging diseases in public health education:
The case of field epidemiological trainings
P. Crépey¹, **A. Flahault**²
¹Paris (France), ²Rennes (France)



PARALLEL SESSION • SESSION 23

International Meeting on Emerging Diseases and Surveillance 2011

Room: Park Congress • Ground Level

Monday, February 7, 2011

08:30–10:30

Farm to Table: Foodborne Infections

Co-Chairs: Jacques Acar, France
Tam Garland, USA

- 23.001 Salmonella: Epidemics, reservoirs, and resistance
J. Threlfall
London (United Kingdom)
- 23.002 Listeriosis on the rise
F. Allerberger
Vienna (Austria)
- 23.003 Opportunistic food-borne infections: The burden of prevention
J. Torres
Caracas (Venezuela)
- 23.004 The changing epidemiology of noroviruses
M. Koopmans
Rotterdam (Netherlands)

10:30–11:00 **Coffee Break** (Ground Level AND Upper Level)



Room: Klimt Ballroom 2&3 • Upper Level

Monday, February 7, 2011

08:30–10:30

Emerging Infectious Pathogens of Animals & Man (Oral Presentations)

Co-Chairs: Tim Brewer, Canada

Nilufar Rakhmanova, Uzbekistan

- 24.001 Prevalence of campylobacters in patients and poultry in and around Chandigarh, India
C. Vaishnavi, M. Singh, B. R. Thapa, J. Thakur
Chandigarh (India)
- 24.002 SARS-Coronavirus ancestors foot-prints in South-East Asia: Bat colonies and the biodiversity refuge theory
M. Le Guoil¹, S. Puechmaille², J.-P. Gonzalez³, E. Teeling², P. Kittayapong⁴, J.-C. Manuguerra¹
¹Paris (France), ²Dublin (Ireland), ³Franceville (Gabon), ⁴Nakhon Pathom (Thailand)
- 24.003 Sentinel organisms as biomonitors for emerging zoonotic pathogens at the environmental interface of humans, wildlife, and livestock
D. B. Conn¹, T. K. Graczyk²
¹Mount Berry, GA (USA), ²Baltimore, MD (USA)
- 24.004 Zoonotic arboviruses threatening wildlife in Southern Africa
M. Venter, J. Styel, S. Human, C. van Eeden, S. Smit, J. Williams
Pretoria (South Africa)
- 24.005 Emergence and spread of human adaptation markers in avian influenza viruses during an HPAI A(H7N7) virus outbreak
M. Jonges¹, A. Bataille², R. Enserink¹, J. A. Stegeman², G. Koch³, A. Meijer¹, M. Koopmans⁴
¹Bilthoven (Netherlands), ²Utrecht (Netherlands), ³Lelystad (Netherlands), ⁴Rotterdam (Netherlands)
- 24.006 Origin and genetic evolution of swine influenza A virus isolated during winter of 2008–2010 in Zhejiang province, China
L. Jiang, Q. Jiang, Y. Zhou, X. Lv, Q. Shi, Y. Gao, X. Zhu, L. Ju
Shanghai (China)
- 24.007 Surveillance of leptospirosis in an urban slum: Using animal population surveillance data to assess human risk
J. Halliday¹, D. Knobel², B. Agwanda¹, S. Cutler³, B. Olack¹, R. Breiman¹, K. Njenga¹, S. Cleaveland⁴, M. Bronsvoort⁵
¹Nairobi (Kenya), ²Kisumu (Kenya), ³London (United Kingdom), ⁴Glasgow (United Kingdom), ⁵Edinburgh (United Kingdom)
- 24.008 Epidemic Intelligence (EI): Assessing event-based (EB) tools and users' perception in the GHSAG community
L. Vaillant¹, P. Barboza¹, R. R. Arthur²
¹Saint Maurice (France), ²Atlanta, GA (USA)



PARALLEL SESSION • SESSION 24

International Meeting on Emerging Diseases and Surveillance 2011

Room: Klimt Ballroom 2&3 • Upper Level

Monday, February 7, 2011

08:30–10:30

24.009 Discovery of *Mycobacterium mungi* sp nov.: A novel, emerging *M. tuberculosis* complex pathogen affecting banded mongoose living at the human-wildlife interface
K.A.Alexander¹, P.N. Laver¹, A. L. Michel², M. Williams², P.D. Van Helden³
R. M. Warren³, N. C. Gey van Pittius³
¹Blacksburg, VA (USA), ²Pretoria (South Africa),
³Tygerberg (South Africa)

24.010 Zoonotic pathogens present in South African bat species
W. Markotter, M. Geldenhuys, M. Tjale, M. Moller, S. Mcculloch, J. Coertse, L. Nel
Pretoria (South Africa)

10:30–11:00 **Coffee Break** (Ground Level AND Upper Level)



PLENARY LECTURE • SESSION 25

International Meeting on Emerging Diseases and Surveillance 2011

Room: Park Congress • Ground Level

Monday, February 7, 2011

11:00–11:45

Identifying New and Emerging Viruses of Bat Origin

Chair: Larry Madoff, USA

25.001 Identifying new and emerging viruses of bat origin
L. Wang
Geelong (Australia)



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SESSION 01 (Plenary)

Plenary Lecture 1

Friday, February 4, 2011

Room: Park Congress • Ground Level

14:20–15:00

1.001 Monitoring Emerging Disease Threats in Europe

M. Sprenger
Stockholm, Sweden

NO ABSTRACT RECEIVED

SESSION 02 (Symposium)

Diseases at the Wildlife-Human Frontier

Friday, February 4, 2011

Room: Park Congress • Ground Level

15:00–16:30

2.001 Public health and conservation: collision or collaboration

J. Childs
Yale University Medical School, New Haven, CT, USA

NO ABSTRACT RECEIVED

2.002 Looking at bats for emerging infectious agents

S. Zhang
East China Normal University, Shanghai, China

Bats have been identified as a natural reservoir for an increasing number of emerging zoonotic viruses, including rabies viruses, lyssaviruses related to rabies virus, henipaviruses, SARS-like coronaviruses, Ebola viruses etc. Several reasons might explain why bats are hosts of so many emerging viruses, including these mammals' abundance and colonial nature, roosting behaviors, diversity and wide distribution, ability to fly and seasonal migration, hibernation, food diet, life span etc, but some other potential reasons such as evolution and immunology of bats are also discussed.

2.003 Rabies threats to people and endangered wildlife: If everybody benefits, who pays?

R. Woodroffe
Institute of Zoology, Regent's Park, London, UK

Background: As well as threatening human health, rabies has contributed to the extinction or near-extinction of several important wildlife populations, including those of endangered African wild dogs and Ethiopian wolves. I therefore review the potential for rabies control to benefit both people and endangered wildlife in African rangelands.

Methods: I monitored a population of African wild dogs living alongside people and domestic dogs, as well as wild carnivores such as jackals and hyaenas, over a ten-year period. Combining these data with published information on rabies control in domestic dogs allowed an evaluation of alternative management scenarios.

Results: Field data suggest that rabies infection was persisting in local domestic dog populations, but not in wild carnivores. Infrequent contact between packs of wild dogs meant that rabies would probably wipe out infected packs before any opportunity arose to transmit to another pack, leading to rapid fadeout. Because domestic dogs appeared to be

acting as a reservoir of rabies infection, vaccinating domestic dogs could potentially benefit both people and wildlife. However, the high costs of vaccinating domestic dogs in rural vs urban areas mean that public health organisations might not prioritise rabies management in wildlife areas.

Conclusion: In African rangelands, both people and endangered wildlife could benefit from rabies vaccination targeted at domestic dogs. However, because public health programmes may not prioritise such extremely rural areas, they may not represent suitable funding sources for interventions likely to benefit wildlife conservation.

SESSION 03 (Plenary)

Plenary Lecture 2

Friday, February 4, 2011

Room: Park Congress • Ground Level

16:30–17:15

3.001 Wildlife and emerging diseases: Drivers, maps and the road ahead

P. Daszak¹, T. Bogich¹, P. Hosseini¹, K. Olival¹, C. Zambrana-Torrel¹, W. Karesh¹, J. Mazet², S. Morse³
¹EcoHealth Alliance, New York, NY, USA, ²UC Davis, Davis, CA, USA, ³Columbia University, New York, NY, USA

New zoonoses seem to emerge from wildlife in a random, unpredictable pattern, but with increasing frequency and impact. Work over the past two decades has shown that the process of zoonotic disease emergence is essentially an ecological one in which anthropogenic factors drive the spillover and spread of wildlife microbes in human hosts. Because these 'drivers' are measurable, and to some extent their future trajectory is known, analyzing them provides a basis from which to predict the patterns of future zoonotic disease emergence. Targeting these regions for surveillance will enable the best use of scant global resources - a 'Smart Surveillance' strategy. In this talk, I present an approach to identify the regions where the next emerging infectious diseases (EIDs) are most likely to emerge (EID 'hotspots') and our current efforts to refine our recently published work (Jones *et al.* Nature 2008), with updated driver data, and new analyses. This research may provide a cost-effective strategy for pandemic prevention, by allowing us to allocate global resources to the regions where the next pandemic is most likely to originate. We are involved in a large scale effort to collect samples from wildlife in these hotspots regions and discover new pathogens that could potentially become zoonoses. This "PREDICT" program is funded by USAID as part of a larger Emerging Pandemic Threats (EPT) program. As part of this strategy, we have set up a series of large-scale transects across disease 'hotspots' which represent gradients of deforestation, population density, biodiversity (of hosts and pathogens), agricultural intensification, and other factors that are important in disease emergence. The aim is to ultimately produce far more accurate predictions of where the next emerging zoonoses are most likely to originate, and from which species of wildlife.

SESSION 04 (Early Morning Session)

GIDEON

Saturday, February 5, 2011

Room: Klimt Ballroom 2–3 • Upper Level

07:00–08:00

4.001 GIDEON: A global web-based system for disease simulation and informatics in the field of geographic medicine

S. Berger
Tel Aviv Medical Center, Tel Aviv, Israel



Background: 347 generic infectious diseases are distributed haphazardly in time and space; and are challenged by 342 drugs and vaccines. Over 3,000 pathogenic bacteria, viruses, parasites and fungi have been described in human disease.

Methods and Materials: An ongoing project (*GIDEON*, <http://www.gideononline.com/>) for decision-support and informatics will serve as a paradigm to demonstrate current trends in web-based systems for Geographic Medicine.

Results: The first module of *GIDEON* generates ranked differential diagnoses based on signs, symptoms, laboratory tests, exposure history, country of acquisition and incubation period; and can be used to diagnose or simulate any infectious disease scenario. Additional capabilities include bioterrorism simulation and syndromic surveillance.

- The second module follows the epidemiology of individual diseases, including their global status and occurrence in each endemic country. As of 2010, this module contains 3 million words of text in 19,000 country-specific text notes; 32,095 graphs; 5,100 images (clinical, microscopic, life cycle, etc); 347 maps; 250,000 linked references; 20,200 outbreaks and 21,101 disease prevalence and serosurveys. An additional submodule is designed for Informatics and Consultation in the field of Tavel Medicine.

- The third module follows the pharmacology and usage of all anti-infective drugs and vaccines; and the fourth is designed to identify and characterize all species of bacteria, mycobacteria and yeasts.

- During the coming months, a sub-program of *GIDEON* will release electronic books (e-books), each of which presents a complete review of all data for a specific country or disease. The series consists of 411 individual books—95,000 pages (<http://www.gideononline.com/ebooks/>) and will be updated yearly.

Conclusion: This system is currently used by WHO, CDC and academic departments and agencies in over 40 countries. The background and functions of *GIDEON* will be reviewed through a series of screen-shots; and the application of web-based systems for use in diagnosis, surveillance and education will be discussed.

according to pre-existing biases. Such episodes can have adverse consequences for those fearful of retribution if they seek out medical care during an epidemic as well as the public health authority's responses.

Influenza pandemics appear to be different from most contagious crises in that the scapegoating associated with them has been much more fleeting and has had far less staying power, especially as it spreads around the globe. But public health and government officials still need to be on guard against society's impulses to blame and the repercussions of this age-old habit.

5.002

Influenza transmission: Pigs to people and back K. Van Reeth

Ghent University, Ghent, Belgium

Pigs are naturally susceptible to the same influenza A virus subtypes as humans and H1N1, H3N2 and H1N2 viruses are endemic in swine populations worldwide. However, the epidemiology of swine influenza is complex, because swine influenza viruses (SIVs) have a different history and origin in different regions of the world.

Human influenza viruses, H3N2 viruses in particular, regularly transmit from humans to pigs. H3N2 SIV lineages in Europe and North America have a human haemagglutinin (HA), but they have acquired other viral genes from swine-adapted or avian viruses through the process of genetic reassortment. These SIVs are thus genetically distinct from their human counterparts, and they also show slower drift in their HA. Pigs can therefore serve as "reservoirs" for older human influenza viruses. The other way round, SIVs occasionally transmit from pigs to humans. Most humans with SIV reported a recent exposure to pigs, and they had a mild influenza-like illness or pneumonia.

While the number of proven SIV cases in humans remains small compared to the total number of humans with occupational exposure to pigs, serological studies for SIV antibodies in humans suggest that zoonotic SIV infections are much more widespread and that many asymptomatic infections go undetected. Unfortunately, the interpretation of such studies is disputed, because of technical limitations of differentiating between swine and human influenza viruses by serology.

Most important, there is little evidence for person-to-person spread of swine-lineage viruses and the swine-to-human transmissions have been epidemiologically dead end events. The single known exception is the pandemic H1N1 2009 influenza virus. Unlike other swine-origin viruses, this virus clearly spreads readily between humans, and we don't know why it has this capacity.

As a swine influenza virus researcher, I will present my personal viewpoint on the public health significance of influenza in pigs. I will tackle some timely questions. Should we worry about zoonotic SIV infections in humans? What do we really know about the species barrier between humans and pigs? What have we learned from the 2009 pandemic? Will the next influenza pandemic come from pigs or from birds?

5.003

Pandemic influenza: The early days in New York City

A. Fine

Bureau of Communicable Disease, New York, NY, USA

The sudden and unexpected arrival of a novel influenza virus in New York City (NYC) in April 2009 posed immediate challenges to the NYC Department of Health and Mental Hygiene (DOHMH). Previous pandemic planning in NYC had focused on a scenario in which a pandemic virus arrived in NYC weeks to months after its first emergence as a serious threat, and on a virus with lethality comparable to the 1918 pandemic virus.

Initial objectives of the DOHMH response included the rapid implementation of surveillance methods to determine the extent of transmission in the community, estimate the incidence and severity of disease, describe the geographic and age distribution of both mild and severe illness, and to monitor trends over time. Secondary objectives focused on estimating case fatality rates, determining risk factors for severe disease and gathering sufficient data to be able to make informed recommendations regarding infection control measures for

SESSION 05 (Parallel Session)

H1N1 Pandemic

Saturday, February 5, 2011

Room: Park Congress • Ground Level

08:30–10:30

5.001

The 2009 A/H1N1 influenza pandemic and the "Blame Game": A brief history

H. Markel

University Michigan, Ann Arbor, MI, USA

Background: The term scapegoat originates from Leviticus 16. It refers to a goat driven off into the wilderness and was part of the ceremonies for Yom Kippur, the Day of Atonement, conducted by the Jews in Exodus and well after the construction of the Temples in Jerusalem. Exiled from the community, the goat carried away their sins. Medical historians have since come to use the word "scapegoat" to describe those blamed for epidemics.

Methods and Materials: Historical review of the media generated during the 2009 pandemic.

Results: After Mexico announced its outbreak, reports blaming Mexicans begin appearing on U.S. media outlets. Within days, anti-Mexican charges in the U.S. (and soon after around the world) media included illegal aliens, undocumented workers settled immigrants as the causes of both imported disease and economic ruin. Soon after, other scapegoats were suggested including government officials, President Obama, the media, public health officials, and scientists, and pork products.

Conclusion: Scapegoating social groups during (and after) epidemic outbreaks are not new phenomena. There can be more than one scapegoat during an epidemic event Those blamed are often stereotyped



both healthcare and community settings, and regarding the clinical management of both mild and severe influenza-like illness.

This presentation will focus on strategies employed by DOHMH to meet these challenges and will discuss lessons learned for the early management of future pandemics.

5.004 One health, one flu?

I. Capua¹, C. Giovanni²

¹Istituto Zooprofilattico Sperimentale delle Venezie, Padova, Padua, Italy, ²Istituto Zooprofilattico Sperimentale delle Venezie, Legnaro (Padova), Italy

Background: The emergence and spread of the pandemic H1N1 2009 virus from the animal reservoir raises questions on the future approach to influenza virus infections. Evidence demonstrates that influenza virus genes migrate across continents and animal species assembling themselves in combinations which threaten animal and human health, resulting in panzootics like H5N1 or pandemics H1N1 2009. The latter originated from the animal reservoir, containing a unique combination of genes from three species and two hemispheres. Mapping gene movements across species and national borders and identifying mutations and gene constellations with pandemic potential or virulence determinants is essential to enact prevention and control strategies at a global level.

Methods and Materials: Vast improvements in capacity building have been achieved following the H5N1 global crisis. Thousands of viral isolates with zoonotic potential have been obtained through surveillance efforts, although the genetic information has not been exploited fully. Furthermore, the circulation of influenza viruses in certain species including dogs, pigs and horses has been neglected.

Results: "One Flu" is a novel approach to influenza virus infections, in line with the "One Health" vision, abandoning prefixed compartments linked to geographical origin or species of isolation, aiming at analysing the influenza gene pool as one entity. It would capitalise on existing achievements and investments to develop an international network and a permanent observatory to improve our understanding of the dynamics of the influenza virus gene pool in animals and humans. This will generate crucial information to support both public and animal health.

Conclusion: The "One Flu" initiative would also result in international synergies, bridging gaps between medical and veterinary scientists, permanent monitoring of virus evolution and epidemiology and the best exploitation of investments in capacity building. Above all it could be a challenge and opportunity to implement the "One Health" vision, and possibly act as a model for other emerging zoonotic diseases.

Results: Malaysia was the first to approve and conduct semi-field trials to assess the mating competitiveness and mating compatibility of sterile male mosquitoes from the lead RIDL strain of *Aedes aegypti* (called OX513A), as well as the world's first study on the relative susceptibility of females from this transgenic and wild type strains to key viruses such as CHIKV and DENV-2. In addition, extensive bionomic studies have been conducted to confirm that the transgenic strain did not differ from the wild type strain in morphology or life history traits, and that there is no evidence for successful interspecific cross-mating of transgenic *Aedes aegypti* with wild type *Aedes albopictus* (its closest species). Outside the United Kingdom and its Overseas Territories, Malaysia was also the first country to approve and conduct open-field trials involving this transgenic mosquito strain, setting the precedent in the world for regulatory approval and public engagement pertaining to open release of transgenic mosquitoes. These trends are consistent with the role Malaysia has played in the last two decades -- from introducing biosafety provisions in the Convention on Biological Diversity in 1992, hosting the first Meeting of Parties (MOP1) to the Cartagena Protocol on Biosafety, enacting and enforcing the Biosafety Act 2007, to playing a key role in the adoption of the Nagoya-Kuala Lumpur Supplementary Protocol on Liability and Redress (2010) to the Cartagena Protocol on Biosafety.

Conclusion: This paper summarises these important developments in the context of reducing the burden of dengue and chikungunya in the world.

6.002 First report of concomitant leptospirosis and hantavirus nephropathy, and of an as yet unknown hantavirus in Sri-Lanka

J. Clement¹, N. Sunil-Chandra², M. Van Esbroeck³, P. Maes⁴, M. Van Ranst⁴

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Background: Leptospirosis and hantavirus nephropathy are two mainly rodent-borne infections, occurring both worldwide. Sri-Lanka is highly endemic for leptospirosis, but so far no hantavirus cases have been clinically documented.

Methods and Materials: Patients hospitalized in Kelaniya for leptospirosis ("lepto")-like symptoms were screened with IgM ELISA for lepto, and for hantavirus ("hanta") with European prototype *Puumalavirus* (PUUV) and Asian prototype *Hantaanvirus* (HTNV).

Results: A prospective study comprised 39 patients, aged 13 to 74 years (mean 35), 34/39 being males, with a history of rodent exposure in 34/39. IgM ELISA in 31/39 acute sera was positive in 9 (29%) cases for lepto only, 2 (6.5%) for hanta only, whereas 13 (41.9%) were negative for both, but 7 (22.6%) were simultaneously positive for both pathogens. IgM seropositivity was for PUUV only in 2/9, for PUUV predominantly in 5/9, and for HTNV predominantly in 2/9. Convalescent sera 2-3 weeks later confirmed acute PUUV-like infection in 4/31 (12.9%) cases, but picked up additionally 8 lepto IgM-positive cases, thus finally resulting in 17/31 (54.8%) acute lepto-only cases. Compared to seronegative or lepto-only cases, clinical symptoms were more severe in all 9 hanta-positive cases, with 78% jaundice, 56% hepatomegaly, 56% hematuria, and 33% cough. Serum bilirubin (1.7-16.2, mean 6.9 mg/dL), and blood urea (36-305, mean 118.8 mg/dL) was likewise more elevated.

In a second retrospective study, an additional 23/24 lepto-like patients appeared IgG ELISA lepto positive. Of these, 10 were also IgG ELISA hanta positive, again with a net predominance (9/10) for PUUV.

Conclusion: Lepto and hanta can clinically mimic each other perfectly, and can occur simultaneously, probably after transmission from the same (here still unknown) rodent reservoir. These dual infections could explain "treatment failures" of lepto with antibiotics. This is worldwide the first report of concomitant or successive lepto-hanta infection in a total of 17 patients, and of seroconfirmed hantavirus nephropathy in Sri-Lanka. In neighbouring India, we found likewise PUUV-like predominance in similar and fatal cases. However, they were RT-PCR negative for all hitherto known pathogenic hantaviruses. Proven PUUV-infections occurred only in Europe so far, and the responsible rodent reservoir *Myodes glareolus* is absent from both India and Sri-Lanka.

SESSION 06 (Parallel Session)

Vectorborne Diseases (Oral Presentations)

Saturday, February 5, 2011

Room: Klimt Ballroom 2-3 • Upper Level

08:30-10:30

6.001 Transgenic mosquitoes to control dengue and chikungunya in Malaysia

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²Institute for Medical Research, Kuala Lumpur, Malaysia

Background: Dengue and chikungunya have put more than half the world's population in over 124 countries at risk.

Methods and Materials: Malaysia has taken the lead in regulating and evaluating the biosafety and efficacy of the RIDL-Sterile Insect Technique—a new tool developed at Oxford University (United Kingdom) and its part-owned company Oxitec—to suppress the *Aedes aegypti* vector population and thus combat dengue and chikungunya.

**6.003 West Nile Outbreak in the Mediterranean Region, August–November 2010**

P. Barboza¹, S. Iloos¹, F. Ait-El-Belghiti¹, V. Gauthier¹, G. La Roche¹, I. Capek¹, M. Dente², R. Vorou³, M. Gastellu¹

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Background: In summer 2010, West Nile (WN) spread all around some of Mediterranean countries. EpiSouth, which is a network of 27 Mediterranean and Balkans countries for the control of public health threats, reported WN outbreaks in 8 EpiSouth countries since August 2010. Data regarding numbers of human and animal cases, and the nature of WN surveillance implemented in those 27 countries were collected to document WN circulation in this area.

Methods and Materials: A questionnaire was sent to EpiSouth focal points in all the network countries to collect information on WN surveillance systems and availability of WN laboratory, epidemiological context and recent cases. Background information previously collected by EpiSouth work-packages in charge of zoonoses was integrated and official reports issued by OIE and ministries of health were also considered for cases counts.

Results: On 15 of November 2010, 17 countries provided information: 375 human cases including 34 deaths were reported by 5 countries (Greece, Israel, Italy, Romania and Turkey). Only 5 countries (Bulgaria, Greece, Italy, Morocco, and Spain) reported equine WN cases.

14 countries have access to a WN reference laboratory, 13 have a permanent or seasonal human surveillance. Regarding veterinary surveillance, 6 countries have permanent or seasonal WN surveillance among horses and 4 among birds, 7 countries have neither human nor veterinary surveillance.

Conclusion: Since August 2010, outbreaks have been identified on all major birds' migratory routes crossing Mediterranean region but also in the Volga basin (Russia) which is a major bird nesting area. The WNV circulation documented during the autumn the Mediterranean Basin and neighbouring areas is unprecedented.

WN surveillance systems and access to laboratory facilities across EpiSouth countries drastically vary. In this context early alerting and rapid information exchange is essential especially for countries with limited facilities. This highlights the importance of maintaining such a cross border Network with efficient laboratory components and real field surveillance so that appropriate control measures can be implemented.

6.004 Mosquito flavivirus survey in Portugal, 2006–2009

L. Zé-Zé¹, H. C. Osório¹, F. Amaro¹, I. M. Chelo², REVIVE Workgroup¹, M.-J. Alves¹

¹National Institute of Health Dr. Ricardo Jorge, Águas de Moura, Portugal, ²Instituto Gulbenkian de Ciência, Oeiras, Portugal

Background: West Nile virus (WNV) is currently recognized as Europe's most important mosquito borne virus. In Portugal, it was demonstrated to be circulating since the 60's and was first isolated in 1969 from mosquitoes. No clinical cases were reported until the summer of 2004 when two tourists acquired WNV disease in the Southern province of Algarve. In a way to access the potential WNV infection risk to the human population, a mosquito surveillance programme was developed by the Portuguese National Institute of Health and the Regional Public Health Authorities in 2006 and at a National level from 2008 (REVIVE program).

Methods and Materials: The surveillance actions started in 2006 and 2007 only in the region of Algarve. In 2008 mosquitoes' collection was extended to cover most of mainland Portugal. Mosquitoes were collected from June through October with CDC light-traps, identified and unfed females were pooled for RNA extraction and screened by RT-PCR for the presence of WNV by partial NS5 gene amplification using flavivirus specific primers. PCR amplicons were sequenced and identified by homology searches within GenBank database using Blast algorithm.

Results: A total of 20,878 adult females comprising 13 species and belonging to six genera were screened for flaviviruses in 576 pools. The most common species were *Culex pipiens* s.l. L. (53.3%) and *Ochlerotatus*

caspius Pallas (26.0%), followed by *Culex theileri* Theobald (15.6%). Twenty nine pools were found to be positive for flaviviruses. Significant scores were found by BLAST for 21 pools, from *Culex* and *Ochlerotatus* mosquitoes, with sequences of mosquito flaviviruses detected in *Oc. caspius* in Italy (isolate OccaFV2) and eight pools of *Cx. theileri* with sequences of "Wang Thong virus" detected in *Cx. fuscocephala* in Thailand. A preliminary analysis of the phylogenetic relationships was performed using non-structural protein NS5 partial gene sequences and both sequences cluster within the insect-only flavivirus group.

Conclusion: During the course of this study, two new insect flavivirus sequences were detected in *Culex* and *Ochlerotatus* mosquitoes. Our results agree with previous suggestions that a large number of flaviviruses, namely in the insect-only cluster still remain unknown.

6.005 Characterization of Chikungunya infection in an in vitro primary human skeletal muscle model

K. Mohamed Hussain, M. L. Ng, J. J. H. Chu

National University of Singapore, Singapore

Background: Chikungunya virus (CHIKV) is a mosquito-borne virus known to manifest itself with an acute febrile phase followed by a prolonged arthralgic disease, affecting the joints of the extremities which may persist for weeks or months, or in rarer cases, years. Despite this knowledge, the pathophysiology of CHIKV infection has not been widely studied to date.

Methods and Materials: In view of the classical tropism of CHIKV infection, primary-derived human skeletal muscle myoblasts (HSMM) were selected as potential susceptible hosts. Infectability of these cells with CHIKV was established by plaque assay, quantitative real-time PCR and double immunofluorescence labelling analyses. The mode of CHIKV replication as well as the role of CHIKV-induced apoptosis in these cells was also investigated.

Results: We noted that the CHIKV-infected HSMM cells produced viral titres comparable to BHK-21 cells. Transmission electron microscopic studies of CHIKV-infected cells revealed morphological changes typical of alphavirus infection, including the proliferation of endoplasmic reticulum membranes and large cytoplasmic vacuoles, containing viral replication complexes. At various infection periods, enveloped mature virions were also observed to be budding at the plasma membrane. Furthermore, as characterized by morphological assessment and terminal deoxynucleotidyltransferase-mediated dUTP nick end labelling (TUNEL), CHIKV infection of these skeletal muscle cells triggered an apoptotic cellular response, with nuclear disintegration and DNA fragmentation observed.

Conclusion: The establishment and characterization of this cellular model would assist in contributing to a better understanding of CHIKV pathogenesis and enable future development of anti-viral strategies against CHIKV infection.

6.006 Detection of rickettsia and anaplasma in lizards ticks, Algeria

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Background: Our results raise the possibility that these agents transmitted to the human by the tick where the reservoir can be our biological model.

Methods and Materials: *Study Area:* The study was conducted in El-kala National Park (North East of Algeria) humid bioclimatic zone (72%–78, 9%). *Tick and Lizard Collection:* This survey was conducted from April 2008 to April 2009. Lizards were hand captured in the site or using a special pitfall in the complex zone. Ticks were removed from each lizard using forceps and stored in 70% ethanol for later identification to species and life stage using taxonomic keys (IPTM, version1.0 "AFPMB" and confirmed by Pasteur Institute of Tunis). *DNA Extraction:* DNA was extracted from ticks composed of males and unfed females, using the QIAmp DNA Mini Kit (QIAGEN GmbH, Hilden, Germany).



Results: 184 lizards were captured belonging to tree species: 125 *Psammotromus algerius*, 07 *Iacerta pater*, 52 *Podarcis hv*, were checked for attached ticks. In total 422 nymph and larval ticks were removed and further identified as *I. ricinus*. Moreover, 10 tails and 52 skin biopsy specimens were taken from the captured lizards.

DNA isolation was further analyses for the presence of *Rickettsia*, *Anaplasma*. 37% ticks carried *Rickettsia*, 4% *Anaplasma* and 3% unknown pathogens. None of the tested tails were positive only one of the 52 skin biopsy specimen was positive. The vast majority of pathogens detected were *R. helvetica* (15%), 12% *R.monacensis*, the rest are unknown *Rickettsia* (*Rickettsia* sp). 4% were *A. phagocytophilum* and 3% unknown pathogens.

Conclusion: In the conclusion of our work further studies are needed to confirm the role of lizards in cycle transmission of all these pathogens transmitted by *Ixodes ricinus* to humans. Until we do we can considerate the lizards as a platform for ticks feeding and mating. However, the apparent contributions of various other hosts to pathogen transmission highlight the need for a community approach to understanding vector-borne zoonoses. Future methods will generate information for approaching a variety of topics of pressing concern to public health, including the potential impact of anthropogenic landscape change on human risk of exposure to zoonotic pathogens.

6.007 First autochthonous dengue virus infections in south-east France in a context of a sharp increase in imported dengue cases in 2010

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Background: In Europe, the last dengue epidemic was reported in 1927-1928 in Greece, *Aedes aegypti* was the vector and since disappeared. Since the 1970s, *Ae. albopictus* has become increasingly established in European countries. This mosquito species is established since 2004 in south-east France. A national plan against the spread of dengue and chikungunya viruses in metropolitan France has been implemented since 2006.

Methods and Materials: As part of this plan, imported dengue cases are monitored through a laboratory network surveillance system since January 2006. Furthermore, enhanced surveillance is implemented each year from May to November in the districts where *Ae. albopictus* is established, allowing the reporting and the confirmation of suspected cases to be accelerated.

Results: The laboratory network surveillance system detected around 350-400 imported dengue cases per year between 2006 and 2009 (381 cases in 2009) in metropolitan France. During the same four-year period, 33 were reported by enhanced surveillance (including 11 cases in 2009). Between 1 May and 26 November 2010, 2,080 and 167 imported cases were reported by the laboratory network and by the enhanced surveillance system, respectively; this represents an 18-fold and a 15-fold increases, respectively, when compared with the entire 2009 season. These increases are mostly related to the epidemics in the French West Indies, Martinique and Guadeloupe, in 2010.

In September 2010, the enhanced surveillance identified the two first cases of autochthonous dengue infection ever diagnosed in metropolitan France, in Nice (south-east). The investigation found imported cases of dengue in the neighborhood. The hypothesis of an introduction of the virus through imported viremic cases from West Indies is the most likely.

Conclusion: The clustering of cases of locally transmitted dengue fever in Nice is a significant but not unexpected public health event. This highlights the importance of detecting cases by adapted surveillance and of anticipating the transmission by the development of a national plan. This event showed the advantages of such preparedness as it allowed the implementation of adequate and rapid measures of surveillance and control.

6.008 Laboratory based surveillance of dengue viral infection in a tertiary care hospital of Pakistan

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Background: Dengue haemorrhagic fever (DHF) is an acute mosquito-borne viral infection, caused by four immunologically distinct serotypes of Dengue virus. The disease is worldwide in distribution and a major health issue. In 1994, first dengue epidemic was recorded in Karachi, Pakistan. It was first time detected in city of Lahore during 2006. In year 2008 another epidemic was reported in same city while during the year 2010 a fulminating and massive epidemic occurred in Lahore, the capital of densely populated province Punjab, and directly connected to the epidemic area through daily based mass movement. Hence a lab based surveillance was conducted in a public tertiary care hospital of Lahore, Pakistan.

Methods and Materials: The study was conducted in the Microbiology department of Mayo hospital, Lahore. Blood samples of clinically suspected patients from emergency, indoor and out patient departments were tested by using IgM and IgG capture ELISA method. The major epidemiological parameters like age, gender, weekly increase in patient number were included in the study.

Results: During the year 2010, from a total of 4,210 suspected cases, 2690 cases were found reactive against Dengue virus-1 and 2 serotypes. Of the positive cases 51% were reactive to IgM, 36% to IgG while 13% for both IgM and IgG dengue. Of the reactive cases 78.92% were male and 21.08% were female. Among dengue cases, 15.24% were less than the age of 15 years, 43.86% were (16-30)yr, 21.58% were (31-45)yr, 15.24% were (46-60)yr, 2.97% were (61-75)yr and 1.11% were more than the age of 76 years. Majority of patients reported during October and November.

Conclusion: DF/DHF has emerged as the most important vector-borne viral illness in Lahore, Pakistan. There was substantial evidence of exposure to mosquitoes resulting in Dengue epidemic, and the serological tests demonstrated IgM, that is a highly sensitive marker of acute dengue infection. The epidemiology of dengue virus infection is not well reported in Pakistan. The trend of disease reflects its endemic status in the country. There is a need to establish an active laboratory-based surveillance system in dengue endemic areas. The only means to control this disease is to interrupt the transmission of the virus.

6.009 Re-emerging mosquito-borne diseases in Europe

W. Van Bortel, E. Warns-Petit, K. Leitmeyer, T. Mollet, H. Zeller
European Centre for Disease Prevention and Control, Stockholm, Sweden

Background: The number of recent notifications of mosquito borne diseases in the EU Member States in 2010 is a matter of concern to ECDC.

Methods and Materials: This presentation will review the epidemiological situation of mosquito-borne diseases in the EU, discuss the future risk and the actions for preparedness.

Results: In Greece the first large outbreak of West Nile Virus (WNV) in humans occurred in Europe since the Romanian outbreak in 1996-1997 and WNV circulation in other EU Member States (Romania, Hungary, Italy and Spain) and neighbouring countries (Russia, Israel, Turkey) seemed intensified. In 2010 new areas were infected with WNV and the outbreak showed an early onset. In France and Croatia the first autochthonous cases of dengue fever in continental Europe were reported since the outbreaks of 1927 and 1928 in Greece. Furthermore two autochthonous cases of chikungunya were notified in France, while Spain reported a local malaria case.

Conclusion: These events involved different types of pathogens of which some are considered typical for tropical areas. Moreover different groups of mosquito species, exotic as well as native, were involved. The



risk of transmission of the above mentioned mosquito-borne diseases is variable and depends on different drivers related to the pathogen, the vector, the host and the ecology.

These recent notifications strengthen the need for integrated surveillance systems and response plans, and to improve our knowledge on the disease transmission in Europe. This includes raising awareness of medical doctors of the clinical presentation of WNV, and of the import of dengue, chikungunya and malaria cases. Moreover, strengthening the understanding of the local and exotic vector species and transmission cycles would be of value.

6.010 West Nile: An emerging viral disease in North East (NE) India

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²Regional Medical Research Centre, Dibrugarh, Assam, India

Background: West Nile virus (WNV), an arthropod borne virus belongs to the family Flaviviridae, genus Flavivirus. In India, WNV activity has been reported from southern, central and western regions. Northeast (NE) India comprises of 8 states including Assam which is the most populous state harboring almost half of the 38,857,769 population of the region. Here, the leading cause of Acute Encephalitis Syndrome (AES) is JE, endemic since 1976. Large numbers of AES cases are JE negative which include death cases as well. During the year 2006, of 167 AES samples collected, 13 cases from 4 districts were positive for WNV infection. This is the first evidence of WNV activity in Eastern India. The present study is aimed to determine the emergence and spread of WNV in NE India.

Methods and Materials: From January 2007 to June 2010, 721 AES samples were collected from various hospitals of NE India. All the sera samples were tested with WNV specific IgM capture ELISA (PanBio, Australia) and JEV specific IgM capture ELISA (NIV, Pune, India). Paired sera were collected from WN and JE positive patients and subjected to viral neutralization test (VNT).

Results: Out of 721 sera tested, 10.40% were found positive for WNV IgM antibody. Among these WN positives (n=75), 96% showed cross reactivity with JEV IgM antibody. The WNV positive cases belonged to 14 districts spread over the states of Assam, Arunachal Pradesh and Meghalaya. A fourfold rise in WNV neutralizing antibody titer was observed in 11 cases. The remaining paired sera samples showed neutralizing antibodies to both WNV and JEV. Fever and altered sensorium were the most common symptoms recorded. WNV isolated from one human CSF sample relates to lineage 5.

Conclusion: Our findings suggest that WN, an emerging arboviral infection in the context of NE India, is another cause of AES. Cross reactivity in serological tests viz. ELISA and neutralization is a concern for diagnosis of the etiology. Development of a diagnostic tool with appreciable specificity is warranted in regions where two or more closely related arboviruses are circulating. A detail study of characterization of virus, vector incrimination and epidemiology is necessitated.

6.011 Emergence and explosive spread of West Nile virus infections in Europe—a matter of both public health and veterinary concern

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Background: In summer 2004 a lineage 2 West Nile virus (WNV) emerged for the first time in Europe (south-eastern Hungary; Ref.). Before that, lineage 2 WNVs were restricted to sub-Saharan Africa.

Methods and Materials: WNV surveillance systems were set up in several European countries.

Results: In 2005 and 2007 further WNV cases were observed in the same region. In summer 2008 the infection suddenly spread all over Hungary and to the eastern part of Austria, affecting several different species of birds (however mainly goshawks and other birds of prey), horses and humans.

Interestingly, in summer 2008 a widespread WNV outbreak was also observed in northern Italy, though the etiologic virus of the Italian outbreak was a lineage 1 WNV, which circulated in Europe already for a long time. It seems that in 2008 there were extremely favourable conditions for the spread of WNV in central Europe.

In 2009 West Nile disease was observed in the same large areas as in 2008.

In summer and autumn 2010 a significant WNV outbreak occurred in central Macedonia (northern Greece) with 191 laboratory-diagnosed human neuroinvasive cases including 32 fatalities. The etiologic virus of this outbreak was the Hungarian/Austrian lineage 2 WNV, which, however, exhibited increased neuropathogenicity for human beings, possibly associated with a certain amino acid exchange.

Also in summer 2010 a widespread WNV outbreak with many human cases was observed in the Volgograd region in Russia, which was caused by a lineage 2 WNV, different to the one circulating in Hungary, Austria and Greece.

Again in summer 2010 WNV outbreaks were seen in Romania, which were—at least in certain areas—caused by the Volgograd strain!

Conclusion: Since 2008 at least one lineage 1 WNV and two different lineage 2 WNV strains have been circulating in Europe and have been causing widespread and severe West Nile disease in humans and animals. As a consequence, WNV monitoring systems should urgently be established or extended in Europe, and the awareness of the general public must be increased.

Reference: Bakonyi *et al.* (2006): Lineage 1 and 2 strains of encephalitic West Nile virus, central Europe. *Emerg Infect Dis.* 12: 618-623.

SESSION 07 (Plenary)

Plenary Lecture 3

Saturday, February 5, 2011

Room: Park Congress • Ground Level

11:00–11:45

7.001 Emerging Arenaviruses

R. Swanepoel
National Health Laboratory Service, Johannesburg, South Africa

Background: Following the opening of a BSL4 laboratory in Johannesburg in 1980, antibody surveys were conducted on selected human, livestock and wild animal populations in order to establish which of the known viral hemorrhagic fevers occurred in South Africa and neighbouring countries. Some findings were reported, but progressive engagement of the laboratory in the investigation of outbreaks of hemorrhagic fever elsewhere in Africa led to suspension of further publication of surveys. The results of a survey on 5,363 rodent sera, together with details of the isolation of arenaviruses from seropositive species will be discussed in relation to the 2008 nosocomial outbreak of disease in Zambia and South Africa associated with the novel Lujo virus. Reference will also be made to information on emerging arenaviruses elsewhere.

SESSION 08 (Parallel Session)

Emerging Diseases and Public Communication

Saturday, February 5, 2011

Room: Park Congress • Ground Level

14:30–16:00



8.001 Health security communicators network of the EC and lessons learned from H1N1

G. Thinus
European Commission, Luxembourg

Background: The HSC communicator's network, created in 2008, brings together communicators from the 27 EU Member States, the 4 EFTA countries, EU agencies [ECDC, EMA, EFSA, ECHA] and WHO. Its mandate focuses on crisis communication, including communication preparedness aspects, on issues related to health threats, including CBRN and pandemic influenza. The network communicates about measures taken by crisis managers, health related recommendations, and risk management.

Methods and Materials: The HSC Communicators' Network played a key role during the H1N1 pandemic. It sought to share the communication challenges with which the members were confronted, while providing support and advice to each other in the writing of common guidelines as well as in the development of the messages on key subjects. It organised about 40 virtual and 7 face-to-face meetings over the period of the pandemic.

Results: The network succeeded in identifying lessons to be taken forward for tackling future health crisis. These lessons learned have already been acknowledged by the EU Health Council in September 2010.

These lessons can be summarized as follows:

- In decision-making on future policies, the HSC must take into account communication factors,
- The existing tools available to the Network must be improved and adjusted accordingly to the needs [e.g. HEDIS and MediSys (<http://medua.jrc.it>)].
- Identifying and establishing a relationship with stakeholders and the media before a pandemic is essential,
- The use of new social media (Web 2.0) is increasing ever more rapidly and will offer new possibilities for reaching specific target groups
- Polls and surveys are essential tools for understanding the perceptions and behaviours of citizens in a health crisis. They also help to assess whether the right messages are passed.

Conclusion: The network has been recognised as an important asset of the crisis management process and its future work plan intends to strengthen the network and to foster the development of common communication strategies and key messages. It will also reflect further work on the lessons learned from the H1N1 pandemic.

Communication, and subsequently the HSC Communicators' network, will be a constituent of the upcoming Health Security Initiative due for end of 2011.

8.002 Using data from social networking sites to predict the spread of pandemic influenza

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Background: Pandemic influenza poses a dire threat for mankind. Combined with early detection, knowledge of infection routes can serve as an effective guide for rapid deployment of counter-measures, potentially saving millions of lives. However, many attempts to predict global spread of pandemics have rendered dubious results, largely due to insufficiencies in the variables used to proxy global human interaction. This paper introduces the first global proxy of human interaction containing data from social networking sites (SNS) on the Internet. Using both the new SNS proxy and the traditionally used air-traffic proxy, we simulate the global spread of A/H1N1 in 2009. Correlation analyses between simulated and reported incidence cases indicate that the SNS-proxy does the best job in recapitulating the 2009 spread of A/H1N1. The results suggest that the spread of future pandemic influenza can be predicted with a considerable increase in accuracy obtained by implementation of SNS-data.

Methods and Materials: Human interaction on YouTube has been recorded. The recorded interaction is used as a country to country interaction matrix.

Using flow of air passengers between countries (IATA), and human interaction on YouTube as proxies of human interaction, a deterministic model of spread of A/H1N1 (WHO GAR) is developed.

In our simulation of spread, A/H1N1 spreads globally in accordance with the communication patterns in Mexico at time t_0 , and in accordance with the communication patterns in any affected country at time $t+$.

Results: Results indicate that the simulated estimate using the SNS-proxy is more correlated to the reported incidence count (WHO GAR) than the air traffic proxy estimates.

Conclusion: Using social networking on Internet as proxy for human interaction is better than using traditionally used proxies for human interaction when predicting spread of global pandemics.

8.003 'OMG, are we all gonna die?' – Covering the 2009 flu pandemic, from confusion to indifference, with stops at journalistic poverty, White House intimidation, Google-worship, summer camp and the video game formerly known as sneeze

D. G. McNeil Jr.
The New York Times, New York, NY, USA

NO ABSTRACT RECEIVED

SESSION 09 (Parallel Session)

Biosecurity and One Health

Saturday, February 5, 2011

Room: Klimt Ballroom 2–3 • Upper Level

14:30–16:00

9.001 Animals as detectors of bio-events

B. Vallat
OIE, Paris, France

Background: Solidarity for living, bind animals and humans. For 25 years the changing face of infectious diseases in humans and animals has challenged our systems of prevention, control and therapy. It has prompted the need for surveillance and for early detection of emerging, re-emerging infections and of possible threat of bioterrorism. Humans and animals share a common environment and zoonotic pathogens are responsible of most of human infectious diseases and some of them have been used as bioweapons.

Methods and Materials: Animals as sentinels are an essential part of an integrated surveillance system. Outbreaks of animal diseases are often the forerunner of human diseases. In case of weaponised pathogens, animals might manifest clinical signs prior to humans. In natural, accidental, or deliberate outbreaks in humans, it may become critical to recognize and follow the pathogens in animals; since the containment of the human outbreak will require to control the spread and the amplification of pathogens in animals.

It is desirable to establish a co-analysis system of human and animal diseases (food animals; companion animals; wildlife).

Results: The OIE plays a key role at the intergovernmental level in global surveillance, early warning and in mitigating risks posed by animal diseases, including zoonosis. Global security from animal diseases needs universally strong and well governed veterinary services because disease events, deliberate release of a pathogen or a breach in laboratory biosecurity in one country can threaten the biosecurity of many other countries.

Conclusion: OIE is committed to global bio-threat reduction. Considerable efforts are made to improve existing alert systems (eg WAHIS) to promote international transparency, to enhance interagency cooperation (OIE /FAO/WHO; BTWC) and to create adequate global networks and mechanisms (GLEWS; OFFLU; CMC-AH, etc).



9.002 Biosecurity and plant pathogens

I. Sache
INRA, Paris, France

Background: Biosecurity of crops, forests and natural plant stands has become a major issue over the last decades. Phytosanitary crises breaking out worldwide have highlighted the socio-economical and ecological threats represented by the uncontrolled establishment and spread of plant pathogens, especially emerging ones. In contrast with natural epidemics, agroterrorism, that is the deliberate use of plant pathogens in malevolent acts, is often considered as a minor plant biosecurity issue. Even if state-sponsored programs on such biological weapons have been officially stopped, the threat of agroterrorist acts perpetrated by individuals, organizations or states, is still a matter of debate and speculation.

Methods and Materials: Several lists of plant pathogens of potential interest for agroterrorism exist, but only a few studies have assessed the real risk represented by these pathogens. Such an assessment should consider not only the pathogen biology but also the potential motivations of the perpetrators, the feasibility of the acts and their socio-economical consequences.

Results: Case studies show that the use of plant pathogens for agroterrorist purposes would require much more skills than usually believed. However, the biosecurity risk represented by agroterrorism should not be neglected and awareness should be raised among the agencies and individuals in charge of plant and food protection. The use of emerging plant pathogens would have even more negative consequences because of the lack of knowledge, expertise and preparedness in the areas where they would emerge.

Conclusion: In practice, experiments on emerging pathogens are hardly feasible, but concern and preparedness can be increased by learning lessons from the natural emergence and spread of plant diseases. Recent examples such as the introduction of soybean rust in the Americas and the emergence of the *Ug99* virulent strain of wheat stem rust in Africa and Asia, highlight the need of anticipation and quick, international reaction to mitigate the effects of disease.

9.003 Twinning between laboratories will improve disease security worldwide

K. Hamilton
OIE, Paris, France

Background: Twinning has been used extensively to facilitate capacity building and networking, and to bring communities together. The OIE is applying the concept to laboratories with the aim of building capacity for detection and control of the most important animal diseases and zoonoses in priority regions. The results will strengthen global surveillance networks for animal disease agents, zoonoses, and new and emerging pathogens.

Methods and Materials: Through its network of OIE Reference Laboratories, which provide expertise for a named disease, and OIE Collaborating Centres, which provide expertise in a designated sphere of competence, the OIE provides essential diagnostic and technical support to countries worldwide. The distribution of this network currently favours developed countries in the northern hemisphere and through twinning OIE aims to redress the imbalance and provide more even geographical coverage, allowing more countries to access high quality diagnostic testing and expertise essential for early disease detection and rapid control.

Results: Each twinning project links an existing OIE Reference Laboratory or Collaborating Centre with a selected candidate laboratory. Knowledge and skills are exchanged through this link allowing the candidate laboratory to develop capacity and expertise for a disease or topic that is a priority in its region, and to better comply with OIE International Standards. Eventually the candidate laboratory will be able to provide support to other countries and may apply to become an OIE Reference Laboratory or Collaborating Centre in its own right; this is the ultimate goal of twinning.

Integral to all twinning projects are essential generic areas of competence such as laboratory biosafety and biosecurity, so twinning plays a role in global biothreat reduction.

Conclusion: With 30 projects underway OIE twinning is gathering a body of experience that can be used to improve the programme itself, and allow this model to be applied to other capacity building initiatives.

9.004 Bees, agricultural health and food security

M.-P. Chauzat
ANSES, Maisons-Alfort, France

Background: The concept of One Health is highly relevant when it comes to study bees in general. Pollinators are essential for pollinating 35% of the agricultural crops of global importance which are food for humans. Among the pollinators, the social honeybees (*Apis mellifera*) have an economic value mainly due to their marketable products, as well as their pollination activity in agricultural areas. In many countries now, decreases of several species of bees from crop fields and from other areas have been described worldwide.

Methods and Materials: Several reasons have been reported for bee losses, mainly classified in three categories: pesticide exposure, disease outbreaks and environment alteration. All these three main factors also interact between themselves. *A. mellifera* has been—and still is—the subject of many studies because it is the only ubiquitous bee species that can be easily reared. However, other bee species should not be neglected.

Results: Since the massive use of pesticides after the Second World War, much concern has been raised on insecticide interactions with honeybees. Monitoring the residues and assessing the impact of small amounts of pesticides on honeybee health are the key issues that should be studied more frequently concomitantly with other factors. Honeybee diseases are known since humanity consumes honey. Nevertheless changes in virulence of the common pathogens have been reported, together with multiple introductions of exotic parasites and diseases. Although none of the disease can affect mammals, mankind is concerned by their great influence on honeybee colony health. In addition, environment modifications affect bees by disturbing nest and feeding habitats. These alterations are directly linked to human activities.

Conclusion: Consequently causes and consequences of bee decline are highly correlated. Therefore, pulling honeybee health and public health together is a good worldwide example that could result in the improvement of health care for humans, animals and the environment.

SESSION 10 (Parallel Session)

New Vaccines and Old Foes: Emerging Issues in Vaccine Preventable Diseases

Saturday, February 5, 2011

Room: Park Congress • Ground Level

16:30–18:00

10.001 Polio—Vaccine end game strategy

R. Sutter
WHO, Geneva, Switzerland

The over-riding objective for the post-eradication area of work is to prevent or minimize the risk of paralytic disease due to poliovirus to future generations. The most important decision—the cessation of oral poliovirus vaccine (OPV) after certification of eradication—has been suggested in 2004, and endorsed by WHO technical oversight committees in 2006 (Advisory Committee on Poliomyelitis Eradication [ACPE]) and in 2008 (Scientific Advisory Group of Experts [SAGE]). In addition, the six pre-requisites for stopping OPV have been elaborated. In 2008, the World Health Assembly (WHA) requested WHO to "...develop appropriate strategies and products for managing risks, including safer processes for IPV production and affordable strategies for its use..." A process is under way to devise the immunization policies for the post-eradication era, led by a SAGE working group, and expected to conclude



with the publication of a new WHO position paper on polio vaccines in 2012. In terms of timelines, even if polio eradication can be achieved by the end of 2012, it is unlikely that OPV will be discontinued before 2017, to account for the national, regional and global certification processes which should result in certifying the world as polio-free. To make IPV affordable for developing country use, a number of strategies are being pursued, including 1) schedule reduction (fewer doses); 2) dose reduction with fractional doses; 3) antigen reduction with adjuvant; 4) production of Sabin-based IPV in developing countries; and 5) process optimization for Sabin-IPV production. In terms of maintaining an immunity base against polioviruses in the post-eradication era, the use of IPV either indefinitely or during a 5-10-year transition period is being considered. Substantial efforts are under way to compile the scientific base to assist decision-makers in finalizing the strategies for the post-eradication era.

10.002 Vaccination towards the global control and eradication of foot-and-mouth disease

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¹Agricultural Research Service USDA, Orient, NY, USA,

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Foot and mouth disease (FMD) is a highly contagious disease of livestock (e.g. cattle, pigs, small ruminants, water buffalo) that negatively affects animal production and is a constant drain to the livelihoods of millions around the world. The disease has been controlled in developed countries through sustained use of vaccination and strict animal quarantines at a cost of trillions (US\$). Although vaccines that protect against clinical disease have existed for decades, millions of animals are killed in efforts to rapidly control and eradicate the disease. The causing virus (FMDV) is a highly variable RNA virus occurring in seven serotypes (A, O, C, Asia 1, Sat 1, Sat 2 and Sat 3) some of which comprise a large number of subtypes. FMD vaccines based on inactivated virus induce little to no cross protection and short live immunity requiring re-vaccination every 6 months. Existing vaccines have limited shelf life and easily degrade without refrigeration. FMDV still thrives in endemic regions that lack the resources to control it. FMD is a global problem, one of the main limitations to eradication is the lack of vaccines designed for the purpose of eradication, capable not only of protecting against clinical signs but also capable of preventing infection and interrupting the natural transmission cycle. These vaccines need to be inexpensive to produce, easy to deliver and long-term and broad immunity against multiple serotypes and subtypes. There is also a need for better integrated strategies that fit the specific needs of endemic regions. Global eradication of FMDV will require not only the appropriate vaccines, diagnostics and control strategies but also political and economic support for a coordinated and sustained global effort.

10.003 Measles—Is eradication feasible?

C. A. de Quadros

Albert B. Sabin Vaccine Institute (SVI), Washington, DC, USA

Background: Measles is one of most infectious diseases. Before the introduction of the measles vaccine, practically all children in the long run contracted measles.

By the end of the 1980s most countries of the world had incorporated measles vaccine into their routine vaccination programs.

Methods and Materials: Globally, some 500,000 deaths due to measles still occur every year, half of them in Africa. Eradication of measles would play an important role in improving child survival.

The goal to eradicate measles from the Americas was set by the Pan American Sanitary Conference in 1994.

Results: Progress to date has been remarkable. Measles is no longer an endemic disease in the Americas and interruption of transmission has been documented in most countries. As of December 2010, eight years have elapsed since the detection of the last indigenous case in the Americas, which occurred in Venezuela in September, 2002. This experience shows that interruption of measles transmission can be achieved and sustained over a long period of time and that global eradication is feasible if appropriate strategy is implemented.

Conclusion: Even in a new paradigm in which eradication is not followed by the discontinuation of vaccination, eradication of measles will be a good investment to avoid expensive epidemics and save the half million children that die every year to infection with the measles virus. It is not a dream to think that we will see a world free of measles by the year 2020.

SESSION II (Parallel Session)

Antibiotic Resistance

Saturday, February 5, 2011

Room: Klimt Ballroom 2–3 • Upper Level

16:30–18:00

11.001 Emergence of resistance in the clinic

G. Cornaglia

Sienna, Italy

NO ABSTRACT RECEIVED

11.002 Surveillance of antimicrobial resistance and antibiotic use in humans and animals

O. Heuer¹, K. Grave², P. A. Beloeil³, H. Goossens⁴, H. C. Wegener⁵

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Antwerp, Belgium, ⁵Technical University of Denmark, Copenhagen, Denmark

Background: Antimicrobial resistance occurs in bacteria in many different and even overlapping reservoirs and resistant bacterial pathogens constitute a serious and increasingly important public health hazard. Throughout different human, animal or environmental reservoirs, the use of antimicrobial agents is recognised as the main driving force behind the emergence of antimicrobial resistance.

Methods and Materials: Surveillance of antimicrobial resistance and antimicrobial use is important to provide data on the occurrence and spread of antimicrobial resistance and the consumption of antimicrobial agents. These data are a prerequisite for targeted interventions to reduce or halt the spread of antimicrobial resistance, and subsequently to document the effect of interventions. Several international surveillance programmes for collection of data from humans, animals and foods of animal origin are currently in place or under establishment.

Results: European data on antimicrobial resistance in selected human pathogens are collected through a number of surveillance networks managed by the European Centre for Disease Prevention and Control (ECDC). Likewise, data on the occurrence of antimicrobial resistance in bacteria from animals and foods of animal origin is collected by the European Food Safety Authority (EFSA). Data on the use of antimicrobial agents in humans are collected by the European Surveillance of Antimicrobial Consumption (ESAC) managed by University of Antwerp, and a new surveillance network collecting data on antimicrobial use in animals are being established by the European Medicines Agency (EMA).

Conclusion: Antimicrobial resistance is an international problem influenced by increasing frequency of international travel and trade. Scientific evidence regarding interaction and exchange of resistant bacteria between various reservoirs indicates that for some bacteria and antimicrobial agent combinations, effective interventions should be based on integrated use of data from human and non-human sources. Specific efforts should be directed towards prevention of resistance to antimicrobial agents regarded as critically important for use in human medicine.

**11.003 Shared resistance determinants in humans and animals****A. Andremont**

University of Paris, Medical School, Paris, France

Transmission of bacterial resistance between animals and humans has been a concern since it has been recognized that the selective pressure imposed by the various human usages of antibiotics was impacting the global microbiota, irrespective of it was primarily intended to treat humans, animals, or plants.

Multiple epidemiological reports have stressed the relationship between global antibiotic usage and bacterial resistance in human pathogens and selected ones have clearly demonstrated that when selective pressure is applied to animals, let it be pets or farm ones, it can influence resistance of bacteria causing diseases in humans.

Conversely, some reports have shown that animals could become infected by resistant human pathogens. Recently, the question rose as to whether it was bacteria, genes or mobile genetic elements that were transmitted between species. The question is of particular interest when one deals with transmission of species which, like enterococci or enterobacteria, are commensals of the intestinal tract of humans, in which they can be potential pathogens, but also of several animal species.

Only bits of answers to this question are currently available and they will be reviewed. Certainly a definite answer will wait for the results of ongoing European studies which will use metagenomics and extensive sequencing to characterized and relate or not strains, plasmids and genes that circulate between mammal hosts.

11.004 Common epidemiological cutoffs (ECOFFs) for surveillance of resistance: Is it feasible?**G. Kahlmeter**

Chairman of EUCAST, Växjö, Sweden

Background: Antimicrobial resistance surveillance is hampered by the fact that breakpoints differ between breakpoint systems (CLSI vs. EUCAST), between countries, between humans and animals and that they may change over time. Changes in a breakpoints result in artificially altered resistance rates.

In 2002 EUCAST was tasked with developing a system for collecting and displaying MICs for bacteria and fungi from all over the world, from many species, from human and veterinary medicine and from all different time periods in order to define MIC and zone diameter distributions in organisms lacking resistance mechanisms.

Methods and Materials: Investigators from all walks of life were invited to submit MIC distributions. MICs were obtained from human and veterinarian resistance surveillance systems, breakpoint committees, pharmaceutical companies, manufacturers of susceptibility testing material, individual investigators, and from the literature. A software was developed to harbour and display all distributions. At the end of 2010 the database contains more than 20 000 distributions and its size is constantly growing.

Results: Using statistical and biological methods it was possible to define the MIC distributions of isolates lacking resistance mechanisms. Each distribution was categorized by an epidemiological cut-off value (ECOFF) corresponding to the highest MIC-value in organisms without resistance mechanisms to the agent.

The distributions and the ECOFFs for benzylpenicillin and *Streptococcus pneumoniae* and ciprofloxacin and *Klebsiella pneumoniae* are freely available on the EUCAST website (www.eucastr.org).

Conclusion: The distribution and the ECOFF provide a sensitive and universally useful epidemiological tool for sensitive detection of resistance in phenotypic test systems. It can be used to measure and compare resistance as a biological phenomenon, irrespective of origin of isolates. Its use requires species identification, the measuring of MICs or zone diameters and the use of a standardized method to determine MIC (mg/L) or inhibition zone diameters (mm). The ECOFF does not, in contrast to clinical breakpoints, change over time or with different breakpoint systems.

SESSION 12 (Poster Presentations I)

Saturday, February 5, 2011 • 11:45–14:00

Room Bruckner/Mahler/Brahms / Upper Level:

12.001 – 12.038 Antimicrobial resistance

12.039 – 12.048 Bioterrorism and biological warfare

12.049 – 12.052 Climate change and ecological factors in disease emergence

12.053 – 12.085 Diseases at the interface of humans, wildlife and other animals

12.086 – 12.116 Foodborne and waterborne diseases

12.117 – 12.126 Infections related to travel and migration

Klimt Ballroom I / Upper Level:

12.127 – 12.166 Influenza and other respiratory infections

12.167 – 12.174 New pathogen discovery

12.175 – 12.176 Outbreak modeling

12.177 – 12.182 Sociopolitical factors in disease emergence

12.001 In vitro evaluation of the effect of hops (*Humulus lupulus*) alcoholic extract on sensitive and resistant strains of *Mycobacterium tuberculosis***B. Nasr Esfahani¹, K. Kermanshahi², J. Esmi³, G. Asghari⁴**¹Isfahan University of Medical Sciences, Isfahan, Isfahan, Iran, ²Alzahra University, Tehran, Iran, ³Islamic Azad University, Gom, Iran, ⁴Isfahan University of Medical Sciences, Isfahan, Iran

Background: Tuberculosis (TB) causes nearly 2 million deaths worldwide each year and there were an estimated 8.9 million new cases worldwide. Because of limitation of useful antituberculosis drugs, it is require finding some effective new drugs. It has been determined that pharmaceutical plants, hops (*Humulus lupulus*), contain some antibacterial effect. In this study the antimycobacterial effect of hops alcoholic extract on sensitive and resistant strains of *Mycobacterium tuberculosis* were determined.

Methods and Materials: Ethanolic extract of hops was prepared by using maceration. Two different concentrations of the extract (4 and 8 mg/ml) was prepared. The effect of the alcoholic extract against resistant a sensitive strains to Rifampin and Isoniazid *Mycobacterium tuberculosis* were determinate by using proportion method.

Results: Three groups of *Mycobacterium tuberculosis* strains, sensitive to Rifampin and resistant to Isoniazid, sensitive to Isoniazid and resistant to Rifampin and resistant to Rifampin and Isoniazid, were used in this study. The results showed that different concentration of hops ethanolic extract (4mg/ml and 8mg/ml) have a remarkable inhibitory effect on sensitive and resistant strains of *Mycobacterium tuberculosis*.

Conclusion: With the increase of worldwide resistance to antimycobacteria drugs, there is a need to access new and complementary approaches to antimycobacterial therapy. The results of this study showed that an alcoholic extract of hops has a strong antimycobacterial effect on all sensitive or resistant to Isoniazid and Rifampin *Mycobacterium tuberculosis* strains. Identification of the effective fraction of *Humulus lupulus* as an efficient anti *Mycobacterium tuberculosis* is a further step to be studied.

12.002 Antibacterial susceptibility patterns and contributing factors to nosocomial and ventilator associated pneumonia in ICUs, Shiraz, Iran**A. Japoni¹, A. Vazin², M. A. Davarpanah³, M. Afkhami Ardakani⁴, A. Alborzi¹, S. Japoni¹, N. Razaatpour⁵**¹Shiraz University of Medical Sciences, Shiraz, Iran, ²Shiraz University of Medical Sciences, Shiraz, Iran, ³Shiraz University of Medical Sciences, Shiraz, Iran, ⁴Shiraz University of Medical Sciences, Shiraz, Iran, ⁵Shiraz University of Medical Sciences, Shiraz, Iran



Background: In the intensive care units (ICU), nosocomial pneumonia (NP) and ventilator associated pneumonia (VAP) are more frequently noticed. The present study seeks to determine the etiological agents of NP and VAP, their antibacterial susceptibility patterns and to evaluate the factors contributing to the mortality of patients. Besides, the impact of appropriate therapy in terms of three parameters (body temperature, PaO₂/FiO₂, leukocyte count) were assessed.

Methods and Materials: This study was conducted in 2008–2009 (9 month period), on 836 adult patients admitted to ICUs, Nemazee hospital, Shiraz, Iran. The inclusion criterion was the commencement of infection at least 48 hours following the hospital admission. Clinical parameters including, core temperature, leukocyte count and PaO₂/FiO₂ ratio were evaluated. MICs of the isolated bacteria to the panel of antibiotics were determined using E-test.

Results: Of the 836 cases, only 58 (6.9%) cases of NP were diagnosed, from which 42 (72%) were VAP. *A. baumannii*, MRSA, *P. aeruginosa* and MSSA were the most prevalent bacteria. Significant correlations between previous antibiotic therapy (P=0.04), use of corticosteroid (P=0.02) and attributable mortality were found. A strong correlation between fever abatement and the ratio of PaO₂/FiO₂ with responses to the treatment and the outcomes was also evident.

Conclusion: Combined treatment with meropenem/imipenem, ciprofloxacin and vancomycin seem to be appropriate and could cover all the possible infective agents. To reduce mortality rate, reasonable prescription of antibiotics and corticosteroid could be effective. Furthermore, adopting a strategy to reduce body temperature and PaO₂/FiO₂ ratio could be beneficial in patients' outcomes.

12.003 Periodontitis and antibacterial susceptibility patterns of *Porphyromonas gingivalis* isolated from adult patients

A. Japoni¹, A. Vasin², S. Noushadi¹, F. Kiany¹, S. Japoni¹, A. Alborzi¹
¹Shiraz University of Medical Sciences, Shiraz, Iran, ²Shiraz University of Medical Sciences, Shiraz, Iran

Background: To test the antimicrobial sensitivity of *Porphyromonas gingivalis* to a panel of eight orally administrable antibiotics in periodontal diseases and to evaluate factors associated with periodontitis in adult patients.

Methods and Materials: A total of fifty strains of *P. gingivalis* were isolated from one hundred and twenty adult patients with chronic periodontitis. Identification of bacteria was carried out by anaerobic culture and biochemical tests. Selected colonies of *P. gingivalis* were used to evaluate the antibacterial activities of penicillin, metronidazole, amoxicillin, amoxicillin/clavulanic acid, clindamycin, doxycycline, ciprofloxacin and azithromycin.

Results: Most of the patients were female, age ranging between 40 to 50 years. Majority of the patients frequently had scaling and depths of periodontal pockets in infected teeth were 5-8 mm and most of them had hemorrhage during sampling. Susceptibility testing revealed a sensitivity of 100% of *P. gingivalis* to azithromycin, doxycycline and amoxicillin/clavulanic acid but lower susceptibilities were found for the rest of antibiotic agents evaluated.

Conclusion: Frequent scaling in women aged between 40-50 years had positive correlation with chronic periodontitis. The application of antibiotics in conjunction with mechanical debridement, may reflect in the level of resistance of *P. gingivalis* in patients with chronic periodontal infections. This could suggest periodical antibiotic susceptibility testing is necessary to determine the efficacy of antimicrobial agents if the perfect curing of chronic periodontal diseases after mechanical debridement is meant. Further clinical studies are required to confirm the *in vitro* results. The only limitation in this study was identification of bacteria to species rather than subspecies level.

12.004 Frequency and antibiotic susceptibility of Gram-positive bacteria in Makkah hospitals— Saudi Arabia

A. Asghar

Umm Al-Qura University—Hajj Research Institute, Makkah, Saudi Arabia

Background: Gram-positive bacteria are important nosocomial pathogens. The objective of this study was to estimate the frequencies and resistance rates of Gram-positive pathogens isolated from hospitals in Makkah, Saudi Arabia.

Methods and Materials: This prospective study included clinical isolates from 1087 patients with Gram-positive bacterial infection at three Makkah hospitals- Saudi Arabia in 2008–9. The patients' demographic and laboratory data were collected. Standard microbiological methods were used to identify the organisms and test antimicrobial susceptibility. The results were interpreted according to the Clinical Laboratory Standards Institute (CLSI) guidelines.

Results: Gram-positive pathogens infected all age groups but had no gender predominance. *Staphylococcus aureus* was the most common cause of wound infection and accounted for more than half of the clinical isolates (688 cases). Coagulase-negative staphylococcus (CONS) was a common isolate from blood cultures. Wounds were the most common site of infection (37.6%). *Enterococcus* spp. and *Streptococcus agalactiae* were the second most common bacteria (26%). The resistance rates of *S. aureus* and CONS isolates were 39.4% and 82.4% for oxacillin, respectively. Among the streptococci, the resistance rates of *Streptococcus pneumoniae* were 21.1% and 16.7% for ampicillin and erythromycin, respectively.

Conclusion: *S. aureus* infections were very common in the Makkah hospitals. Infection prevention, control measures, and continuous monitoring for antibiotic susceptibility are necessary to reduce these and other nosocomial infections

12.005 Recovery of a Tn402-like class 1 integron with a novel cassette array and flanking miniature inverted-repeat transposable element-like structures

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Background: Integrons are genetic elements that contribute to lateral gene transfer. They possess a site specific recombination system that captures and expresses genes as a part of mobile gene cassettes. Class 1 integrons are of most clinical importance, being responsible for transmission and ongoing acquisition of new antibiotic resistance genes. In this project, I aim to determine the abundance of integrons and antibiotic resistance genes in aquaculture and natural environments and the potential for retransmission of class 1 integrons carrying new genes into humans.

Methods and Materials: Bacteria were cultured from individual digestive tracts of uncooked prawns, and the resulting mixed cultures screened for the presence of class 1 integrons using PCR specific for integron-integrase genes (*intI*). Most prawns tested were positive for class 1 integrons. Genomic DNA of *intI1* positive isolates was used for PCR amplification of cassette arrays followed by cloning and sequencing. Sequencing of one of the amplicons revealed an unusual structure. Molecular typing of this strain was carried out using 16SrDNA sequencing, which identified it as a species of *Acinetobacter*. A fosmid library was constructed to obtain the complete sequence of the *intI1* positive clone and flanking regions.

Results: The recovered integron possessed features typical of Tn402 class 1 integrons, containing a truncated *tni* module and 3'-conserved segment. However, rather than being bounded by inverted repeats IRi and IRt, the integron was flanked a direct repeat of a miniature inverted repeat transposable element (MITE). The recovered class 1 integron contained two gene cassettes. The second cassette encoded AadA2, which confers



resistance to *streptomycin* and spectinomycin, and is commonly found in clinical integrons. The first cassette was novel, consisting of three genes, *msrB*, *msrA* and a gene encoding a hypothetical protein. The *msr* genes encode methionine sulfoxide reductase which is involved in the repair of protein damage during oxidative stress.

Conclusion: This observation suggests that Tn402-like class 1 integrons are recruiting new gene cassettes when they are released into the environment, and that these encode phenotypes unrelated to the neutralization of antibiotics. *Msr* genes, in particular, have the potential to enhance bacterial colonization and pathogenicity.

12.006 Presence of multidrug-resistant vibrio species isolated from molluscan shellfish in the coastal environments of Canada

S. Banerjee, L. Bakouche, J. M. Farber
Health Canada, Ottawa, ON, Canada

Background: The emergence of antimicrobial resistance (AMR) in foodborne bacteria is a growing concern worldwide. This surveillance study reports the pattern and diversity of AMR detected in halophilic *Vibrio* species isolated from molluscan shellfish harvested in Eastern and Western Canada.

Methods and Materials: *Vibrio* species, particularly *V. parahaemolyticus* (Vp), *V. vulnificus* (Vv), *V. fluvialis* (Vf) and *V. alginolyticus* (Va), isolated from molluscs such as oysters, clams and mussels, were tested for susceptibility to 19 common antibiotics following the 'Clinical and Laboratory Standards Institute' (CLSI) protocol using the Kirby-Bauer's disc diffusion method. Filter discs, each containing a known amount of an antibiotic, were laid on a lawn of the bacteria on Mueller-Hinton agar (MHA) plates, and incubated at 35°C for 18–24 h. Standard strains were used for comparing the zones of inhibition and for assigning the resistance profiles to the tested strains.

Results: We found that asymptomatic molluscs accumulate *Vibrio* species which are indigenous to the estuarine environment, including some with multidrug-resistance (MDR) and/or virulence traits. During the summer months of 2006 to 2009, 455 strains of *Vibrio* species (Vp, Vv, Vf and Va) were isolated, with only 4.2% being found sensitive to all 19 drugs. A total of 19.2, 21.1 and 26.5% of the halophilic *Vibrio* spp. were MDR (four to six drugs) in 2006, 2007 and 2008, respectively, but the incidence of MDR dropped to 5.8% in 2009. Resistance to fluoroquinolones was rare. Two Vp strains, one in 2008 and one in 2009, were potentially virulent as well as MDR.

Conclusion: (i) The presence of AMR/MDR *Vibrio* spp. in the Canadian estuaries is an indication that selective pressures are present in Canadian coastal environments.

(ii) The detection of potentially virulent Vp strains which are MDR warrants further investigation and monitoring.

(iii) Fluoroquinolone resistance was not that common in the AMR patterns of *Vibrio* spp. isolated in this study.

(iv) A drop in the MDR *Vibrio* spp. in 2009 is an interesting finding which should be further investigated.

12.007 Infection/colonisation with methicillin-resistant *Staphylococcus aureus* (MRSA), penicillin-resistant *Streptococcus pneumoniae* (PRP) and vancomycin-resistant enterococci (VRE), Oppland and Hedmark Counties, Norway 1995–2009

V. Hasseltvedt
Sykehuset Innlandet Trust, Lillehammer, Norway

Background: MRSA and PRP infection/colonisation was made notifiable in Norway in 1995 with the implementation of the The Infectious Diseases Control Act as of January 1, 1995 - URL: <http://www.lovdato.no> (in Norwegian). The same was done for VRE, in 1996, URL: <http://www.msis.no>. Our laboratory serves the two counties, Oppland and Hedmark with a population of approximately 370 000 – as of 2009.

Methods and Materials: Our laboratory tests *Staphylococcus aureus*

utilizing traditional methods. St. Olavs Hospital in Trondheim performs the reference testing for MecaA, nuc, spa-typing as well as MLST typing/MLST repeats. Strains of *Streptococcus pneumoniae* are, primarily, tested for optochin and bile esculin susceptibility – as well as E-tests® - when there is a possibility of increased resistance. Reference testing is performed at The Norwegian Public Health Institute – including capsule serotyping. VRE is reference tested at The University of Tromsø – for PCR detection of the various van-genes.

Results: Our findings per year were as follows (number of cases notified to MSIS),

Norwegian Public Health Institute:

	'95	'96	'97	'98	'99	'00	'01	'02	'03	'04	'05	'06	'07	'08	'09
PRP	0	0	0	1	0	1	1	0	0	0	13	6	3	0	0
VRE	0	0	0	0	0	0	0	1	0	1	3	0	0	1	0
MRSA	1	1	1	4	0	2	2	8	9	5	21	18	28	19	19

Conclusion: The MRSA situation in Oppland and Hedmark counties reflects that of the Norwegian epidemiological situation. The increase after 2005 is mainly due to colonisation being notifiable, in addition to infection, which was the only entity made notifiable from 1995.

In 2005 our laboratory detected 13 cases caused PRP strains. A cluster was detected in a family where three members had the capsular serotype 23F. The other strains comprised 9V (3), 14 (2), 19 (2) and 19F. This cluster is one of the few Norwegian clusters known. The PRP incidence in our two counties was, in year 2005, almost three times more than the national incidence in 2004. The incidence of VRE cases, in our two counties, remains low, whereas, in Sweden, this is a problem of a much higher magnitude.

12.008 Changing trends in antimicrobial resistance in *Salmonella* serovar Typhi: An epidemiological study

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Background: Enteric fever is a major health problem despite the use of antibiotics and development of newer antibacterial drugs. *Salmonella enterica* serovar Typhi in the last decade has rapidly developed resistance to first-line drugs, fluoroquinolones and third-generation cephalosporins.

Methods and Materials: A prospective study of the prevalent aetiology of enteric fever was undertaken at a tertiary care hospital, New Delhi (India). Blood samples were collected from febrile patients prior to initiation of antibiotic therapy and inoculated directly into blood culture bottles containing brain heart infusion broth and samples were processed according to standard recommended techniques. A detailed clinical and treatment history was elicited from all of the patients. Antibiotic sensitivity was tested by the Kirby–Bauer technique according to Clinical and Laboratory Standards Institute guidelines. Statistical analysis was performed using the chi-square test and Student's paired t-test.

Results: *Salmonella* spp. were isolated from 174 (7 %) patients; 140 (80 %) patients were infected by *Salmonella enterica* subspecies *enterica* serovar Typhi (S. Typhi) and 16 (9 %) by *S. enterica* serovar Paratyphi A; the remaining 11 % were infected by other *S. enterica* serogroups, Typhimurium, Paratyphi C and Senftenberg, and other group E salmonella. Multidrug resistance (resistance to chloramphenicol, ampicillin and co-trimoxazole) sequentially increased from 34 % in 1999 to 66 % in 2005. Moreover, 8 % of the S. Typhi isolates were found to be presumptive extended spectrum β -lactamase producers. No resistance was observed to fluoroquinolones in 1999, while 4.4 % resistance was observed to sparfloxacin, 8.8 % resistance to ofloxacin and a high resistance, 13 %, to ciprofloxacin in 2005. Further studies after 2005 at this site showed changes in the proportion of S. Typhi and S. Paratyphi A with MDR, including reductions in the proportion of isolates with MDR.

Conclusion: It is of paramount importance to limit unnecessary use of fluoroquinolones and third generation cephalosporins so that their efficacy against salmonella is not jeopardized further. Multidrug resistance in S Typhi has decreased indicating that the first line antibiotics have a role to play in the treatment of enteric fever.

**12.009** Assessing the rising cases of methicillin-resistant *Staphylococcus aureus*: Hospital and community-associated cases

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Background: Methicillin-resistant *Staphylococcus aureus* (MRSA) has since become a major cause of illness and death in our healthcare setting. Risk factors for HA-MRSA include hospitalization, older age, invasive devices, and residence in long-term care facility, including exposure to antimicrobial agents. HA-MRSA isolates are often resistant to several antimicrobial drug classes in addition to beta-lactams. The CA-MRSA infections usually affects young, healthy persons and associated with sharing towels or athletic equipment, participating in contact sports, living in unsanitary and crowded areas, using illegal intravenous drugs.

Methods and Materials: Directions were given out for clinical microbiology laboratories to submit invasive isolates of MRSA to our unit, where we perform antimicrobial drug susceptibility tests on all isolates and characterize all isolates that were resistant to <3 non-beta-lactam antimicrobial drug classes. Most isolates were obtained from blood cultures.

Results: The full model for predicting invasive infection with CA-MRSA compared with HA-MRSA included age, seasonality, and hospital exposure, plus specimen type. The only significant predictors of CA-MRSA infection compared with HA-MRSA were age <69 years, which was associated with increased risk ([OR] 5.1, 95% [CI] 2.06-12.64), and hospital exposure (OR 0.07, 95% CI 0.01-0.51), which was associated with decreased risk. Most patients were hospitalized for their infections and the proportion of patients admitted to intensive care units did not vary by strain. Patients infected by MRSA were younger than those infected by other strains.

Conclusion: The number of invasive MRSA infections reported and the number of invasive infections caused by CA-MRSA is on the increase. The increase of CA-MRSA poses a unique public health threat. It is now clear that CA-MRSA no longer causes only SSTIs but now causes an increased proportion of invasive infections in a rural state.

12.010 Antibiotic sensitivity and resistance patterns of *S. typhi* isolated from Khairpur, Sindh Pakistan

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Background: Enteric fever (typhoid and paratyphoid fever) is a systemic infection caused by several *Salmonella enterica* serotypes including *S. Typhi*. Antimicrobial drug resistance has become increasingly common in Khairpur, which can complicate therapy. The aim of this study was to investigate the sensitivity and resistance profile of *S. Typhi* isolated from clinical blood samples.

Methods and Materials: Blood cultures (n=40) of patients presented with typhoid fever to District hospital and Diagnostic and Research Center (DRC) Department of Microbiology Shah Abdul Latif University, Khairpur. The cultures were initially grown in Blood culture bottles (Oxoid) and on 7th day, the positive cultures were subcultured on *Salmonella* - *Shigaella* agar. The characteristic colonies, motility test and biochemical test using API-20E confirmed *S. Typhi* that were subjected to antimicrobial study by Kirby-Bauer disc diffusion. The sensitivity and resistance patterns against each antibiotic tested was noted as per zone criterion according to disc manufacturer instructions.

Results: Antimicrobial activity of 17 antibiotics from different drug categories was tested against 22 confirmed isolates of *S. Typhi*. MDR and nalidixic acid resistance was found in 70-90% of *S. Typhi* isolates. There was resistance to >5 classes of antimicrobial drugs, where 75% isolates were resistant to Naladixic acid alone.

The multidrug-resistance (MDR) pattern was NACTG (resistance to Nalidixic acid, Ampicillin, Cephadrine, Tetracycline, Gentamycin). In present study, 75% (30/40) isolates were resistant to Nalidixic acid. A significant percentage (82.5%) of isolates remained susceptible in vitro to Ciprofloxacin, Ofloxacin (60%), Ceftriaxone (60%) and Aztreonam

(70%). The only cephalosporin which gave in vitro promising results was Ceftriaxone, where against Chloramphenicol, 27.5% isolates shown intermediate response and the same percentage (27.5%) of isolates shown resistance.

Conclusion: Keeping in view the cartilage damaging effect of Quinolones in children, Aztreonam could be a suitable alternate in present set up of MDR typhoid. Our study indicates increase in the prevalence of the MDR phenotype in Khairpur, it appears that MDR serovar *Typhi* strains have been spreading and are gradually replacing the fully sensitive strain.

12.011 Characterization of extended-spectrum β -lactamases in the isolates of *Enterobacter cloacae* from Split, CroatiaB. Bedenic¹, I. Franolic-Kukina², S. Sardelic³, M. Ajman⁴, J. Vranes⁵¹School of Medicine, University of Zagreb, Clinical Hospital CenterZagreb, Zagreb, Croatia, ²Lika Institute of Public Health, Gospić,Croatia, ³University hospital Split, Split, Croatia, ⁴Teaching Institute ofPublic Health of Primorsko-Goranska County, Rijeka, Croatia, ⁵School of Medicine, University of Zagreb, Zagreb Institute of Public Health "Andrija Stampar", Zagreb, Croatia

Background: Recently an increase in the prevalence of ESBL positive *Enterobacter cloacae* was observed at the University hospital in Split, Croatia.

Methods and Materials: During 2009–2010, thirty ceftazidime resistant isolates of *E. cloacae* were collected at the University Hospital in Split. Production of ESBLs was tested by double-disk synergy test and confirmed by CLSI combined disk test. Susceptibility to a wide range of antibiotics was tested by disk-diffusion and broth microdilution method. Transfer of cefotaxime resistance was determined by conjugation (broth mating method) using *E. coli* A15R- strain resistant to sodium azide. Molecular characterization of ESBLs was performed by PCR with primers specific for TEM, SHV and CTX-M β -lactamases. Multiplex PCR was used to determine the group of CTX-M β -lactamases. Plasmids encoding ESBLs were extracted with Macherey Nagel mini kit.

Results: There were 60% of the strains resistant to ceftazidime, 56% to ceftazidime, 50% to cefotaxime and 40% to cefepime. All strains were susceptible to combination of cefotaxime with clavulanate and piperacillin with tazobactam. No resistance to carbapenems was observed. Among non β -lactam antibiotics high resistance rate was found for gentamicin (70%). Only 33% of the isolates were resistant to ciprofloxacin. The most potent antibiotics were meropenem and imipenem with MIC₉₀ of 0.06 and 1 mg/L respectively. The least potent antibiotics were ceftazidime, cefotaxime and ceftriaxone with MIC₉₀ of 256 mg/L. All strains transferred cefotaxime resistance to *E. coli* recipient strain with the frequency ranging from 1 to 5 x10⁻⁶. The strains were shown to possess CTX-M β -lactamases by PCR. Multiplex PCR revealed group 9. CTX-M β -lactamases were encoded on the large plasmids of approximately 150 kb which were transferable to *E. coli* recipient. Plasmid extractions yielded PCR products with primers specific for CTX-M β -lactamases.

Conclusion: This study demonstrated clonal outbreak of CTX-M group 9 positive *E. cloacae* at the University hospital Split.

Carbapenems are the antibiotics of choice for the treatment of infection caused by our ESBL positive *E. cloacae* strains.

Finally, the spread of CTX-M producing Enterobacteriaceae in Croatia in a manner similar to that observed in other countries may indicate difficulty in controlling these emerging resistance determinances.

12.012 Detection of plasmid-mediated AmpC β -lactamase producing *Klebsiella pneumoniae* in blood cultureS. Luk, W. K. Wong, T. K. Ng, W. K. To, S. Lo
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Background: Plasmid-mediated AmpC β -lactamases have arisen through the transfer of chromosomal AmpC β -lactamases of *Citrobacter freundii*(CMY), *Morganella morganii* (DHA) and *Aeromonas species* (FOX, MOX, CMY) etc. Their prevalence among *K. pneumoniae* varied from 4% in China to 58% in Singapore.



Methods and Materials: There were 881 non-duplicate blood culture isolates of *K. pneumoniae* isolated in the microbiology laboratory in Princess Margaret Hospital, Hong Kong, in 2004–2008. Isolates were screened for production of AmpC β -lactamase by either non-susceptible to cefoxitin, amoxicillin-clavulanate, cefotaxime or ceftazidime. The non-susceptible isolates (n=168) were tested by disk approximation, AmpC disk test, boronic acid inhibitor based method, a three-dimensional extract test and multiplex PCR. For isolates positive of plasmid AmpC β -lactamases, the minimal inhibitory concentrations (MIC) of 3rd generation cephalosporins, carbapenems and fluoroquinolones were determined by E tests.

Results: *blaDHA* was present in 52 (5.9%) isolates. The AmpC disk test was the most sensitive phenotypic test, which detected 98.1% of *blaDHA* positive isolates, while the inhibitor method and the three-dimensional extract test detected 92.3% and 90.4%, respectively. The disk approximation performed the worst, which only detected 65.4% of *blaDHA* positive isolates. All *blaDHA* positive isolates were susceptible to cefepime, imipenem, meropenem and doripenem. Most isolates, however, were resistant to fluoroquinolones. Susceptibility towards 3rd generation cephalosporins is variable.

Conclusion: The prevalence of plasmid-mediated AmpC β -lactamase among *K. pneumoniae* blood culture isolates was 5.9% and the predominate plasmid was *DHA*. Using the new CLSI breakpoints, there is still a significant number of *blaDHA* positive isolates being classified as susceptible to 3rd generation cephalosporins, for which treatment failure in serious infections have been reported. The rationale of obliterating the need for resistance mechanism testing by lowering the MICs of 3rd generation cephalosporins seems not to be applicable here. Simple phenotypic test like the AmpC disk test can detect most of the *blaDHA* positive isolates and should be performed for all *K. pneumoniae* isolates resistant to amoxicillin-clavulanate causing severe infections.

12.013 Antimicrobial susceptibility acinetobacter species

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Background: Prolonged hospitalization and antibiotic therapy creates predisposition to *Acinetobacter* infections, colonization and multi-drug resistance. *Acinetobacter* can be highly resistant to antimicrobials; it causes multi-drug infections and is sensitive to few antibiotics. *Acinetobacter* infection is rarely associated with meningitis, pneumonia, endocarditic, peritonitis, urinary and blood tract infection.

Methods and Materials: The aim of this study was to evaluate the antimicrobial resistance of a panel of 130 clinical *Acinetobacter* species isolated from hospitalized patients, clinically different patient samples in the routine microbiological work and identified by standard microbiology methods. Samples consisted of: sputum and respiratory secretions, wounds, urines, bloods. The determination of antimicrobial susceptibility of *Acinetobacter* by using Mueller Hinton Agar, based on the agar diffusion method a standard NCCLS method, with the 25 BBL Sense-disc.

Results: The results indicate that most strains of *Acinetobacter* species were multi-resistant and relatively few antibiotics are active against this organism. Antimicrobials to which *Acinetobacter* usually is % sensitive are shown in the table:

Antimicrobial Agent	Resistant	Intermediate	Susceptible
Colistin CI - 10	0	19 (14,62%)	111 (85,38%)
Ampicillin/Sulbactam SAM - 20	20 (15,4%)	24 (18,5%)	86 (66,1%)
Meropenem MEM - 10	52 (40%)	7 (5,38%)	71 (54,62%)
Netilmicin NET - 30	65 (50,0%)	6 (4,62%)	59 (45,38%)
Imipenem IPM - 10	62 (47,69%)	10 (7,69%)	58 (44,67%)
Cefepime FEP - 30	41 (31,54%)	51 (39,23%)	38 (29,23%)
Amikacin AN - 30	82 (63,0%)	16 (12,38%)	32 (24,62%)
Trimethoprim/ Sulfametoxazole SXT	62 (47,70%)	46 (35,38%)	22 (16,92%)
Nalidixic Acid NA - 30	112 (86,15%)	0	18 (13,85%)
Gentamicin GM - 30	111 (85,38%)	7 (5,39%)	12 (9,23%)

Antimicrobial resistance limits greatly the therapeutic options for patients who are infected with this organism, especially if isolates are 100% resistant to the following antimicrobial agents: Amoxicillin/Clavulanic acid, Ampicillin, Cefotaxime, Cefoxitine, Ceftazidime, Ceftriaxone, Ciprofloxacin Chloramphenicol, Ertapenem, Nitrofurantoin, Norfloxacin, Piperacillin, Piperacillin/Tazobactal, Tetracycline and Trimethoprim.

Conclusion: Eradication of *Acinetobacter* spp. requires adherence to good infection control practices and prudent antibiotic use, as well as effective antimicrobial therapy. Susceptibility testing is required for each clinically significant strain before antimicrobial treatment. Multidrug-resistant *Acinetobacter* is a rapidly emerging pathogen in healthcare settings.

12.014 Multidrug-resistant organisms in a military medical facility in Masar-e-Sharif

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Background: Military Missions in the field of international conflict prevention and crisis management are special challenges for military hygiene.

In medical facilities of the German Federal Armed Forces in Afghanistan ill and wounded German, ISAF, Afghan soldiers and policemen are being treated, as well as native patients are treated.

Methods and Materials: The presentation shows the principles of data collection, analysis and risk management in a German military medical facility in Masar-e-Sharif. Measures will be presented which protect against the infection.

Results: Multidrug-resistant organisms are very common in these groups of Afghan patients. Among these patients are frequently diagnosis of antibiotic-resistant organisms especially such as extended-spectrum β -lactamase-producing species, *Acinetobacter baumannii*, methicillin-resistant *Staphylococcus aureus*, *Escherichia coli* and *Pseudomonas aeruginosa* are made.

Conclusion: Health promotion and prevention of diseases and injuries are elementary conditions for a "healthy troop," which is physically and mentally strong and thus well prepared for the deployment.

The limited infrastructural and personnel resources of a field hospital are enormous challenges and limiting factors for a good prevention.

The key factor for the successful protection of the soldiers and patients against an infection with multidrug-resistant organisms are risk communication, epidemiological networks, national as well as multinational co-ordination of prevention, control strategies and a pragmatic conversion of the national hygiene guidelines adapted to the operational conditions.

12.015 Surveillance of antiretroviral resistance among HIV patients receiving ART in Georgia

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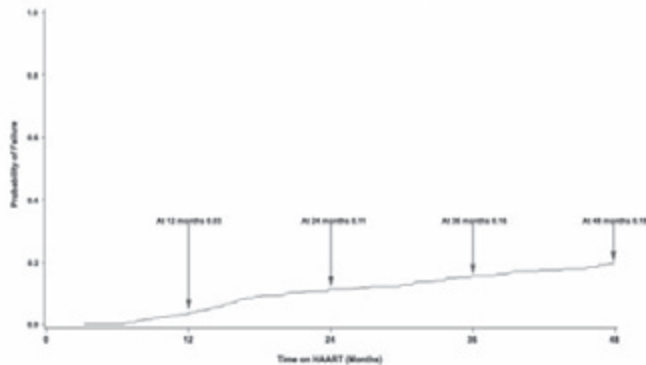
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Background: HIV drug resistance (HIVDR) has been recognized as major threat to sustained effectiveness of antiretroviral therapy (ART). The driving force of the spread of resistant HIV is the evolution of resistant variants in patients failing on ART. Since 2004 Georgia ensure ensured universal access to free ART. We report findings of surveillance of antiretroviral resistance among HIV patients receiving ART.

Methods and Materials: Analysis included 99 patients experiencing virologic failure defined as confirmed plasma HIV-1 RNA >50 copies/ml 12 months after starting therapy in a patient who is on potent ART. According to national guidelines plasma HIV-1 RNA is measured every four months to monitor response to treatment. Patients not achieving viral suppression are tested for HIVDR. For genotypic resistance testing the TruGene HIV-1 Genotyping Kit was employed according to the manufacturer's instructions using OpenGene DNA Sequencing System. Mutations listed by the International AIDS Society-USA Panel were considered.



Results: Of 876 patients enrolled in free ART program, 99 (11.3%) patients experienced virologic failure. Probability of failure at 12, 24, 36 and 48 months were 0.04, 0.11, 0.16 and 0.19 respectively. Of these 99 patients 79 (79.8%) had mutations consistent with antiretroviral resistance. Median number of mutations was 2. The most commonly detected NRTI mutation was M184V/I (65.7%). Frequency of thymidine analogue mutations (TAM) was relatively low, with only 16.2% patients having virus with any TAM. Only six (6.1%) patients had viruses with ≥ 3 TAMs. G190S/A was the most frequent NNRTI mutation (43.4%), followed by K103N (29.3%). Time trend analysis showed no statistically significant differences in the occurrence of common drug resistance mutations. Only L74V mutation showed marginally significant increase in cumulative frequency from 4.4% to 14.6%. This difference was consistent with increased use of Abacavir.



Kaplan-Meier probability of virologic failure

Conclusion: Low median number of resistant mutations and low frequency of TAM indicate effectiveness of routine viral load monitoring in preventing accumulation of mutations. Monitoring of HIVDR should be continued both in treatment-naïve and treatment-experienced patients to inform ART program planning and to optimize its effectiveness.

12.016 Tuberculous Meningitis: Novel ways to evade antimicrobial resistance

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Background: Tuberculous meningitis (brain TB) is a growing concern world over. A cumbersome therapy of around 2 years (Tuberculous Meningitis) with old enough ATDs, high on dose dependent side effects and low on cerebral permeability is raising WHO's eyebrows for an estimated 2.6 million new cases of MDR-TB by 2015. The slow prognosis of the disease leading to long term therapy and dawdling pace in development of newer ATD, it becomes all the more important to improve the efficacy of the existing agents. The present investigation proposes ways to improve the efficacy of these agents.

Methods and Materials: A NDDS system with targetability potential (solid lipid nanoparticles; SLNs) was selected. SLNs are lipophilic matrix systems which improve permeability of drug molecules across biological membranes. Suitable lipids were selected following IR spectroscopy and DSC studies. The SLNs were prepared by microemulsification technique and characterized for particle size, entrapment efficiency and total drug content. Emphasis was laid on developing nanosized particles below 200 nm so as to circumvent detection by RES (reticuloendothelial system). The efficacy of these agents was evaluated in a suitable animal model.

Results: A significant improvement in entrapment efficiency of ~80% with average particle size of 120 nm (essential for long circulation) was achieved. Effect of various process parameters like drug loading on entrapment efficiency and type of lipid on particle size were studied. A controlled drug release was obtained in 48 hrs. The release kinetics followed Higuchi model (r^2 0.997).

Conclusion: A *trifold benefit* of improved *targetability*, *permeability* (both of these are achieved because of the lipidic nature of SLNs; small size nearing 100 nm which overcomes the sieving of these particles by RES, hence ensuring an improved circulation) and an *achievement of*

a *sustained/controlled effect* were achieved. The current formulation can strengthen the existing antitubercular therapy by improving efficacy, reducing side effects and convenient dosing than can be achieved with the conventional ATD therapy, by increasing their **permeability** to reach the cerebral regions (targetability) to a greater extent (increased permeability).

12.017 Rates of methicillin resistant *S. aureus* bloodstream infections and infection control policies in California hospitals

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Background: Healthcare-associated Infections (HAI) caused by methicillin resistant *Staphylococcus aureus* (MRSA) are associated with significant morbidity and mortality in the acute care setting. The purpose of this analysis was to identify infection control practices used by California hospitals to prevent MRSA after the implementation of mandatory reporting requirements and targeted MRSA screening requirements in the state in January 2009

Methods and Materials: A cross-sectional survey of infection control departments from acute care California hospitals was conducted in the Spring of 2010. Respondents were asked to report the presence of specific policies directed at MRSA including the use of surveillance cultures, screening for MRSA upon admission and periodically after, use of presumptive isolation/contact precautions for patients with pending screens and for culture-positive patients and screening of microbiology results to identify cases. MRSA bloodstream infection (BSI) rates were also collected. Descriptive statistics were conducted to examine rates of MRSA BSI and the presence of MRSA infection control policies.

Results: 180 hospitals completed the survey (response rate =54%). The mean MRSA BSI rate was 1.50 per 1000 central line days (n=92, median=0, range=0-98) and 0.96 per 1000 inpatient days (n=108, median=0, range=0-5.1). Most hospitals (87.3%) reported the use of targeted screening; the most frequently screened groups included readmissions within 30 days (89.4%), transfers from nursing homes (96.0%), ICU patients (86.8%), dialysis patients (76.8%) and patients with specific medical conditions (55.0%). Only a third of hospitals (34.3%) reported use of isolation/contact precautions for patients with pending screens. The majority of hospitals (93.3%) reported presence of a policy to implement contact precautions for culture-positive patients, and 70% reported performing surveillance of microbiology results to identify new cases of MRSA. The most frequently used surveillance method for MRSA was standard culture (36.7%), MRSA selective agar (32.2%) and PCR (23.9%).

Conclusion: This study represents a snapshot of the infection control practices aimed at MRSA utilized by California hospitals after implementation of mandatory reporting. Most hospitals are involved in activities to decrease MRSA; however, there is variation in the specific type of activities utilized.

12.018 Risk factors for multidrug-resistant invasive pneumococcal disease in South Africa, 2003-2008

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Background: Resistance to antimicrobials among *Streptococcus pneumoniae* is of concern in South Africa as it complicates management of pneumococcal infections. Several risk factors for multidrug-resistant (MDR) invasive pneumococcal disease (IPD) have been reported, although few reports on risk factors from South Africa exist.



Methods and Materials: Data from laboratory-based surveillance for IPD conducted in South Africa from 2003 through 2008 were analysed. Pneumococci displaying resistance to three or more classes of antibiotics were defined as MDR. Risk factors for multidrug resistance were evaluated using multivariable logistic regression.

Results: From 2003 through 2008, 27732 IPD cases were reported. Of the 20100 (72%) cases with viable isolates, 3708 (18%) were MDR. The percentage of isolates that were MDR increased from 16% to 20% ($p < 0.001$). Serotypes included in the 13-valent conjugate vaccine (PCV13) accounted for 94% of MDR strains. Significant risk factors for MDR on multivariable analysis were age < 1 year (416/1652; 25%; OR, 2.1; 95% CI 1.8–2.4), 1–4 years (386/1458; 26%; OR, 2.0; 95% CI 1.7–2.3), and ≥ 65 years (39/239; 16%; OR, 1.5; 95% CI 1.0–2.1) vs. 13% (571/4327) aged 15–64 years; PCV13 serotypes (1486/6407; 23% vs. 85/2067; 4% non-PCV13 serotypes; OR, 6.2; 95% CI 5.0–7.8); HIV-infection (975/4636; 21% vs. 172/1028; 17% HIV-uninfected cases; OR, 1.4; 95% CI 1.2–1.7); antibiotic use in the previous 24 hours (98/375; 26% vs. 1107/6184; 18% with no antibiotics; OR, 1.4; 95% CI 1.1–1.9) and in the previous two months (242/803; 30% vs. 792/4773; 17% with no antibiotics; OR, 1.6; 95% CI 1.3–2.0); hospital admissions in the last year (579/2450; 24% vs. 722/4472; 16% with no admissions; OR, 1.2; 95% CI 1.0–1.3) and residence in urban Gauteng province (883/4375; 20% vs. 15/138; 11% in rural Limpopo; OR, 1.6; 95% CI 1.4–1.8). MDR was not associated with specimen type, clinical syndrome, or outcome.

Conclusion: MDR IPD is increasing in South Africa. Risk factors associated with multidrug resistance—increasing year, age < 5 and ≥ 65 years, HIV, previous antibiotic use, previous hospital admissions, and urban location—may correlate with greater antimicrobial exposure. Because PCV13 serotypes account for most MDR infections, pneumococcal vaccination may reduce multidrug resistance, in addition to reducing the burden of vaccine serotype disease.



Figure 1: Sites at which Greater Flamingo (*Phoenicopterus roseus*) cloacal swabs were taken for antibiotic sensitivity testing (from west to east): Rio Odiel, Spain; Fuente de Piedra, Spain; Ebre Delta, Spain; Camargue, France; and Comacchio, Italy.

Results: In preliminary analyses with a subset of samples, resistance to all six antibiotics has been detected, a significant finding given that they represent several classes of antibiotics. If further analysis indicates inter-site variation in resistance profiles - suggesting the influence of land-use and landscape characteristics - potential sources and mechanisms of transfer of ARB through a given environment can be investigated.

Conclusion: Through our use of the Greater Flamingo as a sentinel, we provide strong evidence of the prevalence of ARB in European natural environments. By using a multi-site approach, we are able to undertake comprehensive analysis of spatial variability and as a result, have generated a novel dataset from which trends in antibiotic resistance will be assessed.

12.019 **Antibiotic resistance in wild greater flamingos (*Phoenicopterus roseus*): Results from a network of Mediterranean sites provide evidence of spatial variability**

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Background: The widespread use of antibiotics in recent decades has resulted in antibiotic resistance becoming an issue of increasing concern, recognized – both within the scientific literature and by international bodies such as the World Health Organization – as a serious threat to human health. Indeed, antibiotic resistant bacteria (ARB) are of critical importance because they undermine the potential success of antibiotics. Initially recognized as a problem within urban areas, recent research has provided evidence of the spread of ARB into natural environments. Much of this research has been based on single-site studies and as such, has limited spatial analyses of resistance profiles (the suite of antibiotics to which an organism is resistant). As a result, determining the extent to which land-use and landscape characteristics drive spatial variability in antibiotic resistance has proven difficult. The current research aims to investigate spatial trends in antibiotic resistance through use of a multi-site approach, using the Greater Flamingo (*Phoenicopterus roseus*) as a sentinel.

Methods and Materials: A total of 350 cloacal swabs were taken from pre-fledgling Greater Flamingos during July and August 2010 at five sites within its Western Mediterranean metapopulation (Camargue, France; Comacchio, Italy; Ebre Delta, Fuente de Piedra, and Rio Odiel, Spain). Swabs were transported to the laboratory in Amies transport medium, and antibiotic susceptibility testing was undertaken using disc-diffusion methodologies for six antibiotics: ampicillin (10µg), amocyclin/clavulanic acid (30µg), erythromycin (15g), imipenem (10g), tetracycline (30g) and streptomycin (10g).

12.020 **Effectiveness of porcine lysozyme as a candidate antibacterial agent to supersede antibiotics**

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Background: Recently, the abuse of the antibiotic induces the appearance of the drug resistance bacteria. Therefore, it is necessary to develop an alternative way that takes the place of antibiotics. Lysozyme, an anti-bacillus protein of nature, is one of the promising candidate. Because anti-bacterial mechanism of the lysozyme and antibiotics are different, the lysozyme is effective against the antibiotic-resistant bacteria. In order to spread this useful protein as a practical anti-bacterial medical agent, it is necessary to reduce the production cost. To establish cost effective mass-production system, recombinant porcine lysozyme was produced by insect cell using the synthetic gene.

Methods and Materials: Porcine lysozyme (PLY) gene (length: 488bp) was synthesized from 9 short DNA oligomers (length: 70-80mer) by SPR method and PCR extension. This artificial gene was expressed in 3 insect cell lines (BmN4, Sf-9, expresSF+) with baculovirus expression system. The anti-bacterium activity of each cell culture medium was measured. 3D structure of PLY was analyzed by the structure prediction software (FAMSD, In-Silico Sciences).

Results: In the productivity of PLY, the expresSF+ cell is most excellent (more than 50mg/L) than other cells. The PLY in culture medium of expresSF+ cell was purified by ultrafiltration and cation-exchange column. As the result of N-terminal sequencing and mass spectrometry, it was physicochemically the same as the natural PLY. In the comparison of PLY with the human lysozyme (HLY) and the chicken lysozyme (CLY), against various bacteria containing the antibiotic resistant bacteria (*Enterococcus*, *Enterobacter* etc.), PLY showed strong anti-bacterial activity from 2 to 10 times in the minimum inhibitory concentrations. Moreover, PLY exhibited significantly wide optimal pH range and resistance to higher ionic strength conditions. The 3D structure of PLY showed that the number of basic residues on the surface of PLY was more than that of other lysozymes. It presumably works advantageously in strength of the positive charge on the surface of PLY interacting with bacteria.



Conclusion: PLY, efficiently produced in expresSF+ cells, has stronger anti-bacterial activity against the antibiotic resistant bacteria, wider optimal pH range and higher resistance to the ionic strength than HLY and CLY.

12.021 Antimicrobial susceptibility in children with urinary tract infection in a pediatric hospital of Western Venezuela

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Background: Urinary tract infections (UTI) take second place in incidence of pediatric bacterial infection. Occurrence of UTI below two years of age, delay in starting treatment and presence of vesico-ureteric reflux or obstruction are main risk factors associated with renal scarring.

Methods and Materials: A retrospective investigation was performed comprising all patients between 0-14 years old, admitted to the pediatric hospital of Barquisimeto, Venezuela, with the diagnosis of UTI during the period January 2004- December 2009. Epidemiological characteristics were reported; all clinical relevant variables were considered. Uroculture and uroanalyses were evaluated. Descriptive statistics were generated for the epidemiological data. Qualitative and quantitative comparisons were made for the time periods. SPSS® statistical software was used; level of confidence of 95%, p significant <0.05.

Results: 400 patients were treated during the study period. 53,8% of them were female and 46,3% were male with a mean age of 19 months. UTI were most common in females between 1-6 years old and in males between 0-12 months. 17% of patients had a pathologic ultrasound. UTI were more common in patients with hydronephrosis (4,5%), obstructive uropathology (5%), megaureter (4,5%) and lithiasis (2,3%). 51% of available urocultures were positive. *E. coli* was the most common causal agent (66%), followed by *Klebsiella spp.* (9%), *Proteus spp.* (7,5%) and *Pseudomonas aeruginosa* (3,7%). Antimicrobial susceptibility showed that the majority of *E. coli* cases were resistant to ampicillin (81,6%), cefalotine (77,8%), ampicillin-sulbactam (67,8%) and amoxicillin-clavulanic (59,25%); ampicillin showed high resistance also in *Proteus spp.* (66%), *Klebsiella spp.* (100%) and *Pseudomonas aeruginosa* (100%) infections. Cephalosporins showed resistance ranging from 9 to 50%. All pathogens were susceptible for imipenem, carbapenem and aztreonam (100%), also all of them except *Streptococcus spp.* were susceptible for meropenem and ertapenem. 22,4 % of patients required a change of treatment, third generation cephalosporines were the most common final treatment (61,5%).

Conclusion: The current goal of management of UTI is to prevent detrimental effects by early detection and treatment; this objective could be affected by the increase of antimicrobial resistance. Periodic evaluation of pathogen resistance in each geographical area could decrease the time of hospitalization and increase treatment response.

12.022 WHO Global Foodborne Infections Network external quality assurance system (EQAS) for antimicrobial susceptibility testing of *Salmonella* isolates

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Background: The WHO Global Foodborne Infections Network (GFN) builds global capacity to conduct integrated, laboratory-based surveillance, detection and response to outbreaks of foodborne and other infectious enteric diseases through a number of components. One such component is the international External Quality Assurance System (EQAS) for the antimicrobial susceptibility testing of *Salmonella* species which was initiated in 2000 by GFN. EQAS enhances the capacity of national reference laboratories to obtain reliable data for surveillance purposes worldwide.

Methods and Materials: Nine EQAS iterations were conducted between 2000 and 2009. In each iteration, participating laboratories submitted antimicrobial susceptibility testing (AST) results for eight *Salmonella* isolates through a secured website and received an instant report with suggestions for corrective action if needed. The use of the reference strain for quality control is essential when performing AST. For this purpose the EQAS-organizers provide the *E. coli* ATCC 25922 to each participant.

Results: In the EQAS iterations from 2001 to 2009, a total of 323 laboratories in 119 countries participated in AST at least one EQAS iteration (the 2000-data are not included as they were not uploaded to the database). The eight strains are selected to cover a variety of antimicrobial resistance profiles, especially emerging phenotypes like plasmid-mediated quinolone resistance and extended-spectrum beta lactamase-producers (ESBL). Cumulatively, 92% of the uploaded results on the test isolates were in agreement with expected results. The percentage of laboratories uploading data for the quality assurance strain ranged by iteration between 72% to 99% with 41% to 56% of the laboratories having all values within the acceptance limits.

Conclusion: The results from the GFN EQAS, one of the largest of its kind in the world, show that most laboratories worldwide are capable of correctly performing antimicrobial susceptibility testing of the *Salmonella* isolates included in the proficiency panel. However, this study also indicates a continuing need for improvement. Future training efforts should be aimed at enhancing the quality control of the assay stressing the importance of the QC strain, the true indicator of the quality of AST performance, and at enhancing the ability to detect emerging resistance phenotypes, e.g. plasmid mediated quinolone resistance and ESBL.

12.023 Clinical mastitis in cows and their response to in vitro sensitivity

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Background: 50 samples from Tripoli were subjected to microbiological examination. *Staphylococcus spp.* was the predominant causative organism and *E. coli* the next and *Streptococcus spp.* Where as 3 cases are caused by non bacterial agents. The isolates bacteria were tested for their in-vitro susceptibility to different antimicrobial agents used in commercial intramammary infusion products. Antibacterial susceptibility testing showed that the best antibiotic was ciprofloxacin

Methods and Materials: *Sample collection:* Milk samples were collected from 50 cows affected with mastitis in Tripoli. Mastitis was identified by swelling, hardness, warmth and/or abnormal secretions (abnormal color or consistency and/or presence of clots or flakes). *Bacterial isolation and identification:* Each sample was streaked on blood agar, MacConkey's agar and nutrient agar. The plates were incubated aerobically at 37°C and examined for growth after 24 and 48 h. The gram stain was performed to distinguish Gram-positive and negative organisms and to reveal the bacterial. *Biochemical tests used to identified bacteria—Susceptibility testing:* The isolated bacteria that were sensitive to antibiotics were tested using Mueller Hinton agar and the antibiogram was determined by the disc diffusion method. The antibiotics tested were ciprofloxacin, enrofloxacin, cefotaxime, deoxycillin, chlorphenicol, ampicillin, amoxicillin, vancomycin and fusidic acid. After 18–24 h of aerobic incubation at 37°C, the diameter of the zone of inhibition was measured by a ruler and classified as resistant, intermediate or susceptible according to the Quinn *et al* procedure.



Results: The isolation frequency of the bacterial strains is summarized in Table (1). The susceptibility of the bacterial species isolated in the present study to the antimicrobial agents used in intramammary infusion products summarized in (Table 2)

Table (1): Bacterial isolates from milk samples obtained from the mastitic quarters.

Bacteria	Number of isolates	%
<i>Staph.</i>	18	36
<i>E. coli</i>	12	24
<i>Strepto.</i>	3	6
No bacterial growth	12	24
Mixed cultures	5	10

(Table 2): Sensitivity pattern of mastitis milk samples

Antibiotic	Percent Sensitivity
ciprofloxacin	100
enrofloxacin	96
cefotaxime	90
deoxicillin	88.8
chlorophenicol	66.5
ampicillin	62.5
amoxicillin	50
vancomycin	42
fusidic acid	33.3

Conclusion: In the present study we found that the most bacteria distribution in the area of the study was *staphylococcus*, and the best antibiotic for treatment was ciprofloxacin.

12.024 Shiga toxin-producing *Escherichia coli* (STEC) isolates from different origins showed high antimicrobial susceptibilities

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Background: *Escherichia coli* carrying the *stx* gene is an important food-borne pathogen, which can cause severe illnesses in humans like bloody diarrhea, hemorrhagic colitis or hemolytic uremic syndrome. Ruminants are regarded as the main reservoir. Human infections can be due to ingestion of raw or insufficiently cooked meat. Increasing high antimicrobial resistance in *E. coli* of animal origin, especially against ampicillin, tetracycline and sulphonamides, has been reported. The objective of this study was to examine if STEC isolates show similar antimicrobial patterns to those of *E. coli* using 13 antimicrobial agents.

Methods and Materials: Antimicrobial susceptibility of 88 STEC isolates (54 from deer and 34 from small ruminants) collected between 2006 and 2010 in Germany (76) and Switzerland (12) were studied using broth microdilution method (CLSI 2008). Antimicrobial susceptibilities were tested for ampicillin, cefotaxime, ceftazidime, chloramphenicol, ciprofloxacin, florfenicol, gentamicin, kanamycin, nalidixic acid, streptomycin, sulfamethoxazole, tetracycline, and trimethoprim.

Results: All STEC isolates were susceptible to ampicillin, cefotaxime, ceftazidime, chloramphenicol, ciprofloxacin, gentamicin, kanamycin, nalidixic acid, and trimethoprim. Most isolates were resistant to sulphamethoxazole (96%) and florfenicol (85%). Yet, only one isolate (1%) (from a Swiss goat) was resistant to tetracycline and 9 isolates (10%) were resistant to streptomycin. Nine isolates (10%) were also multi-resistant of which 8 were resistant to 3 (streptomycin, sulphamethoxazole and florfenicol) and 1 to 4 (streptomycin, sulphamethoxazole, florfenicol and tetracycline) antimicrobial agents.

Conclusion: Only sporadic resistance to most of the antimicrobial agents tested occurred among most STEC isolates examined. The resistance patterns of STEC differed from the patterns reported among *stx*-negative *E. coli*. Whilst *stx*-negative *E. coli* from animal origin are usually highly resistant to ampicillin, sulphamethoxazole, streptomycin, and tetracycline all STEC isolates studied were sensible to ampicillin,

and almost all isolates were sensible to tetracycline. The resistance to streptomycin was low. Multiresistance was rare among the STEC isolates examined.

12.025 Trends in pediatric bacterial meningitis in Sudan 2005–2006

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Background: A surveillance of epidemiological pediatric bacterial meningitis was carried out between January 2005 and January 2006 in Sudan, in National Reference Laboratory

Methods and Materials: 932 CSF samples were collected from children suspected having bacterial meningitis, gram stain, culture, biochemical tests and serotyping was done,

Results: with the following results: Bacterial meningitis cases numbered (46 boys, 32girls), from a total of 932 children suspected having bacterial meningitis. The age distribution for the infections was the highest under 2 year of age, decreasing with increasing age. *N. meningitidis* was the most common pathogen, followed by *Haemophilus influenzae*, *Streptococcus pneumoniae*, *Staphylococcus aureus* (one isolate). The relationship between causative pathogens and age distribution was as follows: *staph aureus* was isolated from child of 6 months of age and *H. influenzae* and *S. pneumoniae* were major pathogens less than 5 years of age. where meningococci were from more than 5 years of age. Susceptibility tests demonstrated that . 60% of *H. influenzae* isolates and . 58% of *S. pneumoniae* isolates were drug-resistant.

Conclusion: Ceftriaxone an effective against meningococci, where chloramphenicol antibiotics are currently less effective a combination of ampicillin and cephem antibiotics is used first line at many facilities for patients below 4 months of age. A combination of carbapenem which showed effective against PRSP and cephem which showed effective against *H. influenzae* is the first choice in childhood bacterial meningitis for patients above 4 months of age.

12.026 Role of limited access dressing in eliminating Multi-drug resistant organisms capable of forming biofilms in wound infections

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Background: Limited access dressing (LAD) is the combination of intermittent negative pressure & moist wound dressing which is used in the management of both acute and chronic wounds (such as Burn wound, Diabetic foot ulcer, necrotizing fasciitis) by preventing bacterial invasion at the wound site and reduce the hospital acquired infections.

The objective of the present study is to evaluation of the efficacy of LAD in wound care management by checking the bacterial growth before and after the LAD, testing their antibiotic susceptibility including ESBL, AmpC & MBL & ability to form biofilm *in-vitro*.

Methods and Materials: Swabs were collected from wounds of sixty patients according to the conventional microbiological method before applying and after removing the LAD. Identification and antibiotic susceptibility was done using CLSI guidelines. The strains were checked for multi-drug resistant enzyme production using disk approximation method and biofilm formation ability was tested using microtitre well method.

Results: Out of 60 patients evaluated in this study bacterial growth was detected from 57 patients (95%), usage of LAD resulted in NO GROWTH in 34/57 (59.6%) patients, and reduction in the number of organisms in 19/57 (33.33%) patients.

Among isolates (n=93) from the first sample, Biofilm producers were 35 (37.6%), ESBL producers 24 (25.4%), AmpC producers 8 (8.6%), MBL



producers 17(18.2%). LAD effectively removed organisms which produced Biofilm in 34 cases, ESBL 20 cases, AmpC 6 cases and MBL 12 cases.

Other isolates from the PRE-LAD TREATMENT SAMPLE (n=93) were *Pseudomonas* spp.=36(38.7%), *Klebsiella pneumoniae*=13(13.93%), *Klebsiella oxytoca*=7 (7.52%), *Acinetobacter* spp.=9(9.6%). Commonly isolated organisms from the POST-LAD TREATMENT SAMPLE (n=26) were *Pseudomonas* spp.=10(38.4%), *Proteus mirabilis*=6(23.07%), *Klebsiella oxytoca*=4(15.38%).

Conclusion: LAD prevents hospital strains to colonize & cause wound infections and effectively eradicates ESBL, AmpC and MBL and organisms which produce Biofilm. So it opens a new window in treatment of resistant wound infection.

12.027 Isolation resistant Enterococci from hospitalized patients in two years

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Background: Enterococci have gained increasing clinical importance through the 1990s due to changes in hospital patient populations and antimicrobial use patterns. The most frequent clinical enterococcal infections are urinary tract infections and endocarditis. Enterococci are also isolated from polymicrobial intra-abdominal abscesses and wound infections. *Enterococcus faecalis* and *Enterococcus faecium* have traditionally been estimated to account for 90% and 5–10% of enterococcal infections. Enterococci are considered important difficult-to-treat pathogens, due to their intrinsic resistance to several antimicrobial agents and their propensity to acquire resistance.

Methods and Materials: The present prospective study was carried out to determine the antimicrobial susceptibilities of enterococci isolated from clinical samples in a tertiary care hospital of Iran. *Enterococcus* species were identified by standard biochemical tests. Antimicrobial susceptibility testing was performed by the disk diffusion method. Susceptibility testing for 136 antibiotics was performed in a series of clinical enterococci recovered in a teaching hospital shohada tajrish.

Results: The percentages of antibiotic resistance detected were as follows: penicillin (62.3%), erythromycin (59.8%), cloxacillin (100%), streptomycin (100%), trimethoprim-sulfamethoxazole (89.7%), ampicillin-amoxicillin (16.7%), vancomycin (18.5%), gentamicin (51.2%), nitrofurantoin (52.9%) and ciprofloxacin (41.8%) clindamycin(86.5%) cephalothin(52.9%)

Conclusion: Infection control and monitoring of antibiotic sensitivity among isolated hospital strains may prevent the transmission of resistant strains in a hospital.

12.028 Phage Nanobiotechnology, Applications for Defense against Emerging Pathogens

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Background: The rapid identification, treatment and prevention of emerging bacterial diseases remain complex issues. Drug-resistant pathogens are a growing threat to both people and animals. From *Vibrio cholerae* to *Staphylococcus aureus*, *Clostridium difficile*, *Streptococcus suis* and multidrug-resistant *Mycobacterium tuberculosis*, the list is growing. Phage nanobiotechnology, or the use of bacteriophages and their derivatives, may provide a useful alternative or an adjunct to current approaches.

Phages are viruses that destroy bacteria by lysis. The concept of using phage as a therapy for bacterial diseases was first proposed during WWI and since then has been a key tool Eastern Europe. More recently, lytic enzymes have been isolated and expressed in *Escherichia coli*. This has further broadened the potential of phage derived technologies for treatment, prevention, decontamination and diagnosis. The use of these enzymes has been further expanded to include replacement or enhancement of antibiotics to treat disease including those causing animal or agricultural diseases.

Examples and data of various applications of phage nanobiotechnology will be presented. These included applications of lytic enzymes as a spray or fogger for decontamination, incorporation in wound dressings, as well as a preventative for high risk groups.

Methods and Materials: A preparation called *Staphylococcus bacteriophage liquid*, which is a mixture of sterile filtrates of phage lysate active to various strains of *S. aureus* was obtained from G. Eliava Institute of Bacteriophages, applied via oral administration (a spoon of soda solution to neutralize pH of gastric juice was administered prior to phage preparation) 5 ml of preparation twice a day over a period of 7 days and then repeated.

Results: Upon completion of a total 14-day phage therapy, the nasal and pharyngeal swab was tested for *S. aureus*. Samples taken from the patient showed no bacteria in question.

The patient gradually recovered from general fatigue, malaise, sore throat and respiratory infection symptoms. After two weeks, the arthralgia disappeared as well. No side-effects of the applied preparation were observed in the patient

Conclusion: Bacteriophage therapy was successful in treating a long-term MRSA infection. Other applications of phage nanobiotechnology will be presented.

12.029 Multidrug-resistant bacteria in urban surface waters

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Background: Antibiotic resistance is a major public health problem worldwide. There are few data on the occurrence, sources and significance of antibiotic-resistant bacteria in surface waters in metropolitan areas. The Vienna waterside consists of an array of diverse ecosystems such as the Danube river, the deviation of the Danube ("Danube canal"), the Wien river ("Wienfluss") and the "Alte Donau". All these locations are highly frequented recreation areas for diverse water related human activities. Therefore, selected sites in the Vienna metropolitan area were examined for the occurrence of multidrug-resistant fecal indicator bacteria.

Methods and Materials: Bacteria were isolated from water samples by 0.2 µm membrane filtration using antibiotic-supplemented standard media such as MacConkey and Slanetz-Bartely agar. Antibiotic resistance profiles of isolates were determined by the Kirby-Bauer disc diffusion method. Phenotypic identification of AmpC and/or extended-spectrum β-lactamase (ESBL) enzyme production was performed in a second, confirmatory test.

Results: At least two out of ten sites were identified as a potential reservoir for multidrug-resistant bacteria including ESBL-producing strains. The isolates, among others *E. coli*, *Enterobacter* and *Klebsiella* spp., were resistant towards 4 to 12 out of 14 antibiotics tested. Resistance was most commonly found against ampicillin, amoxicillin, cefalotin, sulfonamide-trimethoprim, and streptomycin. In contrast, resistance towards quinolones (ciprofloxacin), aminoglycosides (kanamycin, tobramycin) or tetracycline was infrequently detected.

Conclusion: The investigation suggests that multi-drug resistant bacteria are common in metropolitan aquatic ecosystems. These waters may contribute to the spread of antibiotic resistance. Water quality control should incorporate antibiotic resistance analyses into current methods to improve water management.

12.030 Antimicrobial susceptibility of *Pseudomonas aeruginosa* invasive isolates in Clinical Center of Serbia: 2007–2010

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Background: *Pseudomonas aeruginosa* (PA) is ubiquitous organism and important causative agent of nosocomial infections. Treatment of infections caused by multidrug resistant PA is a growing problem.

Aim of the study was to determine the antimicrobial susceptibility of PA isolates from primary sterile body fluids processed in Bacteriology Laboratory of Clinical Center of Serbia during 2007–2010.



Methods and Materials: Total of 89 PA isolates originating from blood cultures, pleural and cerebro spinal fluids was analysed. The isolates were obtained from patients residing at 12 clinics of Clinical Center of Serbia from 01.01.2007-30.11.2010. Isolation and identification were performed using standard microbiological methods. Antimicrobial susceptibility to: amikacin, gentamicin, cefepime, ceftazidime, ciprofloxacin, imipenem, meropenem, piperacillin, piperacillin plus tazobactam and colistin was determined by Vitek 2 (bioMerieux) with interpretation according to CLSI (Clinical and Laboratory Standard Institute) criteria.

Results: Total number of PA (N=89) made 71 (79.78%) blood culture isolates, 14 (15.73%) pleural fluids and 4 (4.49%) cerebro spinal fluids. Average susceptibility was: amikacin 38,46%, gentamicin 29,21%, cefepime 32,58%, ceftazidime 34,09%, ciprofloxacin 20,22%, imipenem 39,76%, meropenem 42,53%, piperacillin 20,45%, piperacillin plus tazobactam 21,35% and colistin 100%. Isolates were divided in one group, collected from 2007-2009 and in the other group collected in 2010. The first one contained 46 (51.68%) isolates, while the other one contained 43 (48.32%). Antibiotic susceptibility of isolates from these groups was significantly different for cefepime and ciprofloxacin ($p < 0.05$). Isolates were analyzed by the origin: surgical wards (N = 39, 43.82%) and medical wards (N = 50, 56.18%). Statistically significant difference ($p < 0.05$) was demonstrated for sensitivity to ciprofloxacin, imipenem, meropenem among the isolates from surgical and medical wards; the differences in susceptibilities to other antibiotics tested were highly significant ($p < 0.01$). Between the sensitivity of isolates from blood cultures and other samples statistically significant difference has not been found.

Conclusion: The high level of resistance to antibiotics has been found in the tested strains. All of them were susceptible to colistin. Significantly better susceptibility of the isolates was documented for the strains originating from medical wards, compared to surgical. Susceptibility to cefepime and ciprofloxacin in 2010 was significantly increased compared to the previous period.

12.031 Evaluation of antimicrobial Resistance of vibrio cholera obtained from patients and contaminated water of Kashan city 1998–2009

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Background: Cholera is an acute diarrhea that can lead to severe dehydration in a few hours and progressively cause death. Regarding importance of this disease this study was conducted to evaluate antimicrobial resistance of vibrio cholera obtained from patients and contaminated water.

Methods and Materials: In a cross Sectional study, Stool sample gathered from the patients with severe diarrhea, were cultured in TCBS for detection vibrio cholera. Than serotyping and biotyping were done through enzymatic method. After identifying Vibrio in samples, antibiotic susceptibility test was done through disk diffusion method (Kirby Bauer). Qualitative variables were analyzed by constant and relative abundance and quantitative variables by mean and standard deviation. To compare the variables Fisher-exact and Chi-square statistical tests were

Results: Totally 58 samples gathered from patients referred to health centers and 15 ones from contaminated waters in the area. Among the samples, those gathered from contaminated waters had more antibiotic resistance than the others gathered from patients. In the group of water samples only resistance to two antibiotics, Ampiciline (13.2%) and Nitrofurantoin (6.7%), was seen. But in the group of patient sample resistance to all antibiotics, but erythromycin, was seen (max. Ampiciline (31%) and min. Doxycycline, Ciprofloxacin and Tetracycline (1.7%)). The antibiotic resistance was compared upon Vibrio cholera serotypes, age and gender

Conclusion: There was the obvious increasing curve of antibiotic resistance to choice antibiotic for Vibrio. This can be the major concern about cholera because appearing Multi Drug Resistant specing of Vibrio may encounter the treatment with a lot of problems.

12.032 Antibiotic-resistant cholera strains isolated in Kazakhstan

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Background: The cholera microbes are resistant to antibiotics including multi-resistant stains have been registered on the background of high sensitivity of cholera microbes to many antibiotics. The numbers of cholera cases caused by antibiotic-resistant cholera strains have been permanently grown up and the list of potential effective antibiotics has been reducing.

Methods and Materials: In addition of traditional preparations used for cholera treatment, the antibiotics of fluorinolons (ciprofloxacin, lomefloxacin, etc), aminoglucozides (gentamicin, tobramycin, kanamicin, etc.), and combination of antibacterial preparations (doxycycline+ciprofloxacin, ciprofloxacin+rifampicin, etc.) were suggested for alternative treatment of cholera.

The wide-spectrum antibiotic sensitivity of cholera strains isolated in Kazakhstan in 2005 has been studied. 220 of cholera strains were studied. The strains were studied by serial dilution, and disks methods. The toxigen and non-toxigen cholera strains were isolated as from patients as from environment.

Results: The next results were received:

- The strains of epidemic cholera isolated from patients of the South-Kazakhstan Province, Almaty, Kyzylorda, Oral cities were sensitive to tetracycline excepting of one strain isolated in Aktau-city;
- all strains were high sensitive to antibiotic of siflox independently of isolation objects, and using of siflox is more effective for cholera treatment;
- 62% of non-toxigen strains of *V. cholerae non O1* isolated in the South-Kazakhstan Province and Aktau-city were resistant to tetracycline;
- The strains isolated from environment objects in the South-Kazakhstan Province, Aktau, Taraz cities were sensitive to tetracycline, and one strain isolated in Atyrau-city (Oral River) was sensitive to tetracycline and other one was resistant to tetracycline.

Conclusion: Take into account of action of antibiotics in the selection of resistant clones of cholera strains the problem of reasonable applying of antibiotics for cholera treatment and control for antibiotic sensitivity of cholera strains isolated from persons and environment objects have to be carried out.

12.033 Detection of Integron elements and gene groups encoding ESBLs and their prevalence in *E.coli* and *Klebsiella* isolated from urine and stool samples of patients who referred to Mofeed children hospital in Tehran by PCR method

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Background: Antibiotic resistance pertaining of extended spectrum beta lactamases recently has highly increased. It could be seen as daily enhancement. The most observations are for Enterobacteriaceae and early studies were for this family of bacteria. Because, *E.coli* and *Klebsiella* species are amongst the usual clinical isolated bacteria, this study has been performed on these two bacteria. Integron elements are short sequences of DNA like transposons. They can transfer genes such antibiotic resistance among the bacteria. Recent studies have revealed these elements could bear the ESBL genes.

Objectives: Determination of prevalence *E.coli* and *Klebsiella* species including ESBL and their relation with integron sequences

Methods and Materials: 100 *E.coli* and 100 *Klebsiella* have been isolated from urine and stool samples. Then susceptibility antibiotic testing such epsilometry test (E-test), disc diffusion test and MIC has



done with prototypical antibiotics indicative for ESBLs like Ceftriaxon, Ceftazidim, Cefotaxim, Cefpodoxim, Aztreonam and Clavulanate added to Cefotaxim and Cefpodoxim. ESBL bacteria have been preserved in -70 °C freezer and PCR performed on them. The studied gene groups for ESBL were CTX, TEM, SHV and Int.

Results: 33 of *E. coli* were positive for ESBL with frequency include: CTX (30), TEM (15), SHV (25), Int (18). 29 *Klebsiella* were positive for ESBL with frequency such: CTX (28), TEM (24), SHV (20) and Int (14).

Conclusion: it could be perceived that among these strains 48%–54% concomitantly have ESBL genes and Integrons.

12.034 Ambiguity in the diagnosis of pneumococcal infections and emerging of optochin resistance in clinical isolates of *Streptococcus pneumoniae* and in Iran

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Background: *Streptococcus pneumoniae* is one of the most important pathogens in children and in elderly populations, being the most common cause of invasive bacterial infections such as pneumonia, sinusitis, and meningitis. So that accurate identification is crucial for correct diagnosis and treatment of patients. The major test in diagnosis of *S. pneumoniae* is to be susceptible to optochin disk. But optochin-resistant pneumococci have been reported in the last 2 decades. Recent studies show an alerting in *atpA* and *atpC* that encode A and C subunits of F0F1ATPase that is responsible for optochin resistance.

Methods and Materials: 64 isolates were collected from patients of some clinical center in Iran since 1998 till now. After biochemical tests such as bile solubility, α hemolysis on chocolate agar, negative catalase test, and PCR, 64 isolates identified as *Streptococcus pneumoniae*. All isolates were tested for optochin Sensitivity by disc diffusion method. *atpC* gene was targeted with specific primers in PCR assays. The *atpC* gene was sequenced and compared for these isolates. PFGE was done for all isolates.

Results: From all 64 *S. pneumoniae* strains, 12.5% (8 isolates) were optochin resistant (zone was less than 14mm) and bile soluble. 10.9% (7 isolates) were optochin resistant and bile non soluble (with other tests they were determine as *S. pneumoniae*). All of Optochin resistant strain showed replacement of alanine to threonine (A49T) in *atpC* gene. PFGE classification has been shown different patterns for resistant strains.

Conclusion: Susceptibility to optochin is often used in laboratories as the primary and sometimes the only identification method. It may be so harmful if laboratories can't diagnosis *S. pneumoniae* because of optochin resistant. This mutation that we have detected has been reported as one of the major cause of Optochin resistant by other studies. Our results show an emergence of optochin resistance among clinical isolates of *S. pneumoniae* in Iran.

12.035 Emerging of *Streptococcus pneumoniae* isolates with High-level Resistance to Penicillin in Iran

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Background: *Streptococcus pneumoniae* is an important human pathogen that is the most cause of meningitis, pneumonia, otitis media and sinusitis. Penicillin resistance among *Streptococcus pneumoniae* is rapidly increasing. In resistant strains there is a reduction in the capacity to bind to antibiotics in penicillin binding proteins.

Methods and Materials: 65 pneumococcal isolates were collected during the period from 2003 to 2009. Identification of pneumococcal isolates was performed by standard microbiological methods, such as optochin susceptibility, and bile solubility. We used molecular methods such as PCR for accurate identification. Antimicrobial susceptibility testing was done by broth dilution and Etest. The region encoding the transpeptidase domain of *pbp1a*, *2b* and *2x* was amplified by PCR. The nucleotide sequences were determined by direct sequencing. Chromosomal DNA fragments digested by *SmaI* and separated by PFGE.

Results: From all 65 *Streptococcus pneumoniae* strains, 4 isolates (6.1%) were optochin resistant and bile soluble; these isolates had *lytA*, *ply* and *psaA* genes. 16 isolates (24.6%) were penicillin resistant ($MIC \geq 2$ $\mu\text{g/ml}$) and 5 isolates (7.6%) were high-level penicillin resistant ($MIC \geq 4$ $\mu\text{g/ml}$). All of the high-level penicillin resistant strains had T371A/S substitutions in the STMK373 motif and had P432T substitutions close to the SRN430 motif of *pbp1a*. All of the penicillin-nonsusceptible isolates had alterations in transpeptidase domain of *pbp2b*. PFGE analysis showed that high-level penicillin resistant isolates were clonally unrelated.

Conclusion: Our results revealed the increase of penicillin resistance in strains of *Streptococcus pneumoniae*, moreover, prevalence of high-level penicillin resistant strains revealed a crisis in treatment of pneumococcal infections. We showed that alterations in the conserved motifs in *pbps* specially *pbp1a* are associated with high-level penicillin resistant in *Streptococcus pneumoniae*.

12.036 Clinical outcomes of patients with *Klebsiella pneumoniae* carbapenemase (KPC) in a Mexico general hospital

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Background: *Klebsiella Pneumoniae* resistant to carbapenem (KPC) has emerged as significant nosocomial because its substantial morbidity and mortality related. We reported clinical outcomes of patients with *klebsiella pneumoniae* carbapenemase (KPC) in our hospital during 2010.

Methods and Materials: 28 patient isolates of *klebsiella pneumoniae* resistant to carbapenem were detected. Isolates were biochemically characterized and their antimicrobial susceptibilities evaluated using MicroScan 96. For phenotypic test we made modified test Hodge. The carbapenemase genotype was determined by PCR. The resistant profile was evaluated by MicroScan 96, for ertapenem and tigecycline we used disk diffusion and for colistin we used microdilution.

Results: We studied 28 strains. None of the patients were associated with previous travel. Patient clinical samples included: sputum (15), urine (1), blood culture (2), surgical site (5), and abdominal fluid (4) and central catheter (1). In 12 patients, therapy with some carbapenem had been received. All isolates were resistant to carbapenems, susceptible to tigeciclyne and colistin and were modified Hodge test positive and *blaKPC* PCR. 14 of the 28 patients died, 13 of them had pneumonia.

Conclusion: KPC-producing *Klebsiella pneumoniae* infections has emerged an important cause in our hospital with significant mortality in patients with pneumonia even received tigeciclyne.

12.037 Nasal carriage of multidrug resistant *Staphylococcus aureus* in medical personnel of tertiary care hospital in Nepal

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Background: *Staphylococcus aureus* is one of the most common causes of both hospital and community acquired infections worldwide which results in substantial morbidity and mortality. The organism may thrive on human skin and mucous membranes, and can be carried for long periods without causing clinical consequences. The present study was carried out to assess the nasal carrier rate of methicillin resistant *S. aureus* (MRSA) and/or multidrug resistant (MDR) *S. aureus* among medical staffs of tertiary care hospital in Nepal.

Methods and Materials: Nasal swab screenings were performed in 205 hospital personnel. Swabs were microbiologically processed and *S. aureus* were isolated and screened for multidrug resistance by antimicrobial susceptibility testing.



Results: Among 81 *S. aureus* isolates from nasal swab, 39.0% (n=48) were from males and 40.2% (n=33) were from females. The distribution of nasal carriage of *S. aureus* between male and female was not found to be statistically significant. In female, the highest prevalence of nasal carrier of *S. aureus* was found in the age group of 10-19 years (100.0%) while in male, it was found in the age group of 50-59 years (50.0%). Among hospital personnel, high nasal carrier rate was found in ward attendants and sweepers 52.5 % (n=21) followed by volunteer nurses 44.4% (n=8) and nursing staffs 42.4% (n=25). Regarding the department wise distribution of nasal carrier, highest nasal carriage rate of *S. aureus* was from ENT (63.6%) followed by Orthopedic (54.5%). The isolates showed highest resistant to Penicillin (86.4%) followed by Amoxicillin (71.6%), Cotrimoxazole (44.5%), Erythromycin (31.3%), Gentamicin (13.5%), Tetracycline (12.3%), Chloramphenicol (11.1%) and least towards Vancomycin (100.0%). Only 23.5% (19/81) *S. aureus* isolates were MDR. No MRSA was found among the positive isolates of *S. aureus*.

Conclusion: Medical staffs carry a significant high percentage of multidrug resistant *S. aureus* on their nares. Regular nasal screening of hospital staffs and health care personnel for the carriage of methicillin resistant/multidrug resistant *S. aureus* should be done to minimize the spread of the strain to patients.

12.038 National survey on MRSA in pigs in Finland in 2009–2010

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Background: A new Methicillin-resistant *Staphylococcus aureus* (MRSA) type CC398, apparently emerged in pigs, and evidently spreading among production animals in Europe, has been transmitted to humans. Occurrence of MRSA in pig primary production has been assessed EU-wide in 2008, where MRSA was found app. in fourth of the breeding holdings tested (EFSA 2009). In Finland, MRSA was detected in the immediate environment of one of the tested holdings. According to that finding, it was estimated (at that time), that MRSA could occur on a few holdings with breeding pigs in the country. MRSA CC398, which was the predominant MRSA lineage identified in the EU, was also found in Finland. On account of the first detection, the occurrence of MRSA in pigs in Finland was further studied nationally.

Methods and Materials: Sampling of pigs was conducted from September 2009 to August 2010. Nasal swabs were taken from live pigs at slaughterhouses and from dead pigs sent for autopsy (at the investigating laboratory). In total, over 300 pigs representing more than 90 holdings were tested. Of these, nearly 60 represented finisher pig holdings and over 30 breeding holdings. The pigs were tested for the presence of MRSA, and all isolates were sub-typed by *spa*-typing. In a case of a positive result, the holding and the local authorities in question were notified.

Results: MRSA was detected in pigs representing one fifth of the finisher pig holdings, and from pigs originating from one breeding holding. Two MRSA lineages were identified; MRSA CC398 and CC1.

Conclusion: Although, these preliminary results are not sufficient for estimating the true prevalence of MRSA in the Finnish pig production, they show that MRSA is more common in pig holdings than previously expected. MRSA CC398 seems to be the predominant MRSA lineage in both fattening and breeding pigs. Apparently, exposure of humans to pig related MRSA is possible also in Finland.

12.039 Knowledge, attitude and practice (KAP) regarding anthrax among health care workers in some hospitals in Tehran, 2010

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Background: Anthrax is an acute lethal disease caused by the bacteria *Bacillus anthracis*. Although a very rare disease in developed countries, anthrax is still endemic in developing countries. Bioterrorism is one of the main public health categorical domains. Recently, anthrax has been evaluated as one of the most dangerous biological weapons. Outbreaks of anthrax have diverse consequences on society. Establishing the appropriate control strategies is very important and crucial in reducing the socio-economic impact of the disease. Control measures and Public Health system are aimed at breaking the cycle of infection, and their implementation must be adhered to rigorously. In this study, we evaluated Knowledge, Attitude and Practice regarding Anthrax among Health Care Workers (HCWs) in Some Hospitals in Tehran, 2010.

Methods and Materials: A cross-sectional survey was conducted in June–July 2010 among the doctors, nurses and laboratory technicians of some hospitals, Tehran province, Iran. A questionnaire was formulated which included the demographic data of the respondents and their knowledge, attitude and practice towards Anthrax based on review of the literature and checked for completeness, and validated by trained interviewers. A total of 140 responses were collected. Data analysis was done by computer software, SPSS version 11.5

Results: The most range age of the respondents (51% Male & 49% Female) was stand between 26 to 40 years (60%). When education level was controlled, More than 97% of HCWs had at least a college, and transmission methods, prevention and treatment. 86% of volunteers don't have any experience in their work background. More 50% of HCWs declare correct response in "Symptoms" field. Main information sources were from university courses respectively. Interesting result is 82.4 % of HCWs didn't know regarding the treatment protocol of Anthrax. Higher education and working background with better attitude and practice were also significant factors. 50% of HCWs know that B. Anthracis as a biological weapon.

Conclusion: This survey demonstrated that KAP about Anthrax in all fields was acceptable level. So suitable strategies are needed for raising awareness of preventable after repatriation of them in treatment and diagnosis aspects in epidemic especially through brochures and workshops.

12.040 Simultaneous and rapid detection of *Bacillus anthracis*, *Salmonella typhi* and *Yersinia pestis* by multiplex PCR

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Background: Rapid detection of biological agents are prime importance in countering the emerging infectious disease and bioterrorism events.

Methods and Materials: We have tested *Bacillus anthracis* Vaccine strain and *Yersinia pestis* from recombinant clone containing F1 gene for Vaccine purposes but for *salmonella typhi* we used DNA extracted directly from strain obtained from reference laboratory that is isolated from clinical sample.

Results: We report here for the first time the development of a rapid PCR method for simultaneous detection of the *Bacillus anthracis*, *salmonella typhi* and *Yersinia pestis* with Multiplex mixture of 6 specific primer sets designed and tested specifically for these agents.

These methods may provide a rapid tool for the simultaneous detection and identification of the three category A bacterial species listed as biological threats and can be used in reference laboratories, clinical and diagnostic labs and specially for filed analysis of samples or contaminated letters in mobile labs .

Conclusion: These methods may provide a rapid tool for the simultaneous detection and identification of the three category A bacterial species listed as biological threats and can be used in reference laboratories, clinical and diagnostic labs and specially for filed analysis of samples or contaminated letters in mobile labs.

**12.041 Rapid detection of *Bacillus anthracis* by multiplex PCR**

A. Karami
RCMB, Iran

Background: Routine microbiological methods like culture and biochemical tests are useful for identification of *Bacillus anthracis*, but a definitive identification may take 24–48 hours. Further analysis like virulence test will need more time.

Methods and Materials: To establish a rapid and specific detection and identification method for practical applications, the polymerase chain reaction (PCR) was used to identify *B. anthracis* cells by using an assay capable of amplifying specific fragments from the gene that encodes the protective antigen (PA), lethal factor (LF) and edema factor (ED) which are essential for virulence of *B. anthracis*. The sequence specific oligonucleotide primers (two PXO1, PXO2 plasmids and one chromosomally located target) amplified exact fragments only from *B. anthracis* (Stern strain) DNA but not closely related species belonging to the *Bacillus cereus* group including *B. cereus*, *Bacillus Bacillus mycoides* and other bacterial strains tested.

Results: This method was able to detect *B. anthracis* from extracted DNA, direct inoculation of *B. anthracis* cells. Sensitivity analysis by DNA concentration and CFU assay revealed that method is able to detect less than few cells in the sample.

Conclusion: With optimization of sample preparation, PCR conditions and fragment analysis (pre PCR, PCR and post PCR) we were able to develop sensitive, accurate and rapid PCR method for direct detection of *B. anthracis* in less than 2 hours with standard thermo cyclers.

12.042 Challenges to administrative and management facilitation to a research laboratory handling Ebola and Marburg viruses at a virus research institution without BSL3 and BSL 4 facilities in an African country

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Background: Uganda has had outbreaks of Ebola and Marburg viruses during the past six years. Both of these are classified as select agents that can easily be used in bioterrorism. Samples, some of which are positive with these viruses, have been collected from suspected patients and brought to the Uganda Virus Research Institute for diagnosis. This poster describes biosecurity challenges related to handling such samples in a research facility without BSL3 or BSL4 facilities.

Methods and Materials: A physical assessment of Biosecurity needs related to handling Ebola and Marburg viruses was made at the Uganda Virus Research Institute Laboratory handling Ebola and Marburg. The main objective was to ensure that no samples containing Ebola or Marburg viruses are lost or stolen from this institute.

Results: We found that there is a need to strengthen security at the main entrance of the institute by training guards, replacing the existing old gate with a modern electronic-controlled one, fixing surveillance cameras, and improve on methods of visitor vetting and identification. There is a need to isolate the existing laboratory handling Ebola and Marburg viruses from nearby laboratories. Security of the current laboratory must be improved by repairing the front door leading to the enhanced BSL 2 now handling Ebola and Marburg viruses, the corridors must be cleared of the shipments and should no longer be used for storage, the double doors leading to the enhanced BSL2 laboratory should be fixed with access control units, the windows must be strengthened with burglar proofing, and a guard should be positioned at the entrance of the facility. Also, safety of the repository with Ebola and Marburg viruses must be improved by putting the freezers in a brick-walled building with metallic lockable doors, with alarm systems for detecting unauthorised entry. We found that tracking and accountability for Ebola and Marburg samples must be improved by computerising the tracking system and fixing an alarm system to prevent unauthorised removal of samples.

Conclusion: A lot of improvement must be done to the facility handling

Ebola and Marburg viruses at the Uganda Virus Research Institute to prevent the loss or theft of samples of these select agents.

12.043 Early diagnostics for the bioterror agent *Burkholderia pseudomallei*

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Background: The ability to rapidly identify an individual who has been exposed to a Bioterror agent is particularly important so that the correct measures can be implemented. These include treating the individual promptly and correctly and implementing procedures to protect unexposed individuals. Currently, time consuming culture methods are used as a standard diagnostic tool for biological agents. Molecular methods such as real time PCR can drastically reduce analysis time and potentially detect exposure at the pre-symptomatic stage. This study explores the application of PCR assays to the detection of *B. pseudomallei* in relevant clinical samples.

Methods and Materials: A Taqman-based real time PCR assay was designed and optimised to detect *B. pseudomallei*. Mice were exposed to *B. pseudomallei* via the inhalational route and blood and tissues harvested at 24, 48 and 72hr time points. DNA was extracted using the Qiagen Blood and Tissue DNeasy kit. An extraction control was included in the process to improve reliability. Real time PCR was performed on the samples and a Ct value recorded. Culture plate counts from each sample were also prepared and these compared to PCR results.

Results: The limit of detection (LOD) of the *B. pseudomallei* assay on purified DNA is 100 fg, equating to ~8 genomes. Using blood samples the assay could reliably detect *B. pseudomallei* at 48 hours equating to ~1930 genomes per 100 μ l of sample. The assay could detect *B. pseudomallei* in lung and spleen samples 24 hours after exposure. Throat swabs were also tested and could detect *B. pseudomallei* at 48 hours.

Conclusion: The PCR assay could reliably detect the presence of *B. pseudomallei* 48 hours after exposure in blood samples and at 24 hours in tissues. Cultures taken from blood samples were able to detect the presence of *B. pseudomallei* 48 hours after exposure, however culture required at least 72 hours for the result to be confirmed, whereas PCR could potentially produce an accurate result within 5 hours. Molecular methods such as PCR can detect low bacterial numbers and be used as a rapid, early and sensitive diagnostic method for *B. pseudomallei* exposure.

12.044 Comparison of real time PCR and ELISA tests for clinical diagnostics

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Background: Real time PCR and antibody-based ELISA assays have been developed for BW agents. The limit of detection (LOD) of these assays has not been determined in relevant models of infection. Using animal models of infection, the LOD of a real time PCR assay and an ELISA assay targeting the bioterror agent *Francisella tularensis* was determined and compared against one another and the traditionally used culture method.

Methods and Materials: A real time Taqman PCR assay was developed and optimised against *F. tularensis*. An ELISA assay was optimised using combinations of antibody capture and detection pairs to determine the most suitable pairing for use. The LOD of the two assays was determined using blood spiked with a known dilution series of *F. tularensis* Schu4 culture. Clinical samples were received from mice studies. Mice were exposed to Schu4 and blood and tissues harvested at 24, 48, 72 and 96 hours. DNA was extracted using a Qiagen DNeasy blood and tissue kit and real time PCR performed using Cepheid Smartcyclers. A sandwich ELISA was carried out using the same blood and tissue samples as used for real time PCR.

Results: Real time PCR assay had a LOD of 40 fg for purified Schu4 DNA. This is equivalent to 20 genomes per PCR reaction. The PCR



assay could reliably detect the presence of *F. tularensis* 48 hours in blood and 24 hours post exposure in organs such as the lung. The ELISA assay could detect *F. tularensis* at 72 hours post-exposure in blood samples. Culture methods could detect *F. tularensis* at 48 hours post-exposure.

Conclusion: All three methods could reliably detect *F. tularensis* in blood and tissues. However, culture methods require a further 72 hours for confirmation of the presence of the target organism. PCR methods are the least time consuming and most sensitive, although sample preparation is required. However, even with sample preparation, PCR can provide an answer within 5 hours. ELISA and PCR methods have the potential to be used as alternative methods to culture for the early detection of *F. tularensis* in clinical samples.

12.045 Electrostatic detection and characterization of bio-nanoparticles and intact viruses

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Background: Electrostatic size classification of airborne particles has been exploited in aerosol research for a number of years. The extension of the working range of this method into the sub-10 nm size range where it merges with chemical analytical methods opens new fields of applications. Combined with an aerosol generation using nano-electrospray (nano-ES), this method (GEMMA - gas phase electrophoretic mobility molecular analyzer) has been proven very useful to characterize functional protein complexes and intact viruses with attached antibodies.

Methods and Materials: The GEMMA combines the benefits of the low charge levels per particle with the process of dispersion from the solution by means of nano-ES process. It utilizes a differential mobility analyzer for the separation of singly charged particles by their electrophoretic mobility at atmospheric pressure. A condensation particle counter is used for the detection of the individual separated singly charged particles (ions). A direct relationship between molecular mass and diameter was obtained allowing the use of the nES-GEMMA to determine the molecular mass of high molecular weight proteins and non-covalent protein complexes. This system was also used to study the influence of different pH values on the stability of the selected functional protein complexes.

Results: Due to the fact this electrostatic technique functions at ambient pressure it offers an opportunity for a real-time measurement, sampling and enrichment of airborne nanoparticles, biomacromolecules or viruses and complements bioanalytical tools such as e.g. mass spectrometry or size exclusion chromatography. The study of human rhinoviruses has demonstrated the capability of the technique to analyze (exact size determination) the intact infectious human-pathogenic viruses and to monitor the dissociation of these supramolecular structures by means of heat as well as to determine the exact number of capsid-protein specific antibody attachments.

Conclusion: The nano-ES- GEMMA method allows a fast real-time and highly sensitive characterization of proteins and their complexes in the range of low kDa to tens of MDa. The GEMMA spectra obtained are pleasingly clean and uncomplicated as a result of the

single charge state of investigated nanoparticles/molecules, making the data interpretation straightforward and providing also an opportunity for airborne virus detection, disease surveillance or in a biological warfare.

12.046 The rise and fall of the bioterrorism 'myth'

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Background: In September 2001, letters containing powdered anthrax sent through the US postal system led to a cluster of 22 anthrax infections and five deaths. Although the strain of anthrax used in the letters had come from a US military laboratory, the anthrax letters and the alleged threat of further bioterrorism was used to build a conceptual bridge between the 9/11 terrorist attacks and the justification for the invasion of Iraq in 2003. US funding for research into 'biopreparedness' reached an astonishing \$5.2 billion in 2004 alone, transforming neglected public health into a central component of US national security.

Methods and Materials: I examined the discourse around bioterrorism from its appearance after the first Gulf war in 1991 to the present, using papers published in established mainstream medical and scientific journals, including themed issues from *JAMA* and *Emerging Infectious Diseases* and a dedicated journal—*Bioterrorism and Biopreparedness*. (See Washer, P (2010) *Emerging Infectious Diseases and Society*. New York, Macmillan)

Results: The ever increasing pitch of the alleged bioterrorism threat came to dominate US public health discourse after 9/11. Funding for biopreparedness was said to be 'dual use', in that it would also improve preparedness for naturally occurring infectious disease threats. By 2005, it was clear that the promised 'spin offs' from bioterrorism research were not forthcoming. A mutinous open letter was published in *Science* to the Director of the US National Institutes of Health from over 700 NIH funded signatories. It argued that instead of attracting funding and talent to neglected public health, bioterrorism was diverting attention away from diseases with any significance, particularly those infectious diseases that affected the poorest people in the world.

Conclusion: Since 2005, within public health and infectious diseases, there has been increased attention to 'neglected diseases of poverty'. At the same time, interest in, and publications about, bioterrorism and biopreparedness has declined dramatically. I argue that we are witnessing the end of the bioterrorism 'myth'.

12.047 Biological threat prevention—approaches for increased international co-operation

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Background: Current scientific research provides important benefits. The spread of scientific results is rapidly providing easier access to knowledge to state and non-state actors worldwide. Advances are continually being made within the life sciences as more tools and technologies are developed to help work designed to increase the understanding of infectious diseases; how they spread, how they infect, and how they operate in humans, animals and plants, as well as how they mutate and become drug resistant. The biotechnology toolkit has inherent dual use potential.

All these developments pose new challenges to international and national authorities in their efforts to regulate the acquisition of knowledge, especially with regard to these highly sensitive materials and technologies. Research and clinical laboratories are rapidly spreading throughout the world with inherent hazards.

Measures are being put in place to restrict access to pathogens of concern by tightening physical access, providing safer storage of collections, increasing surveillance of facilities, and specific requirements for transport. Nevertheless opportunities for incidents remain despite these and other efforts.

Methods and Materials: The International Science and Technology Centre (ISTC), based in Moscow, is an intergovernmental and non-profit organization that finds practical ways to redirect the creativity and intellectual capabilities of former weapons scientists in Russia and the Commonwealth of Independent States (CIS). As part of our work we have initiated a Targeted Initiative in Science and Technology in the Prevention of Biological Threats. This initiative aims to promote more effective coordination inside and outside the CIS including the promotion of international scientific cooperation.

Activities carried out under this initiative have involved workshops and development of international projects in food security, disease surveillance, monitoring technologies and pathogen control technologies.

Results: Results indicate that activities to improve disease surveillance capability within Russia and the CIS are necessary and well received. It has been shown that increased interaction and forthright discussion on an international basis between relevant scientists and representatives of political bodies is important in order to create practical solutions to help prevent biological threats.

Conclusion: Increased international co-operation is an effective strategy for improvement of biosafety and biosecurity both for individual countries and globally.



**12.048 United States Department of Agriculture (USDA):
Application for permit to import or transport
controlled material or organisms or vectors**

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Background: The mission of the Animal and Plant Health Inspection Service is to protect and improve the health, quality, and marketability of US animals, animal products and veterinary biologics by preventing, controlling, and/or eliminating animal diseases, and monitoring and promoting animal health and productivity. The National Center for Import and Export mission includes facilitating trade, monitoring the health of animals presented at the border and regulating the import and export of animals, animal products and biologics.

Methods and Materials: Infectious micro-organisms are hazardous materials that are under control in all countries and are declared "dangerous goods". The materials are shipped across the world using various means. They are sent for identification, reference, research, or production purposes from researcher to researcher. Materials in-transit will put carriers and recipients at risk and government regulations have evolved to counteract carelessness and negligence by the shippers. Risk of exposure to dangerous materials should be minimal or nil. Various classifications systems of materials exist in the world to help in the protection of the carriers and recipients.

Results: In the US, the Health and Human Services and the Department of Agriculture created a Select Agent and Toxins List found in livestock, plants, and human. The Select Agent and Toxins transport is regulated by the National Select Agent Registry Program administered by the Agriculture and Human Services. The Program requires registration of facilities that possess, use or transfer material that pose risk for human, animal, and plant health. In addition, the US Department of Agriculture requires permits to import and transport in the territory of material that may represent a health risk to livestock and poultry. The permittee shall agree in writing to observe restrictions listed in the permit for public and livestock and poultry health protection.

Conclusion: The registration of facilities possessing, using and transferring infectious agents is part of the U.S. government's efforts to improve the ability of the United States to prevent, prepare for, and respond to bioterrorism and other public health emergencies and is required under the Public Health Security and Bioterrorism Preparedness and Response Act of 2002.

**12.049 Teschen disease emergence and environment
pollutions**

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Background: During Teschen disease (TD) emergency (1992–1998) its prophylaxis in Russia hasn't success until to introduction of Navlya-96 vaccine. In 1998–2000 we demonstrated clue significance of new agent's variant for TD prophylaxis on its Post-Chernobyl's nosoareal. New strain has some specials in its genome and ecology behavior. Transformation of Ukrainian piggeries on small size mode is coexisting with raise of TD morbidity in 14 regions: 46 outbreaks in only Central Regions covered at least 3575 pigs during 5 last years. The objective of this work is highlighted TD epidemiology in Ukraine on base of own experimental dates.

Methods and Materials: Swine and rats inoculation with TD virus was performed using virus contaminated water polluted with guinea pigs feces infected with Butcha strain of agent (low-passages virus which isolated from Poltava Region in 2003). The same method was used for pigs inoculation with cultural seed of Butchatch strain (high-passages clone of Navlya-96 strain). The final concentrations of TD viruses in drink water were about 1000TCID₅₀/l and 100000TCID₅₀/l respectively. Agent's infectious activity was determined on PK15 cells. Rat's γ -irradiation was performed with 5 R doses.

Results: All domestic pigs (n=21, age - 4–24 months) infected with faecal polluted water were ill and 18 from them were dead with classical clinical signs TD during 9–27 days post infection (p.i.). Domestic pigs infected

with high-passages cultural TD virus weren't diseased (OR=96,00; P<0,00). Less one-year-old wild boars demonstrated the weak TD signs and recovering during 45–55 days p.i. 3 years old pigs dead with strong TD signs on 13 day p.i. Adult wild boars (5–7 years old, n=3) had no TD signs during 3 month p.i. γ -Irradiated rats (n=5) demonstrated intensive reproduction of TD agent in gastro-intestinal tract and virus shedding with feces without clinics. Intact rats (n=15) didn't demonstrate any features of TD virus shedding (OR=75,00; P<0,00).

Conclusion: The combined virus-irradiation environment's pollutions have dramatically and diversely influence on TD epidemiology. Irradiated rodents became virus' reproduction source and some species were viral enhancers in TD epidemiological chain. High passages TD virus variant hadn't neurovirulence for pigs that explains TD outbreaks mainly distribution among small piggery holdings

**12.050 Impact of agricultural development on
the emergence of visceral leishmaniasis in
Central Tunisia**

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Background: Until the 80's, the mean annual incidence (MAI) of visceral leishmaniasis (VL) in Tunisia haven't exceed 15 cases. Since, a drastic increase was observed with about 100 cases yearly. Such expansion is associated with a large-scale spread from the northern regions to the central ones. The aim of this work is to study the involvement of agriculture and irrigation in this new epidemiological situation.

Methods and Materials: VL cases registered until 1995, were computed from bibliography owing to the epidemiological monitoring of VL cases prevailed in Tunisia. Those reported from 1996 to 2006 were directly recorded from the medical departments of the endemic areas. Data related to the Tunisian population allowed the calculation of the MAI rate (MAIR) in each governorate and each age group. Information concerning hydraulic resources were obtained from the ministry of agriculture. Statistical analysis was performed using Epi Info 6.04d.

Results: Children less than 5 years old revealed the most affected by VL (82.6%, p<0.001). The MAI showed a gradual increase from approximately 3.1 cases (1904–1956) to reach 99.6 cases (1996–2006). The current MAIR (9.6/100000 children under 5 years) is one of the highest in Mediterranean area. Central Tunisia, rarely involved before the 80's, is at present registering more than 40% of all cases.

The usable water volumes showed a progressive increase from the 70's to reach nowadays almost 4000 Mm³. Likewise, the irrigated areas have gradually increased: 120000ha in the 70's, 334000ha in 1996 to reach currently 400000ha. About a third of these areas are located in the Center of Tunisia where VL has recently emerged. A significant positive correlation is found between the cumulated number of waterworks (dams, hill lakes, wells) built between 1996 and 2002 in each governorate and the corresponding MAIR (r=0.47, p<0.001).

Conclusion: The emergence of VL in Tunisia is probably associated to the promotion of water restraints in the arid areas of the center. In spite of their benefits on agriculture, water plans induce environmental changes that are generally auspicious to sandflies and dogs, respectively vectors and reservoirs of *Leishmania infantum* the causative agent of VL.

12.051 Trendy of leptospirosis in Albania

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Background: Leptospirosis is now identified as one of the emerging infectious diseases. It is a zoonotic spirochetal disease of global importance. This disease continues to have a major impact on people living in rural areas of developing countries with inestimable morbidity and mortality.

Methods and Materials: Clinical history, signs and symptoms are analyzed in TUHC, Albania. All cases were considered confirmed if the serological examination with ELISA (enzyme-linked immunoassay) were positive for IgM antibodies in Institute of Public Health, Tirana, Albania.



Results: We investigated 52 patients from January 2002–November 2010. Most of them were males, 86.5% and 13.5% were females. Mean age at the time of diagnoses was 44.15 years old with 14.76±DS range 16–68. Distribution according to the season was: spring (11.5%); summer (34.6%); autumn (26.9%); winter (26.9%). 53.8% of cases occurred between September to February. 53.8 % of the cases were diagnosed from January 2009 to November 2010, but since 2002 to 2008 two to three cases were diagnosed every year. 84.6% of patients lived or worked in village as farmer, mechanic or driver. 46.1% of cases were from Tirana and 83.3% of them lived in rural area. Mortality was 3.84%.

Conclusion: Males are more at risk from Leptospirosis in Albania due to their work activity. The disease is more frequent during summer. The increase of cases during the last years (2009–2010) should be further investigated related to climate change or other factors. We didn't investigate if there was any correlation between the rainfall as an epidemiological risk factor and the increases of the cases during last years but during two last year has been an increase of the rainfall in Albania.

12.052 Soil-helminthiasis and schistosomiasis prevalence before and after rainy season

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Background: A cross-sectional study was carried to determine the prevalence of soil-helminths and of the fresh-water parasite, *S. haematobium* in the sahelian village of Pongonon, Mali. Our study was conducted at two time points: at the debut and end of the rainy season.

Methods and Materials: Our study was carried in Pongonon, a rural Dogon village in Mali where climate consists of two main seasons. The dry season lasts from November to May and the rainy season from June to October with annual rainfall between 300 to 600 mm. Investigations were performed in July and November 2007. Urine and stool samples were collected from 305 patients in July and 278 patients in November. The Kato-Katz method and the Watman filter-paper filtration method were used to search for soil-helminths and *S. haematobium* eggs, respectively.

Results: The population consisted mostly of children aged 6 to 15 years (44.6%). Soil-helminth prevalence in July and November was 2.9% and 7.6%, respectively. Only two species of soil-helminths were found in July: *Hymenolepis nana* and *Ancylostoma duodenale* with 7.2% and 0.4% prevalence, respectively. In November, three species were found: *Hymenolepis nana* (7.2%) *Ancylostoma duodenale* (0.4%) and *Ascaris lombricoïdes* (0.7%). *S. haematobium* prevalence was 7.6 % in November. No infections were found in July. Co-infection was seen only in November with the following prevalence: *S. haematobium* + *H.nana* (6.3%) and *S. haematobium* + *A. duodenale* (5.0%). Younger children (3 to 15 years) were more often infected with soil-helminths and urinary schistosomiasis parasites than those 15 to 80 years.

Conclusion: Soil-helminth and *S. haematobium* are still detectable in villages where children have been treated with IPT (intermittent-preventive therapy) since 2005, when IPT for these infections was first introduced in Mali. Timing IPT programs during periods of measured high-prevalence may improve chances of eliminating these parasites over the arbitrary biannual or triannual treatment campaigns currently in place.

12.053 A search for the rodent hosts of Leishmania major in Southern Iran: Demonstration of the parasite in Tatera indica and Gerbillus sp., by microscopy, culture and PCR

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Background: Zoonotic cutaneous leishmaniasis (CL) caused by *Leishmania major* occurs widely in Iran, where several species of rodent serve as the parasite's 'reservoir' hosts. In an attempt to identify the rodent hosts in the Larestan region, which lies in the Fars province of southern Iran (where the incidence of human CL has been rising)

Methods and Materials: Thirty-two rodents (20 *Tatera indica*, eight *Meriones crassus*, four *Gerbillus* sp.) were caught and checked for leishmanial infection. Using two detection methods (the microscopical examination of stained tissue smears and the culture of tissue samples) and a PCR to identify any leishmanial parasites detected

Results: *L. major* was identified in six of the rodents caught: two male *T. indica* from Alamarvdasht, two female *T. indica* from Lamerd, and two females of the genus *Gerbillus* (one caught in Lamerd and one in Lar). Although the samples were too small to prove that *M. crassus* is not a significant host of *L. major* in Larestan, they were large enough to indicate that *T. indica* and members of the genus *Gerbillus* serve as reservoir hosts of *L. major* in the region.

Conclusion: *Tatera indica* appears to be an important host of *L. major* across much of Iran but this appears to be the first time that the genus *Gerbillus* has been found to be involved in the epidemiology of CL in the country.

12.054 Tatera indica as reservoir host of Leishmania major in Estahban, Southern Iran

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Background: Leishmaniasis is mainly the disease of the underdeveloped countries and more than 25 countries and territories in the American continents and 75 countries and territories in Africa, Mediterranean region, the Middle East, the Southern part of Russia and Asia are endemic foci of infection. To identify the infected rodent hosts to *Leishmania major* in Estahban town, Fars Province in southern Iran during 2004-2005, 13 rodents were trapped alive close to houses

Methods and Materials: Parasite presence was demonstrated by microscopy, culture, PCR and enzyme electrophoresis. Among captured rodents, 8 were *Tatera indica* (5 male and 3 female Indian gerbils) and 5 were *Rattus rattus* (3 males and 2 females)

Results: One female *T. indica* was just smear positive for amastigotes in Mohammad Abad village of Estahban town. This rodent was also found culture positive for leishmanial infections which were confirmed by PCR and enzyme electrophoresis. At histological and ultrastructural levels, many clusters of amastigotes were noticed in the foamy macrophages of the femoral bone marrow

Conclusion: Our results showed that *T. indica* may be one of the rodents that can play a role as a potential reservoir host of *L. major* in the region. It was also shown that femoral bone marrow was the tissue of choice to confirm the presence of macrophages containing the amastigote form of the parasite

12.055 Rattus norvegicus as reservoir host of Leishmania major in Fars Province, Southern Iran

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Background: Zoonotic cutaneous leishmaniasis is an important health problem in Iran and a great economic burden on the health resources. In southern Iran (Fars Province), *Meriones libycus* was reported as the main reservoir of zoonotic cutaneous leishmaniasis in Arsanjan and Marvdasht cities, and *Tatera indica* and *Gerbillus* spp. were the reservoirs reported in Larestan and Kharameh districts. Because of an increase in human cutaneous leishmaniasis in Fars Province, this study was performed to identify the rodent hosts in this region

Methods and Materials: From April 2004 to April 2006, live traps were used to catch rodents in different parts of Fars Province. Fifty-seven *Rattus norvegicus* were caught and checked for *Leishmania* infection using a combination of microscopy, culture, nested polymerase chain reaction (PCR), and enzyme electrophoresis

Results: One female *R. norvegicus* was found to be smear positive for amastigotes in Giemsa-stained skin sample of sole, and it was also culture positive for *Leishmania*. Results of PCR and isoenzyme electrophoresis indicated that this infected rodent was harboring *Leishmania major*. PCR



was also positive for *L. major* in biopsy of soles, ear, liver, and spleen of 29 other *R. norvegicus* hosts that were negative in smears and cultures. There were no lesions seen in any parts of infected rodents' bodies

Conclusion: As *L. major* has not been previously reported in *R. norvegicus* in Iran or elsewhere, the rodent can be considered as a possible reservoir in transmission of the disease in Fars Province, and it should be brought into consideration when planning for preventive measures

12.056 Tatera indica as reservoir host of *L. major* in Shiraz, Southern Iran

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Background: Cutaneous leishmaniasis (CL) with diverse clinical manifestations is prevalent and remains a major public health problem in Iran and its incidence has been doubled over the last decade. The present study is about the potential role of rodents in the epidemiology of CL in Kharameh district in Shiraz, Southern Iran

Methods and Materials: From April 2004 to April 2005, a total of sixteen rodents were collected in live traps from the endemic area of CL in Kharameh district in Shiraz. Evans medium was used for culture. Specific polymerase chain reaction and isoenzyme electrophoresis methods were performed to characterize the parasite

Results: The rodent species were *Tatera indica*. Three samples from *Tatera indica* were found positive (2 males and 1 female in Kafdehak and Sejel-Abad villages) for *L. major*. Macrophages in the bone marrow of femoral bone were infected with the amastigote form of the parasite

Conclusion: It seems that *T. indica* is the reservoir host for CL in Kharameh (a district in Shiraz, Southern Iran). It was shown that the bone marrow of the rodents is the tissue of choice for light and ultrastructural studies of *L. major*

12.057 The survey of drug resistance and prevalence of Urinary Tract Infections amongst hospitalized infants and neonates in the west of Iran (Ilam) during 2008–2010

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Background: Urinary Tract infection is one of the most common infections amongst infants and neonates. Previous Studies were shown that 2.7% of boys and 0.7% of girls who suffered from Urinary Tract infections (UTI) are less than 1 year old. The aim of current study was to evaluate the frequency of bacteria causing UTI and their relevant drug resistance amongst infants and neonates hospitalized in Ilam province, west of Iran during 2008–2010.

Methods and Materials: Overall, 220 cases of UTI enrolled in this cross-sectional retrospective study. A standard checklist was used for demographic and clinical data to be collected from their health records. Data then was analysed using SPSS version 17.0.

Results: Totally 220 cases were assessed, among which more than two third (64.8%) were female. *E. coli* (44.5%), *Klebsella* (18.6%), *Enterobacter* (15 %) and *Staphylococci spp.*, (12.7%) were the most common microorganisms isolated from UTI respectively. High rates of resistance to tetracycline, ampicillin, and nalidixic acid were observed among these isolates.

Conclusion: Similar to other studies, *E.coli* was the most common bacteria caused UTI and showed a high rate of resistance to most of antimicrobial agents. Using appropriate antibiotics against UTI and establishment of annual surveillance programs on antimicrobial sensitivity of routinely used antibiotic can be helpful for physicians in choosing a proper treatment in patients suffering from UTI and also to reduce the complications related to serious UTI.

12.058 *Yersinia pseudotuberculosis*, iron and disease

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Background: *Yersinia pseudotuberculosis* is the cause of pseudotuberculosis in humans and animals. Animals, and the environment, can be a source of infection for humans but, although the organism is widely spread, the prevalence of pseudotuberculosis in the human population is low. Although many predisposing factors may affect the clinical course of disease caused by *Yersinia* spp. i.e. presence or absence of virulence characteristics in the bacteria, exposure dose, route of infection, concurrent disease in the host, debility, physiological stress, it has been recognised that the severity of infection with *Y.pseudotuberculosis* and *Y.pestis*, is often linked to the availability of iron. This is especially of interest with the observation that the severity of infection, as well as the extent of distribution of lesions seems to be more severe in animals, including birds and humans, with hemosiderosis,

Methods and Materials: A calibrated scintillation system using saponin to lyse chick spleen phagocytic cells previously incubated for two hours with 5×10^6 *Yersinia pseudotuberculosis* (virulent) or *Yersinia frederiksenii* (non virulent), with or without Iron dextran, Imferon (C), and radiolabelled Uracil - H 3 at 37° C was used to enumerate released intracellular yersiniae.

Results: When a two-way analysis of variance and the student's t test was used it was found that the scintillation counts were significantly higher ($P < 0.001$) following lysis of iron loaded phagocytic cells than following lysis of untreated phagocytic cells at all times of incubation with *Y. Pseudotuberculosis*. The relative increase in the scintillation counts obtained for *Y. frederiksenii* were less pronounced ($P < 0.05$).

Conclusion: In this study it has been found that pre-treating chicken phagocytic cells with iron dextran resulted in an increase in the number of intracellular yersiniae released following cell lysis. The results of this and other studies support the hypothesis that the availability of iron is an important factor in deciding the outcome of host-pathogen interactions but that the relationship is complex depending on the ability of host and pathogen to acquire available iron. The relative effect of iron availability as compared with other important variables, which may upset the balance between host and pathogen is often difficult to establish but should always be considered.

12.059 Pathogenic Leptospira in rodents in the Canary Islands

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Background: Leptospirosis is an important zoonotic emerging infectious disease with a worldwide distribution. It is characterized by fever, renal and hepatic insufficiency, pulmonary manifestations and reproductive failure. Humans are infected by close contact with animals and contaminated water with the urine of infected animals. Rodents, *Mus* species and rats (*Rattus norvegicus* and *Rattus rattus*), are important reservoir hosts. In the Canary Islands (Spain), leptospirosis has been detected in human. However, to the present there were no available data about *Leptospira* in reservoir hosts.

Methods and Materials: A total of 171 wild rodents (85 *R. rattus* and 86 *Mus musculus domesticus*) from five of the Canary Islands were analyzed.

Urine samples and the urinary bladder were preserved in 100% ethanol. DNA extraction was carried out using the Fast DNA (BIO 101 Systems) kit. Samples were analyzed by a PCR which targets the *Leptospira lipL32* region. Positive control, *L. interrogans* serovar Icterohaemorrhagiae, was used. Amplicons of interest were cloned in the pGEM-T Easy vector and sequenced. A BLAST search was used to analyze the homology with other published sequences.

Results: Thirty samples were positive, therefore, the general prevalence obtained in the rodents was 17.5%. Although the prevalence was higher



in rats (21.2%) than in mice (13.9%) it was not significantly different (χ^2 test). Positive samples were obtained from all the studied islands and for both host species in all of them. The prevalence of the infection was similar between islands and also between host species per island, except in one island where rats showed higher infection percentage than mice. The BLAST analyses showed high homology with *L. interrogans* and *L. borgpetersenii*.

Conclusion: The *lipL32* fragment is only amplified in pathogenic *Leptospira*. In the Canary Islands, and from the epidemiological point of view, it is relevant that in all the studied islands, pathogenic *Leptospira* species were detected, suggesting that it is widely spread all over the Archipelago. Furthermore, the high incidence of *Leptospira* among rodents, both rats and mice, suggests that rodent population could play an important role in the transmission of human leptospirosis via environmental contamination in the Canary Islands.

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12.060 Digestive Tract Disorders in Leptospirosis

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Background: To highlight the frequency and structure of gastroenteric syndrome of the leptospirosis.

Methods and Materials: Includes 181 cases of leptospirosis aged 14–76 years, followed during 1984–2009, who suffered from evident digestive tube pathology. Diagnosis of leptospirosis is confirmed by the RMAL test and after 2002 by ELISA.

Prospective collection of data, identifying the number of cases of gastrointestinal disorders: type, timing and the course of disorders

Results: Abdominal pain occurred in 42 cases, in 25 cases the pain was localized in upper part of the abdomen in 12 cases in the right hypocondrium, in 3 cases in the left hypocondrium in 2 cases the pain was in periumbilicus, right iliacus pain in one case, whole abdominal pain in one case. The pain emerged during the first week of illness with aggravating and constricting features of low to moderate intensity; 1 case presented with severe pain abdomen's rectus muscle,

- Vomiting occurred in 37 cases at first 3–4 days, with foodstuff or biliar nature 2–10 times daily. One case presented hemorrhagic vomiting.

- Not dysenteric diarrhea occurred in 13 cases, in the first week of illness, 2–5 times daily.

- Enterorhagia was present in 5 cases, lasting 2–5 days. It appeared in the first 10 days of the illness.

- 18 patients presented with severe anorexia at the beginning of the disease and continued for 8–12 days

- Constipation was present in 6 cases. Combined symptoms were present among 52 patients. In 12 cases predominated digestive symptoms, so that the cases were considered as gastroenteritis, enteritis, or acute abdomen.

Conclusion: 1) Disorders of the digestive tube were present in 28.7% of cases of leptospirosis. 2) 7 different syndromes occurred: abdominal pain 23%, vomiting 20%, diarrhea 7%, nausea 10.4%, anorexia 9%, enterorhagia 2%, constipation in 3.3% of cases. 3) The diagnosis was difficult to establish in 6.2% of cases.

12.061 Serological confirmation is decisive for the diagnoses of Dobrava virus infection. Case report

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Background: Hemorrhagic fever with renal syndrome (HFRS) is a disease caused by viruses of the family *Bunyaviridae*, genus *Hantavirus*. It's a very rare disease in Albania. During last ten years we have had only six cases. Clinical aspects aren't pathognomonic. Serological confirmation is decisive for the diagnosis.

Methods and Materials: A 25 years old male admitted at our service of infectious disease having: fever, nauze, vomiting, abdominal and lumbar

pain, myalgia, oligoanuria and testicular pain. The physical examination noted intoxicated facies, conjunctival injection, tendency to hypotension (90-60mm Hg), hiccup, sensitive abdomen in all quadrants; right test was edematous and painful. The skin was without bleeding phenomena. Radiologic examination showed free abdominal liquid and orchitis. We didn't find any pulmonary involvement. Laboratory examinations: white blood cell count 9200/ μ L (range 4x10³-10x10³), with segment 79.1%, red blood cell 5.94x10⁶/mm³ (range 4.5x10⁶- 5.2x10⁶), platelet count 58x10⁹/ μ L (range 150-450x10³), hemoglobinemia 16.4 mg/dL (range 14- 16.5), glicemia 127 mg/dL, kreatinemia 2.57 mg/dL (range 0.66-1.44), azotemia 85 mg/dL (range 10.0-43.0), AST 163 UI/l (range 0-45), ALT 111 UI/l (range 0-45), and other examination was normal. The blood was tested at the *IPH* according to the rules for transportation of contagious substances for Hanta virus profile 1 (EUROLINE). We did a lot of examination for infective and non infective diseases: leptospirosis, typhus, brucellosis, renal and hematological diseases, acute abdomen etc.

Results: Serologic examination reported that the patient was positive IgM and IgG for Dobrava virus infection.

Conclusion: Serology is still the first choice for the diagnosis of Hemorrhagic fever with renal syndrome by Dobrava virus infection. HFRS should be considered in differential diagnosis along with a series of other acute infectious diseases, especially scrub typhus, murine typhus, spotted fevers, leptospirosis and non infectious disease: hematological and renal diseases, and acute abdomen. Transmitter of the diseases in Albania is *Apodemus flavicollis*.

12.062 Current status of Q fever in Ukraine and needs for expand surveillance of *Coxiella burnetii*

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Background: Since the 1950s, the incidence and distribution of Q fever has been monitored in Ukraine. Local outbreaks of the disease have been identified. Only sporadic cases have been identified among the human population. The majority of these were in areas of southern Ukraine where intensive sheep breeding is located, with aerosolization serving as the primary means of transmission. The study was aimed to assess the present seroepidemiological situation of Q fever in western Ukraine.

Methods and Materials: This study (project P364/UP-1) was conducted as a component of a larger serosurvey of zoonotic diseases in Ukraine. Serologic assays (ELISA, IFA, CFT) were used to assess antibody levels against *Coxiella burnetii* in serum samples from healthy volunteers (n=1000) collected in a survey at a single region in western Ukraine. Samples were screened with a commercial ELISA and by IFA to confirm the reaction.

Results: Of the 1000 serum samples, 36 samples reacted positively in the screening ELISA. Of those screen positive samples, only one individual gave positive IFA tests. While this study indicated a seroprevalence in this area, we are going to study the contribution of *C. burnetii* to acute febrile illness in future. It is possible that some individuals, such as Ukrainian residents who work in agriculture in Europe, may become infected while working and/or living in Q fever enzootic areas outside of Ukraine. However, it is known that *C. burnetii* still circulates in natural foci within Ukraine despite a decrease in morbidity among the population. The pathogen was transmitted by vectors from enzootic areas in some parts of Ukraine to other regions thereby creating new foci. Thus, further understanding of natural maintenance of *C. burnetii* in ticks, reservoir hosts, and the contribution to human disease in Ukraine is critical to the future study and implementing appropriate epizooto-epidemiological prevention and control measures.

Conclusion: The importance of Q fever has been increasingly recognized in Ukraine. The current status of Q fever requires further epidemiological investigation. This preliminary study provides the basis for future efforts aimed at improving the ability to detect Q fever among acute patients and to enhance our understanding of the natural foci of infection.

**12.063 Equine Herpesvirus-5 associated with Equine Multinodular Pulmonary Fibrosis in 4 Horses**

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Background: Equine Herpesvirus type 5 (EHV-5) belongs to the subfamily of Gammaherpesvirinae and was recently associated with a disease termed Equine multinodular pulmonary fibrosis (EMPF). EMPF was first reported in 2005, has been observed in the USA and Europe up to now and presents the first association between a viral infection and lung fibrosis in veterinary species.

Methods and Materials: Cases: A 14-month-old Arab filly (1) with depression and anaemia, which died. A 2-year-old Warmblood filly (2) with neurological signs and a 22-year-old Warmblood mare (3) with T-cell leukaemia, which were both euthanized. A 22-year-old Warmblood gelding (4) with recurrent pyrexia, dyspnoea, hyperfibrinogenaemia, intranuclear inclusion bodies in macrophages of bronchoalveolar lavage (BAL) and disseminated interstitial pulmonary fibrosis, diagnosed by thorax radiographs and lung biopsy. The horse recovered after treatment with valacyclovir (40 mg/kg TID per os) and is still alive and asymptomatic.

Results: Pathohistology of the lungs (1-3) showed numerous, variably sized, homogeneous, grey-white-coloured, dense, sharply demarcated nodules up to 6.5 cm with an extensive thickening and fibrosis of the interstitial tissue and inflammatory infiltrations, predominantly lymphocytes, most prominent in perivascular and interlobular spaces. Within airways there was abundant detritus with numerous macrophages, neutrophil granulocytes and some multinucleated giant cells as well as proliferation of type II pneumocytes. A few macrophages contained eosinophilic intranuclear inclusion bodies.

EHV-5 DNA was identified by PCR in all cases either of lung specimen (1-3) or BAL (4). Attempts at localizing EHV-5-specific nucleic acid sequences by *in situ* hybridization at the sites of the lesions have been unsuccessful so far.

Further findings except EMPF in our cases include severe anaemia, haemorrhagic diathesis, subcutaneous oedema (1); chronic lymphatic leukaemia (2); non-suppurative panencephalomyelitis of unknown aetiology (3).

Conclusion: The prevalence of EHV-5 in horses is quite high, but just a few seem to develop EMPF. The specific role of EHV-5 in the pathogenesis of EMPF is unclear, but an aberrant host immune process and inflammatory response could be relevant. Also in humans herpesvirus (e.g. Epstein Barr Virus) might play a role in initiating or perpetuating fibrotic lung diseases. However, it is still unclear if a definitive causal relationship exists.

12.064 Diagnosis of a human parapoxvirus infection in Austria, in 2010

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Background: Human infection with parapoxvirus generally arises from direct contact with infected ruminants. We report on the diagnostic procedures employed in a case of parapoxvirus infection occurring in Austria. In spring 2010, a woman from a cattle farm was hospitalised because of a large local finger lesion, which progressed through a typical pattern of erythema, macula, papula, pustule and scab. The patient later came down with a generalized rash of pustules. The necrotic biopsy material of finger lesion and the pustules were sent to our institute for laboratory diagnosis.

Methods and Materials: For rapid analysis and confirmation, electron microscopy (EM) and molecular biological methods were used. Crust

material and swab of the finger lesion, and pustule samples were analysed by negative staining followed by ultrathin sectioning. Molecular diagnosis of parapoxvirus was performed by PCR following the methods of Inoshima et al., 2000 (J. Virol. Meth. 84:201) and Kottardi et al., 2006 (J. Virol. Meth. 134:119). Orthopoxvirus was excluded by a specific real-time PCR, and by a PCR specific for the HA gene of *Cowpox virus*. Direct DNA sequencing was followed by phylogenetic analysis and comparison to other parapoxvirus strains (Kottardi et al. 2006, Vet. Microbiol. 116:310) published at the NCBI GenBank.

Results: EM diagnosis enabled a rapid and an accurate diagnosis of parapoxvirus infection. The ovoid virions differed from the orthopoxvirus group by a distinct surface filament design exhibiting a crisscross transverse spiral coat pattern. Sections of epidermal lesions showed swellings of keratinocytes which resulted in ballooning degeneration, central cytoplasmic lysis, vacuolation and nuclear pyknosis. Intense keratinocyte proliferation led to marked acanthosis. Poxvirus structure and morphogenesis was identical with other poxviruses. Parapoxvirus DNA was successfully identified by the two PCRs. Sequence analysis confirmed PCPV; molecular biological methods specific for orthopoxvirus and respectively *Cowpox virus* were negative. A phylogenetic tree of parapoxviruses is presented. Pustule samples were negative for poxviruses in both, EM and PCR.

Conclusion: Human parapoxvirus infection, a rare, self-limiting, zoonotic disease, often lacks for a reporting system. However, diagnosis of parapoxvirus infection is important as this infection may be combined with outcome of other microbial diseases (Larcher et al. 2009, Eur. J. Dermatol. 19(4):375).

12.065 Emergence and re-emergence of smallpox

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Background: Smallpox is a dangerous infectious disease, known to the mankind since ancient times, which has taken more lives than any other infections or numerous wars. Previous RFLP analysis divided smallpox (variola) virus (VARV) strains into two subtypes, one of which included West African and South American isolates. This allowed us a dating to be introduced for the first time in estimation of the VARV evolution rate.

Methods and Materials: The archive data on smallpox, history of ancient civilizations, and the most recent data on the genome organization of orthopoxviruses, their evolutionary relationships, and the time moment of smallpox emergence were summarized.

Results: The performed analysis provides the grounds for the hypothesis that smallpox could have emerged several times as a result of evolutionary changes in the zoonotic ancestor virus and disappeared due to insufficient population size of ancient civilizations. Smallpox reemerged in the Indian subcontinent approximately 2500-3000 years before present, which resulted in endemization of this anthroponotic infection, which had been preserved until the smallpox eradication in the 20th century AD.

Conclusion: Potential possibility of future VARV reemergence, presenting a great menace for the mankind, as well as the need in the development of new safe smallpox vaccines, design of anti-smallpox drugs, and activation of the control of zoonotic human orthopoxvirus infections are suggested.

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12.066 Campylobacter and Salmonella occurrence in young greater flamingos (Phoenicopterus ruber roseus) in northeastern Spain

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Background: *Salmonella* spp. and *Campylobacter* spp. are the leading agents of zoonotic enteric infections in developed and developing countries. Wild birds have been considered natural vertebrate reservoirs of zoonotic agents, and due to their great mobility, may function as



effective spreaders of disease through fecal contamination of the environment. However, limited information exists on the occurrence of zoonotic bacteria of public health importance in wild flamingos. A colony of over 2000 breeding pairs of Greater flamingos are present all the year in Ebro Delta (northeastern Spain). Since they may represent a reservoir of these bacteria, a study was conducted to determine the prevalence of *Campylobacter* and *Salmonella* in these wild birds.

Methods and Materials: On August 2010, during the ringing operation of greater flamingos at Ebro Delta, duplicate cloacal swabs were obtained from 44 chicks and placed in Amies charcoal medium, transported to the laboratory and cultured using standard methods to isolate *Salmonella* and *Campylobacter*. *Campylobacter* isolates were identified to the species level by PCR and analyzed by enterobacterial repetitive intergenic consensus (ERIC)-PCR to determine the diversity of strains.

Results: No *Salmonella* was isolated from chick flamingos, but a prevalence of 9.1% of *Campylobacter coli* was found with a low diversity of strains. These bacteria could have originated either from contact with the parents or other species frequenting the same habitat or from the water. The early feeding of chicks by the adults may insure a transfer of the organisms. Also, soon after hatching, the chicks leave the nests and form nurseries under the supervision of a few adults. These nurseries consist of all the chicks in the colony and in Ebro Delta can reach numbers of up to several hundred birds, thus providing a good environment for the transmission of zoonotic bacteria.

Conclusion: Results indicate that Greater flamingos at Ebro Delta represent a reservoir of *Campylobacter* species and may be of public health importance in the geographic area studied.

12.067 Prevalence of Canine Visceral Leishmaniasis in Dogs (*Canis lupus familiaris*) in Palestine

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Background: Dogs (*Canis lupus familiaris*) are considered the main domestic reservoir for *Leishmania infantum* parasites causing human visceral leishmaniasis (VL). In Palestine, the disease mainly is affected children with average annual incidence 3.02/100000. This study aimed to investigate the prevalence of canine VL in Palestine.

Methods and Materials: The prevalence was established using ELISA, *in-vitro* cultivation and ITS1 PCR. In total, 215 dogs were tested. The examined dogs were from different Palestinian districts including Al-Khalil and Bethlehem in the south, Ariha (Jericho) in the center and Jenin, Salfeet, Qalqilia and Tubas in the north.

Results: Of the 215 tested dog sera, 16 (7.4%) were seropositive. The seropositive cases were distributed as follows: 31% from Jenin, 25% from Al-Khalil, 19% from Salfeet, 13% from Jericho and 6% each from Tubas and Bethlehem. Among the seropositive dogs 12 (75%) were males, 7 (44%) were of local breed. The average age of the seropositive dogs was 3.4 yr ranging from 1 to 5 yrs. Three different dog samples produced promastigotes in culture, of which one was seronegative. ITS1-PCR followed with restriction analysis using *Hae III* enzyme revealed that the causative agent as *L. donovani* complex. ITS1-PCR showed 5/54 (11%) positive for *Leishmania* DNA. The overall prevalence using the *in-vitro* cultivation, ELISA and ITS1-PCR was 9.3%.

Conclusion: Canine VL is present in all Palestinian districts included in this study which poses a threat to the Palestinian public. *L. donovani* complex is the causative agent. Results agree with previous studies done in specific regions in Palestine. Jenin and Al-khalil districts were the most prevalent for CVL infections which is in agreement with the high prevalence of human VL cases.

12.068 Hepatitis E in Belgium: an imported disease or a viral zoonosis?

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Background: In industrialized countries, hepatitis E (HEV) is considered as an imported disease related to travel to endemic regions. However, increasing evidence indicates that HEV also occurs in patients in developing countries who have no history of travel, and that swine may act as a possible reservoir. The virus is mainly transmitted by faecal-oral route through contamination of drinking water. Nevertheless, HEV transmission by blood transfusion has also been described.

More evidence suggests that HEV could be a viral zoonosis with swine as an animal reservoir. In Japan, HEV transmission was associated with consumption of raw or undercooked wild boar or deer meat.

Hepatitis E infection causes an acute self-limited or fulminant hepatitis that does not evolve into chronicity, except in organ transplant recipients. The mortality rate is low, ranging from 1 to 3 percent, but in pregnant women the mortality 25 percent. The seroprevalence in blood donors from non-endemic countries ranges from 1 to 3 percent. A higher prevalence was seen in persons working with swine.

Methods and Materials: The major objectives of our study are the 1) molecular characterisation of HEV strains circulating in Belgium in humans and animals to establish a zoonotic risk profile in Belgium and 2) estimation of the transmission risks from swine to humans.

Therefore, HEV laboratory diagnosis at the National Centre of Viral Hepatitis of the Belgian Institute of Public Health has been elaborated. HEV IgM antibodies are detected by an ELISA and confirmed by Western blot. HEV RNA is detected by a nested RT-PCR. Genotyping assay is currently in optimization in order to determine the HEV risk profile in Belgium.

Results: Since 2008, 2009 and 2010, respectively 8/210 (4%), 9/264 (3%) and 18/206 (8.7%) of submitted human serum samples were HEV positive. Epidemiological studies have shown that some of these HEV infections were imported. However preliminary genotyping results on HEV PCR positive samples indicate the presence of genotype 3 in Belgium.

Conclusion: These sequences show a homology with the strains of swine isolates in the Netherlands.

Finally, we will be able to provide data to health authorities on the potential zoonotic transmission of HEV in humans.

12.069 Emerging infectious diseases: a long term multidisciplinary study in the Camargue

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Background: Emerging infectious diseases are actually of major concern worldwide. Most of them are zoonotic and their epidemiology must consequently be studied conjointly in humans and animals. We present here a long-term research program lead in the Camargue. This area situated in the Rhone delta, crossroads of many birds' migration routes is a biodiversity hotspot. It appears vulnerable to disease emergence due to its key location and to the common use of wetlands by wild and domestic animals as well as humans.

Methods and Materials: Since 2004, a health ecology program is lead in the Camargue mainly focusing on Influenza A viruses.

Results: First, pathogen dynamics are studied in their wild reservoir. For example, a seasonal pattern of avian influenza A virus circulation in waterfowl was highlighted, an infection peak being generally observed in early fall, probably due to the massive arrival of young and possibly immunologically naive birds. Seasonality of avian Influenza viruses is currently studied in gulls. Second, pathogen transmission between wild and domestic birds is investigated. Interestingly, no highly pathogenic avian influenza virus was detected in wild birds of the region from 2006 to 2009 suggesting that migrating birds do not play an important role in the transmission of these viruses. On the other hand the potential impact of domestic ducks release for shooting on avian influenza A viruses



dynamics in wild waterfowl is currently studied. Finally, researches are lead on pathogen exchange between wildlife and humans. Antibio-resistant bacteria, similar to those circulating in humans in France have been detected in gulls showing that they could be contaminated by human pathogens.

Conclusion: This multidisciplinary program already proved that animal health, human health and ecology issues can be fruitfully linked to gain insight in the epidemiology of emerging pathogens. Besides it highlights that long-term studies are needed to be able to face emerging health issues, rather than short term studies limited to crisis periods which are necessarily insufficient.

12.070 Detection of Chikungunya Virus from domestic animal samples collected from epidemic and non-epidemic areas in Thailand

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Background: Chikungunya is an arboviral disease transmitted by *Aedes* mosquitoes and the disease is widely spread in many countries. So far, monkeys, rodents, birds and unidentified vertebrates had been reported as the main reservoirs for Chikungunya virus (CHIKV). Many studies found an evidence of CHIKV-neutralizing antibodies in wild monkeys, pigs and chickens, but none from Thailand has been reported. Domestic animals are identified as the reservoir of many zoonotic diseases since they share both habitats and vectors with humans. This study aimed to detect the presence of CHIKV in domestic animals in both Chikungunya epidemic and non epidemic areas in Thailand.

Methods and Materials: Serum samples were collected from domestic animals, especially dogs, cats, chickens in Rayong and Nakhon Sawan which were considered as Chikungunya epidemic and non-epidemic areas respectively. The total of 306 bp of glycoprotein E1 gene of CHIKV was used in RT-PCR detection of field collected samples.

Results: In Chikungunya epidemic area, 22 of 149 (14.77%) of serum samples from domestic dogs were positive for CHIKV. None of the serum samples from three cats and one chicken were positive. In non-epidemic area, 16 of 633 (2.53%) of the serum samples from domestic dogs were positive for CHIKV.

Conclusion: This is the first report of CHIKV infection in domestic dogs in Thailand. Sylvatic transmission involving domestic animals may play an importance role in the emergence and re-emergence of Chikungunya infection. However, the role of domestic animals as the reservoir of CHIKV need to be further investigated.

12.071 Domestic and wild mammals as possible reservoirs hosts of *Leishmania* spp. in Darién region of Colombia

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Background: To improve our understanding about the epidemiology of American Cutaneous Leishmaniasis, and to use that knowledge in prevention and control strategies, there is necessary to unveil both the domestic and wild reservoirs. The aim of this study was to determine which species of domestic and wild mammals are hosts of the parasite and which is the most probably reservoir in the Darien region of Colombia.

Methods and Materials: The area of study was the Darien region, Colombia, South America, that is located in the Chocó biogeographical region that borders with Panama. Cage traps baited with fruits were used to capture wild mammals. Those houses with active or history cases of leishmaniasis were surrounded with cage traps in a systematic fashion. Samples of several tissues was taken under anesthetics and several animals were sacrificed for the taxonomic voucher.

With the owner's consent, dogs were sampled under anesthetics. The DNA extraction was done with a commercial kit and for *Leishmania* spp. diagnostic we used the amplification of kDNA minicircles with primers

JW11 (5'-CCC ATT TTA CAC CAA CCC CCA GT-3') and JW12 (5'-GGG TAG GGG CGT TCT GCG AAA-3'). The fragments were visualized in 2% agarose gels. Additionally, IFAT and Xenodiagnostic in dogs and xenodiagnostic in wild mammals were used as diagnostic tools. Capture of sandflies and patient attention was also performed in the study area.

Results: A total of 112 wild mammals from nine species were captured. Of those, on *Choloepus hoffmani*, one *Didelphis marsupialis* and one *Proechymis semispinosus* were positive by PCR and 2 *Didelphis marsupialis* were positive by xenodiagnostic and PCR. From the 83 dogs sampled two dogs were positive by PCR and showed a prevalence of 23% by IFAT.

Conclusion: *Choloepus hoffmani* is a good *Leishmania* spp. host, and perhaps the main reservoir in Darien Region of Colombia. Despite low detection by PCR in *Didelphis marsupialis*, the relative abundance and a couple of animals positive by xenodiagnosis makes this species a potential secondary reservoir. The role of *Proechymis semispinosus* is unknown. We propose the infection cycle for leishmaniasis in the region.

12.072 Potential economic impact of poultry restructuring in Vietnam using an ecohealth approach

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Background: More than 80% of small scale rural households in Vietnam own some form of livestock, and most of those households own poultry. The poultry sector in Vietnam provides low cost nutrition, steady income, and a means for reducing agricultural risk. The rapid rise in the poultry sector was severely damaged economically in the last five years due to the emergence of highly pathogenic avian influenza (HPAI). Lowest income producers with the lowest proportion of disposable income were most vulnerable to economic damage.

The structure of traditional backyard livestock production also results in high exposure to risks of newly emerging infectious diseases nEIDs including HPAI. Awareness of HPAI is high, but knowledge of options for change to production less risky to human, animal, and environmental health (ecohealth options) is low. This paper examines the impact of restructuring the poultry sector in Vietnam using an ecohealth approach.

Methods and Materials: The backyard poultry sector of Vietnam was modeled using a combination of data gathered by the author and in the literature. Restructuring of the sector was modeled to incorporate an ecohealth approach under three scenarios, in which production inputs were shifted primarily to: 1) other livestock; 2) other livestock and vegetable production; 3) poultry, other livestock, and vegetable production. Rice production and off farm income was assumed unchanged. Using simulation, economic impact was measured for changes occurring under the three scenarios.

Results: Net household income over a 1 year horizon was increased under all three scenarios (1=38%; 2=147%; 3=110%). Shifts in production were assumed driven by supporting policy change encouraging adoption of ecosystem approaches to health management. Major constraints to structural change were identified as: access to finance; lack of management skills; reluctance to change; and, high dependence on poultry income.

Conclusion: An ecosystem approach to integrated agriculture appears to result in increased income for small scale poultry producers in Vietnam. Such changes in production embrace an ecohealth approach to small scale farming consistent with reduced risks of nEIDs. Supportive policy is needed to drive such structural change including access to microcredit and skills training.

12.074 Current epidemiologic situation with dangerous bacterial and viral diseases in Azerbaijan

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Background: Republican Anti Plague Station currently working with such extremely dangerous infections as plague, cholera, anthrax, brucellosis, tularemia, rabies, bird flu, swine flu, tick-borne encephalitis, viral



hemorrhagic fevers and other, and the epidemiologic situation is:

There have been identified three natural focuses of *Plague* in Azerbaijan, and the degree of epidemiologic danger has increased in recent years due to the invasion of vast enzootic plague areas of the republic which are used for farming, building, construction of transport, oil and gas pipelines and others.

56 cases of cutaneous *Anthrax* have been registered among the people over the period of 2005–2010. The majority of those who have recently fallen ill with anthrax is composed of livestock owners and their family members as well as people who bought meat from individual sellers.

Methods and Materials: For the investigations were used the standard epidemiological, microbiology, virology and statistic methods.

Results: The last enzootia of the *Plague* among the rodents was recorded in 2001, in the Garabagh mesofocus.

The *Anthrax* registered with children under 14 years old (8,2%) is of interest which is likely connected with the living conditions in rural areas where children have direct contacts with the meat of dead animals infected with anthrax.

Rabies. According to the analysis of epidemiologic and epizootic situation in the republic it should be pointed out that substantial deterioration has been recently observed in this respect. The number of people who applied for medical aid because of being bitten by animals has been constantly growing. In 2006 the number of those bitten by animals came up to 9062 persons, in 2007 10419 persons, in 2008 11554 persons, in 2009 11991 persons. Among people there were registered 4 cases in 2005, 2 cases in 2006, 2 cases in 2007, 4 cases in 2008, 7 cases in 2009, over the 6 months 6 cases in 2010.

5 cases of *Tularemia* have been registered among the population over the period of 2005-2009.

Conclusion: Serology investigations also showed that the degree of spread of antibodies to some infectious agents increased, and is for: Leptospirosis - 6%, Rickettsiosis group of epidemic typhus -16%, Crimean - Kongo hemorrhagic fever - 6%, Tick-borne encephalitis - 0,7%, Western Nile virus - 5%.

12.075 Cowpoxvirus infection in farmed llamas in Italy

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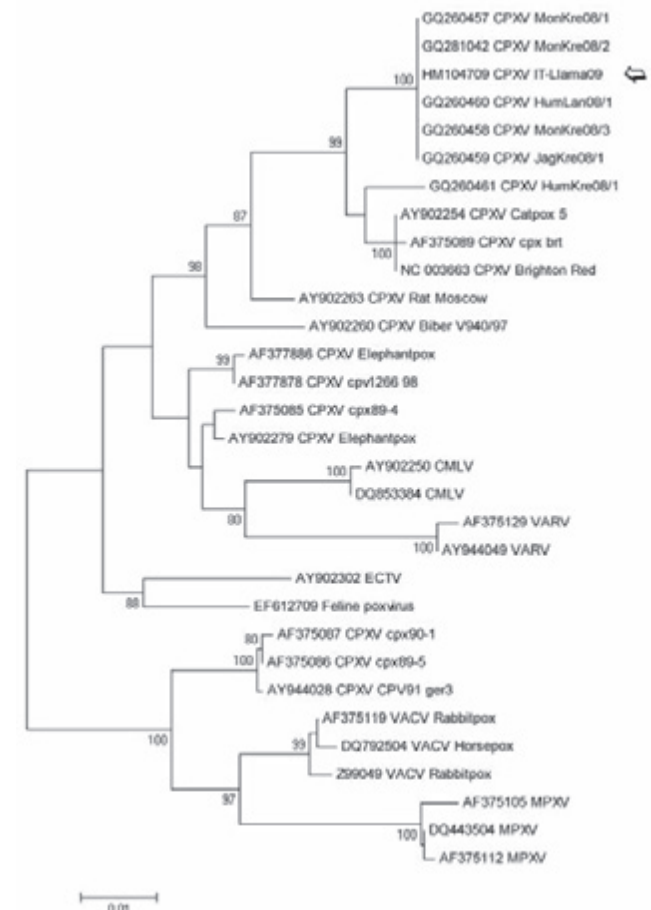
Background: In July 2009, 5 adults of 7 llamas in a farm around Viterbo in Central Italy exhibited skin lesions at different sites (palpebral conjunctiva, auricles, teats, around mouth and anus) evolving from nodules to crusts; some of them had a crater morphology typical for pox lesions. On the farm, there are present many species of birds (local and exotic) and mammals (goats, cattle, pigs, donkeys, horses), none of which showed any of the above mentioned symptoms.

Methods and Materials: Suspecting a poxvirus, the skin lesions were processed for Electron Microscopy techniques. Two mammal cell lines were used for virus isolation from skin lesions collected from 1 of the 3 dead animals and from the remaining 3 llamas still alive. Two lots of mice imported from a big farm in Germany, were sampled (31 animals in total) for laboratory analysis together with 44 wild grey rats (*Rattus rattus*) captured in the farm.

Samples of skin lesions were fixed, embedded, cut and stained for histological examination. Serological analysis for the detection of CPXV antibodies were conducted in cattle, horse, donkey, goat, llama and human sera collected about 3.5 months after the 1st observation of the episode. Total viral DNA was extracted from both homogenized crusts and cells supernatant and a Real-Time PCR targeting a region of the cytokine response modifying protein B (crmB) gene, was performed identifying an Orthopoxvirus. For the phylogenetic analysis, two classic PCRs targeting the complete gene of the hemagglutinin (HA) and crmB were made.

Results: Transmission electron microscopy revealed brick particles typical of orthopoxviruses. Cell cultures developed focal areas of cytopathogenic effect with complete lysis of the monolayer. Histologically,

the skin lesions showed eosinophilic, intracytoplasmic inclusion bodies in basal and spinous layers of epidermis. CPXV-Antibodies were detected from llama and human sera. A Cowpoxvirus, homologous to CPXV-MonKre08/1-2-3 strains isolated in Germany in 2009, was identified by PCR and sequencing.



Conclusion: Cowpoxvirus is distributed in Europe with an increasing number of reports. As it is responsible of human cowpox affecting a wide range of wild and domestic animals, CPXV is considered a pathogen of public health importance.

12.076 Blood variation in Brucellosis

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Background: Brucellosis is a zoonosis especially important in Albania and its neighbours because of variability of clinical picture. Laboratory findings consist of changes in peripheral blood such as anemia, normal or low WBC, and rarely thrombocytopenia. Erythro sedimentation rate is normal or higher. Pancytopenia is a rare finding, its cause are granulomas in bone marrow or cytophagocytosis that some times like as Robb-Smith syndrome.

The aim of the authors is to study the variability of peripheral blood changes and their relations with the hepato-lienal syndrome.

Methods and Materials: consist of 340 patients, hospitalised in the Dpt. of Infectious diseases in the UHC of Tirana, Albania during the period Jan 2000–Dec 2009. They all were diagnosed with brucellosis according to their serological confirmation (RB +, Wright >1:160). This is a retrospective and prospective study.

Results: Hepatomegaly was found in 96% of cases, splenomegaly in 62%, and hepatosplenomegaly in 62%. Enlarge lymph nodes were found in 11.8 % of cases. The frequency of splenomegaly was 65% in the acute stage, versus 48% in subacute stage (p=0.036).



WBC were between 2000–17000, less than 4000 were found in 19% and more than 10000 in 9.2%. In 91% of cases was found lymphocytosis and in 71% anemia. Erythrosedimentation rate > 20 were in 58% of cases. Pancytopenia was observed in 3% of cases. Bone marrow aspiration was made in 15% of cases with normal results, except in one case with coinfection Brucellosis + Leishmania. 8% of patients with blood changes had hepato-splenomegaly

Conclusion: Brucellosis have to be considered when periperal blood changes as anemia, low WBC and lymphocytosis, thrombocytopenia and sometimes pancytopenia are found. Serological tests are important for diagnostic confirmation.

12.077 Junin, Machupo, and Guanarito: Patterns of New World Arenaviruses

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Background: Viral hemorrhagic fevers are some of the newest and most lethal viruses worldwide. Arenavirus genus is composed of 25 viruses with global distribution, of which at least six viruses cause viral hemorrhagic fever in humans. Divided genetically and geographically, Old World viruses are mostly endemic to Africa and Europe while New World viruses are endemic to the Americas. South American agents, including Junin, Machupo, and Guanarito, are members of the same phylogenetic clade, as well as several nonpathogenic arenaviruses. Arenaviruses are generally rodent-borne, associated with a species and habitat.

Methods and Materials: A comparison of literature regarding arenavirus microbiology and taxonomy, as well as personal accounts of outbreaks.

Results: The emergence of Junin, Machupo, and Guanarito viruses exhibited 3 common traits: change in agricultural activities, rural location, and a rodent reservoir impacted by societal developments.

In the Pampas of Argentina, farmers began using herbicides, which allowed for growth of tall grasses as agricultural workers entered the fields. The taller grasses provided sustenance to *Calomys musculinus*, which carries Junin virus.

Residents of remote towns in Beni province converted grazing land to farming and began storing grains after revolution disrupted river trade and food deliveries. In time, *Calomys callosus* acclimated to live in homes and feed on grain storage.

The extension of agricultural activities into new lands in Portuguesa, Venezuela and the related migration to rural areas produced ecological changes favorable for the increase of wild rodent populations, specifically *Zygodontomys brevicauda* whose population density correlate with endemic and epidemic cycles of Venezuelan hemorrhagic fever among humans.

Conclusion: The similarities and differences among the emergent outbreaks of Junin, Machupo, and Guanarito viruses provide a starting point for controlling Venezuelan hemorrhagic fever. While rodent vector controls have been effective in controlling Machupo virus, Junin virus shows that traps are not effective control for viruses exposed in fields during agricultural labors. Similar to Junin, protection should be through a vaccine. Candid #1 vaccine did not cross protect against Guanarito virus but immunological cross-reactivity of Guanarito and Pirital viruses is one example of the possibilities for using a virus from a different clade.

12.078 Human Hantavirus outbreak in Bavaria, Germany in 2010: An emerging problem?

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Background: Notification of human hantavirus infections has been mandatory in Germany since 2001. Bavaria, the southernmost federal state of Germany is endemic for hantavirus infections. In general the incidence remains below 0.5 cases per 100,000 per year. Unexpectedly high number of cases of human hantavirus infections were observed

in Bavaria in January and February 2010, suggesting an emerging epidemic. In addition to recommendations on awareness and prevention for doctors and the Bavarian population, real-time surveillance of the emerging situation was at the core of the control strategy. This poster describes the results of the hantavirus surveillance in Bavaria in 2010.

Methods and Materials: Human hantavirus infections are reported by medical doctors and laboratories via the local health office to the Bavarian Health and Food Safety Authority (LGL), according the national case definition. Case records were extracted from the Bavarian infectious disease database for analysis.

Results: In 2010, 425 cases of hantavirus infection were reported in Bavaria to date (8th dec 2010), resulting in the highest annual incidence (3.4/ 100,000 population) since the introduction of mandatory case reporting in 2001. In total, 69% of cases were hospitalised. There were no fatalities. The majority of cases (69%) were between 30 and 60 years of age. Nearly 75% of cases were male. The cases were clustered geographically, occurring mainly in the known endemic foci.

Conclusion: In 2010 the highest number of human hantavirus infections since the introduction of mandatory case reporting (2001) was reported in Bavaria. Increasing numbers of hantavirus infections have been linked to high densities of the host population (bank vole). Future control of the disease continues to be dependent on early recognition of impending outbreaks through existing surveillance systems as well as effective public health communication on risk and prevention measures to the population. Further research to investigate the complex interactions between reservoir host, environment and pathogen is required to inform prevention strategies.

12.079 Orthopoxviruses seroprevalence among cats from different areas of Friuli Venezia Giulia, Italy

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Background: Recently, 2 cases of zoonotic infections, in veterinary personnel scratched by cats, occurring in Northern Italy, have been referred to the National Institute for infectious Diseases for etiological diagnosis, leading to the identification of an orthopoxvirus (Cowpox). Zoonotic orthopoxvirus infections has been reported in several European countries, in the north-eastern Italy systematic surveillance of orthopoxviruses circulation in cats has been started, it is important to acquire data on this issue to evaluate the extent of the problem and to envisage possible strategies to circumvent it.

Methods and Materials: To investigate the seroprevalence of orthopoxvirus in cats 140 blood samples from wild and domestic cats of a selected area of Friuli Venezia Giulia were collected to test signs of previous exposure to orthopoxviruses by using microneutralization assays.

A standardized questionnaire was also used to record the past history, as well as to evaluate the risk factors.

Results: The seroprevalence rates among cats was 35% with a different distribution among rural and urbanized territories.

Conclusion: Circulation of orthopoxviruses in wild and domestic animals, together with decreased immunity in humans, may lead to increased occurrence of human cowpox, especially in atopic and immunocompromised persons who are at risk for generalized infection. To know the real extent of orthopoxvirus circulation accompanied by an early diagnosis and prompt recognition of the virus is essential for treating and differentiating cowpox, from other orthopoxvirus and herpesvirus infections, especially in severe cases.

**12.080** Ten years of fox variant rabies epidemiology in Nunavik, Québec, 1999–2009C. Aenishaenslin¹, T. Forde², C. Fehlner-Gardiner³, I. Picard⁴, D. Bélanger⁵¹Université de Montréal, Saint-Hyacinthe, QC, Canada, ²University of Calgary, Calgary, AL, Canada, ³Canadian Food Inspection Agency, Ottawa, ON, Canada, ⁴Ministère de l'Agriculture, des Pêcheries et de l'Alimentation du Québec, Québec, Qc, Canada, ⁵Université de Montréal, Saint-Hyacinthe, QU, Canada

Background: Although no human rabies cases have been reported in Nunavik over the last 30 years, fox rabies is endemic in this isolated region of Northern Quebec and remains a public health threat. Each year, several cases of animal aggressions cause grave injuries to local residents and require expensive interventions such as post-exposure prophylaxis for the prevention of rabies. Since 1983, the provincial ministry of agriculture, ministère de l'Agriculture, des Pêcheries et de l'Alimentation du Québec (MAPAQ) has offered an annual canine vaccination program for Inuit municipalities, since there are no veterinary clinics in this northern area. However, the dearth of epidemiological data makes it difficult to assess the program efficacy.

Methods and Materials: This is a descriptive study of fox variant rabies epidemiology in Nunavik from 1999 to 2009, including domestic and wild animal cases.

Results: A total of 80 samples from Nunavik were analyzed by the Canadian Food Inspection Agency (CFIA) from 1999 to 2009, under a passive surveillance program (cases involving human or domestic animals exposures only). According to the CFIA case investigations, sixty-two of the samples (78%) were associated with a human exposure. Twenty-six (33%) of the 80 samples submitted were positive for fox variant rabies; as expected, no other rabies variants were detected. A peak of occurrence is noted in the month of March, an observation compatible with rabies case reports from other arctic regions. The positive cases consisted of 14 red foxes (50%), six dogs (23%), four arctic foxes (15%) and two wolves (12%).

Conclusion: This descriptive study confirms that fox rabies remains an important threat for human health in Nunavik. The high proportion of positive samples suggests that the real number of cases is underestimated and provides arguments for enhanced surveillance for rabies in the region in order to better evaluate the risk and the epidemiology. To the authors' knowledge, this study is the first publication on rabies epidemiology in Nunavik. It provides essential baseline data for further research such as an evaluation of the protective efficacy of the canine rabies control program on human risk of exposure.

12.081 The U.S. Armed Forces Health Surveillance Center: Efforts in disease surveillance at the human-animal interfaceK. Vest, R. L. Burke
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Background: Greater than 60 percent of emerging infectious diseases are of zoonotic origin, including influenza, leishmaniasis and Q fever. To promote global health, the U.S. Armed Forces Health Surveillance Center supports programs conducting surveillance at the human-animal interface with a central objective of rapid detection of new diseases and outbreaks.

Methods and Materials: Supported efforts include surveillance in animal reservoirs and high-risk populations, predictive surveillance, and pathogen discovery.

Results: Reservoirs: Since the Korean War, zoonotic diseases such as hantavirus, leptospirosis and scrub typhus have affected military forces on the peninsula. These studies have quantified prevalence levels in known reservoirs and identified new organisms (rickettsial and anaplasma) and reservoirs. Similarly, in the Mediterranean region, various viral hemorrhagic and encephalitis pathogen prevalence levels have not been recorded. An AFHSC study reported the prevalence of zoonotic pathogens in an Egyptian abattoir including *Leptospira* (29%–50%), *Brucella* (1–10%), CCHF (0–2%), Q fever (0–30%), and RVF (0–3.3%) in ruminants and camelids.

High Risk Populations: Gaining outcomes of disease surveillance is of higher likelihood when following up individuals at high-risk of infection due to work practices, living conditions and behaviors. Q fever seroprevalence was determined among military veterinarians, as well as influenza exposure among humans occupationally exposed to animals in seven countries, identifying risk factors for zoonotic transmission. Additionally, zoonotic disease prevalence among (acute febrile illness (AFI) patients in Ghana and Djibouti was determined.

Predictive Surveillance: Prevention and zoonotic disease outbreak intervention has successfully provided early warning of RVF outbreaks in the Horn of Africa.

Pathogen Discovery: Discovery efforts are ongoing in eastern European hospitals within rural/farming communities, by screening samples from AFI patients that were negative for traditional bacterial and viral pathogens. Additionally, in Peru where jungle habitat modification is associated with road building, mining and farming, other efforts are focusing testing for new viruses that may reside in potential animal reservoirs and vectors.

Conclusion: Disease surveillance within the human-animal interface may provide early warning for pathogen emergence. Nevertheless, the presence of disease in humans may suggest there is an unidentified animal reservoir within the community.

12.082 Cowpox virus outbreak in pet ratsD. Thaller¹, P. Wohlsein², J. Kolodziejek³, H. Lussy⁴, H. Weissenboeck⁵, N. Nowotny⁴¹Institute of Pathology and Forensic Veterinary Medicine, University of Veterinary Medicine, Vienna, Vienna, Austria, ²Institute of Pathology, University of Veterinary Medicine Hannover, Foundation, Hanover, Germany, ³Clinical Virology, University of Veterinary Medicine, Vienna, Vienna, Austria, ⁴University of Veterinary Medicine, Vienna, Austria, ⁵Institute of Pathology and Forensic Veterinary Medicine, Vienna, Austria

Background: Laboratory and wild rodents are the reservoir hosts of cowpox virus (Orthopoxvirus). Virus transmission to cats and humans from infected rats is occasionally reported. Clinical signs in infected rats range from inapparent infections to dermal or pulmonary or mixed lesions. Animals showing only the dermal form have a higher survival rate than animals with pulmonary or mixed lesions.

Methods and Materials: Within a five month interval two massive outbreaks of cowpox virus infections occurred in a large group of rats held as pet animals. Clinically, the animals showed signs of acute dyspnoea as well as skin lesions for several days and died spontaneously. Necropsy, pathohistological, bacterial and virological examinations as well as immunohistochemical staining were conducted.

Results: Whereas in the first outbreak the submitted adult rats showed mild skin lesions with intramuscular bleeding and purulent inflammation, the juvenile animals during the second outbreak presented distinct skin lesions of the limbs and the head with ulcerative inflammation, bleeding and bacterial infection. All animals showed severe pulmonary changes ranging from purulent to hemorrhagic or necrotizing pneumonia. Bacteriological examination of the lungs in the first outbreak also revealed an infection with *Mycoplasma pulmonis* and *E. coli*. Due to the severe bacterial infection and the mild skin lesions in the first outbreak cytoplasmic inclusion bodies were better visible by immunohistochemical staining. The diagnosis was confirmed by PCR amplification of cowpox virus DNA in lung and skin samples.

Conclusion: The most likely cause for the outbreaks was the acquisition of clinically inapparently infected animals. However, because the rats were bought in different pet shops the actual source or origin of the infection remained undetected. Attention must be given to the fact that this is a zoonotic disease and that also cats can act as host species. Human infections of private pet rat owners as well as professionals working with laboratory rats have repeatedly been found.



12.083 **Farmed wildlife surveillance: The missing link in understanding the ecology and diversity of pathogens posing risks to people, free-ranging wildlife, and livestock**

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Background: Emerging infectious diseases of humans, livestock or wildlife pose significant threats for public health and livelihoods. Global surveillance systems typically monitor pathogen loads in people, livestock, but relatively few wildlife species, and this usually when livestock or public health is threatened. Wildlife farming systems are a growing sector that serve as a local protein resource for communities and also have large economic values associated with marketing and exports. Wildlife that is farmed can range from frogs, to civets to disease free buffalo, used for varied purposes including ornamental pets, consumption, hunting, or medicinal purposes. While it is recognized that ensuring the health of wildlife that is farmed requires proper husbandry practices, biosecurity, and disease monitoring, these farming systems are often overlooked by authorities as they do not fall directly within the mandates and responsibilities of either the Ministry of Agriculture or Wildlife/Natural Resources. The result is a largely unregulated farming and marketing system with little hygiene associated with slaughtering and consumption.

Methods and Materials: Understanding the prevalence of avian influenza and other viruses in farmed wild birds is crucial for evaluating the potential avian virus transmission among wild and domestic birds. Molecular and serological studies were carried out on seven species of farmed wild birds from farms near wild bird inhabited wetlands.

Results: Results of this study reveal avian influenza viruses exist in farmed wild birds and present a possible explanation about the potential virus transmission among poultry, farmed wildlife and wild birds. Wetlands and rice fields which domesticated wild birds and wild birds share are the likely virus transmission medium. It is possible these farmed wild birds play an important role in virus transmission among wild and domestic poultry.

Conclusion: In the future, as human populations increase, farming systems expand and intensify, and ecological systems undergo greater encroachment, it is vital that global disease surveillance systems increase their focus on the role of wildlife as disease reservoirs, and as indicator species that acquire diseases from livestock or people. In particular, farmed and marketed wildlife serves as an area that needs to have greatly enhanced surveillance as well as regulatory dimensions put into place.

12.084 **Isolation, identification, serotyping and evaluation of diagnostic test on *Leptospira* from urine of slaughtered cattle**

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Background: Leptospirosis is currently identified as a worldwide public health problem. Increase in the incidence of the disease has been recorded in countries where leptospirosis surveillance exists (WHO, 2009). It is an occupational hazard for people who work outdoors or with animals such as farmers, sewer workers, veterinarians, port workers, dairy farmers and military personal (CDC, 1998).

Methods and Materials: A cross-sectional study was carried out to investigate the incidence of the *Leptospira* species in cattle urine from slaughtered cattle. The population targeted during the sampling period was 7,200 cattle at the age of 10 years old. A total of 150 urine samples were randomly selected. 20ml of urine samples were taken for each collection individually, immediately after slaughtered by direct bladder puncture. Collected 25 samples were for each visits at 2 weeks interval. Isolation and identification of *Leptospira* species from slaughtered cattle was done according to the instruction described by Norris (1999). Modified Ellinghausen and McCullough (EMJH) medium (Johnson

and Harris, 1967) was prepared. A few drops of urine were aseptically added to EMJH medium supplemented with antibiotics on a bedside-the -cow basis. The remaining urine was neutralized with N/10HCL or N/10NaOH. All urine samples collected individually from each visit were examined directly under dark field microscope (DFM). Urine samples were inoculated onto EMJH media supplemented with antibiotics. All isolates were serotyped by Microscopic Agglutination Test (MAT) against 12 serotypes of standard known references antisera provided by National Institute of Animal Health, Thailand.

Results: The *Leptospira* positive samples detected by DFM and EMJH were 45/150 (30%) and 32/150 (21.3%), respectively. The performances of these tests were interpreted by using a standard 2^A-2 table (Martin et al., 1997). True prevalence was 21.3%. The relative sensitivity, specificity, positive predictive value and negative predictive value of DFM was investigated as 100%, 90%, 71% and 100%, respectively while EMJH method was introduced as a reference test. Based on the kappa statistic for determination of overall agreement between the direct DFM and EMJH was 0.7, indicating substantial agreement between the two methods for *Leptospira* examination. The *Leptospira* isolated from cattle was identified by MAT against 12 serotypes of standard known references antisera and the most predominant serovar were *L. pomona* (31.3%) followed by *L. icterohaemorrhagiae* (21.9%), *L. canicola* (18.8%), *L. grippityphosa* (15.6%) and *L. sejroe* (6.3%). These findings indicated that cattle can be infected by several pathogenic *Leptospira* serovars, although they are the maintenance hosts of the serovar Hardjo.

Conclusion: The study approved cattle represent as an important reservoir for the transmission of *Leptospira* infection to humans for potential zoonotic disease since they excrete *Leptospira* organisms in their urine into the environment for prolonged periods.

12.085 **Pathogen Spillover, Zoonotic Disease, and the Use of Modeling Tools to Address Public Health Needs**

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Background: The threat of novel, emerging infectious disease has captured the attention of the public as well as public health specialists across the globe. Given that the majority of emerging infectious disease originates from wildlife reservoirs, there has been an increased focus on understanding zoonotic pathogen dynamics at the human-wildlife interface. How and under what circumstances will pathogens move from wildlife reservoirs to human populations? Where should we focus disease surveillance and research efforts? What is the most appropriate public health response to control an outbreak of infectious disease of zoonotic origin? Mathematical models provide an important tool to make the intractable elements of infectious disease research tractable. Explicit definitions of the interactions and parameter values of a system in an interactive and dynamic environment allow experimentation with the system. When applied to infectious diseases emergence, mathematical models can facilitate the evaluation and identification of important elements of the spatial and temporal features of disease spread and their public health implications. Often, however, there is a great divide between scientist conducting empirical studies on emerging zoonotic disease at the human-wildlife interface and the skill-base necessary to choose, develop and apply models to evaluate these systems. Which modeling approach should one employ?

Methods and Materials: We review the process of pathogen spillover and zoonotic disease emergence. Using zoonotic disease examples, we assess the application of agent based models (ABM) versus compartmental models to these systems.

Results: Using this examination, we provide general guidelines for model selection in zoonotic disease investigations and public health control activities.

Conclusion: Understanding and managing public health threats associated with the emergence of zoonotic disease will increasingly require scientists to fully engage modeling approaches that allow assessment across disciplines, animal communities, people and environments. Both agent-based models (ABM) and compartmental modeling approaches



have their strengths and weaknesses, with model selection being driven by the computational capacity of the researcher, the nature of the system under study and the type of questions being asked.

12.086 The antimicrobial properties of silver nano particle on food-borne pathogens

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Background: There are several micro organism that have the most effect on diseases caused by food industry. despite much progress, these micro organism are still very important and more or less illnesses are reported caused by theme. The anti – microbial properties of nano – silver cloadial particlens on several important food-borne pathogens such as *Pseudomonas aeruginosa* ATCC 9027, *Staphylococcus aureus* ATCC 6538, *Escherichia coli* ATCC 8739, *Candida albicans* ATCC 10231 and *Aspergillus niger* ATCC 1604 were investigated.

Methods and Materials: After preparation of different concentration of the nano particle, they were subjected to the standard level of the indicator organism A significant Reduction in the level of the viable organism counts were indicative of the particles anti – microbial properties. Peptone water, Ringers saline solution, and saline solution containing polysorbate were is diluents.

The microorganisms were grown in Typical soy agar or nutrient agar for 18–24 hr at 37 . The yeast cells were cultivated at 26 for 48 hr in TSA. They were then subcultured into peptone water tube and the turbidities were adjusted to 0.45 with 425 nm light. This level of turbidity roughly accounts for 1 10⁸ bacterial cells and 1 10⁷ yeast cells per ml .

For preparation of fungal suspension a rich solid growth of the cell were transferred into saline solution and following through suspension, it was passed through a filter membrane . The resulting spore suspension was counted with a graduated counting gloas slide . The fungal spore suspension count was adjusted 1 10⁷ / ml .

Results: The most sensitive bacterial cell was found to be *E.coli* in which a 9 ppm concentration of the nano silver particle completely inhibited its growth . *Pseudomonas aeruginosa* was found to be the most renitent organism able to resist up to 18 ppm concentration of silver particle.

This amount resistance was for *Staphylococcus aureus* And *Aspergillus niger* 11ppm And *Candida albicans* 13 ppm.

Conclusion: Using Nano Silver with considering its enormous power (less than 20ppm thickness) and cheap price, with this low thickness is suggested as instead of food conservators.

12.087 Effect of pasteurization on microbial characteristics of liquid eggs in Iran: The first comprehensive study

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Background: Pasteurized products come to be important while we take a look at the food poisoning occurring worldwide. Pasteurization of food products constrains the growth of pathogenic microbes. The process of pasteurization is currently applied in many industries particularly for milk, fruit juice, egg products, etc. Pasteurization condition of eggs is a striking affair because of the quick coalescence. Accurate devices are required for pasteurization of eggs within a low temperature and a long time. Thus, importing of such industry and technology into a country can reduce the health risks related to contaminated eggs and provide food safety as well. Meanwhile, the liquid egg pasteurization was first imported into Iran by private sector in 2006. We found no study on this product since its first production in Iran.

Methods and Materials: In our study, around 1000 samples of pasteurized liquid eggs (3 samples were chosen randomly from each batch comprising 10 tons).

We examined the total count of aerobic mesophilic bacteria, coliforms, *Escherichia*, *Salmonellae*, mold and yeast in the samples before and after the pasteurization according to the national standard protocol of Iran.

Results: No growth of coliforms, *Escherichia*, *salmonella*, mold and yeast was observed in the cultures. Pasteurization could drastically decrease the count of aerobic mesophilic bacteria. It should be noted that accepted total plate count of eggs being <100000 according to national standard protocol of Iran. Whereas by pasteurization of eggs, the count numbered around 650 and 1200 cfu/ml in 2007 and 2008, respectively.

Conclusion: It is the first study in this field in Iran. Precise and controlled egg pasteurization could completely obviate the problem related to the presence of pathogenic bacteria like coliforms, *Escherichia* and *Salmonella* especially in foods with cold process such as mayonnaises, etc. It also leads to reduced amount of preservative consumption in egg-associated foods.

12.088 Campylobacteriosis in Oppland and Hedmark Counties, Norway, 1981–2009

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Background: Campylobacteriosis is a notifiable condition to the Norwegian Notification System for Infectious Diseases (MSIS). The Norwegian epidemiological situation has some general features. Norwegian case-control studies have demonstrated the following risk factors, consumption of contaminated surface water, consumption of chicken which has not been heated sufficiently, as well as daily contact with dogs and cats.

Methods and Materials: Campylobacter is diagnosed in our laboratory under standard conditions utilizing specific media under capnophilic conditions. Previously strains of genus Campylobacter were submitted to the Norwegian Public Health Institute for reference testing, including biotyping. This has been discontinued. Reference testing of strains belonging to genus Campylobacter is usually performed only on special occasions, e.g. under outbreak conditions.

Results: The total number of cases was 2152. Oppland had 1134 notifications, whereas Hedmark had 1018 cases – from 1981 to the end of 2009. Around 60 % of the cases are domestically acquired. Around 55% of the cases were amongst males and 45% amongst females. The age groups mostly affected were 20 - 50 years, as well as children. Amongst people over 70 years of age there were few cases. Most cases occurred June through September.

Oppland and Hedmark counties have experienced two consecutive outbreaks of campylobacteriosis in connection with the bicycle race “Mjøsa rundt” around year 2000. Another outbreak, in 1998, which also affected persons from our two counties, was amongst approx. 1200 Norwegian and other Nordic health care workers participating in a sports competition, the so called “Sykehuslekene”, where crab meat contaminated by feces from seagulls was the most likely source. Approximately 40-50 of the competitors were infected.

Conclusion: There has been a steady increase in notified cases 1981-2009. Some of this may be due to increased awareness of the condition and improved diagnostic methods. Other contributing factors may comprise more travel abroad, increased import of food products with higher risk of contamination with campylobacter. Around year 2000 there is probably some impact of increased rainfall – resulting in contamination of surface water. There has been an improvement concerning data on place of acquisition of campylobacteriosis throughout the period described. This has to do with upgrades of the MSIS system, including a better notification form.

12.089 Globalisation and the food supply

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Background: The exchange of food and animal products across regions, nations, and continents has occurred for centuries. Many of the diseases that have grown in importance in human medicine in recent



decades are transmitted via the food and water supply. In the globalized political economy of the late 20th century, increasing social, political, and economic interdependence occurred as a result of the rapid movement of people, produce and other commodities across national borders. A consequence of increased trade, travel and migration is the growing risk of transmitting biological and other hazards from country to country on a large scale. With greater connectedness, new and emerging diseases have the potential to travel very fast and trace back and control is often difficult.

Methods and Materials: The international circulation of food products as commodities along with the transnational expansion of food-based co-operations resulted in the need for global governance of food safety and quality. To a large extent this has occurred through the World Trade Organization (WTO) and the implementation of standards outlined in the Sanitary and Phytosanitary (SPS) Agreement and the Codex Alimentarius.

Results: Global outbreaks of foodborne disease can have socio-economic impacts on consumer food choices and other behaviour. In this presentation we will examine how our understanding of the epidemiology of foodborne diseases has evolved in recent decades corresponding, in part, to improvements in pathogen detection and reporting systems. In addition, we will discuss how new pathogens have emerged to correspond with a changing food supply, an increase in the number of people with heightened susceptibility to foodborne diseases and a greater diversity of food preparation practices and food preferences. This has posed a number of challenges for the veterinary profession and public health agencies.

Conclusion: Current SPS requirements emphasise the importance of science-based risk assessment and hazard control programmes for the continued reduction of pathogens at relevant points of the 'farm-to-fork' food production chain. This recommendation, along with good consumer education about food preparation and handling practices is likely to be the best approach for reducing risks to human health in the modern globalized society.

12.091 Yersiniosis in Oppland and Hedmark Counties, Norway, 1990–2009

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Background: Yersiniosis has been notifiable to the Norwegian Notification System for Infectious Diseases (MSIS) since January 1, 1975. The two main epidemic clones consist of *Yersinia enterocolitica* serogroups O:3 and O:9. Whereas salmonellosis mostly are imported infections in Norway, yersiniosis is, in general, domestically acquired. Amongst risk factors are consumption of contaminated surface water and meat products originating from swine. Partially due to improved slaughter techniques when it comes to animal husbandry, especially swine, the incidence of domestically yersiniosis has decreased since the late 1990s.

Methods and Materials: The Laboratory for Medical Microbiology, Sykehuset Innlandet Trust diagnoses *Yersinia enterocolitica* using standard bacteriological cultivation/identification methods.

Results: Yersiniosis in Oppland and Hedmark counties by year 1990–2009 (year and number of notifications)

1990	1991	1992	1993	1994	1995	1996	1997	1998	1999
12	11	22	28	16	20	10	20	24	21
2000	2001	2002	2003	2004	2005	2006	2007	2008	2009
13	12	10	10	17	10	11	5	4	3

The number of cases was 292. Oppland had 159 notifications. Hedmark had 133—1990–2009. Most cases occurred in June, July and August. During the rest of the year fewer cases were notified.

Conclusion: The trends in Oppland and Hedmark counties are similar to that of the epidemiological situation in Norway—in general. The decrease in incidence in the two counties, as well as in Norway, co-incides, throughout the period from the late 1990s and after, with improved slaughtering techniques and compliance to hazard-analyzes critical control point (HACCP)-related practices, mentioned above. The test algorithms for *Yersinia enterocolitica*—in the Norwegian medical microbiological laboratory setting may have changed marginally, but not to any level of significance. Thus most of the decline observed is likely, to be due to improved slaughtering techniques of swine. The significance of differences in the quality of surface water remains uncertain. This may be due to the small proportion of such cases and the lack of data on what kind of water has been consumed throughout the period described. Some of the seasonal variation might be due to outdoor consumption of meat and lower hygienic standards in that context.

12.092 A study of allergic sensitization to *Anisakis* species in experimental mice

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Background: Hypersensitivity to *Anisakis* species is a worldwide medical problem. The aim of this study was to detect the immunological response in experimental mice, through measurement of Immunoglobulin E (IgE) antibodies in their lymphocytes by flow cytometry, following the ingestion of *Anisakis* crude antigen.

Methods and Materials: Sixty Swiss albino mice were divided equally into control and experimental groups, and each of them were further subdivided into five subgroups, six mice each. The percentage of IgE antibodies was measured in the lymphocytes of their splenic suspensions at zero, 1st, 3rd, 5th and 7th weeks post inoculation using Fluorescein isothiocyanate (FITC) anti-mouse IgE, and were analyzed on a FACS Calibur flow cytometer Becton Dickinson equipped with an argon-ion laser apparatus operating at 488 nm.

Results: The percentage of IgE antibodies was enhanced in lymphocytes of animals exposed to *Anisakis* antigen from the first week, peaking three weeks following initial exposure, starting a decline by week five and decreased more by the seventh week, as compared to the control group.

Conclusion: The results obtained from this study proved the efficacy of flow cytometry in detecting the sensitization against *Anisakis* species through the measurement of IgE antibodies.

12.090 Outbreak of gastroenteritis in Tibetan transit school, Dharamshala, Himachal Pradesh, India, 2006

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Background: On 28th June, 2006 we investigated an outbreak of gastroenteritis among the hostellers of Tibetan Transit School to identify the source, propose control and preventive measures.

Methods and Materials: We defined a case of gastroenteritis as occurrence of more than three smelly loose motions between 28th June to 2nd July, 2006 among some sections of the hostellers. We determined age and sex specific attack rate. We hypothesized it as a food borne beef meat outbreak. We conducted case control study and collected the information about the food items consumed inside and outside the hostel at dinner using the standardized questionnaire. We calculated floor wise incidences of four hostels, odds ratios and attributable fractions. We interviewed food handlers. We lifted seven rectal and four water samples for culture and sensitivity.

Results: We identified 116 cases patients. Overall attack rate (AR) as 14% with maximum AR (16%) and floor wise incidences as highest (40%) in the youngest group (15–20yrs) and nil in staff, median age 20 yrs (Range 17–40 yrs). Sex specific attack rate was more (18%) in females. Of the six edible items examined, food specific AR was highly statistically significant in the beef meat eaters (82% with PAF 71%; OR 19.19; 95% C.I. as 9.3–140). The food handlers and cooking conditions were unhygienic. *Escherichia coli* were detected in the given samples. No fatality was reported.

Conclusion: The beef meat purchased from outside was implicated for the explosive common source outbreak. The school authorities were counseled for hygienic food handling.

**12.093 Evaluation of the co-agglutination test in diagnosis of experimental microsporidiosis**

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Background: Microsporidiosis is an emerging and opportunistic infection associated with wide range of clinical syndromes in humans. Confirmation of the presence of Microsporidia in different samples is laborious, costly and often difficult. The present study was designed to evaluate the utility of Co-agglutination test (Co-A test) for detection of urinary, fecal and circulating microsporidial antigens in experimentally infected mice.

Methods and Materials: One hundred and twenty male Swiss albino mice were divided into non infected control and infected experimental groups which were further subdivided into two equal subgroups; immunosuppressed and immunocompetent. Microsporidial spores were isolated from human stools and identified to be *Encephalitozoon intestinalis* by the molecular methods. They were used to infect each subgroup of mice, then their urine, stool and sera were collected at the 1st, 3rd, 5th, 7th and 9th days post-infection (PI). Co-A test, using prepared hyperimmune serum was used to detect antigens in all collected samples. The cross reactivity of microsporidial hyperimmune sera with antigens of *Cyclospora cyatenensis* and *Cryptosporidium parvum* was investigated by Co-A test.

Results: The results proved that Co-A test was effective in detecting microsporidial antigen in stool of immunosuppressed infected mice from the 1st day PI, and in urine and serum from the 3rd day PI till the end of the study. While in immunocompetent subgroup, Co-A test detected microsporidial antigens in stool, serum and urine of mice from the 1st day, 3rd day and the 5th day PI, respectively till the end of the study, without cross reactivity with *Cyclospora cyatenensis* or *Cryptosporidium parvum* in both subgroups.

Conclusion: Co-A test proved to be simple and suitable tool for detecting microsporidial antigen in different specimens and did not need sophisticated equipments. It is very practical under field or rural conditions and in poorly equipped clinical laboratories.

12.094 Seroepidemiology of Cryptosporidium and variation over time associated with changes in the treatment of drinking water

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Background: Drinking water contaminated with *Cryptosporidium* parasites is an internationally recognised risk factor for human illness. *Cryptosporidium* sp. contamination of drinking water can arise from a variety of sources including the contamination of raw water and post-treatment contamination with oocysts (infectious stage) from infected humans, livestock and feral animals present in the catchment. Inadequate treatment of drinking water can permit oocysts to be transmitted to susceptible consumers of that water, posing a risk to public health. Continuous low-level exposure to oocysts via unfiltered water might result in a higher background level of immunity to *Cryptosporidium* among consumers. Paradoxically, low-level exposure to oocysts via unfiltered surface water may stimulate a protective effect among people subsequently exposed to *Cryptosporidium* from other sources e.g. zoonotic transmission or foreign travel. The unintended consequence of introducing filtration might therefore reduce the level of 'herd immunity' to *Cryptosporidium* in the relevant population.

Methods and Materials: Implementation of a water filtration system for the city of Glasgow (Scotland) allowed comparisons of this cohort with with an existing control population, Dundee. Serological evidence was derived from blood donors, testing for IgG isotypes to the 27-kDa antigen. The study was longitudinal which enabled the level of seropositivity in individuals to be tracked over the duration of the study. Donors donated blood twice before and after implementation of the water filtration system and donors were questioned on their behaviour on each occasion e.g. water consumption, recreational activity, pet ownership etc. Mixed effects regression modelling was performed for this complex dataset.

Results: Introduction of filtration to the Glasgow municipal water supply resulted in a temporal reduction of antibody to *Cryptosporidium*. Consumers of private water supplies and those who swam on a regular basis had higher levels of antibody to the 27-kDa antigen. Pet owners had lower levels of antibody to this particular antigen.

Conclusion: Introduction of enhanced physical treatment of municipal surface water supplies is expensive but should prevent large waterborne outbreaks of cryptosporidiosis. However, unfiltered drinking water may contribute to herd immunity to this pathogen and the recent increase in swimming pool outbreaks in Central Scotland suggests small outbreaks of cryptosporidiosis may increase. The implications for drinking water improvements has world-wide relevance.

12.095 Molecular epidemiological analysis of Campylobacter infection in Fukuoka, JapanS. Fujimoto¹, F. Kojima¹, Y. Harada¹, S. Higashida², M. Shigematsu³¹Kyushu University, Fukuoka, Japan, ²CRC, Inc., Fukuoka, Japan,³National Institute of Infectious Diseases, Tokyo, Japan

Background: *Campylobacter* spp. is frequently isolated and important pathogens of acute enteritis in Japan. Nation-wide surveillance of food poisoning cases is run by the government, but a surveillance system for sporadic cases has not been established. The aim of this study is to investigate the molecular epidemiological features of the organisms isolated from the sporadic cases in Japan.

Methods and Materials: One hundred of the *Campylobacter* clinical strains those were isolated from the persons who visited hospitals in Fukuoka area were analyzed. The strains were isolated from fecal samples and were identified as *Campylobacter* spp. by culture-based methods and microscopic features. The information such as the age and gender of the person was obtained from those was attached to the clinical specimens for the culture (fecal samples). The isolates were identified those species by PCR using the primers those were reported by Wang et al and Samorsornuk et al. Flagellin gene (*fla*) typing of *C. jejuni* and *C. coli* was done by the method by Nachamkin et al.

Results: 1) Age and sex distribution of the cases.

Eighty-one cases with good patients information were analyzed. The cases included all age groups but approximately 70% of them were children under 15 years old and about half of them was under 10 years old. A peak occurred in youth aged 10 to 19 years. About under 20 years old, the rate of *Campylobacter* infection for children younger than 1 year was substantially lower than for other age groups. The incidence was approximately 1.5 times higher in males than in females.

2) Distribution of *Campylobacter* species

PCR using species-specific primer sets for *Campylobacter*s showed that 86% of the strains were *C. jejuni* and 11% was *C. coli*.

3) *Fla* typing of the *C. jejuni* and *C. coli* isolates.

Of the 91 *C. jejuni* and *C. coli* isolates studied, fifty strains could be successfully amplified. Twenty-one distinct *fla* RFLP patterns were observed when the 50 isolates were studied.

Conclusion: This study showed that *Campylobacter* infection is very common not only as food poisoning but also sporadic enteritis in Japan and also suggest the unique aspect of *Campylobacter* enteritis in Japan.

12.096 Non-typhoidal salmonellosis in Oppland and Hedmark counties, Norway, 1990–November 20, 2010

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Background: Salmonellosis are notifiable to the Norwegian Notification System for Infectious Diseases (MSIS) - since January 1, 1975. The Norwegian epidemiological situation has some general features. The two main serovariants causing infections are *S. Enteritidis* and *S. Typhimurium*, the first serovariant representing mostly imported cases, whereas cases caused by *S. Typhimurium* have a large proportion of indigenous cases. Other serovariants occur much more sporadically. The epidemiological situation in Hedmark and Oppland reflects that of the national situation.



Methods and Materials: Salmonella is cultivated at The Department of Medical Microbiology, Sykehuset Innlandet Trust, Lillehammer utilizing standard media and conditions. The reference testing is performed at The Norwegian Institute of Public Health—in accordance to the EU's Zoonosis Directive (Directive 92/117 EEC).

Results: Salmonellosis in Oppland and Hedmark by year 1990–20/11/2010 (year and number of cases)

1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	
71	38	49	58	84	60	72	67	94	67	
2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010
82	104	77	85	90	90	107	105	110	85	59

The total number of cases was 2 048. Oppland had 1022 notifications, whereas Hedmark had 1026 cases—throughout the time span described.

The were 1095 females and 948 males. For 5 cases no information of gender was available. Most cases occurred in September—294 cases (14.3%). The lowest total was in February—with 80 (3.9%). The highest total was notified in 2008 with 110 cases (7.7%), whereas there were only 10 cases (0.7%) notified in 1978.

Outbreak-associated serovariants—throughout the timespan comprise, S. Oranienburg, S. Typhimurium and S. Livingstone.

Conclusion: The Oppland and Hedmark situation is that of an area low endemicity for salmonellosis. Few domestic cases are encountered. The increase in incidence throughout the timespan correlates very well with travel abroad. There were relatively few cases in 1991–92 which is the same time period as the first Gulf War. With the increase of package tours sold throughout the late 1990s and after the turn of the millenium, with more than 1 million charter travels per year the incidence of salmonellosis is also rising.

Conclusion: Cat exposure affects *Toxoplasma* infection rates. Despite the limited number of animals tested, there appears to be genetic diversity of this parasite in Israel.

12.098 Seroprevalence of antibodies against HEV in slaughter pigs in Southern Bavaria, Germany

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Background: Hepatitis E virus (HEV) is an emerging pathogen predominant in developing countries causing enterically transmitted hepatitis in humans. In industrialized countries, infections with HEV occur sporadically and they have been considered as traveller's disease to endemic regions. Recently, reports on indigenous infections in industrialized countries have increased and zoonotic transmission from domestic pigs to humans is suggested. Also, domestic pigs and wild boars are considered as a reservoir for HEV worldwide. In Europe, the seroprevalence of anti-HEV antibodies in domestic pigs ranges from 30% to more than 90%. This wide range might either be due to different infection rates among the pig farms tested or due to the assays used. Most of the tests use antigens of HEV Genotyp (GT) 1 only. The objective of this study was to assess the seroprevalence of antibodies against HEV in blood and meat juice samples from slaughtered pigs in Germany using a newly developed ELISA assay based on GT1 and GT3 antigens.

Methods and Materials: In 2009, 516 serum samples and 198 corresponding meat juice samples from fattening pigs were collected at four slaughterhouses in Southern Bavaria, Germany. They were tested for anti-HEV antibodies using the recently developed ELISA assay based on recombinantly produced GT1 and GT3 antigens of HEV (Mikrogen GmbH, Germany). The obtained results were compared with the results obtained using an ELISA which uses a peroxidase conjugated HEV-antigen as detection molecule (HEV Ab, Axion Diagnostic, Germany) and verified by a HEV line-immunoassay (*recomLine* HEV IgG, Mikrogen GmbH, Germany) adapted to pig samples which also uses antigens of GT1 and GT3.

Results: The seroprevalence of anti-HEV IgG using blood samples was 68%, 73%, and 71% using the recently developed assay, the Axion assay and the line-immunoassay, respectively, and 7% for anti-HEV IgM using the line-immunoassay. Also, 68% of the meat juice samples were positive with the newly developed assay. Thus, the correlation coefficient between blood and meat juice samples was 0.94.

Conclusion: The seroprevalence was high in pigs at slaughter in Bavaria. The recently developed ELISA assay is suitable for testing for anti-HEV antibodies in both blood and meat juice samples.

12.099 Localization of proteases in amoeba of the genus Acanthamoeba

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Background: Among the emerging protozoa group, our study has been focused on opportunistic parasitic protozoa of the genus *Acanthamoeba*. Their presence has been described in all types of water, animals, contact lenses, human nasal epithelia, and other places (Visvesvara & Stehr-Green, 1990). These protozoa are causative agents of human diseases such as granulomatous amoebic encephalitis and amoebic keratitis which mainly affects contact lens wearers. Moreover they produce disseminated infections involving a wide range of organs in immunocompromised patients (Armstrong, 2000). Recent studies about the pathogenic character of these protozoa have suggested the role of several extracellular proteases and cellular receptors in the infection mechanisms of *Acanthamoeba* (Khan & Tareen, 2003). Immunological

12.097 Toxoplasma seroprevalence and genotypes in cats and ground feeders of Israel

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Background: A *T. gondii* seroprevalence study of cats and ground feeding animals in Jerusalem was conducted in order to determine the degree in which cats and their infective feces play a role in disease transmission by environmental contamination.

Methods and Materials: Jerusalem cats (1062) and 1612 sheep, poultry and pigeons from various locations were serologically surveyed by ELISA or MAT for *Toxoplasma* antibodies. Jerusalem cats were also surveyed for *Toxoplasma* oocyst excretion by copro-PCR (Salant *et al.*, 2007). *Toxoplasma* DNA isolates from local animals and a human were sequenced and analyzed by PCR-RFLP at the SAG2 locus.

Results: Amongst Jerusalem cats, 16.8 % were *Toxoplasma* seropositive, suggesting a substantial potential of ground contamination by oocysts. Seropositivity rates in cats increased with age from 11 days ($p < 0.001$). Rates were also significantly greater in cats captured from east- compared to west Jerusalem ($p < 0.001$), were higher in summer compared to other seasons ($p < 0.001$), and in cats that were of "strict domestic indoor habitat compared to those of different habitats ($p < 0.006$). Nine percent of cats surveyed were oocyst shedders determined by copro-PCR

Amongst ground-feeding animals, 8.9% south- raised and 37.5% north-raised sheep, respectively, were *Toxoplasma* seropositive. Amongst poultry, infection rates were 35.4% of Jerusalem battery raised chicken egg-layers, 12-44% of free-range chickens from various regions, 9% slaughtered turkeys in the north, but none of 58 poultry breeding stock, nor 50 broilers from Jerusalem raised in high biosecurity conditions, were observed to be *T. gondii* seropositive Also, 4 % pigeons from various locations were *Toxoplasma* seropositive.

It was possible to differentiate 24 native isolates at the SAG2 locus using PCR-RFLP analysis. Although most native animal isolates tested were of types II and III, two cat isolates were of type I.



diagnostic methods have become the most widely used techniques for the detection and characterization of useful proteins for the identification of pathogens.

Methods and Materials: A liter of water sample was filtered through a cellulose filter, the membranes were removed and incubate in plates. These plates were monitored for outgrowth of *Acanthamoeba*. After DNA extraction by the phenol-chloroform method, this DNA was amplified using genus-specific primer pairs (Vodkin *et al.* 1992). Protein purification was carried out as previously described (Khan *et al.*, 2000). The purified proteins were employed to obtain polyclonal antibodies through subcutaneous inoculation in Balb/c mice. The specificity and effectiveness of the obtained serum was tested by Western-Blot against the same purified proteins, which had been inoculated. Indirect immunofluorescence stainings were performed with the sera developed in mice previously and an anti-mouse IgG antibody FITC conjugated as a secondary antibody.

Results: Amoeba from the genus *Acanthamoeba* were identified in tap water samples from different points of Tenerife and Gran Canaria (Canary Islands) by PCR with the specific primer pair. We detected the presence of proteases in the extracellular medium and could obtain specific antibodies in mice against these proteases. Using the IIF technique we could observe different locations depending if the amoeba was in its infective form or resistance form.

Conclusion: In the infective form of *Acanthamoeba*, proteases are localized in granules and in the resistance form, proteases are scattered throughout the cytoplasm and around the cell wall.

12.100 Occurrence of Potentially Pathogenic Bacteria in Kuwait Fish Market

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Background: Vibriosis occurs in cultured and wild marine fish in salt and brackish water, particularly in shallow waters like the Arabian gulf during late summer, and the contact between fish seems to be an important factor for the spread of pathogen. Therefore, the presence of potentially pathogenic strains of bacteria was investigated in fish market across Kuwait.

Methods and Materials: Different fish species and ice samples were analyzed for food-borne pathogens using 16S ribosomal DNA sequencing.

Results: The results showed that 45% of bacteria isolated from different fish market are vibrio sp. Other species such as *Aeromonas* sp, *Alishewanella* sp, *Morganella morganii*, *Edwardsiella tarda*, *Photobacterium damsela*, *E.coli*, *Staphylococcus sciuri* and *Exiguobacterium* sp were found in different marine organisms.

Conclusion: The occurrence of these pathogens suggests that the fish commercialized in Kuwait fish market represent a health risk to the consumers additionally the need for following strict hygiene during handling and processing fish is highly required to prevent the transfer of potentially pathogenic bacteria to humans.

12.101 Evolution of RepFIB putative virulence plasmids of *Cronobacter* spp.

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Background: *Cronobacter* spp. are emerging opportunistic pathogens that cause meningitis, necrotizing enterocolitis, and septicemia, particularly among neonatal infants and elderly persons. The genus, previously classified as a single heterogeneous species, *Enterobacter sakazakii*, was recently established and divided into 6 species groups, based on a polyphasic genetic and phenotypic scheme. Members of the genus include *C. sakazakii*, *C. malonaticus*, *C. turicensis*, *C. dublinensis*, with 3 subspecies, *C. muytjensii*, and a *C. genomospecies* 1. To date, whole genome sequencing has been completed on two strains, *C. sakazakii* BAA-894 and *C. turicensis* z3032. We recently performed an in silico analysis of two large RepFIB plasmids found in each of these

genomes, pESA3 and pCTU1. We found that this plasmid was ubiquitous among *Cronobacter* spp. strains and that it harbored a number of putative virulence factors.

Methods and Materials: In this study, we sequenced a RepFIB plasmid from five other *Cronobacter* spp. strains, representative of the majority of the other species groups and subspecies. Comparative in silico analysis of these new plasmids with pESA3 and pCTU1 was performed.

Results: We identified an approximately 68 kb conserved backbone of this shared plasmid. Phylogenetic analysis of this plasmid backbone agreed with that of a partial chromosomal core genome phylogeny supporting our hypothesis that this plasmid was acquired long ago in the evolutionary history of *Cronobacter*. Further, its non-self transmissibility has led to an evolution that mirrors that of the chromosome. However, we also identified and describe novel putative genomic islands on these plasmids, many of which are homologous to virulence, host-associated and survival-related genetic elements from other enteric organisms.

Conclusion: The insertion of these differentially present loci has significantly contributed to the speciation of this genus and apparently has led to distinct pathotypes among *Cronobacter* spp.

12.102 Microbiological quality of different snack foods in an urban city of Pakistan

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Background: Problems of food safety in the developed countries differ from those faced by the developing countries like Pakistan and foodborne infections associated with consumption of poor quality food are frequently reported. The contamination of food products with infectious organisms and their persistence, growth, multiplication and /or toxin production is an important public health concern

Methods and Materials: Microbiological quality of various snack foods sold at retail outlets in Lahore, one of the major city of Pakistan was evaluated. A total number of 60 snack food samples comprising of 14 sandwiches, 26 burger and 20 pizzas were processed for various microbiological quality assays. These include Total aerobic plate count, Coliform count, enumeration of *Staphylococcus aureus* and detection of *Salmonella*.

Results: Sandwiches had the highest geometric mean of aerobic plate counts followed by the pizza and burger respectively. In total 73% of the snack foods were contaminated with Coliforms. The Coliforms were detected in 35% of the sandwiches, 23% of the burgers and 15% of the pizza samples processed. Staphylococcal contamination was higher as compare to coliforms contamination. The contamination level of snack foods was above the permissible level in 50% of the sandwiches, 27% of the burgers and 45% of the pizza when compared with the reference guidelines for grading of Ready to Eat Foods in Hong Kong & U.K. However *Salmonella* was not detected in any of the food sample tested. Foodborne infections associated with consumption of contaminated and poor quality food are frequently reported as an important public health concern. Hygienic measures necessary to reduce or prevent the contamination are also discussed to decrease the contamination level.

Conclusion: Bacteriological quality of snack foods consumed by low income people was determined in this study. Poor hygiene practices and favorable environment for the growth of bacteria due to use of meat as common ingredient are main reasons of food contamination. Hygienic manipulation practices, such as washing of hands, utensils and dishes, disinfection of usable things, protection of food from insects, flies and rodents, hygienic meat with proper refrigeration, are recommended to decrease the contamination level.

12.103 Application of enzyme linked immune-sorbent assay in diagnosis of neurocysticercosis in endemic region of Nepal

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Background: Human and porcine taeniasis/cysticercosis is reported to be among the major zoonotic diseases in Nepal. Many cases remain undiagnosed due to lack of expertise and lab facilities. Confirming the diagnosis in neurocysticercosis is always challenging due to wide variation in clinical presentation and limited availability of the tests in areas where the disease is endemic. The availability of noninvasive diagnostic confirmation in cases of suggestive clinical and imaging data has become even more important. Antibody detection by test procedure such as Enzyme-linked immunosorbent assay (ELISA) has been used with variable results.

Methods and Materials: one hundred patients with neurocysticercosis and 100 controls with other neurological disorder and healthy individual were prospectively studied in western region of Nepal where the disease is endemic. Case definition was made based on clinical findings, neuroimaging studies and epidemiological data. Serum samples from all individuals were obtained at admission and before any treatment was given. Samples were processed by the commercially available plate ELISA kit.

Results: The cysticercus antibodies could be demonstrated by ELISA in the sera of different groups of NCC and controls. ELISA detected antibodies in 96.3% cases with CT scan confirmed cases and 73.9% with clinical suspected cases. The test showed sensitivity of 87%, specificity of 84%, positive predictive value of 84.47% and Negative predictive value of 86.6%. The performance of ELISA also depended on number and type of lesion. ELISA had higher sensitivity (95.24%) in cases with multiple lesions compared to those with single cyst (81.03%) which is statistically significant ($p < 0.05$). And also higher sensitivity (97.5%) in cases with active lesions. 16% of the control population were seropositive.

Conclusion: The detection of specific antibody against *T. solium* cysticercal antigen using enzyme linked immune-sorbent assay (ELISA) is considered important diagnostic element for neurocysticercosis especially when neuroimaging technique are unavailable or inconclusive. Even in endemic region, ELISA can be used in diagnosing or confirming the diagnosis of neurocysticercosis. This study shows that ELISA can be used in any settings for diagnosis of neurocysticercosis.

12.104 WHO Global Foodborne Infections Network (GFN): Over 10 years of strengthening national capacities to detect and control foodborne and other enteric infections globally

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Background: The WHO Global Foodborne Infections Network (GFN), launched as WHO Global Salm-Surv in 2000, strengthens national capacities to conduct laboratory-based foodborne disease surveillance and response. GFN promotes collaboration between epidemiologists and microbiologists working in the public health, animal, and food sectors. Technical and financial support is provided by eleven Steering Committee Partners and GFN Regional Centers of Excellence.

Methods and Materials: Activities used to build surveillance and response capacity include international training courses which promote skill acquisition, critical thinking regarding surveillance systems, networking, and advocacy; an external quality assurance system (EQAS) which tests laboratories' abilities to conduct serotyping and antimicrobial susceptibility testing; a passive surveillance system for *Salmonella* serotype data (Country Databank); focused regional and national projects (including enhanced surveillance work); reference services; and an electronic discussion group (EDG) and other forms of communication to keep GFN Members informed and connected on foodborne disease issues.

Results: As of November 2010, GFN has conducted 74 international courses at 18 sites, providing training to more than 1,200 microbiologists and epidemiologists from more than 140 countries on topics such as isolation and identification of foodborne and other enteric pathogens

such as *Salmonella*, *Campylobacter*, and *E. Coli* 0157; antimicrobial resistance; how to strengthen surveillance systems; mass gathering surveillance; burden of illness estimation; outbreak response; source attribution; antimicrobial susceptibility testing; and epidemiology exercises for outbreak detection and response. EQAS has 180 laboratories participating in its current cycle. More than 250 EDG messages have been distributed, and the Country Databank reports 1633 members from 180 countries and 1081 datasets from 84 countries. Projects include microbial characterization and enhanced surveillance initiatives in Asia, Africa, and Central America. To date, more than 25 articles have been published on GFN projects in the international peer-reviewed literature.

Conclusion: GFN has increased the capacity of nations to effectively conduct laboratory-based surveillance and response. Future network initiatives will focus on continued enhancement of systems, data collection, focused projects and training course follow-up.

12.105 Prevalence and Antimicrobial Resistance of *Listeria spp* Isolated from Foods in Behshahr—Iran

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Background: *Listeria spp* is a ubiquitous organism that is widely distributed in nature including soil, sewage, and plant foods, unpasteurized dairy products. Among the species of *Listeria*, only *Listeria monocytogenes* is pathogenic to humans, causing serious infections such as meningitis or septicemia in neonates, immunocompromised patients and pregnant women

Methods and Materials: 380 samples were collected from June 2009 to June 2010. *Listeria spp* were isolated from (95) cheese, (80) yoghurt, (75) salad, (70) milk products, and (60) meat. Samples were collected and processed according to international standards methods of the Food and Drugs. Biochemical tests were performed to confirm the diagnosis. Antibiotics susceptibility pattern of *listeria* strains was determined by disk diffusion method.

Results: All strains showed susceptibility to the sulfamethoxazole-trimethoprim and vancomycin. 25.7% of *listeria spp* showed resistance to penicillin G; 35.8% to ampicillin and 4.2 % to erythromycin. Among the different foods for isolation of *Listeria spp*, cheese showed a higher number of strains resistant to antibiotics

Conclusion: As *L. monocytogenes* can develop into antibiotic resistant gradually by achievement of recognized antibiotic resistance genes from Gram-positive bacteria, a continual investigation of emerging antimicrobial resistance in *listeria spp* is significant to insure treatment effectiveness of human listeriosis. These data can be beneficial in building up background information on antibiotic resistance of strains isolated from food and food natural and for epidemiological and public health studies of *L. monocytogenes*.

12.106 Cpa, the outer membrane protease of *Cronobacter sakazakii* activates plasminogen and mediates resistance to serum bactericidal activity

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Background: *Cronobacter spp.* are emerging neonatal pathogens in humans, associated with outbreaks of meningitis and sepsis. To cause disease, they must survive in blood and invade the central nervous system by penetrating the blood-brain barrier. *C. sakazakii* BAA-894 possesses a ~131 kb plasmid (pESA3) that encodes for an outer membrane protease (Cpa) that has significant identity to proteins that belong to the Pla subfamily of omptins. Members of this subfamily of proteins degrade a number of serum proteins, including circulating complement, providing protection from the complement-dependent serum killing. Moreover, proteins of the Pla subfamily can cause uncontrolled plasmin activity by converting plasminogen to plasmin and inactivating the plasmin inhibitor α 2-antiplasmin (α 2-AP). These reactions enhance the spread and invasion of bacteria in the host.



Methods and Materials: In this study, a *cpa* isogenic mutant was constructed in *C. sakazakii* BAA-894 by allelic exchange mutagenesis and tested for resistance to serum, and complement cleavage, as well as plasmin activation and inactivation of α 2-AP in comparison to the wild-type parent strain.

Results: We found that an isogenic *cpa* mutant showed reduced resistance to serum in comparison to its parent *C. sakazakii* BAA-894 strain. Over-expression of *Cpa* in *C. sakazakii* or *E. coli* DH5 α showed that *Cpa* proteolytically cleaved complement components C3, C3a and C4b. Furthermore, *Cpa* over-expressing *C. sakazakii* strain caused a rapid activation of plasminogen and inactivation of α 2-AP.

Conclusion: Our results strongly suggest that *Cpa* may be an important virulence factor involved in serum resistance, as well as spread and invasion of *C. sakazakii*.

12.107 A case of autochthonous hepatitis E in Austria

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Background: We present the case of a 79 year old man with acute hepatitis E. The patient sought medical attention because of jaundice, malaise, anorexia and nausea and was admitted to the surgical ward of our hospital because of a suspected tumour lesion on the first ultrasound scan of the abdomen. However, a consecutive CT and an MRI ruled out both a tumour and any other cause of biliary obstruction. Aminotransferases were markedly elevated (maximum ALT level of 1241 U/l and AST of 892 U/l) with liver synthesis parameters being at no time impaired.

With symptomatic supportive therapy the patient made a complete clinical recovery after one week; liver enzymes and bilirubin returned to normal levels after 39 days.

Methods and Materials: Diagnosis was established by serology (anti HEV IgG and IgM positive) and PCR from blood after infection with hepatitis A, B, C, CMV, EBV and leptospirosis and other conditions like autoimmune hepatitis had been ruled out. Further molecular analysis revealed that the virus was genotype 3 (which is associated with milder disease).

Results: The most intriguing aspect about this case is that the patient had not been outside Austria in the last years before he fell ill, which means that this is a case of autochthonous hepatitis E. The exact mode of acquisition remains elusive, however, as the patient had not consumed deer or wild boar or undercooked pork meat or internal organs of animals, his wife was negative for hepatitis E and there was no other index case of hepatitis E, either.

Conclusion: In conclusion, we propose testing for hepatitis E in any patient who presents with so-called cryptogenic hepatitis even if there is no history of travelling abroad.

12.108 Epidemiological study of intestinal parasitic infestation in rural village of Nepal

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Background: About 70.0% of health problems and deaths in Nepal are attributed to infectious diseases. Outbreaks of diarrhea, dysentery, cholera, enteric fever and jaundice occur every year and are associated with contamination of drinking water. Environment is highly contaminated and most people are infected with some kinds of intestinal parasites. Intestinal parasitosis is one of the major public health and socio-economic problems in Nepal. It is ranked among the top 10 morbidity in Nepal.

Methods and Materials: An epidemiological study of the prevalence of intestinal parasites in rural village of western Nepal was carried out during the period August 2009 to July 2010. Fecal samples were collected from

the patients attending to different hospitals and private laboratories throughout the district. Direct smear method for microscopic examination was used to all samples.

Results: A total of 985 participants were included in the study. The age ranged from 1 to 86 years. Commonly affected age group was of below 15 years. Male to female ratio was 1.3:1. The general prevalence of infection with different types of intestinal parasites was 14.7% (145). The fecal examination revealed different types of helminthes (7.2%) and protozoan (7.5%). *Giardia lamblia* was the most common parasite (5.5%), followed by *Entamoeba histolytica* 2.0%, *Ascaris lumbricoides* 4.0%, *Ancylostoma duodenale* 1.8%, *Trichuris trichiura* 0.8%, *Hymenolepis nana* 0.4% and *Taenia spp* 0.2%. Multiple parasites were observed in 11 samples. Higher prevalence rates of parasitic infections were seen among children and were also found to be associated with families with lower income and lower education level.

Conclusion: Intestinal parasitosis is one of the common morbidity in Nepal although regular deworming is practiced in some part. It is more common in younger age group (<15 years). *G. lamblia* was the commonest protozoan infection while *A. lumbricoides* was the commonest helminthes infection. Further field survey is needed to determine the prevalence of carrier state of intestinal parasite in general population in rural Nepal.

12.109 Statistical modeling of risk factors of *Escherichia coli* O157:H7 contamination in a beef processing plant

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Background: Risk factors for *E. coli* O157:H7 (or EHEC or enterohemorrhagic *E. coli*) are a combination of farm to fork variables. By analyzing commonly collected data from a beef packing plant, we hoped to find new risk factors for *E. coli* O157:H7 contamination.

Methods and Materials: A dataset covering 484 process days was compiled for analysis. Variables included day of week, number of lots per day, number of organ condemnations, processing errors and carcass quality measures. Using counts of positive *E. coli* tests as our dependent variable, a negative binomial model was fitted to the data. Forward selection with a cutoff p-value of 0.30 was used to include variables into the model. After selecting the initial variables, interaction variables and confounders were analyzed.

Results: Three variables were included in the initial forward selection: percentage of bagging errors, percentage of liver condemnations, and percentage of choice carcasses. No significant interaction between these variables was found. Two additional variables (number of lots per day and percentage of heads condemned by dentition) were added into the model as confounders because they changed one or more variable coefficients by >10%.

Final model interpretations:

1. On days with bagging errors, the rate of positive test results increased by 2.26 [1.12-4.55, p = 0.022].

2. On days where >75% carcasses grade choice, the rate of positive test results increased by 2.57 [1.01-6.57, p = 0.048].

3. All categories of increased liver condemnations were associated with an increased rate of positive test results; 19-22% increased rate by 3.28 [1.31-8.22, p = 0.011], 22-27% increased rate by 3.89 [1.50-10.08, p = 0.005], and >27% increased rate by 3.58 [1.31-9.77, p = 0.013].

Conclusion: Bagging errors can result in fecal contamination of the carcass, so association with increased positive tests is expected. Increased positives associated with condemned liver percentages as well as grade is interesting and suggests risk factors in management at the pre-harvest level. We only had data on a day level, but with individual level data, this mode of analysis might be able to clarify more control points for *E. coli* O157:H7 contamination.

**12.110** **Detection of indicator bacteria from multiple drinking water sources—West Amhara, Ethiopia, 2005–2009**

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Background: In developing countries, control of the microbiological quality of drinking-water is an important factor in the control of waterborne diseases. Fecal contamination of drinking water can transmit a number of infectious diseases including cholera, *Escherichia coli* (*E. coli*), and shigellosis. In Ethiopia water quality monitoring is not well developed and there is limited availability of laboratory data for comprehensive intervention and trend monitoring. The aim of this study is to assess the bacteriological content of drinking water from multiple sources in West Amhara, Ethiopia during 2005–2009.

Methods and Materials: Drinking water samples were collected from 36 districts and a variety of different sources in West Amhara from 2004–2009. Samples were tested for water quality indicator bacteria using the multiple tube method as per standard microbiologic techniques. Most probable number (MPN) determination of *E. coli* and total coliforms was used to assess water quality. Data was transcribed from hand written logbook to an electronic data base and analyzed using Epi-Info v3.3.2.

Results: A total of 475 drinking water samples were analyzed. The majority (64.8%) were collected from piped sources (Table 1). The prevalence of total coliforms from all samples obtained was 47.4%; prevalence of *E. coli* was 28.2%. *E. coli* was isolated from all sources of water; 47.3% of samples obtained from well water were positive for *E. coli*. In 53 (11.2%) samples, the MPN count was >180/100ml indicating the water is contaminated. Chlorination showed statistically significant protective association with the presence of *E. coli*. (unadjusted OR=0.29, 95% CI=0.2-0.44, $p < 0.001$) and presence of coliforms (uOR=0.25, 95% CI=0.17-0.37, $p < 0.001$). Piped sources of drinking water compared to all other sources had a significantly protective association with presence of *E. coli* (uOR= 0.3, 95% CI=0.2-0.46, $p < 0.001$). Rural water sources were significantly associated with presence of *E. coli*. (uOR= 3.6, 95% CI=2.1-6.6, $p < 0.001$)

Conclusion: Fecal contamination is present in all types of drinking water sources in Western Amhara. Therefore, this study reinforces the need to rigorously maintain and monitor chlorination levels in drinking water and to strengthen other water sanitation strategies to improve drinking water safety.

12.111 **Etiological investigation of diarrheal diseases in the suburbs of Nairobi, Kenya**

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Background: Etiological investigation of diarrheal diseases was carried out on the children of under 5 year of age in the surrounding area of capital Nairobi in Kenya from 2008 to 2009.

Methods and Materials: Diarrheal stool samples were collected from those who visited health facilities complaining of diarrhea at least more than three times a day. Samples from healthy controls which correspond to the diarrheal cases were collected from children of same age and sex living in the same area after confirming no diarrhea for a week. All samples were examined for etiological agents causing diarrhea such as enteropathogenic *Escherichia coli*, *Campylobacter* sp and Rota virus and so on, as well as *Vibrio* sp., *Shigella* sp. and *Salmonella* sp. For the detection of enteropathogenic *E. coli*, multiplex PCR was applied. Isolation rates among two groups are statistically analyzed by McNemar test.

Results: A total of 595 paired samples were analyzed bacteriologically and molecular biologically. Classical diarrheagenic pathogens like *Shigella* sp. *Salmonella* sp. and *Vibrio cholerae* were not isolated in this study. The detection rate of Rota virus among diarrheal cases and control group was 169 (28.4%) and 1 (0.17%), respectively. Isolation rate of enteropathogenic *E. coli*, enterotoxigenic *E. coli* and enteroaggregative *E. coli* from diarrheal cases and control group were 14 (2.4%) and 16 (2.7%), 37 (6.2%) and 38 (6.3%), 88 (14.8%) and 111 (18.7%), respectively. McNemar test reveals that Rota virus only is closely related with occurrence of diarrhea but other pathogens are not associated with those of diarrhea.

Conclusion: In the suburbs of Nairobi, a major causative agent of diarrheal diseases was Rota virus and classical enteropathogens seemed to be no longer major diarrheagenic agents. It is also suggested that significance of enteropathogenic *E. coli*, enterotoxigenic *E. coli* and enteroaggregative *E. coli* as diarrheagenic agents is unclear.

12.112 **The enemy of good is perfect; Saccharomyces fungemia in a patient taking probiotic**

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Background: Probiotics are typically considered a safe product, however the possibility of a life threatening fungemia exists with their use. Composed of varying strains of bacteria or yeast and touted as “beneficial”, “natural”, and “non-pathogenic”, probiotics are available to the general public over the counter. They have been generally accepted as preventative therapy for antibiotic associated diarrhea as well as adjunctive therapy for infectious diarrhea, primarily focused on *Clostridium difficile*. Inclusion of these products into the already established and effective antibiotic treatment regimen for *C. difficile* infections may cause more harm than good.

A 34 year old female with a history of Hirschsprung’s Disease status post total colectomy with ileostomy had frequent hospital admissions for stricture of her ileostomy, requiring endoscopic dilatation by her Gastroenterologist. She was plagued by frequent infections with *C. difficile*. For this reason she was started on Florastor, a probiotic which utilizes *Saccharomyces boulardii* as its active yeast. Within weeks of its initiation she was again hospitalized for nausea, vomiting, and dehydration which was found to be related to another stricture. She was again taken to the endoscopy suite for dilatation. Following the procedure she developed fever and chills.

Methods and Materials: Blood cultures were drawn from a mediport.

Results: Blood cultures grew three fungal species, one of which identified as *Saccharomyces cerevisiae* later subspecies by molecular identification to *Saccharomyces boulardii*. Her fungemia was initially treated with Fluconazole, however subsequent to Infectious Disease consult she was changed to a 14 day course of Voriconazole and advised not to restart Florastor or consume other probiotics.

Conclusion: While it is rare for probiotics to cause harm including potentially fatal fungemia, it does occur as this case illustrates. This patient was not an ideal candidate for probiotic use. She had several potential risk factors for *S. boulardii* fungemia including chronic central access via her mediport, frequent gastroenterological manipulations and alterations in the gastrointestinal barrier via her ileostomy. Physicians should be aware of the potential harms and risk factors and caution high risk patients against their use. Evidence shows that current antibiotic treatment regimens for *C. difficile* are effective and safe when used appropriately.

12.113 **Ethiological spectrum of foodborne infections in Timis Country, Romania**

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Background: Because of their acute evolution and unexpected complications, foodborne infections represent an important public health



problem. The purpose of paper is to determine the etiological spectrum of foodborne infections in a group of patients from Timis Country, Romania.

Methods and Materials: There were retrospectively analyzed the medical records of 182 patients with various foodborne infections at Hospital of Infectious Diseases Timisoara in 2009. Diagnosis was established based on epidemiological aspects (the onset of foodborne infection after food consumption from restaurants, family party, group party with the establishment of infectious outbreaks), physical examination (fever, repeated shivers, nausea, vomiting, headache, multiple diarrheic fetid stools, abdominal colic, pyrosis, dizziness, paresthesia of lower limbs etc.), laboratory tests (erythrocyte sedimentation rate, blood counts, fibrinogen, glycemia, blood cultures, lingual swabs, throat swabs, stool cultures, stool parasitological examinations, natremia, kalemia, calcaemia) and different explorations (abdominal echography, electrocardiography). Data of the epidemiological survey were collected from the Institute of Public Health from Timisoara. The statistical processing was done using Epi Info 3 software.

Results: From the total number of patients, 80 (43.95%) were residents in rural areas and 102 (56.84%) were residents in urban areas. There were registered 7 epidemic outbreaks which occurred after the collective consumption of potato mayonnaise, ground beef meatballs with beer, duck eggs, cheese, cream cakes with egg, salami pizza etc. Symptomatology included: fever (170 patients), shivers (182 patients), sweating (182 patients), nausea (182 patients), vomiting (172 patients), diarrhea (182 patients), abdominal colic (175 patients), muscle cramps (150 patients), headache (182 patients), and asthenia and loss of appetite (182 patients). From the study group, the etiological agent has been identified only in 110 (60.43%) cases: *Staphylococcus aureus* (25 patients), *Salmonella* (42 patients), *Schigella* (23 patients) and *Escherichia coli* (20 patients). Seventy-two of the patients received antibiotics prior to hospital admission and all patients required endovenous hydroelectrolytic replacement with glucose, saline and Ringer, along with symptomatic medication (analgesics, antipyretics, antispasmodics, antacids etc).

Conclusion: Knowledge of the etiology of foodborne infections allow the usage of an efficient antibiotics therapy along with the specific prevention and control measures with clinical and laboratory optimal results.

12.114 Multiple outbreaks of norovirus gastroenteritis linked to an infected post-symptomatic food handler

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Background: Norovirus strains of the GII.4 genotype have become the predominant cause of norovirus gastroenteritis outbreaks over the past decade in the United States, Europe, and Oceania. Contamination of food by infected food handlers can lead to outbreaks of norovirus gastroenteritis. We report a series of outbreaks linked to an asymptomatic catering company food worker infected with norovirus genotype GII.4.

Methods and Materials: An outbreak investigation was undertaken, comprising retrospective cohort studies of attendees at events receiving food from the catering company, using standard questionnaires. Faecal and environmental specimens were collected for microbiologic analysis. An environmental investigation of the catering company premises was also conducted. Specimens were tested for RNA of norovirus genogroups I and II, and strains were further characterised by genetic sequencing.

Results: Outbreaks of gastroenteritis in four separate events were linked to food prepared by the same catering company during the period 20-22/09/2010, with a total of 52 cases. The attack rate among people exposed on 20/09/2010 was 30%, and this declined significantly over the next two days to 5% for those exposed on 22/09/2010. Three food items had significant independent association with illness. An uncommon GII.4 norovirus strain was identified from faecal specimens of symptomatic event attendees, from an environmental specimen collected from a toilet door handle at the catering company premises, and from a faecal specimen from a food handler who had a history of gastroenteritis symptoms that resolved 18 hours before preparing food for the events: all isolates were indistinguishable.

Conclusion: Results strongly suggest that these four outbreaks were linked to a single infected food handler preparing food less than 24 hours after resolution of symptoms. This outbreak emphasises the impact that infected food handlers can have on amplifying transmission of norovirus. Exclusion of infected food handlers from the workplace until 48 hours following resolution of symptoms is warranted.

12.115 Food-borne *Listeria monocytogenes* outbreak associated with a traditional herring product, Germany 2010

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Background: *Listeria monocytogenes* (*Lm*) can cause food-borne outbreaks with symptoms of bacteraemia and meningoenephalitis with high fatality rates in risk groups such as elderly or immunosuppressed patients and fetuses. In Germany, laboratory diagnosis of *Lm* is notifiable; additional genotyping of isolates is not mandatory.

Between January and November 2010, patient isolates for 47 of 56 listeriosis cases (84%) reported in Baden-Wuerttemberg were submitted to the Robert Koch-Institute and the Binational Austrian-German Consiliar Laboratory for pulsed-field gel electrophoresis (PFGE) genotyping. In October 2010, two cases of listeriosis were reported in a couple that had consumed "slices of salted herring in oil", manufactured in Baden-Wuerttemberg according to Russian tradition. *Listeria* with an identical, so far unobserved PFGE-pattern were found in samples taken from the store where the product was purchased. The product, distributed via grocery stores for Russian food items in Germany and Belgium, was recalled from the market in November 2010.

Methods and Materials: To investigate the extent of this outbreak, cases were ambispectively identified by comparing the PFGE-patterns of the herring product to patient isolates submitted to the national reference laboratory. Additional case finding was performed by local public health officers through contacting cases and identifying other persons with concomitant herring product consumption. Confirmed cases were defined as patients with laboratory confirmed *Lm* infection with the outbreak PFGE-pattern (Ascl/Apal), probable cases were household contacts with a *Lm* positive stool sample who reported consumption of the herring product since September 2010.

Results: As of December 8th, 2010 we found 7 confirmed cases, including a neonate, and one probable case. There were 5 male cases and the age ranged from 0 to 75 years (median 55 years). Five cases suffered from pre-existing chronic diseases. One elderly patient died. All cases had a family history of immigration from Russia or other members of the Commonwealth of Independent States.

Conclusion: The importance of consistent use of genotyping in listeriosis surveillance is underlined by this investigation. This report also emphasizes the added value of molecular typing for outbreak investigations, especially in a setting with broad geographical case distribution and where language barriers may limit the outcome of questionnaires.



12.116 A field laboratory method for the recovery of *Vibrio cholerae* isolates from food and environmental samples suitable for epidemiological investigations in developing countries

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Background: Cholera is endemic in countries of the world where socio-economic conditions are poor. On the occasion of outbreaks, it is essential to investigate the reservoirs and the infection sources. Therefore, there is a need for a simple, low cost and rapid method of isolation and identification of *Vibrio cholerae* species.

The aim of this work was to validate the presumptive identification driven by a two steps screening protocol (growth without NaCl, positive oxidase reaction) applied to environmental isolates obtained after isolation on TCBS agar.

Methods and Materials: Two different isolation procedures (enrichment at 41°C in saline alkaline peptone water during 18h followed by spreading on TCBS plates vs direct spreading) were respectively applied to 2875 environmental samples (1400 surface waters, 115 sediments and 325 cockles) and 10 water samples. 825 isolates were collected according to the tested screening procedure.

The confirmation of the presumptive identification of these isolates was done by two methods (API20E & PCR).

Results: The proposed screening procedure seemed to be very efficient since the identification confirmation rate by the two methods was more than 85%, whatever the nature of specimens or its treatment before spreading on TCBS agar.

The use of the trait "sucrose fermenting" alone, is not sufficient for a presumptive identification of *Vibrio cholerae* with environmental samples: it was observed that only 51 out of 93 yellow colonies on TCBS agar give a presumptive identification of *Vibrio cholerae* according to the 3 traits.

But to use TCBS agar as selective medium is probably a key pre-condition for making the proposed selection of strains effective for good presumptive identification.

Conclusion: This protocol provides reliable identification of the species *Vibrio cholerae* with basic laboratory equipment and a minimum of expensive consumable products. The identification is obtained within 72h.

This confident recovery of *Vibrio cholerae* allows reduction of the number of agglutinations with O1 O139 anti-sera in order to identify the agent of cholera. Moreover strains are available for further comparisons.

At the opposite, PCR methods applied directly on food or environmental samples are faster but require specific equipment, expensive reagents and controlled laboratory environment. Overall, they don't provide strains for epidemiological investigations.

12.117 The incidence rate of travel-associated infectious diseases among Japanese travelers by destination country

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Background: A total of 2–3% of returned travelers present with fever, which demands prompt attention. Therefore the information on the incidence rates of travel-associated infectious disease by destination country is of great help for both travelers and health care providers in pre- and post-travel risk assessment. In this study, we estimated the incidence rate by destination country of major travel-associated febrile illness such as malaria, dengue and enteric fever (typhoid and paratyphoid) among Japanese travelers using the national surveillance data between 2006 and 2009.

Methods and Materials: To estimate the incidence rates of malaria, dengue and enteric fever by destination country, we used the number

of cases diagnosed between January 2006 and December 2009 and reported through the national surveillance system as numerators. The number of Japanese travelers visiting individual countries obtained from Japanese National Tourism Organization (JNTO) was used as denominators.

Results: In Southeast Asia, dengue had the highest incidence rate in all countries, followed by enteric fever and malaria. In South Asia, enteric fever was dominant in most countries, whilst in Pakistan and Maldives, the disease of the highest incidence rate was malaria and dengue respectively. In Sub-Saharan Africa, malaria mostly caused by *P. falciparum* showed by far the highest incidence rate. In Central America, the incidence rate of dengue was the highest, whilst it was different for each country in South America. In Oceania, malaria had the very highest incidence rate in Papua New Guinea and *P. vivax* was the major causative agent. In the other countries in this region, however, no malaria cases were reported and dengue was dominant.

Conclusion: The incidence rate of malaria was by far the highest in Sub-Saharan African countries and Papua New Guinea. However dengue or enteric fever was dominant in most of the other countries. Both travelers and medical providers can use these incidence data for pre- and post-travel risk assessment. Continuing update for the data would be expected.

12.118 Imported Cases of Chikungunya Fever in the Czech Republic

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Background: Chikungunya fever is an emerging infection which has spread widely in the Indian Ocean region and South-East Asia in recent years. Due to its prevalence and high attack rates during outbreaks, chikungunya represents a significant risk to travellers to endemic countries. The symptomatology of dengue and chikungunya fever is similar and therefore many cases of chikungunya virus (CHIKV) infection can be misdiagnosed.

Methods and Materials: In a prospective surveillance study at Bulovka University Hospital in Prague there were evaluated patients with febrile illness returning from tropical countries between December 2004 and November 2010. Acute CHIKV infections were diagnosed using complement fixation (CFR), indirect immunofluorescence, ELISA and RT-PCR. Data on travel destination, clinical and laboratory features were collected in all patients with confirmed infection.

Results: In the study period the acute CHIKV infection was diagnosed in 8 patients (3 men and 5 women, aged from 29 to 54). The hospital stay required 6 patients and 2 were observed as out-patients. The travel destinations in the study group were: Mauritius (4x, 2006), Maldives (1x, 2009), Malaysia (1x, 2009), Burma (1x, 2009) and India (1x, 2009). The predominant symptom was fever (lasting from 1 to 5 days) and arthralgia, which were observed in all patients. Rash was described in 6 patients, followed by gastrointestinal symptoms (4), myalgia (3) and cephalgia (3). Laboratory findings at admission were: decreased WBC (range 2.0–6.8; median 3.45×10³/μl) and platelets counts (range 103–275; median 151 × 10³/μl) with moderate elevation of liver transaminases: AST (range 17.4–72.0; median 40.8 IU/l), ALT (range 13.2–75.6; median 24.6 IU/l). CRP ranged from 0.6 to 94 (median 7.65 mg/l). The outcome of all patients was favourable, only 3 patients complained of prolonged arthralgia.

Conclusion: Arboviral infections range among the most emerging in the tropical countries. Due to increasing risk of import of these infections to non-endemic areas, it is necessary to improve the diagnostic approach to febrile patients returning from tropical countries. Furthermore, the travellers from developed countries can serve as sentinel population providing data on epidemiological situation in endemic regions.

**12.119 A case of severe typhus in a man returning from Africa**

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Background: With continuous increase of migration and mobility worldwide, severe rickettsial illness as emerging infectious disease needs to be considered as differential diagnosis in cases of fever in returning travellers.

Methods and Materials: A 20-year old Somali student (UK resident) presented with one-week history of fever, rigors and myalgias. He had headaches with mild neck pain and photophobia, and dry cough. He denied shortness of breath, sore throat or rash/bleeding/other symptoms. Symptoms had started one day after returning from Addis Ababa/Ethiopia (had stayed with relatives for one month). Well throughout stay, no insect bites/contact with animals. He had not taken malaria prophylaxis.

Past medical history included treated pulmonary/spinal tuberculosis and epilepsy. Except for Khat use, he denied alcohol, cigarette or intravenous drugs use. He was married and lived with his wife and his child, all well.

On admission appeared unwell: Conjunctival infiltration, temperature 39.0°C, hypotension (90/55mmHg) and pulse rate of 120bpm. Pulsoximetry oxygen saturation 98% (air), respiratory rate 18/min. Three centimetre tender hepatomegaly, but rest of abdominal examination, cardiovascular, respiratory and neurological examination normal, no meningism, rash or eschar.

Results: No malaria parasites on blood film, normal arterial blood gas results. Platelets 84, otherwise normal CBC. Prothrombin time 17.4. C-reactive protein >300, ALP 177, Na 130, Albumin 18, otherwise normal liver/renal parameters. Cyptococcal antigen, HIV/hepatitis and streptococcal/legionella urinary antigen tests all negative.

Electrocardiogram - sinus tachycardia; Chest radiograph, unenhanced CT head and CSF results (glucose 3, blood glucose 5.9, protein 0.24, WBC<1) all normal.

Differential diagnosis acute bacterial or viral infection, Ceftriaxone/ Doxycycline initiated. Subsequent deterioration (agitation, hypotension and ARDS) with patient requiring intubation, ventilation, inotrope treatment, broadened antibiotic cover (Meropenem, Linezolid and Ciprofloxacin), IVIG and parenteral feeding.

Reference laboratory test results showed positive rickettsia-PCR, epidemic typhus group IgM and IgG antibody. Patient stabilised by day six of his admission with improving blood parameters. He was extubated and antibacterial de-escalated to oral Doxycycline. Full recovery two weeks after admission.

Conclusion: Severity/epidemiology of case suggests infection with *Rickettsia prowazekii* (gram negative, intracellular organism transmitted by human body louse *Pediculus humanus corporis*) and highlights importance of prompt diagnosis/initiation of effective antibiotic treatment in suspected cases of imported rickettsial illness.

12.120 Dengue infections in travellers to Thailand: Risk estimates

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Background: Dengue is an arthropod-borne infection caused by a Flavivirus spread by the *Aedes* mosquitoes. Dengue is endemic in most tropical and subtropical countries, many of which are popular tourist destinations. Dengue has emerged as a frequent problem in international travelers, in particular those to Asia. Thailand is one of the countries with the highest risk for dengue.

Methods and Materials: Using mathematical modelling, we set out to estimate the risk of non-immune persons to acquire dengue when traveling to Thailand. The model is deterministic with stochastic parameters and assumes a Poisson distribution for the mosquitoes' biting

rate and a Gamma distribution for the probability of acquiring dengue from an infected mosquito. From the force of infection we calculated the risk of dengue acquisition for travelers to Thailand arriving in a typical year (averaged over a 17 years period) in the high season of transmission.

Results: The risk of acquiring dengue for a traveller arriving in the high season of transmission and staying for 7 days is 0.2% (95% CI: 0.16%–0.23%), whereas the risk for travel of 15 days duration and 30 days is 0.46% (95% CI: 0.41%–0.50%) and 0.81% (95%CI: 0.76%–0.87%), respectively.

Conclusion: Our data highlight that the risk for non-immune travelers to acquire dengue in Thailand is substantial. The incidence of 0.81% is similar to those found in a prospective seroconversion study in Israeli and Dutch travellers. Risk estimates based on mathematical modelling will help the travel medicine provider give better evidence based advice for travelers to dengue endemic countries.

12.121 Imported malaria: experience of a referral center in Tokyo

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Background: Malaria is a common and important infectious disease in international travelers. The aim of this study was to review the current trends in imported malaria at a referral center for patients with tropical infectious diseases in Tokyo.

Methods and Materials: We have conducted a retrospective chart review of malaria cases seen at the National Center for Global Health and Medicine, a 750-bed acute care teaching hospital with a highly infectious disease isolation unit between April 2007 and September 2010.

Results: A total of 55 malaria cases were reported during the study period; 32 (58%) of them were due to *Plasmodium falciparum*, 16 (29%) were *P. vivax*, 5 (9%) were *P. ovale*, and 1 (2%) was *P. malariae*. Forty-four (80%) cases were Japanese and eight (15%) were from African countries. Significant seasonality in the incidence was not observed. The median age was 30 years old (range: 18-67). Most (76%) of infections were acquired in sub-Saharan Africa, especially in West Africa. The most common reasons for travel were for volunteer/aid work (44%), for tourism (22%), or to visit friends/relatives (16%). There were no cases who had taken appropriate antimalarial chemoprophylaxis. Mefloquine and artemether-lumefantrine were the most commonly prescribed antimalarial drugs for uncomplicated falciparum malaria. In falciparum malaria, four cases met the criteria for severe/complicated diseases. Acute renal failure and jaundice were the main manifestations. Time from symptom onset to diagnosis in these severe cases was longer (median: 4 days) than that of uncomplicated malaria and was partly due to doctors' delay in diagnosis. Intravenous quinine and/or rectal artesunate, which are not licensed in Japan but we are allowed to use, were used in those cases and no deaths were reported.

Conclusion: We have seen over 50 cases of imported malaria in Tokyo over the past three years. *Plasmodium falciparum* was the most common species. The risk of contracting malaria is likely to be highest in West Africa even during the dry season when Lassa fever epidemics sometimes occur. Major concerns are the low use of antimalarial chemoprophylaxis in travelers, the delay in diagnosis of malaria, and the limited availability of parenteral antimalarial drugs.

12.122 Concept of operation for emergency response plans at United States Airport point of entry

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Background: The United States (U.S.) Point of Entry (POE) concept of operations for response to communicable disease is based on the World Health Organization (WHO) Phases. The WHO Response Phase declaration is based on the current geographic spread of the influenza pandemic virus throughout the world.



Methods and Materials: If POE waited for the WHO to declare a Phase to initiate interventions, the POE will most likely find itself delaying necessary actions to control the transmission of the virus. Additionally, POE may be requested to initiate pharmaceutical and non-pharmaceutical actions at the request of the Federal Government, prior to confirmation of the virus arriving in the U.S.

Results: Due to the unique nature of U.S. POEs, the concept of operation for response plans should be developed to incorporate international, federal, state and local response. Most U.S. POE concept of operations was based on the sustained human-to-human transmission occurring overseas, and utilized the World Health Organization (WHO) Phases. This was found to be inadequate during the 2009-H1N1 pandemic.

Conclusion: Emergency Response and Global Security Solutions developed a comprehensive concept of operations for pandemic influenza for the Fort Worth International Airport (DFW), a U.S. POE. What makes this plan unique is that it is based on the severity and geographic spread of the disease and accounts for local and international response in one emergency response plan. This simplification of approach and execution allows the DFW Airport to manage an incident internationally as well as locally.

12.123 Migration and the globalization of disease: The reemergence of cholera in the Americas

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Background: *Vibrio cholerae* appeared on Hispanola for the first time in over 50 years following recent flooding. Although, bacterial genetic studies isolated the organism in river water, there was international concern that the disease was imported by foreign assistance workers. Local laboratories and the CDC confirmed that the form of cholera detected in Haiti is commonly found in South Asia and Africa. Recent epidemiological studies determined that the outbreak originated from contaminated water near a UN base outside Mirebalais that housed Nepalese troops. Septic tanks and pipes aided in the conclusion. While details of the disease origin have vacillated, the exportation of the disease is of particular concern as the migration of humans has led to sporadic clusters of cholera cases in new and previously unaffected regions.

Methods and Materials: By 9 November, confirmed cases in Port-au-Prince proved the disease spread from outlying areas to the capital city. By 16 November, the Dominican Republic detected its first cases of the disease in a migrant worker who recently returned home. Due to the porous nature of the border, officials tightened security to prevent the spread of the disease to the neighboring country. Previous experience with cholera in Latin America in the 1990s suggested the disease is highly mobile and could incubate in human hosts for several days before presenting symptoms. Using previous models, up to 200,000 cases in the Caribbean could be affected in the next 18 months.

Results: In 2010, the globalization of infectious disease is a major threat to international travel and public health systems. Unsubstantiated suspected cases of cholera were reported in Panama, Chile, Peru, and confirmed imported cases have been reported in North America (Florida).

ReliefWeb reported that the majority of Caribbean populations are susceptible to cholera due to a lack of natural immunity. The figure highlights countries under the geographical scope of this risk.

Conclusion: Due to the failing infrastructure, many Haitians migrated to other American countries, particularly the Dominican Republic, Mexico and Chile. These international bonds, the ease of direct flights, and better medical and professional opportunities abroad have turned the outbreak into a multifocal disease event.

12.124 Chagas disease in Murcia (Spain): A major emergent infection

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Background: Chagas disease (CD), is a parasitic zoonosis endemic in 21 countries of Latin America produced by *Trypanosoma cruzi*. Diagnosing infected persons represents a challenge for non-CD-endemic

receiving countries because this is a disease that health services are unaccustomed to managing.

Methods and Materials: A total of 1967 patients who attended the Unit of Tropical Medicine (UTM) of the Virgen de la Arrixaca Hospital in Murcia (Spain) suspected of being infected by *T. cruzi* were screened for CD from January 2007 through December 2009. Most patients were from Bolivia (1460; 74.2%), followed by Ecuador (260; 13.2%). A total of 148 (7.5%) tested patients were children born in Spain to infected mothers.

Patients with positive results for both serological tests (IFI and ELISA) were considered infected by *T. cruzi*. When appropriate, patients were submitted for electrocardiography or X-rays.

Results: In the 1967 patients tested for *T. cruzi*, 606 (30.8%) were positive in both serological tests. The mean (\pm SD) age was 34.3 years \pm 11.2 years.

The vast majority of infected persons came from Bolivia 508 out of 1460 patient tested (34.8%) followed by Ecuador with 12 of 260 patients (4.6%) and other Latin American countries.

In the screening of 148 children born in Spain to infected mothers 5 cases of congenital CD were detected. This represents a 3.4% rate of vertical transmission in our experience.

Apart from the 5 congenital cases, all patients (601) had chronic CD. Of those, 334 (55.6%) were asymptomatic and 267 (44.4%) symptomatic. In total, 123 (20.5%) were only cardiac, 56 (9.3%) also had both cardiac and digestive disorders and 88 (14.6%) had only digestive disorders.

Conclusion: In Murcia, CD is an important challenge because we have diagnosed CD in 606 patients in less than three years. Our patients show cardiac and digestive symptoms of CD, which comes at a considerable clinical, social and economical burden, particularly in areas with a large immigrant population.

In Europe, where CD is an emerging infection, mother-to-child transmission could represent a real problem. Screening of mothers and infants at risk is recommended to prevent congenital transmission in non-CD-endemic countries.

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12.125 Use of malaria imported cases in non endemic countries to assess the return of chloroquine susceptibility of *P. falciparum* strains from Senegal

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Background: Early treatment with effective anti-malarial drugs is the best strategy for those infected by malaria. However, concern is growing about the emergence of resistance to antimalarial treatments. In compliance with WHO recommendations, African countries have discontinued chloroquine, as it becomes ineffective, and now promote artemisin-based combination therapy (ACT), as first-line treatment for uncomplicated malaria. In Senegal, chloroquine was recommended as first line treatment before 2003. But faced with an average chloroquine treatment failure of 25%, Senegal changed its national malaria policy from chloroquine (CQ) to ACT (amodiaquine/artesunate). It is assumed that travelers and immigrants coming from Senegal and collectively infected by a wide variety of strains of *Plasmodium*, could be an effective tool for detecting the evolution of resistance onsite. The aim of the study is to describe, through imported cases from Senegal, the evolution of chloroquine-resistance in the region after a decrease of drug pressure.



Methods and Materials: The study will be conducted by the Malaria National Reference Centre in France in collaboration with the WorldWide Antimalarial Resistance Network (WWARN). The database will collate in vitro response of reference and clinical isolates for CQ. In total, 128 clinical isolates were tested from 1996 to 2003 and 120, from 2004 to 2009.

Results: Mean estimated 50% inhibitory concentration (IC50) for CQ was 133nmol/L (95% confidence interval [CI], 106 to 159) (threshold 100nmol/L) from 1996 to 2003 versus 95nmol/L (95% CI, 78 to 113) from 2004 to 2009 ($p=0.02$). The IC50 isolate/*Pf3D7* ratio was 5.90 (95% CI, 4.63 to 7.17) (threshold =3) versus 2.95 (95% CI, 2.38 to 3.52) ($p<0.001$), before and after 2003, respectively. The strains showed an increased susceptibility to CQ between these 2 periods.

Conclusion: A reduction in resistance to CQ following official withdrawal in 2003 was observed in imported cases from Senegal. A return of the Chloroquine-susceptible *P.f* is consistent with results observed in Malawi, even if the studied period, after the CQ was withdrawn, was shorter in Senegal than in Malawi (6 years versus 12 years). A confirmation by genotyping *pfprt*, *pfmdr-1*, *dhps* and *dhfr* genes of these samples will be done.

12.126 Increasing Trends in Hospitalizations for Dengue in the United States

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Background: Worldwide the number of cases of dengue infection has increased dramatically with a concomitant rapid geographic expansion. Until the recent outbreak in Florida, risk of dengue infection to U.S. residents has been primarily posed by travel. Population-based estimates of incidence and disease trends have been difficult to determine due to variable surveillance methods. We sought to determine trends in dengue fever among hospitalized U.S. patients.

Methods and Materials: We conducted a retrospective cohort analysis. The study population included all National Inpatient Sample discharges from 2000 to 2007 with dengue fever diagnoses (ICD-9-CM code 061). For each yearly incidence rate, we calculated a 95% exact binomial confidence interval. To determine if there was a statistically significant trend in hospitalized dengue fever cases during the study period, we fit a logistic regression model using yearly incidence as the dependent variable and year as the independent variable. To accommodate the temporal association in the yearly incidence, we fit the model using generalized estimating equations, assuming an autoregressive correlation structure. Also, we calculated the ratio of the yearly incidence rates at the beginning and end of the study period (i.e., rates in 2000 and 2007). We tested whether this incidence ratio is significantly different from one using Fisher's exact test, and computed a 95% exact confidence interval for the corresponding odds ratio using the hypergeometric distribution. Finally, we used the Monte Carlo variant of the Fisher exact test to investigate whether there is geographic variation in the incidence rate among the four different U.S. census regions.

Results: The number of hospitalized dengue cases more than tripled during the study period. There was a clear upward and significant trend in the incidence of patients hospitalized with dengue. Incidence rates for the four census regions were homologous except for 2004 and 2007, when the Northeast Region had higher rates.

Conclusion: Incidence rates of patients hospitalized with dengue fever have increased dramatically from 2000 to 2007. Regional incidence rates indicate that travel is the most likely source of this increase.

12.127 Evaluation of the rapid influenza diagnostic tests and bioinformation analysis for 2009 A (H1N1) strain in Taiwan

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Background: Since a novel swine origin influenza virus A (H1N1) is spreading worldwide and become pandemic. The commercially available

rapid influenza diagnostic tests (RIDTs) are important for forming preventative strategies and directing initiation of anti-viral therapy decision.

Methods and Materials: Phylogenetic evolutionary models and analytical bioinformatics tools were used to evaluate 4 groups of RIDTs. While, 1609 nasopharyngeal samples were collected from influenza-like symptoms patients to test the influenza A+B antigen detection tests and randomly selected 40 positive samples for H1N1 RT-PCR.

Results: In predicting immunogenicity, second structure prediction and protein topology analysis, the New jersey/8/76 (H1N1) was most similar to the sequence of A (H1N1). Moreover, one signature change residue at position 100 of nucleoprotein exhibited a dominant change (V-I) in A (H1N1) epidemic strains. Total of 303 (18.8%, 303/1609) samples were positive for influenza rapid antigen analysis. In H1N1 RT-PCR that 51.6% (16/40) of samples were determined with H1N1 infection.

Conclusion: Even A (H1N1) influenza viruses may shift the virus genetic diversity and recombination; we reported that the prediction of bioinformatic tools can conveniently provide a rapid method for evaluation of the influenza RIDTs.

12.128 Pandemic 2009 influenza A H1N1 infection among Iranian Hajj pilgrims 2009: A real-time RT-PCR and serological based study

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Background: Hajj is the massive ritual congregation undertaken annually in Mecca Saudi Arabia, in which millions of world Muslims gather to rededicate themselves to their divine teachings. Hajj 2009 took place in the context of pandemic 2009 influenza A/H1N1 (pH1N1), and seasonal types of it. The potential role played by the pilgrimage to Saudi Arabia could cause a remarkable mortality among them there, and appearance of new wave of infection in their respective countries upon returning home. The present study was an attempt to determine the pH1N1 and other influenza A in pilgrims' respiratory tracts and also the serologic test of corresponding antibodies among them upon returning home

Methods and Materials: Throat swabs and sera were collected from 305 pilgrims arriving at Shiraz airport, southern Iran. Following RNA purification, the pH1N1, and other influenza A viruses were detected using TaqMan Real-Time PCR. In cases of pH1N1, the sensitivity to oseltamivir was also evaluated. The Hemagglutination-inhibiting antibodies against pH1N1 were titrated in pilgrim's sera by Hemagglutination-inhibition Test (HAI)

Results: The pH1N1 was found in 5(1.6%) pilgrims and other influenza A viruses in 8(2.6%). 258(84.6%) of the pilgrims had the minimum HAI titer of 1:40. All the pH1N1 2009 were sensitive to oseltamivir

Conclusion: While only five cases were with pH1N1 in their respiratory organs and that 84.6% of them had HAI antibodies against pH1N1, which could be due to infection developed during the pilgrimage or pre-existing antibodies, it seems that the pilgrims' arrival home would not cause a new wave of infection in the community. In addition, thanks to pre-existing antibodies and restrictions on the high risk groups to Hajj, the mortality and the incidence of severe diseases were negligible

12.129 Comparison of five genotypic techniques for identification of Optochin-resistant pneumococcus

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Background: Three PCR techniques (amplification of the *psaA*, *ply*, and *lytA* genes) and a commercial kit (AccuProbe [GenProbe, San Diego, Calif.], based on hybridization with the 16S rRNA gene), all four of which claimed to be specific for *Streptococcus pneumoniae*, were used to identify 51 alpha-hemolytic streptococcal isolates suspected of being pneumococci.



Methods and Materials: The definite phenotypic identification of these organisms as *S. pneumoniae* was difficult when optochin susceptibility and the presence of a capsule were taken as markers. Furthermore, *RsaI* digestion of the amplified 16S rRNA gene was applied. All 51 strains were optochin resistant. Thirteen of these were encapsulated and were identified as pneumococci by all tests. Twenty of the 38 unencapsulated strains were unambiguously identified as nonpneumococci by all tests. The identities of another 18 unencapsulated strains remained inconclusive due to highly variable reactions for all phenotypic and genotypic techniques applied.

Results: The AccuProbe test was positive for seven strains for which the results of the other tests were inconclusive. *RsaI* restriction of the amplified 16S rRNA gene confirmed the AccuProbe result for all strains, while the result of the *psaA*-specific PCR was in concordance with encapsulation for all strains. The results presented here indicate that identification problems continue to exist for some strains, despite the application of genotypic and phenotypic tests in combination.

Conclusion: We found the *psaA*-specific PCR to be the genotypic technique best suited for the identification of genuine pneumococci and optochin-resistant pneumococci.

highest percent of specimens testing positive, virologic surveillance can reveal variations in the impact of influenza by virus type/subtype and age group.

Methods and Materials: Influenza virologic surveillance in the US consists of World Health Organization (WHO) (N=80) and National Respiratory and Enteric Virus Surveillance System (NREVSS) (N=60) collaborating laboratories. An increasing number of WHO laboratories systematically report the number of specimens tested and the number positive by virus type/subtype and age group (≤ 4 , 5-24, 25-44, 45-64, and >64 years). We examined the percent of specimens testing influenza positive by age group and virus subtype for seasons from 2000-2010.

Results: The impact of influenza varied according to both age group and predominant virus type. Among all ages, the percent of specimens testing influenza positive was consistently highest among school aged children (5-24 years), regardless of virus type, ranging from 27 to 48%. Over the last decade, school aged children accounted for 45% of all influenza positives reported. Prior to the 2009 pandemic, the highest percent positive seasons for children ages ≤ 4 were during H3 predominant seasons (2001-02, 2003-04, 2007-08). Persons aged >64 were also most significantly affected during H3 predominant years when the percent positive ranged from 15 to 21%; the percent positive among persons >64 years ranged from 4.4 to 7.8% during non-H3 years. The trend was similar among individuals aged 45-64, with the percent positive during H3 predominant seasons being roughly twice that of non-H3 seasons. The highest variation between age categories was seen during the 2009 pandemic; the percent positive ranged from 7.4 among those aged >64 years to 48.2% in those aged 5-24.

Conclusion: Age-level analyses of laboratory surveillance data provide information useful for quickly focusing prevention efforts. These data, limited by the number of laboratories reporting age-level data, highlight the need for accurate and timely patient-level data. Resources should be invested at both the state and federal level to facilitate transmission of patient-level surveillance data.

12.130 Survey of influenza-like illness among returning Hajj Pilgrims at Lagos Airport, Nigeria, December, 2009

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Background: Hajj pilgrimage to Mecca, observed by Muslims throughout the world, is an annual mass gathering of over 2.5 million people. Because of concerns of the ongoing 2009 Pandemic Influenza A (H1N1) and high potential for transmission during Hajj, the Federal Ministry of Health (FMOH) conducted airport surveillance for Influenza-Like Illness (ILI) among returning pilgrims.

Methods and Materials: From December 5-21, 2009, a structured questionnaire was administered to one in every five pilgrims arriving from Mecca, at the Murtala Mohammed Airport, Lagos. Information was obtained on current symptoms of ILI, medical history, and knowledge of H1N1. Pilgrims identified with symptoms of ILI were those who self-reported fever, cough and/ sore throat. A pilgrim was considered to be at high risk of influenza if he/she was 65 years of age or older, pregnant, or reported a chronic medical condition. Pilgrims identified as having symptoms consistent with ILI, those who had contacts with other people with ILI, and those with predisposing risk factors were identified for follow-up. Analysis was done using Epi-info software and was based on data from passengers on ten flights.

Results: A total of 889 pilgrims were interviewed with their ages ranging from 21 to 89 years. The median age was 48 years. Of 889 pilgrims interviewed, 527 (59.3%) were males, 455 (51.2%) had heard about H1N1 out of which 181 (39.8%) had knowledge of symptoms, 254 (55.8%) had knowledge of mode of transmission and 347 (76.3%) had knowledge of protection. Sixty-seven (7.5%) of the pilgrims were identified as having symptoms of ILI and 95 (10.6%) as high risk group with predisposing risk factors. Of the 95 pilgrims, 46 (48.4%) had chronic medical condition, 7 (7.4%) were pregnant and 42 (44.2%) aged 65 and older.

Conclusion: The survey identified returning Hajj pilgrims with ILI and individuals at high risk of complications associated with influenza who will require further testing for H1N1. There are gaps on knowledge of H1N1 that need to be addressed by organizing health education.

12.131 A decade of influenza: Trends in WHO collaborating laboratory surveillance data

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Background: The percent of specimens testing positive for influenza provides information on the relative contribution of influenza to acute respiratory disease. While school age children consistently have the

12.132 Social contacts and mixing patterns for influenza illness in Thailand

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Background: Infectious diseases such as influenza can be spread when individuals come into close contact with each other. From reviews, very little detailed information is available about patterns of relevant social contacts, particularly developing countries. This study aimed to conduct a number of population-based surveys of individuals' contact patterns in Thailand. It would represent a major development in our understanding of relevant mixing patterns, and should significantly improve our ability to predict the spread of infectious diseases.

Methods and Materials: Sample size was selected from 4 provinces of Thailand namely, Pathumthani, Lampang, Mahasarakram, and Surat thani. Multi-level sampling was applied for age, sex, and assign contact days. Data was collected by the provincial statistic office under the guidance of field supervisors during February -March 2010. Respondents were interviewed on background information and asked to record their activities and contacts in the diary on certain assigned day. The following interview appointment for contact information would be made a day after the assigned day.

Results: Number of respondents was 2,016 individuals equally among sex and areas (urban and rural). Mean contacts was 9.70 contacts per day (maximum=33). Respondents in rural was 10.35 contacts in average comparing to 9.05 contacts in urban. Number of contacts per day in weekday was slightly higher than holiday, 9.94 and 9.15 contacts respectively. Respondents with aged 13-19, 6-12, and 0-5 years old had 11.40, 11.22, and 9.76 contacts respectively. The contact patterns was mostly found at home (59%), most daily (74%), and 52% had skin contact.

Conclusion: This data contact patterns could be parameters in the mathematical epidemiological models which are increasingly used to guide public health policy-making. The accuracy of the predictions from these models must depend on accuracy of these parameter values used. Additionally, the contact pattern result from this study is probably used as the model assumptions in other developing countries.

**12.133 Extracorporeal membrane oxygenation for (2009) H1N1 influenza in a Belgian University teaching hospital**

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Background: During the (2009) H1N1 pandemic wave in Belgium, Intensive Care Unit (ICU) of a University teaching hospital (400 beds) was called by regional hospitals for transferring four consecutive infected patients with acute respiratory distress syndrome (ARDS) not responding to conventional treatment, and requiring extracorporeal membrane oxygenation (ECMO).

Methods and Materials: Being a reference center for severe respiratory infections and pulmonary transplantation, ECMO treatment was available in ICU and could be instituted in regional hospitals by a specialized ECMO mobile team (ICU medical, nursing, perfusionist).

Regarding the available data from other countries focussing on ICU surge and ECMO treatment (Australia, New-Zealand), we evaluated the internal resources and performed an informal assessment of ECMO capacities in the surrounding acute hospitals, in which there were no ECMO devices directly available, no trained team for ARDS ECMO treatment, and no ECMO mobile team.

We check the availability of material with external firms, assess our ICU limitations and decided to limit the ARDS ECMO treatment to two simultaneous patients, in order to keep capacities for one cardiothoracic patient.

Results: Within a period of 12 days, three patients were successfully transferred on mobile ECMO. They were weaned from ECMO treatment in ICU after 10, 34 and 12 days. There was no significant procedure-related complication. A fourth patient had to be reoriented to another specialized center, for capacities limitations.

The ECMO mobile transfers were time and resource consuming (± 10 hours outside intervention), but allowed safe transportation and survival of the patients.

Conclusion: In our limited experience, use of ECMO for induced (2009) H1N1 ARDS not responding to conventional treatment turned out to be extremely efficient (100% survival and discharge)

The impact of (2009) H1N1 pandemic in Belgium was limited regarding existing data. Considering the same pathogenicity, a higher clinical attack rate should have involved more need for that level of care.

No real-time centralized data exists in Belgium concerning the availability of ECMO trained teams and devices, and ECMO mobile teams.

Comparatively to other European countries, there are resources in Belgium to deal with that issue, but there is a lack of visibility, evaluation and coordination at regional and national levels.

Identification of experienced teams and reference centers should allow better and more care opportunities, *if required*.

12.134 Designing specific real-time RT-PCR assays for Spanish Avian Influenza Virus subtyping

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Background: Avian influenza (AI) is a highly contagious disease caused by influenza virus type A, member of *Orthomyxoviridae* family. To date, 16 AIV different hemagglutinin (HA) subtypes have been described, and specifically H1-H11 and H16 have been detected in Spain. H5, H7, and H9 specific real-time RT-PCR (rRT-PCR) methods are running in the lab. There is a need to develop rapid, accurate and reliable methods to identify other AIV subtypes, which may be associated with disease cases in Spain.

Methods and Materials: Initially, a comprehensive selection of each HA subtype full-length gene sequences available from GenBank was aligned. Primers and TaqMan probes specific for single HA subtype (H1-H4, H6, H8, H10, H11, H16), hybridizing to all European published sequences,

were selected. A collection of 16 reference AIV HA-subtypes from the UE Reference Laboratory (VLA, UK) were used to develop each designed rRT-PCR assay. Collection of recent European AIV isolates, including representative Spanish ones, was tested for evaluation studies.

rRT-PCR assays were optimised separately for each HA-subtype using the commercial *AgPath-ID one-step RT-PCR kit* (Applied Biosystems). Reference rRT-PCR assay targeting AIV M gene was performed for comparison¹.

Results: The analytical sensitivity of each developed HA subtype-specific rRT-PCR was assessed testing replicates of log₁₀ serial dilutions of the corresponding AIV reference subtype. Results were compared by performing AIV M gene rRT-PCR¹, giving similar or even higher sensitivity for each subtype assay. Analytical specificity studies were carried out in separate reactions with AIV reference isolates representing all 16 HA-subtypes. Fluorescence signal was obtained exclusively for homologous HA-subtype. Evaluation studies were then performed analysing a collection of recent European AIV isolates, including Spanish ones, belonging to different HA-subtypes.

Conclusion: This work describes the design and development of a set of subtype-specific rRT-PCR methods for the rapid identification of nine AIV HA-subtypes detected in Spain. These rRT-PCR assays proved to be highly specific and revealed a satisfactory analytical sensitivity. Finally, further validation studies are still required.

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¹Spackman E. *et al* 2002 J.Clin.Microbiol. 40:3256-3260

12.135 Modeling the health impact and cost-effectiveness of an adjuvanted influenza vaccine with enhanced effectiveness in the Canadian population

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Background: The propensity for influenza viruses to mutate and recombine makes them both a familiar threat and a prototype emerging infectious disease. Emerging evidence suggests that use of adjuvanted vaccines in older adults and young children results in enhanced protection against influenza infection and reduced adverse influenza-attributable outcomes compared to unadjuvanted vaccines. We evaluated the impact of introducing a seasonal adjuvanted influenza vaccine in these age groups by comparing the projected health outcomes and costs relative to the currently used unadjuvanted vaccine.

Methods and Materials: We constructed an age-structured compartmental model that simulates the transmission of influenza in the Canadian population over a ten-year period. The impact of influenza on healthcare utilization and costs was estimated based on event probabilities. Main outcome measures were: quality-adjusted life years, costs in 2009 Canadian dollars, and incremental cost-effectiveness ratios (ICERs). The impact of assumptions around relative vaccine efficacies was explored in sensitivity analyses.

Results: Use of adjuvanted influenza vaccine in children under 6 and adults ≥ 65 in the Canadian population, with continued use of unadjuvanted vaccine in the population aged 6-64, was projected to provide substantial health benefits, including aversion of deaths and hospitalizations. In the base case analysis, use of adjuvanted vaccine in older adults was highly cost effective (ICER: \$1970.25/QALY gained). Expanding adjuvanted vaccine coverage to include young children weakly dominated the vaccination of older adults only strategy (ICER: \$296.24/QALY). Sensitivity analyses showed that even small increases in adjuvanted vaccine efficacy were cost-effective: when adjuvanted vaccine efficacy in older adults was 0.21 or greater (compared to the baseline estimate of 0.2 for unadjuvanted vaccine), use of the adjuvanted vaccine was cost-effective at \$43,690.88/QALY. Similarly, expanding the use of adjuvanted vaccine to children was cost-effective (ICER: \$34,669.37/QALY) relative to the use of adjuvanted vaccine in older adults only when vaccine efficacy was increased by 2% (0.51 versus 0.5 for unadjuvanted vaccine in children).



Conclusion: Adjuvanted influenza vaccine is projected to reduce the number of influenza cases and health care resource use and is an economically attractive intervention relative to currently available health interventions.

12.136 **Mycoplasma bovis—an emerging pathogen in Czech cattle herds**

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Background: *Mycoplasma bovis* is a worldwide pathogen of farmed cattle. It causes mastitis, abortion, arthritis, keratoconjunctivitis, otitis and calf pneumonia. The first isolations in the former Czechoslovakia were done in 1975, but only from sporadic cases. After almost 30 years without any mention of this pathogen in our country, we managed to isolate it again in 2007 from a case of bronchopneumonia in calves. The objective of this study was to assess the prevalence of *Mycoplasma bovis* in herds of young cattle in the Czech Republic.

Methods and Materials: Nasal, conjunctival and external ear canal swabs, samples of bronchotracheal lavage and milk were examined by culture and the nested polymerase chain reaction (nested – PCR) based on amplification of the *uvrC* gene sequence specific for *Mycoplasma bovis*. Between November 2006 and November 2010, 318 samples were examined.

Results: From November 2006 to October 2009 we found *Mycoplasma bovis* in 11 samples and between November 2009 and October 2010, six animals were already tested positive.

Conclusion: Our results indicate that *Mycoplasma bovis* is now more frequently isolated than in the past. Last year the number of *Mycoplasma bovis* isolates increased more rapidly than in the previous years. But this pathogen is still often underestimated and we recommend that more attention should be paid to its laboratory diagnostics.

The study was funded from Research Project no. 6215712403, of the Ministry of Education, Youth and Sports of the Czech Republic and from Research Project no.60/2010/FVL, of the Internal Grant Agency, of the University of Veterinary and Pharmaceutical Sciences in Brno.

12.137 **The A(H1N1)2009 influenza pandemic: lessons learned in Latvia**

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Background: The experience and impressions obtained at State agency „Infectology Center of Latvia” (ICL) during the management of the A(H1N1)2009 influenza pandemic in Latvia have induced a will to describe the overall dynamics of the epidemic, main indicators and the risk factors observed in Latvia.

Methods and Materials: Overall, 10,2% of 2,3 million inhabitants of Latvia applied to a doctor. 547 patients were hospitalized in ICL, in 252 of them influenza was verified by identification of virus. Nasopharyngeal swabs, bronchoalveolar lavage and autopsy materials were investigated for A(H1N1)2009 virus by using of RT-PCR as main method (CDC protocol), immunofluorescence method for A influenza virus antigen determination (Imagen Influenza virus A and B, Oxoid, UK), virus was isolated in MDCK (Madin Darby kidney cell) culture.

Results: The first case of the A(H1N1)2009 influenza was laboratory confirmed on June 23, 2009 in-patient inhabitant of Latvia, who arrived from Mexico.

During the next months only some sporadic cases of A(H1N1)2009 influenza occurred in Latvia. During weeks 45-46 number of the diseased persons sharply increased. The peak of the epidemic was registered in week 48 (527,2 cases per 100 000 inhabitants), then – rapid decrease of the number of cases in week 53, and the end of this epidemic in week 6-7, 2010. The common clinical course was mild. Young people (0-14 years) were mainly affected (85,5%), but showed rapid recovery. Hospitalization was higher among 15-64 years old patients.

Risk factors for severe course of A(H1N1)2009 influenza were chronic respiratory and cardiovascular diseases, diabetes mellitus, obesity, pregnancy, immunodeficiency, 35 patients died.

Assessment of A(H1N1)2009 influenza virus diagnostics methods in the laboratory of ICL convincingly showed the preference of real time RT-PCR method for this purpose (sensitivity 88,7%).

In Latvia vaccine against pandemic influenza was not ordered. The main attention was focused on the use of antivirals – Tamiflu and Relenza.

Conclusion: The analysis of patients who died showed that A(H1N1)2009 influenza virus attacks not only upper airways, lungs, but also other organs (gastrointestinal tract, pancreas, kidney etc.). The main laboratory diagnosis of A(H1N1)2009 influenza virus should be performed by using of RT-PCR.

12.138 **Epidemiology of PCR confirmed H1N1 Influenza in South-East Austria**

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Background: Pandemic 2009 influenza A(H1N1) virus has spread rapidly resulting in millions of laboratory confirmed cases and over 18000 deaths worldwide. Compared to previous non-pandemic influenza seasons epidemiology of the H1N1 pandemic in 2009-2010 differed significantly. As sensitivity of currently available rapid antigen tests has shown to be low, PCR is the recommended test for diagnosis and confirmation of infection.

We retrospectively analyzed cases of PCR confirmed H1N1 influenza in South East Austria.

Methods and Materials: This is a retrospective survey of patients with PCR-proven influenza H1N1 infection in South East Austria. PCR confirmed 625 cases of H1N1 influenza. Complete data were obtained from 189/625 (30%) of patients.

Results: Out of 189 cases (113 male, 76 female, mean age 25 years) 15 (8%) required intensified medical care, 125 (67%) were hospitalized, and 48 (25%) presented to outpatient clinic only. Occurrence of a prodrome was reported by 12%. 1% (2/189) had a history of vaccination against H1N1 influenza while 99% had not. Rapid antigen test (BinaxNow, Inverness Medical) was negative in the vast majority of cases (88%). In 63/189 (33%) of cases oseltamivir was initiated within the first 48 hours of infection and antibacterial therapy was administered in 83/189 (44%) of cases. 22/189 (12%) of cases developed pneumonia due to H1N1. Complications occurred in 51/189 (27%) of cases (respiratory insufficiency in 7/63 cases, bacterial pneumonia in 8/63 cases, bacteremia/fungemia in 4/63 cases). 5/189 cases (2,6%) had a fatal outcome, 97% survived. Median age of patients with a fatal outcome was 40,4 years (ranging from 16 to 70 years of age); 2 out of 5 patients with fatal outcome had a history of mild chronic obstructive pulmonary disease.

Conclusion: In accordance with previously published data median age of PCR confirmed cases in South East Austria was comparably low and a high rate of lower respiratory disease associated with influenza H1N1 infection was observed. Case fatality ratio among study population was 2,64%.

12.139 **The role of interaction between influenza viruses in the substitution of epidemic strains**

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Background: New swine-origin influenza A/H1N1 virus (S-OIAV) caused the global pandemic in 2009. In Shanghai, it started to spread in June and rode the crest of a wave in October and November, but declined after that and was replaced by influenza B virus (IBV) in the spring of 2010. Did interaction between S-OIAV and IBV play the role in the substitution besides population immunity?

Methods and Materials: Two IBV in January and February of 2010 and four S-OIAV were selected, and arranged in eight pairs. Equal titer of paired viruses were mixed and inoculated in MDCK cell line, and then the supernatant continued to be incubated in MDCK cell line till the fourth passage. All supernatants of four generations were detected by RT-PCR for S-OIAV and IBV, and sequenced for HA and PB2 segments of S-OIAV and IBV, respectively.



Results: S-OIAV in eight pairs were less and less with the increase of passage, and totally vanished in the fourth generation whereas IBV maintained stable. HA and PB2 segment of IBV were successfully replicated in all four generation without the insertion of S-OIAV. HA and PB2 of S-OIAV were not found the insertion of IBV, but the replication was not effective, especially the anterior 970bp of HA and 1280bp of PB2, which vanished in the third generation.

Conclusion: The replication of these IBV was more effective and successful than S-OIAV in MDCK cell line, which might play a certain role in the substitution of epidemic strains. The study also suggested the possible application of cytological experiment for competitive replication between viruses.

12.140 Indirect impact of the 2009–2010 influenza pandemic on pertussis and gastro-enteritis epidemics

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Background: During the 2009 H1N1-influenza pandemic, non-pharmaceutical interventions were used to control the spread of the disease. The aim of our study was to examine whether these measures had an impact on the incidence of other endemic diseases and to quantify this impact.

Methods and Materials: We estimated the expected incidence of one seasonal disease (acute diarrhea) and one non-seasonal disease (pertussis), in two different settings (France and US) and compared them with the corresponding observed incidence in 2009/2010. Weekly incidence data were obtained from the "Sentinelles network" for acute diarrhea and from CDC database for pertussis. We used data augmentation procedures based on the five preceding years (2004–2009) for acute diarrhea, and on the three preceding years for pertussis (2006–2009) to compute the 95 % bootstrap confidence interval of the expected incidences. Differences were evaluated using incidence rates, number of cases, time taken to reach the epidemic peak, and height of the peak. The endemic period was determined using the Serfling method. Age-specific analyses were also conducted for acute diarrhea.

Results: For acute diarrhea in France, the number of episodes in 2009/2010 was significantly lower than expected until the third week of December (-24% [-36%; -9%]), and then significantly higher (+40% [22%; 62%]), leading to a total increase of 574,440 episodes. The time to reach epidemic status was delayed by 5 weeks. The maximum incidence occurred one week later and was 1.3 times higher. In patients >65 years old, a delayed endemic period was present but without any significant increase in a second period.

For pertussis in the US, the reported incidence was significantly lower than expected from September 2009 to March 2010 (-25% [-41%, 3%]), and higher than expected afterwards (+63% [30%; 114%]) leading to a prolonged rise in the incidence trend.

Conclusion: Our results suggest that the patterns of some endemic diseases have been significantly impacted in 2009/2010. For both studied diseases, number of cases was first significantly lower than expected, and then significantly higher in a second period. The endemic diseases may have been controlled during the beginning of the pandemic, but have later spread faster than expected.

12.141 Determination of an ICU triage protocol in a context of pandemic influenza planning for acute care settings in Belgium

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Background: The impact of a pandemic influenza on intensive care resources has been evaluated in the context of national acute care pandemic planning, by the influenza team of a University teaching hospital.

In a situation of scarcity of resources, even after maximizing processes and implementing surge capacities, an intensive care unit (ICU) triage

protocol could be necessary to prioritize people most likely to benefit from that level of care.

Methods and Materials: International pandemic plans were analyzed, as was reviewed the literature regarding organization of acute care settings during infectious diseases outbreaks (e.g. SARS), and triage modalities in case of overwhelmed ICU capacities.

The impact of a pandemic influenza on Belgian acute care settings was modeled (CDC FluSurge 2.0). Results correlated with most of the published data : a global surge up to 80% of intensive care supply could be necessary in case of severe pandemic.

Modalities of internal surge capacities were defined: prioritisation list of elective surgery interventions requiring post-operative intensive care; possibility of opening and staffing middle care and ICU beds.

Triage protocols already published were reviewed and discussed with the intensivists; a standard operating procedure (SOP) was redacted based on a protocol using the Sequential Organ Failure Assessment (SOFA) score.

Results: Process of prioritisation for elective surgery interventions was validated, as were defined modalities of opening and staffing additional middle care and ICU beds. The ICU triage SOP was discussed with the Board of Belgian Society of Intensive Care Medicine that endorsed it, as did the Belgian Interministry Influenza Committee as part of the operational acute care pandemic planning. The principle of the protocol was in agreement with recommendations from the Belgian Advisory Committee on Bioethics, two years ago mandated for advice on the operational pandemic planning by Public Health Ministry.

Conclusion: It is important to persist in preparation for a pandemic influenza or another highly contagious pathogen, considering a worst case scenario.

Modalities of surge capacities and triage need further research, based on assessment of forthcoming publications.

There is a strong necessity of public information and compliance regarding such disclosures, ethical and legal considerations need to be discussed.

12.142 Rapid differentiation of influenza A/H1N1 pandemic and seasonal strain infections and the analysis of co-infection by multitemperature single-strand conformational polymorphism (MSSCP) technique

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Background: Influenza A virus a member of the *Orthomyxoviridae* family is the most genetically variable human pathogen. Occurrence of recent influenza A/H1N1 pandemic showed that co-infection of a single host with different variants of influenza A virus can lead to the rearrangement of viral gene segments and give rise to a novel reassortant strain with unpredictable properties. We describe a diagnostic method which allows fast differentiation of influenza A pandemic and seasonal strain infections together with detection of co-infections with high sensitivity.

Methods and Materials: A number of conformational forms of a single-stranded DNA can be separated by electrophoresis in native polyacrylamide gels giving a characteristic pattern of electrophoretic bands. Temperature changes during electrophoresis increase the sensitivity of mutation detection in PCR products; this technique was named Multitemperature Single-Strand Conformational Polymorphism (MSSCP). We applied this technique to characterize unique haemagglutinin gene fragments of different origin. A set of specific primers was synthesized after comparison of haemagglutinin sequences of different strains. PCR products were denatured and analyzed by MSSCP method.

Results: The gel patterns of haemagglutinin gene fragments of different seasonal A/H1N1 and pandemic A/H1N1 strains were easy to distinguish after MSSCP analysis. The sensitivity of the minor genetic variant detection during co-infection after MSSCP analysis was 0,1% as determined using a mixture of amplified haemagglutinin gene fragments from seasonal and pandemic strains.



Conclusion: The results of this study show that a new molecular method allowing rapid identification and discrimination of genetic variants of influenza A/H1N1 virus, including the detection of mixed infections can be applied to characterization of new viral variants long before they become dominant.

12.143 Seroprevalence and molecular identification of swine influenza virus: epidemiological implications

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Background: Influenza is the most frequently studied re-emerging disease in the whole world, mainly because of the historical significance of its occurrences. The virus that causes it belongs to the *Orthomyxoviridae* family and infects many animal species. It is present in aquatic birds in the whole world and finds in pigs the possibility of undergoing intense mutations, thus raising the concern about its being a source for potential pandemic viruses. Monitoring viral circulation is a necessary strategy for an early identification of outbreaks and for guiding efficient control measures to ensure human safety and the economic activity associated with the trade of animal origin products.

Methods and Materials: In a study conducted in the State of Parana, Brazil, 675 serum samples from pigs were selected (out of 5327 collected samples). The samples derived from 74 technified properties with a high population density—called farms—and 90 properties with low density of animals and without proper management - named runs. Serum samples were submitted to the Hemagglutination Inhibition test (HI) to detect antibodies against subtype H3N2 of human origin. The results guided the collection of samples of respiratory organs of pigs originating from those regions in the slaughterhouse, to do the PCR.

Results: Out of that total, 24% of the farm samples were positive for H3N2, while only 3% of run samples were positive. Considering all analyzed properties, 46% of the farms were positive while 6% of the runs had at least one positive sample. The distribution of positive samples showed a higher incidence of seropositivity in the coldest areas of the State. Positivity by RT-PCR confirms the presence of the virus and points at the need for sequencing it in order to define which serotype is circulating in that region.

Conclusion: The highest prevalence of seroreagent animals on farms shows the importance of population density on the occurrence of swine influenza. The correlation of the present results with low environmental temperatures allows inferring that workers in the swine trade business should be subject to control.

12.144 Four years of non-sentinel surveillance of respiratory syncytial virus through the Spanish Influenza Sentinel Surveillance System

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Background: Influenza and RSV infections cause a similar symptomatology and both viruses frequently co-circulate around the same time of the year making it difficult to estimate their clinical impacts. In 2006, the Spanish Working Group of Influenza Surveillance agreed to use the infrastructure of the Spanish Influenza Sentinel Surveillance System (SISS) for RSV non-sentinel surveillance as a complementary tool of the influenza surveillance. We aimed to describe the Spanish temporal influenza and RSV pattern from 1997–2006, and to describe the information obtained in these four years of non-sentinel RSV surveillance through the SISS

Methods and Materials: Influenza sentinel data were obtained from SISS (1996–2010) and non-sentinel RSV data from the Spanish Microbiological Information System (MIS) (1997–2006) and SISS (2006–2010).

SISS is formed by sentinel primary care physicians from 17/19 regions who reported the weekly number of ILI cases and obtained a sample of respiratory specimens for laboratory testing. The MIS is the national centralized system in which microbiological information is collected in a voluntary basis from 42 laboratories. Analyzing the weekly percentage of positive samples we characterized the Spanish temporal pattern of circulation of influenza and RSV viruses

Results: RSV circulated 3–9 weeks before influenza viruses from 1996 to 2010 and peaked at the end of the year. In 2003–2004 and 2009–2010, influenza appeared 4 and 10 weeks earlier than RSV, respectively. However, this did not affect the temporal circulation of RSV in the pandemic 2009–2010 season. Spanish and European virus circulation patterns were similar. The percentage of RSV positive samples was 67% in the pandemic season, significantly higher ($p < 0.0001$) compared with the average of the three previous seasons

Conclusion: RSV circulated 3–9 weeks before influenza and peaked at the end of each year studied. The early emergence of the pandemic virus did not affect the RSV temporal pattern described previously. The non-sentinel RSV information through the SISS was timely and was provided by more than 50% of the laboratories integrated into the system and distributed throughout Spain. This information on RSV will allow more precise studies of influenza disease burden in Spain. Moreover, it could be used to better characterize the beginning of the annual influenza epidemic

12.145 Clinical and epidemiological characteristics of deaths attributed to pandemic influenza A (H1N1), 2009–2010, East Ukraine

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Background: We reviewed epidemiological and clinical features of deaths attributed to pandemic influenza A(H1N1) in an industrial region of 2.782 mln population, to determine potential lessons for doctors and public health action.

Methods and Materials: We reviewed surveillance reports and laboratory data for influenza and clinical data to identify characteristics of persons whose deaths were attributed to pandemic A(H1N1) influenza in the industrial region of East Ukraine.

Results: The incidence rate of reported influenza was 69.53/10000 in 2009 and 99.26/10000 for the first 10 months of 2010 and was lower than that seen during the same period in recent years. From November 2009 through February 2010, 65 deaths occurred; giving a case fatality rate of 0.02%. Vulnerable groups included pregnant women, patient with morbid obesity and those with chronic respiratory disease. Studying of the 30 fatal case histories showed a late patient's admission to hospital, the average was 5.63±0.08 days. The mean age of death was 42 years (range: 25–72 years), 50% were men and 19 (30.0%) were with morbid obesity. All deaths had a rapid course of disease, an early appearance of breathlessness was in all cases; in some cases cough of foamy bloody liquids sputum in quantity approximately 300 ml a day was appeared. No pathognomonic symptoms for influenza A(H1N1) were found. X-ray revealed bilateral subtotal or total pneumonia. All patients were treated by non-invasive oxygen therapy under the control of saturation, oseltamivir was administered at 150 mg per day. A predominant damage of vascular endothelium and alveolar epithelium were revealed in lung tissue morphology. Alveolar voids were filled with fibrin strand exudates; hyaline membranes in lung tissue were observed. In 6 fatal cases nasal and/or oropharyngeal swabs were tested by immunofluorescent assay and lung tissue samples were tested by PCR-assays. In 5 cases A(H1N1) virus was founded in the lung tissue samples but was not founded in nasal swabs.

Conclusion: Throughout the 2009/2010 influenza season the low incidence rate and fatality cases rate was observed. Rapid course of disease was observed in deaths. Deaths were young and middle age. Testing of nasal and/or oropharyngeal swabs can't help to decide who require hospitalization.

**12.146 H5N1 avian influenza A—Emergence, trends and pandemic threats in Egypt and Indonesia****J. Malaty**

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Background: H5N1 avian influenza (AI) is a highly contagious disease caused by a virus subtype [influenza A] adapted to birds. Since adaptation is non-exclusive, different species [including humans] are at risk of infection. The disease first emerged among humans in 1997 and spread from East Asia to North Africa.

The age-sex biases for infection and death among confirmed human cases of H5N1 infection in Egypt is significantly different from those recorded in other countries. Although, the case fatality rate (CFR) among human H5N1 cases in Egypt is 34%, versus an average of 66% in other countries and up to 80% in Indonesia. In both countries, case clustering has been identified. Factors may be genetic, behavioral, immunological, or environmental.

Methods and Materials: While there has been some human-to-human spread of H5N1, it has been “limited, inefficient and unsustainable.” However, viral mutations of the past serve as a prologue for the virus’ ability to one day spread from one person to another. If H5N1 were to acquire this ability, a pandemic influenza is imminent.

Results: In 2009, a majority of the cases were reported among young children who had contact with ill or dead affected poultry. Egyptian women may have “more” exposure to the virus as they often perform cullings, slaughtering and de-featherings. Children, who are typically around their mothers, are at a higher risk of exposure to contaminated birds and fomites.

Further, studies have shown that delayed hospitalization due to poor public perception of disease [among agriculture community] attributes to the CFR.

In Indonesia, all clusters have occurred among blood relatives that include children; case clustering may be due to common source poultry exposure.

H5N1 has the potential to evolve into a pandemic strain if there are changes in the HA and NA proteins over time through antigenic drift or shift.

Conclusion: To date, there is no scientific data to suggest major differences in strain virulence in Egypt and Indonesia. However, both countries rates of cluster infections indicate that H5N1 has the potential of evolving into a pandemic strain. Since H5N1 viruses have not infected many humans, there is no natural immunity against the disease.

12.147 H9N2 avian influenza reassortants in live bird retail shops in Pakistan contain signatures of public health concern**M. Chaudhry**¹, H. B. Rashid², A. Angot³, G. Trovò³, A. Drago³, V. Valastro³, M. Thrusfield², M. Hussain⁴, M. Eisler⁵, S. Welburn¹, G. Cattoli³, I. Capua³

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Background: Live bird market system has shown to play a key role in perpetuation of Avian Influenza viruses (AIVs) and are recognised as means by which AI viruses originating from different hosts may spread to households and rural settings via trade of infected terrestrial birds. Currently no information about the genetic make-up of these viruses in live bird retail shops (LBRs) of Pakistan is available. This study was planned to obtain and genetically characterise AIVs identified during LBRs survey in Lahore.

Methods and Materials: A cross-sectional survey of LBRs in Lahore was undertaken between December 2009 and February 2010. Tracheal

swab samples (n=280) were collected and analysed by real time RT-PCR. Virus isolation test was performed according to standard procedures. Viruses identified were characterized by sequencing. The sequences obtained, and sequences from GenBank, were phylogenetically analysed using neighbour joining method.

Results: Thirty four samples were positive for Type A influenza. 28 out of 34, were typed as H9 subtype by molecular investigations. All LBRs were negative for subtypes H5 and H7. Ten H9N2 viruses were isolated and characterized by sequencing of complete HA, NA, NS and M genes. The HA gene of all ten H9N2 viruses contained substitution Q226L at the receptor binding site. This mutation is associated with a preferential receptor binding specificity for sialic acid α 2, 6-linked galactose and displays human virus -like cell tropisms. The HA, NA and M genes clustered within G1 like lineage. The NS gene showed great diversity and clustered with other H9 and one H7N3 virus from Pakistan suggesting the continued circulation of reassortant viruses in Pakistan.

Conclusion: Circulation of H9N2 in LBRs increases the chances of their evolution into new genotypes and of inter and intra subtypic reassortment. All viruses examined to date harbour a mutation that is known to alter a receptor binding profile to one preferentially binds to human receptors. The close contact between human and poultry in LBRs setting suggests that there are no biosecurity barriers to infection of human with animal viruses which have this potential. Continued surveillance of LBR’s in Pakistan is essential to better understand the public health risk posed by H9N2.

12.148 Application of the real-time PCR method for the detection of human influenza A (H1N1) of pandemic potential in Albania**D. Ulqinaku**¹, I. Hatibi², S. Bino³

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Background: In this paper we introduce, for the first time the new technology of the Real-Time PCR in the diagnosis of Influenza. Here we show the high sensitivity of the method and the fast detection of the influenza virus using the one-step reverse transcription Real-Time PCR (rRT-PCR) assay as a method of essential importance in the instigation of appropriate patient and public health management and also for disease surveillance

Methods and Materials: From June 2009 until May 2010 we collected 3167 clinical samples, suspected to contain the influenza virus, including nasal, pharyngeal, nasopharyngeal swabs, and bronchoalveolar aspirates. All the samples were collected from the Sentinel surveillance implemented throughout Albania. For the extraction of the viral ARN we have used the spin columns commercial kit of QIAGEN. Meanwhile for the detection of the influenza virus RNA we used the 1-step TaqMan-based real-time reverse transcription PCR (rRT-PCR) method developed and provided along with primer/probe sets targeting the haemagglutinin genes, from WHO CC for Influenza, CDC, Atlanta, on a platform of ABI 7500 Real-Time PCR machine

Results: We have tested with this protocol 1956 clinical samples suspected to contain the pandemic virus. A total of 1045 samples were tested and confirmed near the Cantacuzino Institute.

Resulted positive to contain the novel pandemic virus A/H1N1 only 545 of them. Some positive samples by rRT-PCR of containing the pandemic A/H1N1, were isolated in MDCK cell line on BSL-2plus facility and the result showed a virus with low titers. As a WHO National Influenza Centre part we sent to WHO-CC for Reference and Research on Influenza, Mill Hill some of the isolates for further phylogenetical analyses. They revealed that the pandemic strain circulating in Albania was the same with the one circulating in all Europe. They also screened the viruses for resistance to the sialidase inhibitors; they were all sensitive to both inhibitors.

Conclusion: Overall, the results revealed that, the RT-PCR methods is the most fastest and sensitive method for the specific detection of influenza, which is an essential need with public health importance to help the clinical management of influenza.

**12.149 Actual issues regarding influenza infection in Romania; the last 2 seasons analysis before pandemic AH1N1**

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Background: Analysis of epidemiological, clinical and virological issues of the last 2 influenza seasons in Bucharest before pandemic AH1N1.

Methods and Materials: Prospective study of the influenza patients (virological confirmed) diagnosed in "Dr Victor Babes" Hospital of Infectious and Tropical Diseases Bucharest during 2007–2009 seasons. Positive diagnosis was based on RT-PCR and MDCK cell cultures (in the National Institute of Microbiology Cantacuzino). The resistance for neuraminidase inhibitors was tested phenotypic using the NA-Star kit (Applied Biosystems, US). The positive and negative controls were provided from WHO Influenza Control Center Laboratory, Australia.

Results: We had 25 patients in 2007/2008 season (all hospitalized) and 106 in 2008/2009 season (50 hospitalized). 51 from all patients were under 18 years of age. During 2007/2008 season 22 were A/H1N1 and 3 were B strains, whereas in the following season 70 were A/H3N2 and 30 also B strains. 1 case had A/H3N2 and B mixed infection. The peak of the influenza seasonal infection was in february–march, with A/H3N2 strain predominance at the beginning of the season and B strain at the end. 23.6% of the patients received antiviral therapy (16% Oseltamivir and 7.6% Zanamivir). The evolution was favorable in all cases. The antiviral resistance was tested by M2 gene sequencing for type A influenza; no mutations were found from the pre existing identified genes for amantadine resistance. No resistant influenza strain (AH1N1 or B) were isolated in 2007/2008 season for neuraminidase inhibitors-Oseltamivir. Apart of our study, other 50 isolated influenza strains were sent from Romania to the WHO Reference Laboratory UK and 4 of them were identified Oseltamivir resistant. One of the AH3N2 strains from 2008/2009 season was identified IC50- 10.45 nM (positive control A/Fukui/45/04 119V with IC50- 6.799 nM). The sequencing of the NA gene was performed.

Conclusion: The study identified semnificative difference concerning the number and type of influenza strains between the 2 seasons but also during 2008/2009 period. Only one quarter of the patients needed antiviral therapy. One influenza A/H3N2 strain resistant to Oseltamivir was identified. The lack of amantadine resistance is probably due to the fact it is not used in Romania.

12.150 Years of life lost associated with influenza seasons in Spain, 1980–2008

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Background: Influenza-associated excess mortality is widely used to assess the severity of influenza epidemics. Recently, it has been proposed to use the potential years of life lost (YLL) as an indicator of influenza mortality burden estimates comparable across influenza epidemic. The purpose of this study was to estimate the YLL due to excess mortality attributable to influenza during the period 1980–2008 in Spain.

Methods and Materials: Mortality data were obtained from the National Statistical Institute (NSI). We used pneumonia and influenza (ICD-9: 480-488 and ICD-10: J09-J18) and all-causes deaths. To calculate mortality rates we used the population projections estimated by the NSI from the Census of 2001. We applied a modified Serfling model to a time series of Spanish monthly influenza and pneumonia and all-causes mortality deaths to estimate influenza-associated excess mortality from 1980–81 to 2007–08 influenza seasons in Spain. To estimated YLL, data of life expectancy from the NSI was applied, using 1991 as reference for the period 1980–1991 and the correspondent year from 1992 to 2008. Information on influenza virus dominant was obtained from the Spanish Influenza Surveillance System and the Microbiological Information System.

Results: During the period 1980–2008 we estimated an annual average of 1,037 (range, 0–4,577) influenza-associated deaths from influenza and pneumonia causes and 10,806 (range, 0–28,353) influenza-associated deaths from all-cause deaths. The annual rate of influenza-associated deaths in Spain was 2.73 per 100,000 for influenza and pneumonia causes and 28.30 per 100,000 for all-cause deaths. The average of YLL due to influenza mortality excess for the entire studied period was 12,283. In those influenza seasons during which the dominant virus was A(H3N2), the YLL average (16,651) was 2.2 times higher than for the seasons that it was not (7,481).

Conclusion: Mortality attributable to influenza varies across influenza seasons. Measurement of YLL allowed discriminating between influenza seasons where the most virulent seasonal virus was prominent in Spain. Studies are underway to estimate mortality excess by age groups with age differences in life expectancy that will assist in describing the health impact of seasonal and pandemic influenza.

12.151 Rapid sequencing and genetic analysis of the pandemic (H1N1)V influenza virus circulating in pigs in Italy

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Background: Emergence of the new influenza pandemic strain (H1N1pdm) will continue to pose challenge to public health and scientific community. General concern exists about possible mutation or reassortment between the H1N1pdm and influenza viruses circulating in human and animal, giving rise to more transmissible or pathogenic viruses. Emergence of resistance during antiviral treatment is a well-recognised phenomenon in influenza viruses; surveillance for emergence of resistant viruses is of importance for monitoring this potential public health problem in the context of the H1N1 pandemic.

Thus preparedness to identify new strains would require fast sequencing of the full genome of virus. Here we present an optimised workflow for rapid sequencing of the entire genome sequence of the H1N1pdm that has been applied to analyse several isolates from different pig influenza outbreaks.

Methods and Materials: We implemented a workflow permitting to analyse the entire virus genome, from sample collection to sequence analysis in just 3 working days. This implies a one step reverse transcriptase PCR reaction, agarose gel electrophoresis, amplicons clean up, sequencing reaction, unincorporated dye removal, capillary electrophoresis and sequences assembly for gene analysis. Amplification of the entire genome has been obtained with 46 primer pairs representing overlapped genetic fragments of the genome.

Results: The method has been applied to monitor genetic variation of H1N1pdm viruses isolated in swine in Italy. Presence of pandemic virus has been confirmed in several swine breeder farms as well as in farm used as Research Facility for preclinical studies. In one of the viruses analysed it has been also evidenced the isolation of a reassortant H1N2 strain. This reassortant derived all genes from H1N1pdm virus, with the exception of the neuraminidase.

Conclusion: The data obtained underline the importance of a genetic surveillance activity aimed at evidencing emergence of new influenza strain, from the animal reservoir, that could significantly alter their overall phenotype.

12.152 Genetic diversity of H1, H2 and H3 subtypes of Influenza A circulating in wild birds in Italy, 2005–2010

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Background: Avian species provide a source of viral HA subtypes antigenically novel to humans. At present, only viruses of the H1, H2 and H3 subtypes of avian origin are known to have caused pandemics in the human population. Recent studies demonstrated that post-seasonal influenza vaccination antibodies do not appear to be cross-reactive with contemporary avian H1 and H3 subtype viruses increasing the likelihood that these subtypes may contribute to the generation of the next pandemic virus. Very limited information on the molecular properties of avian H1, H2 and H3 viruses are available. To shed lights on the molecular characteristics of recently isolated avian viruses of these subtypes, phylogenetic, antigenic site and receptor binding properties of 61 viruses were investigated with bioinformatic tools.

Methods and Materials: The viruses analysed here were obtained as part of surveillance programs in wild birds performed in Italy between 2005 and 2010. The complete haemagglutinin (HA) gene of 61 isolates (31 H1, 13 H2, 17 H3) was sequenced and submitted to a public database. The sequences obtained, together with sequences from GenBank, were phylogenetically analysed using Bayesian methods implemented with the program MrBayes v3.1.2. To infer receptor binding and antigenic site properties, the deduced HA amino acid sequences were analysed.

Results: The topology of the phylogenetic trees obtained for the HA gene of the H1, H2 and H3 subtype viruses sampled from wild birds in Italy revealed the circulation of at least four, five and six distinct genetic clusters respectively. Differences in amino acid composition were found in several antigenic sites of viruses analysed. None of the amino acid substitutions associated with an increased affinity to human receptors were observed in the receptor binding domain of the HA genes analysed.

Conclusion: The wide circulation of H1, H2 and H3 in migratory birds and the identification of a certain degree of intrasubtype genetic diversity emphasize the continuing need to monitor these subtypes. Further studies on their antigenic reactivity, evolutionary dynamic and ability to cross the species barrier will be instrumental to increase our prediction capacities and identify the emergence of novel influenza viruses with pandemic potential.

12.153 The controversial role of *Chlamydia pneumoniae* in chronic infection and vascular disease

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Background: The role of *Chlamydia pneumoniae* (Cp) in atherosclerosis and cardiac complications in Australian cohorts is investigated by means of seroepidemiology, molecular technology and cell culture in chronic diseased sites such as atherosclerotic plaque. Chlamydial cell culture is foreign in Australia with very limited attempts been made worldwide.

Methods and Materials: Investigating the role of *Chlamydia pneumoniae* in the pathogenesis of atherosclerosis and its association in human disease complication. An attempt to detect, isolate and culture *Chlamydia pneumoniae* (Cp) from vascular specimens and blood.

Results: About 79.9% of persons (N=184) with coronary artery disease (CAD) in Australia, show a seroresponse to Cp (59.6%); the seroprevalence of IgA was computed 33.5% of the population studied; with higher seroprevalence among males than in females.

The "age-related" healthy controls (ages 35–95 years) studied (N=125) presented a Cp seroprevalence of 62.4% (MIFIgG) with a lower seroprevalence of IgA Cp (22.4%–34.4%), assay dependent.

We establish the unreliability of 5 different Cp serological assays. No reliable associations were found between circulating IgG and IgA in "age-related" CAD and healthy cohorts, and any significance was assay dependent.

Lack of presence of the organism in re-stenosis CAD patients post stenting, plaque and peripheral mononuclear cells, via culture, antigen and DNA detection was evident.

No correlation of the organism was demonstrated with recognized 'risk factors' and cardiac end points in association with Cp seropositivity.

Elevated triglycerides, hypertension and cholesterolaemia were the closest risk predictors to cardiovascular events; Some risk predictions to CAD, in relation to Cp seropositivity, were yet again assay dependent.

Conclusion: Our findings, in agreement with many other reviews, support our hypothesis that Cp is not a predictive cofactor to CAD

and, in addition, have proven that inconsistencies and flaws do exist in interpretation of data. Often, serologic markers to Cp infection are seen in association with uncomplicated atherosclerosis and other chronic conditions, yet their predictive value for cardiovascular events is not significant. High seroprevalence and even antigen detection do not prove causality in chronicity. We have illustrated that the seroepidemiology data which triggered renewed interest in Cp as a significant agent in the aetiology and pathogenesis of CAD, lacks strength.

12.154 Estimated impact of global antiviral prophylaxis in containing an outbreak of pandemic influenza H1N1 in an isolated first nations community

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Background: The 2009 influenza A-H1N1 pandemic was mild by historical standards, but in Canada appeared more severe in Indigenous communities, including First Nations. First Nations residing in isolated northern communities were at increased risk of severe outcomes and also had limited access to more advanced medical care, and evacuation by air ambulance augmented costs and risks of severe influenza. The antiviral drug oseltamivir was used aggressively in an isolated northern Ontario First Nations community at the onset of an influenza outbreak. We used mathematical modeling to quantify the impact of antiviral therapy on the course of this outbreak.

Methods and Materials: We used a Richards growth model to evaluate the characteristics of the epidemic (projected final size, turning point, and growth rate) using time series for both respiratory visits and influenza-like illness. The expected cumulative attack rate in the absence of effective intervention, and numbers of cases averted, were estimated based on estimation of the basic reproductive number for disease (R0) and the use of the Kermack-McKendrick "final size formula".

Results: The outbreak grew rapidly but declined markedly with initiation of aggressive antiviral therapy. The fit of models to empiric data was excellent; best-fit Richards growth models identified turning points within 24–48 hours of the implementation of aggressive antiviral therapy. Based on usual serial interval estimates of 1.5 to 2 days, estimates of R0 ranged from 4.0 to 15.8, far higher than published estimates for southern Ontario (1.3); we estimate that utilization of aggressive antiviral therapy reduced risk in this community by 45–92%, prevented 296–2122 cases of symptomatic influenza in this community, and may have prevented as many as 54 medical evacuations.

Conclusion: Although not advocated in other settings in Canada, aggressive utilization of antiviral therapy markedly reduced the impact of a pandemic-related influenza A (H1N1) outbreak in an isolated First Nations community in northern Ontario, Canada. The differential risk experienced by Canadian Indigenous communities in the face of infectious disease outbreaks makes tailored interventions, that take into account differential risks associated with elevated attack rates, increased severity of illness, and lack of access to medical services, appropriate.

12.155 Reverse line blot typing and genome evolution of *Bordetella pertussis*

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Background: Despite widespread vaccination, there has been a re-emergence of the respiratory disease known as whooping cough, which is caused by the bacterium, *Bordetella pertussis*. Microarray studies have investigated the genetic composition of the organism in order to determine what has contributed to its re-emergence despite mass vaccination and regions of difference (RDs) have been identified as clusters of genes flanked by insertion sequences. RDs are potential markers of *B. pertussis* evolution.

Methods and Materials: A collection of 41 strains from the pre-Whole Cell Vaccine (WCV), post WCV and acellular vaccine (ACV) eras were



screened for RD variation. Forty three genes representing 30 regions of difference were combined into 5 multiplex PCR. Products were then run on a reverse line blot which was used to determine the absence or presence of genes within each RD.

Results: We developed a RLB assay of forty three genes representing 30 RDs which allows typing of up to 43 strains simultaneously. We used this system to type 41 strains. When mapped against the evolutionary relationships of the strains, two RDs were found to correspond with significant events in *B. pertussis* history. The losses of BP0910-0934 and BP1948-1962 correlated with the significant events of vaccination. The loss of BP0910-0934 coincides with the introduction of whole cell vaccines in the 1950s while the loss of the RD containing BP1948-1962 first emerged after the introduction of ACV in various countries. This RD loss also coincides with the expansion of the most recent cluster of epidemic *B. pertussis* strains.

Conclusion: Reverse line blotting provided a relatively inexpensive and fast method of determining the gene content of *B. pertussis* strains and can be used as a method of typing of *B. pertussis*. We observed that loss of 2 RDs in isolates correlates with the introduction of widespread vaccination.

12.156 Emergence of novel H1N1: India

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Background: The 2009 influenza A H1N1 pandemic appeared in April 2009 and showed rapid spread to all other countries. The first case of Influenza A H1N1 positive case in India was reported on 16th May 2009. On 10th August 2010 WHO declared the pandemic was over and that it was in the post pandemic phase.

Methods and Materials: NCDC is an apex public health institution and during the H1N1 pandemic 2009-2010 it was declared as a nodal agency for testing of samples of H1N1 from all over the country. The study conducted a retrospective analysis of case reports of samples received. The samples were received from all the 11 designated government hospitals in Delhi and from few other states. The samples were then sent to the virology lab for further and processed in BSL -3 lab by PCR using standard CDC reagents and techniques.

The data was analyzed by excel spreadsheets and presented as percentages.

Results: Data from May 09 to September 2010 was compiled and analyzed. A total of 33751 persons were tested for H1N1 of which 7943 (17%) were positive for Pandemic Influenza A H1N1 and 3759 (8%) were positive for Influenza A (seasonal flu). Maximum positive cases in the age group of 20-39 with 37.4% total positives in this age group and 22.5% males and 14.8 % females were affected. Total H1N1 positive cases 2620(25%) of the positive cases were close contacts of positive cases. maximum number of cases reported fever 7005 (88.1%), 6133 (77.2%) reported fever and cough, fever, cough and nasal catarrh was reported in 377 (4.7%) and 362 (4.5%) cases reported fever with shortness of breath. 1 patient reported of diarrhea with other symptoms, 6 positive patients reported of suffering from vomiting, 5 of them reported of having bodyache and 9 reported of headache.

Conclusion: Thus, our study results conclude that the disease was of moderate severity. It showed predominance in the winter months. Adults were affected more and positive cases were reported more in males than in females. High positivity was reported among close contacts. Clinical features showed fever to be the most predominant clinical feature.

12.157 An outbreak of influenza b in a prison in west midlands UK, 2008

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Background: Institutional outbreaks of influenza like illness and influenza are not uncommon. This report describes a large outbreak of influenza like illness in a prison affecting prisoners as well as staff.

Methods and Materials: Cases were investigated by taking pharyngeal swabs for testing by PCR (for RSV, Influenza A&B, enterovirus, Parainfluenza RNA and adenovirus DNA) and viral culture.

Rapid implementation of respiratory illness control measures included isolation of symptomatic prisoners in their cells, suspending work and social interactions between prisoners in other wings, enhanced environmental cleaning, safe disposal of waste and restriction of staff movements between prison wings.

Antiviral (Oseltamivir) was used for prophylaxis and treatment, prisoners in clinical risk groups were given seasonal influenza vaccination

Results: 112 out of 680 prisoners met clinical case definition of influenza like illness.

The epidemic curve confirmed an outbreak with an epidemic, consistent with person-to-person transmission.

Influenza B RNA was detected by PCR from nasopharyngeal swabs taken from ten prisoners, all housed on wing A. Influenza B virus was isolated from one specimen and typed as B/ yamagata like virus strain identifier B/ENG/133/2008. One further specimen was positive for RSV suggestive of a recent infection.

Three prisoners in clinical risk groups required hospitalisation for pneumonias.

36% (25/69) of prisoners considered to be in clinical at risk groups were already vaccinated with seasonal flu vaccination including the 48 year old prisoner with co-morbidities who died during the course of this outbreak.

Higher than usual level of absence was noted amongst the prison staff but the outbreak control team was unable to investigate staff illness any further due to lack of occupational health services facilities for the prison staff.

Conclusion: The outbreak lasted approximately five weeks and remained largely confined to the wing where it started, suggestive of success of control measures.

Virus isolated in this outbreak belonged to B/Yamagata lineage. These are distinct from the B/Victoria lineage virus (B/ Malaysia/2506/2004-like virus) which was included in the 2007/08 northern hemisphere influenza vaccine. This may partially explain lack of protective effect of seasonal flu vaccination and relatively high incidence of secondary complications (pneumonias), three hospitalisations and one death during the course of this outbreak.

12.158 Outbreak of human adenovirus in patients with acute respiratory infection in Korea at 2010

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Background: Human Adenoviruses (hAdvs) are known to be a major cause of acute respiratory infection (ARI) in all age groups. To date, 53 established serotypes of hAdvs have been described and divided into 7 species, A through G, based on various biological and morphological criteria. Respiratory hAdv infections are endemic, with 3.4 % detection rate all the year round (about 0.1~10.5% positivity) in Korea. However, an outbreak of hAdv was observed in nationwide scale, from Jul to Nov 2010. In this study, we describe an outbreak of hAdv and analyze the major serotype of hAdv causing this outbreak.

Methods and Materials: Through KINRESS, a nationwide laboratory surveillance system for respiratory viruses in Korea, throat swabs from outpatients with ARI including influenza-like illness and common cold were collected and performed PCR to detect hAdvs. To obtain viral isolates, A549 cell line was used and serotype was determined using PCR and sequence analysis for Hexon gene.

Results: hAdv was detected 1.167 cases (10.6%) out of 10,996 specimens collected from Jan to Nov 2011. However, the detection rate of hAdv has been increased progressively more than 20% since Jul (ranging



from 8.9% to 31.3%). The major serotype was hAdv type 3 (88.9%) and hAdv type 1, type 5, and type 34 were detected rarely.

Conclusion: The occurrence of hAdv infections in 2010 was seemed unusual outbreak when compared with last four years, 2006-2009. The major serotype causing ADV outbreak was hAdv type 3 which is known the most predominant serotype of ADV, in Korea since 2006. Even though further investigation should be required to explain, outbreak of hAdv in 2010, Korea might be caused by at least three possible factors; firstly, there was a dramatic change in the environment or ecology of viruses; or changing of host immunity; or lastly, the social behavior of patients or clinicians due to pandemic of IFV (H1N1)2009 in Korea.

Acknowledgement: We thank the physicians in peripheral or primary hospitals and the researchers in Health and Environment Research participating in Korea Influenza and Respiratory Surveillance System (KINRESS) and Acute Respiratory Infection Network (ARI-NET)

12.159 Evidence and genetic analysis of swine A (H1N1) influenza viruses circulating in Austrian pigs within the last ten years

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Background: Swine are considered possible reservoirs for influenza A viruses, in certain cases with the potential to infect humans. From the 1930s, when the first swine A(H1N1) influenza virus was isolated, to the late 1990s the classical swine influenza viruses (SIVs) circulating in North America remained antigenetically relatively stable. These classical strains were replaced by new Eurasian SIVs, which resulted from genetic reassortment between swine and avian strains. In 2009 an influenza A(H1N1) virus containing a unique combination of different gene segments, caused worldwide pandemic in humans. The objective of this study was to identify and type SIV strains which have been circulating in Austrian pigs during the last ten years and to determine their genetic relatedness to other SIV strains.

Methods and Materials: Between 2001 and 2010 more than 450 samples from swine with flu-like symptoms were investigated at the University of Veterinary Medicine, Vienna. The samples were tested by specific SIV RT-PCRs in both hemagglutinin and neuraminidase gene regions. PCR-positive amplification products were sequenced. For comparison, the determined sequences of both HA and NA genes were aligned with selected sequences from GenBank database, representing swine, human and bird influenza virus strains of different geographic origin and isolation time. Subsequently a phylogenetic analysis was performed using MEGA 4 software.

Results: During the study period we identified nine (2.0 %) positive swine A(H1N1) influenza samples. Phylogenetic analysis of the selected H1 gene sequences exhibited two major genogroups: the first classical swine clade with American and Asian swine and human influenza viruses and the second group included current Eurasian swine- and American/Asian bird-SIV strains. Phylogenetic investigations on N1 gene sequences computed comparable results. The Austrian A(H1N1) SIV strains belonged without exception to the currently circulating Euroasian SIV family.

Conclusion: Present study indicate that only one swine A(H1N1) influenza virus type was detected in Austrian samples investigated at our University within the last ten years. The phylogenetic analyses exhibited close genetic relatedness of Austrian SIV strains to other currently circulating European A(H1N1) SIVs. Although SIV in Austria seems to have a regressive tendency, continual monitoring is essential for understanding and assumption of future antigenic evolution of influenza viruses.

12.160 Descriptive and comparative epidemiology of influenza type A and B viruses: towards a tetravalent seasonal vaccine?

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Background: In 2001, influenza B virus belonging to the Victoria lineage re-emerged worldwide. Since then, it has been difficult to predict the dominant B lineage and to adapt the seasonal trivalent vaccine that includes only one B lineage. Experts are considering including two B lineages in the seasonal influenza vaccine. The objectives of this review were 1) to describe the circulation of influenza B by season, by age group and by lineage from 1990 to 2009 2) to compare influenza-related morbidity and mortality by influenza virus type 3) to assess the consequences on vaccine effectiveness (VE) of a mismatch between the circulating B-lineage and the vaccine composition.

Methods and Materials: We reviewed 303 articles and surveillance data from the European Influenza Surveillance Scheme and Flunet.

Results: Influenza B circulated every year and accounted for 20% of all influenza isolates worldwide from 1990 to 2009. In more than 50% of seasons, influenza B circulated later than influenza A. Compared with influenza A, there was a higher proportion of influenza B isolates among older children and young adults. The burden of hospitalisations and deaths associated with influenza B was lower than A(H3) but higher than A(H1). The risk of hospitalisation and death among influenza B patients was at least as high as for influenza A. Since 2001 there were five mismatches between the virus included in the vaccine and the dominant B lineage in Europe and the US. A recent review including 9 RTC studies suggested that type B VE was lower when there was a mismatch (31%) than when there was a close match (86%) between the circulating B lineage and the one included in the vaccine.

Conclusion: Our results suggest that while influenza B is associated with lower attack rates, it still represents a significant share of all influenza isolates and it is as severe as influenza A. Further studies on the B strain circulation according to type and lineage are needed to assess more precisely the burden of influenza B strains in the population.

12.161 Evaluation of rapid antigen tests for detection of pandemic influenza H1N1 2009

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Background: Clinical management on influenza is optimized by the use of rapid diagnostic tests (RAT), which facilitate early antiviral use. The objective of this study is to evaluate the performance of selected commercially available rapid influenza antigen detection tests in detecting influenza A/H1N1 2009 virus.

Methods and Materials: 444 Specimens were collected and included in this study.

Three RAT were used: Binax NOW Influenza A&B (Binax, Inc Scarborough, Maine, USA), QuickVue Influenza A+B (Quidel Corporation, San Diego, USA) and InfluenzaTop (All Diag, Strasbourg, France). RT-PCR was used for confirmation of influenza A/H1N1v (Artus influ. /H1 LC/RG RT-PCR). All samples were tested by all methods.

Results: One hundred forty eight cases of PCR-proven influenza A/H1N1 09 were detected (33%). Of these, sixty three samples (42%) were positive for influenza A virus by either RAT assay.

The specificity was 100% for the three RAT assayed. The negative predictive value of the RAT was only 57% for the QuickVue assay. The Binax Now Influenza A&B appears to be more sensitive for the detection of the new H1N1 influenza A virus (87.5% versus 20% and 42.4% for QuickVue and InfluenzaTop respectively).

Conclusion: Performance characteristics of various RAT in the detection of influenza A/H1N1 09 pandemic are uncertain in our study, a marked difference was observed in performance between types of RAT. We suggest that Binax Now Influenza A&B Pandemic may be a useful diagnostic tool for the detection of A/H1N1 2009 in appropriate clinical settings, although a negative RAT may require confirmatory assays of greater sensitivity.

**12.162 Exposure assessment using a novel influenza protein micro-array to detect antibodies against human and animal influenza viruses**

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Background: Influenza A virus is one of the leading zoonotic threats, particularly since the spread of highly pathogenic avian influenza A (H5N1) among poultry and wild birds in Asia, the Middle-East, Europe and Africa. The potential transmission of these and other avian and porcine influenza viruses to humans poses a permanent pandemic threat. However, current surveillance captures new incursions of influenza virus into the human population with low sensitivity, and improved tools are needed for surveillance at the human-animal interface. We developed a novel serological micro-array to detect antibodies against different influenza viruses of subtypes H1, H3, H5, H7 and H9 in small volumes of blood (finger stick) of humans and animals.

Methods and Materials: Recombinant HA1 proteins from 16 different influenza strains belonging to subtypes H1,H3, H5, H7 and H9 were spotted in triplicate on a nitrocellulose coated slide. After incubation of serum, antibody binding to the specific antigens was visualized by a relevant conjugate labeled with Cy5. Assay validation was done using well defined serially collected serum samples from patients infected with RT-PCR confirmed influenza A/H1N1 and H5N1 virus infection, experimentally and naturally infected poultry, and negative control sera from humans and animals.

Results: Use of HA1 subunits as antigens allowed subtype-specific measurement of antibodies in humans and poultry. Low reactivity for H5 in the negative sera was measured in controls compared to naturally infected individuals, and patients infected with the pandemic influenza virus of 2009 showed seroconversions to a range of H1 subtype antigens. Correlations between the antigens on the protein array slide were higher for reactivities within subtype (cross-clade) than between subtypes, ranging from 79% to 96 between different H5 clades when testing human sera from naturally infected (severely ill) patients.

Conclusion: The newly developed micro protein array for detecting antibodies to influenza virus HA can be used for sub-type specific detection of antibodies to a range of influenza viruses. The protein micro-array can be used for population based studies to assess exposure to different influenza viruses.

12.163 Pandemic Influenza on the territory of Skopje, R.Macedonia

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Background: Influenza is an acute infectious disease of the respiratory system that can occur in an epidemic and a pandemic form. During 2009, according to the recommendation of the WHO, R.of Macedonia undertook a lot of activities in order to prevent the spreading and to stop the complications of the new type of Influenza A H1N1. The first cases of the virus were confirmed in the summer months, with patients who returned from their vacation in the neighbouring countries.

Methods and Materials: The epidemiological descriptive method was used. Group weekly reports were used as materials, as well as the weekly reports of the ambulatory and hospital patients in the hospitals in Skopje.

Results: During the season 2009/2010, starting from week 40 until week 13, 17.232 cases of Influenza (Mb = 290.7 /10.000 inhabitants) were registered. The majority of the cases were reported within week 49, from 30/11/2009 until 06/12/2009, when 3.218 cases (Mb = 54.3 /10.000 inhabitants) were registered. The distribution based upon the sex of the patients demonstrates that the most affected age group is from 15-64

years of age, with 9206 cases or 54%. The second age group is from 5–14 years of age, with 4141cases or 24%. Within the period starting 18/11/2009 until 07/03/2010, 16 deaths from Influenza H1N1 were registered, out of which 14 were cases of laboratory confirmed influenza

Conclusion: The Department of Epidemiology at the Center for Public Health in Skopje established a coordination network, assessed the number of necessary vaccines and antiviral medications, completed the assessment of hospital facilities, employees, as well as the personal protection equipment.

12.164 Awareness of H1N1 among Hajj returning Pilgrims, Gombe State, Nigeria 2009

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Background: Hajj activity is a yearly religious rite performed by Muslims all over the world. >2.5million Muslim faithful congregate in Mecca, Saudi Arabia for this activity. In 2009, the H1N1 pandemic coincided with the Hajj period. About 5000 pilgrims were airlifted from Gombe International airport to Saudi Arabia for Hajj 2009.

The government of Nigeria embarked on awareness campaign using various methods to educate Nigerian Pilgrims about the highly infectious H1N1. We assessed the level of awareness of H1N1 among the returning pilgrims.

Methods and Materials: A cross sectional study design was used. All returning pilgrim via Gombe International airport who granted interview were enrolled into the study. We collected data using an interviewer administered structured questionnaire on symptoms of H1N1, mode of transmission and prevention of H1N1 and source of the information.

Results: Of the 5000 pilgrims airlifted we interviewed 2055(41%). Of those interviewed 1302 (63.4%) were aware of H1N1. Cough(43.1%), Fever(25.3%), Catarrh(16.7%), were the commonest symptoms of H1N1 known to the respondent while headache(9.8%), Sneezing(3.9%), Sore throat(0.9%) and difficulty with breathing(0.3%) were the least. 1627 (79.3%) don't know the mode of transmission of H1N1. Of those who had knowledge of preventive measures of H1N1, 267 (55.3%) knew that face masks can be used for prevention. 803 (88.8%) got their information about H1N1 through electronic media.

Conclusion: During disease outbreaks, information about signs and symptoms, mode of transmission and prevention of disease should effectively be communicated to the public. Awareness is key to prevention and control. The choice of an effective and fastest method to educate the public is important. In Gombe, a State in Northern Nigeria, the electronic media is effective in dissemination of information.

12.165 Pediatric Influenza A(H1N1)v infection: insights from virologic surveillance

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Background: On 11th June 2009 the World Health Organization announced the start of the influenza A(H1N1) pandemic. The department of Public Health of the University of Parma is the regional coordination centre for the pandemic surveillance. This study reports data concerning incident cases over a six-month period focusing on the clinical features of paediatric cases.

Methods and Materials: Notification files of suspected cases have been retrospectively analyzed. From April 2009 until September 2009, a total of 542 cases had been notified, 242 of them ≤ 18 year-old. 29.3% were positive for virus A(H1N1)v. Personal data (age, sex and nationality) as well as clinical features (symptoms, time length of symptoms, contacts) were explored. Continuous variables were analysed using t-Student test and categorical ones with Chi square test and calculation of RR and 95%CI.

Results: Paediatric cases had a not significantly shorter symptoms' duration (2.6±4.3 days vs 3.6±5.3 days, p = ns) than adult cases.



Actually, A(H1N1)v+ cases were associated with headache (RR=2.1;95%CI=1.5-3.0), arthralgia (RR 2.0 95%CI1.4-2.9), myalgia (RR=2.3;95%CI1.7-3.3) and dry cough (RR=2.8;95%CI=1.9-4.0). On the contrary, they were at a lower risk of vomit (RR=0.3;95%CI=0.1-0.8). In contrast with adults, body temperature $\geq 38^{\circ}\text{C}$ was not significantly related to A(H1N1)v+ status.

Conclusion: The not significant association between fever and A(H1N1)v+ status could be explained by the clinician's higher degree of suspicion for influenza in pediatric subjects with high body temperature, with a higher number of improperly notified cases. Actually, our results suggests that fever by itself appears as a not significant sign for diagnosis of pediatric influenza.

12.166 Vaccine Effectiveness of Pandemic Influenza A (H1N1) in Korea

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Background: This study was conducted to examine the effectiveness of pandemic influenza A(H1N1) vaccine in six nation-wide hospital workers using cohort study.

Methods and Materials: Hospital workers answered to a questionnaire first, and were followed up 4 months later. Finally, cases of 9,336 participants were analyzed out of 9,355 after excluding 19 subjects that had ambiguous information about being confirmed as an H1N1 infection or receiving H1N1 vaccine.

Results: Vaccine effectiveness using cumulative attack rate was 95.6% (95% CI: 93.3–96.9%), and vaccine effectiveness using density attack rate was 96.0% (95% CI: 94.4–97.2%). Vaccine effectiveness based on the assumption that vaccine is effective after 10 days since vaccination was slightly lower than when vaccine effectiveness after 14 days was assumed. Point values of vaccine effectiveness were all above 90% and statistically significant among subgroups stratified by general and clinical characteristics, seasonal influenza vaccination status, contact history and hygienic habits. Vaccine effectiveness increased as age or body mass index increased, and vaccine was higher among subjects with underlying diseases or those who have received seasonal influenza vaccination, although the difference have no statistical significance. Vaccine effectiveness adjusted for job in hospital, existence of H1N1 patients in family or department, and contact history with H1N1 patients at hospital was the highest among subjects aged 30-39 (98.0%), and these values were similar between male and female subjects. Vaccine effectiveness in October and November of 2009, which was the H1N1 outbreak period (98.5%) was higher than that after December 2009 (86.9%). Vaccine effectiveness in preventing influenza-like illness was 57.6% lower than that in preventing H1N1 infection. The point values of cross vaccine effectiveness of H1N1 vaccine and seasonal influenza vaccine in preventing H1N1 infection were all above 85%, but were lower than H1N1 vaccine effectiveness, so we ascertained that there was no synergic effect between H1N1 vaccine and seasonal influenza vaccine in preventing H1N1 infection.

Conclusion: In this study, we ascertained that the H1N1 vaccine could effectively prevent H1N1 infection. Influenza vaccine for northern hemisphere in 2010/2011 winter season includes influenza A (H1N1) virus as A/California/7/2009 (H1N1)-like virus.

12.167 Wound infection/abscess formation caused by *Eggerthella lenta*

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Background: *Eggerthella lenta* was, up to 1999, known as *Eubacterium lentum*. It is a strict anaerobic, non-sporulating, non-motile Gram-positive bacterium that grows singly, as pairs or in short chains. A MEDLINE search (as of September 14, 2010) gave 23 "hits", using *Eggerthella lenta* as the only search criterium. "*Eggerthella lenta*" and "infection" yielded six "hits", whereas "*Eggerthella lenta*" and "wound infection" gave no results when it comes to peer-review publications.

Methods and Materials: A 75-year-old woman, admitted to Sykehuset Innlandet Trust (hospital), presented with an abscess/wound infection of abdominal origin. Cultures from an abscess/wound infection from the patient proved to be cultivation positive for *Eggerthella lenta*. The cultures were subjected to primary tests at our laboratory using standard media—i.e. blood, chocolate, anaerobe and lactose agars—incubation under aerobic—as well as anaerobic conditions. Primary testing with API 20A (BioMerieux) and VITEK-2 proved inconclusive. 16S rDNA PCR sequencing was performed at Oslo University Hospital.

Results: Cultures demonstrated only growth of a strict anaerobic Gram-positive rod. Utilizing 16S rDNA sequencing the bacterium was identified as *Eggerthella lenta*. There was a 99% homology with a known sequence in The National Center for Biothecnology Information (NCBI) database - using BLAST (version 2.2.17)—URL: <http://ncbi.nlm.nih.gov/BLAST>. The antibiogramme was as follows, clindamycin—MIC 0.32 (sensitive - S), meropenem - MIC 0.125 (S), metronidazole—MIC 0.125? (S), penicillin G - MIC 0.25 (R), piperacillin/tazobactam—MIC 8 (S).

Conclusion: In Norway wounds/abscesses caused by *Eggerthella lenta* has not—to our knowledge been described previously. When it comes to this patient high age was the most likely risk factor for this infection. Our department has, over the years, detected rare bacteria comprising *Actinobaculum urinale*, *Actinobaculum schalii*, *Actinomyces neuui subsp. neuui*, *Clostridium scindens*, *Bulleidia moorei*, *Haemophilus segnis*, *Dialister pneumosintes* and *Anaerobiospirillum succiniciproducens*. Collaboration between local and regional laboratories is essential to diagnose such bacteria.

12.168 Bacteraemia caused by *Varibaculum* species

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Background: Genus *Varibaculum* consists of Actinomyces-like Gram-positive rods e.g. *Varibaculum cambriense*. Herein is a description of what probably is the first documented Norwegian case of bacteraemia caused by *Varibaculum*.

Methods and Materials: Blood cultures from a woman born 1950, admitted to our hospital in June 2008, were subjected primary tests at our laboratory using standard media—i.e. blood, chocolate and lactose agars—incubation under aerobic and anaerobic conditions. The Norwegian Institute of Public Health performed reference testing.

Results: Blood cultures were cultivation-positive for a Gram-positive rod-shaped bacteria later identified to the genus level as *Varibaculum*—most likely *Varibaculum cambriense* at the Norwegian Institute of Public Health, which performed the reference testing, including 16S rRNA sequencing.

Features:

- Hemolysis: None
- Corrosion: None
- Growth on agars:
- Blood aerobic: +
- Chocolate aerobic: +
- Lactose aerobic: -
- Blood anaerobic: +
- Chocolate anaerobic: +
- Metronidazole: Resistant
- Vancomycin: Sensitive

Sequencing: A 496 base pair fragment from the 16S rRNA gene was sequenced, showing a 99% homology with *Varibaculum cambriense*, hence belonging to genus *Varibaculum*.

Conclusion: In Norway bacteraemia caused by genus *Varibaculum* has not—to our knowledge been described before. This is most likely be the first case case report ever in Norway demonstrating genus *Varibaculum* as the cause of a systemic infection such as bacteraemia/septicaemia.



12.169 Infectious pancreatic necrosis (IPN), a new threat of cultured rainbow trout in Iran

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Background: Infectious pancreatic necrosis virus (IPNV), a member of the virus family Birnaviridae, causes an acute, contagious disease with high mortality rate in a number of economically important fish species specially salmonids. During April 2009, one Rainbow trout farm, situated in Gilan province, north of Iran, reported unusually high losses of reared rainbow trout fry with average weight of 560 mg. same mortality were reported from 4 other farms in fryes under 1 gram weight in 2010. Clinical signs included darkening, exophthalmia, distended abdomen, fecal cast and a spiral swimming motion. Cumulative mortalities were more than 90%. Water temperature was between 12 to 16°C. Alive affected fish were delivered to the virology laboratory of Inland water aquaculture institute situated in Bandar anzali for diagnostic investigation. Clinical signs, mortality levels, age and size of fish and necropsy findings suggested that IPNV might be present. The presence of virus was confirmed by virology methods with cooperation of community reference laboratory of fish disease, Aarhus,Denmark.

Methods and Materials: Pools of viscera from each five whole fry were homogenized, re-suspended in medium and clarified by centrifugation at 2000 rpm for 20 minutes in 4°C. Supernatants were inoculated onto monolayers of the BF-2 and EPC cell lines in 24 well multidishes and identified by ELISA, IFAT, NT, Nested-RT-PCR and Chloroform test. The PCR product of an isolate was sequenced and the Phylogenetic tree was constructed from the sequencing data.

Results: CPE was observed 24h post inoculation and IPNV identified by ELISA, IFAT, Nested-RT-PCR and Chloroform test. In neutralization test, the virus showed more closely relationship to the SP (A2) serotype. Through an analysis including to other polyprotein gene sequences deposited in Genbank, a Spanish isolate (ATCC AJ489222.1) was found more similar to Iranian isolate.

Conclusion: Serotype of aquabirnavirus isolated in this study suggesting that the original source of the virus was in Europe. This is the first isolation and identification of IPN virus from rainbow trout fry in Iran.

12.170 Clinical manifestations and outcome in *Bacillus cereus* bacteremia “underestimated complications”

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Background: Although *Bacillus cereus* had not been recognized as actual infections, it had been reported that it can cause number of nosocomial infections such as catheter-related blood stream infection (CRBSI). Gram positive rod bacteremia can cause several complications such as abscess, endovascular infection or osteomyelitis. We investigated clinical characteristics of *Bacillus cereus* bacteremia (BCB) and its complications to assess clinical impact of this organism.

Methods and Materials: We performed a retrospective analysis of BCB at a tertiary care hospital in Kobe, Japan from October 2008 to September 2010. Cases were identified via microbiology laboratory reports, and relevant clinical data were collected from the electronic medical record of each patient. Cases with at least 2 set positive blood cultures were defined as true infection. We investigated clinical characteristics of BCB, type of catheter, types of fluids and patients’ characteristics. We also investigated complications such as sepsis, continuous bacteremia, thrombophlebitis and remote abscess formation.

Results: Thirty nine cases of BCB were identified. Thirty seven cases were CRBSI, whereas 2 cases were followed by surgical site infection. Thirty three cases accompanied sepsis (33/39, 85%). Fifteen cases were complicated with continuous bacteremia (15/39, 38%). Twenty one cases accompanied thrombophlebitis (21/39, 54%). Two cases had remote site infections (septic arthritis and endophthalmitis) (2/39, 5%). One patient died during the treatment of BCB (1/39, 3%). One patient had severe morbidity, i.e. loss of vision by endophthalmitis (1/39, 3%).

Conclusion: Almost all BCB were caused by CRBSI. Although catheter was removed in all CRBSI cases, continuous bacteremia were seen as frequently as *Staphylococcus aureus* bacteremia. Further studies are necessary to determine the risk of *Bacillus cereus* complications.

12.171 Insectivore-borne human hantavirus infections: first report of two (retrospective) cases.

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Background: More than 20 genetically divergent hantaviruses were recently demonstrated in shrews and moles, but worldwide no single human infection was reported so far. We report two cases, each highly suggestive for an acute hantavirus-like infection transmitted by a distinctive representative of these two insectivore families.

Methods and Materials: Indirect immunofluorescence assay (IFA) on 6 different hantavirus strains was used for serodiagnosis.

Results: Patient A: A 50- years old male fish farmer in the Ardennes (South-Belgium) was bitten in July 1987 by a water shrew (*Neomys fodiens*), a known pest in his fish pounds. Three days later, he developed high fever, myalgiae, proteinuria, thrombocytopenia, and acute renal failure (ARF) with a peak creatinine of 4.5 mg%. He recovered without dialysis within 20 days. Patient B: In February 1990, a 46-years old male US military, working in SHAPE HQ, (South-Belgium), decapitated with his spade an European common mole (*Talpa europaea*) in his garden. He was splashed in the face and on his clothes with blood of the animal. Five days later, he was admitted to hospital with high fever, myalgiae, proteinuria, thrombocytopenia, and severe ARF, peaking to creatinine of 6.4 mg%. He recovered fully in 16 days without dialysis. Titers of IFA IgG were:

	HTNV 76-118	PUUV CG18-20	PUUV Hällnäs	PUUV CG13891	PHV	SEOV Tchoupit.
Patient A	512	4096	4096	4096	1024	1024
Patient B	32	16384	16384	16384	1024	16

At that moment, no other laboratory tests were in use for confirmation, but both patients are currently being traced back.

Conclusion: Both clinics and serology are admittedly typical for Puumalavirus (PUUV), transmitted by bank voles (*Myodes glareolus*), common in Belgium. However, the unusual very direct exposure in both cases, and the short incubation time thereafter, are highly suggestive for an insectivore source of infection. Already in early 90 ‘s and with ELISA based on CG 18-20, we demonstrated the presence of a PUUV-like antigen in lungs, and PUUV-like antibodies in the blood of both insectivore species, captured in Belgium. Admitting the distant genetical relationship of all insectivore-borne hantaviruses characterized so far, our predominantly PUUV-like results suggest crossreactions with a new, as yet unknown hantavirus .

**12.172 The first isolation of *Mycobacterium elephantis* from tuberculin-reactive cattle**

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Background: *Mycobacterium elephantis* is a species of atypical mycobacteria recently isolated from a lung abscess of an elephant that died from chronic respiratory disease. The first publication was followed by reports of 14 strains of *M. elephantis* isolated from human sputum, lymph nodes, and bronchial aspirate in Canada, Italy, and Belgium. In livestock, due to the insufficient specificity of tuberculin, atypical mycobacteria provoke positive reactions to tuberculin in cattle and cause significant economic losses. However, the aetiological factor of bovine reactivity to tuberculin remains unknown in many cases.

Methods and Materials: The strain was cultured from lymph nodes of cattle that had reacted to intradermal administration of tuberculin for mammals. The cow was held in a farm with a recent history of a TB outbreak (Kyiv region, Ukraine). On section the cow had no visible TB lesions.

The material was cultured in 7H9 Meadbrook broth, Stonebrink and Ogawa media at 37°C. The culture was stained according to Ziehl-Nielsen procedure.

DNA was extracted, genus- and species-specific PCR, as well as 16S rDNA sequencing were performed.

Results: Growth in broth appeared on the 4th day a.i. On solid media, colonies became visible on the 5th day. The broth was clear with pellicle and yellowish-creamy sediment suggesting that the strain was aerophilic. Colonies were wet and smooth with yellowish-creamy pigment.

Microscopy revealed acid-fast short-to-coccoid rods of pale-red colour.

Genus-specific PCR was positive, whereas all species-specific PCRs were negative.

Hypervariable region A of the mycobacterial 16S rDNA (236 nt) was sequenced and compared with those available from the GenBank database (www.ncbi.nlm.nih.gov/entrez). Sequence analysis revealed 99% similarity to *M. elephantis*.

Conclusion: *M. elephantis*, an "exotic species", was established as a cause of delayed-type hypersensitivity e.g. "positive" reaction for TB in cattle. However, the absence of pathological lesions in the cow indicates low pathogenicity of *M. elephantis* to cattle or none at all.

To our knowledge, this is the first report of isolation of *M. elephantis* from cattle.

12.173 Novel avian orthoreovirus strain associated with runting-stunting syndrome in broilers

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Background: Avian orthoreoviruses (ARVs) are responsible for considerable economic losses in broiler chickens; yet, the genetic characterization of most ARV strains is limited to a few genes, and the full coding region has been determined for only S1133 and 138, two ARV strains associated with tenosynovitis. Recently, in parts of the United States, ARVs with novel neutralization antigen type were isolated from chickens afflicted with runting-stunting syndrome.

Methods and Materials: One such strain, AVS-B, was selected for full genome sequencing and phylogenetic analysis.

Results: The complete genome was 23,494 bp in size and included 12 open reading frames. The lengths of the coding regions, as well as those of the 5' and 3' ends, were fairly well conserved between AVS-B and other reference strains. In pairwise comparisons to the S1133 and 138 strains, the AVS-B strain shared a wide range of sequence identities along each genome segment, i.e., a range of 54-55% for the α C coding region of S1 genome segment and 91-93% for the S2 genome segment. Phylogenetic analyses of individual genes of AVS-B did not identify any single common ancestor among more completely characterized ARV strains for which

sequence data are available. One exception to this lack of identity was strain 138, which shared 90-93% nt identity with AVS-B along seven of ten genome segments; only M2, M3, and S1 segments of these strains shared lower sequence identities.

Conclusion: Collectively, our analyses indicated that multiple reassortment events and strong divergence caused by the accumulation of point mutations could have led to the observed assortment and genetic heterogeneity of the AVS-B genome.

12.174 Emergence of new variants of *Shigella* and their characterization

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Background: Shigellosis represents one of the most severe forms of acute bacterial gastroenteritis and no known *Shigella* spp/subtypes could be isolated from the 40% of clinically Shigellosis cases. Significant number of *Shigella* spp isolated from Bangladesh and in diverse geographical regions between 1999 and 2008 could not be serotyped following the current serotyping scheme. These strains were designated as new variants of *Shigella*. The aim of this study is to identify and characterize these new variants of *Shigella*.

Methods and Materials: All these atypical or new variants/*Shigella*-like organisms (SLO) are confirmed as *Shigella* species using different molecular and phenotypic techniques: serotyping, antibiotic resistance, plasmid profiling, and pulsed-field gel electrophoresis (PFGE).

Results: Of 12,700 strains of *Shigella* species isolated at ICDDR,B in Bangladesh between 1997 and 2008, 4750 strains were characterized phenotypically and genotypically. Twenty-three percent of *S. flexneri*, 8% of *S. dysenteriae*, and 23% of *S. boydii* were identified as atypical since they did not react with either type or group antigen-specific antisera. We found three groups of atypical *S. flexneri* strains as *S. flexneri* 1c, *S. flexneri* 4X, and *S. flexneri* type 4. Of these, *S. flexneri* 1c was predominant (46%), followed by 4X (28%) and Type 4 (26%) respectively. In a population-based study by IVI, Korea in six Asian countries found high prevalence of atypical strains (n=187) in these countries. Of these atypical strains, *S. flexneri* 1c (57%) was the dominant, followed by type 4 (37%) and 4X (6%). Most of the atypical and SLO harbored the 140 MDa plasmid, had the ability to bind Congo red and were positive for keratoconjunctivitis in the guinea pig eye attesting their invasive properties. Two different clones in atypical *S. flexneri* type 4, 3 different clones in 1c and of SLO, two new clusters of *Shigella*, one belonged to *S. boydii* and the other one *S. dysenteriae* were detected in Bangladeshi and in abroad.

Conclusion: The study urges further identification and characterization of these new variants/*Shigella* spp. around the globe with a view to validate the *Shigella* serotyping scheme and to combat *Shigella* outbreaks which in turn will help in designing effective therapeutics and vaccine development.

12.175 Impact of Isoniazid for preventing tuberculosis among non-HIV population in Malaysia: an age-structured model

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Background: Tuberculosis remains as one of the highest unresolved disease burden among re-emerging diseases in Malaysia for the last twenty years. With current treatment protocol emphasizing among the infectives, we seek to find if combination treatment of these active cases with Isoniazid Preventive Therapy for high risk latent tuberculosis infection groups among non-HIV population would give greater impact on reducing incidence.



Methods and Materials: Our study aims to apply the use of infectious disease modelling to study the progression of latent tuberculosis infection among non-HIV population in Malaysia, and to assess the impact of Isoniazid as preventive therapy on reducing incidence. We present a deterministic compartmental age-structured tuberculosis model which incorporates treatment of infectives as well as the preventive therapy. The model assumes that latently infected individuals develop active disease as a result of primary infection, endogenous reactivation and exogenous reinfection. We start by formulating and analyzing the model without any intervention strategy then, we extend to incorporate the preventive therapy and treatment of infectives. The epidemic thresholds known as reproduction numbers and equilibria for the model are determined, and stabilities analyzed. The reproduction numbers for the model are compared to assess the possible community benefits achieved by treatment of infectives, preventive therapy and a holistic approach of combination of both intervention strategies. The model then further quantifies the effectiveness of preventive therapy for early latent tuberculosis infection and demonstrates how effective the therapy has to be to eliminate tuberculosis, when use in conjunction with treatment for active tuberculosis.

Results: Our analyses show that treatment of infectives is more effective in the first years of implementation of preventive therapy as treatment results in clearing active tuberculosis immediately across age categories, hence will do better in controlling the number of infectives due to reduced progression to infectious state.

Conclusion: Our model suggests that Isoniazid Preventive Therapy which identify and treat persons recently infected may have a substantial effect on controlling tuberculosis epidemics in Malaysia.

12.176 Analyzing the Impact of Superspreading Using Hospital Contact Networks

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Background: Super-spreading events have been observed in many community and hospital outbreaks of emerging infectious diseases where a single individual is responsible for the transmission of a pathogen to a large number of people. Hand hygiene control measures have proven to be effective in reducing infection rates in hospitals. Temime et al. 2009, shows using simulations based on a hypothetical intensive care unit (ICU) that noncompliance in a single peripatetic healthcare worker (HCW) can have a substantial effect on the number of patients infected. The purpose of this study is to determine the impact of noncompliant peripatetic HCWs compared to non-peripatetic HCWs using real hospital contact data collected from a wireless sensor network.

Methods and Materials: We used a sensor network to detect and record contacts among HCWs and patients in a 24 bed ICU for one week. Motes, pager-sized devices worn by HCWs and affixed to patient beds, periodically broadcast a beacon to all nearby motes and record beacons received from nearby motes. Then, based on recorded contact data, we ran agent-based simulations modelling the spread of nosocomial pathogens (e.g., MRSA) with various probabilities of transmission. For each shift, we identified the single most and the single least "connected" HCWs based on the number of unique patients each HCW saw during his shift. We then compared the effects of hand hygiene noncompliance between these two HCWs.

Results: The result of each simulation is reported as the average number of patients colonized over 1000 repetitions. In simulations based on 2 different work shifts, the average number of colonized patients was significantly higher when the single most connected HCW did not comply with hand hygiene policies than when the single least connected HCW was noncompliant.

Conclusion: Our results use real contact data gathered in an ICU to corroborate earlier mathematical studies of superspreading and confirm that heterogeneity in HCW behavior is an important factor in pathogen transmission.

Reference: Temime, Opatowskib, Panneta, Brun-Buissonb, Boelle and Guillemotb (2009) Peripatetic health-care workers as potential superspreaders. PNAS 106:43.

12.177 State capacity influences on the epidemiology of neglected tropical and vector-borne diseases in Africa

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Background: Neglected tropical and vector-borne diseases continue to emerge and reemerge in Africa, where a significant number of governments have limited state capacity. The reasons these diseases (specifically leprosy, cholera, yellow fever, malaria, and human African trypanosomiasis [HAT]) resurface are speculative and this problem remains unsolved; however, what little literature does exist suggests that state capacity influences health. This study examines if there is a relationship between state capacity and the epidemiology of neglected tropical and vector-borne diseases in Africa. Specifically, if there is a relationship between state capacity and each of the four categories of dependent variables: disease burden, incidence, prevention/control, and mortality.

Methods and Materials: This ecological, correlational study used archival data that came from the United Nations (UN) Data, a compilation of databases managed by the UN. Data queried from databases were converted to comma-separated values and imported into Microsoft Excel. Multiple regression analyses were conducted using the state capacity variables that were combined into two composite predictors designated as state capacity A, comprised of fiscal resources, and state capacity B, which included sociopolitical measures. The disease categories of burden, incidence, prevention/control, and mortality were the dependent variables. The statistical significance level of .05 was reported as well as the effect size (small importance = .02; moderate importance = .15; large importance = .35).

Results: Statistically significant relationships were revealed between state capacity and the following dependent variables: all disease-burden variables; insecticide-treated nets prevention/control; and all age-related and HAT mortalities. A broad range of effect sizes were observed and the economic and sociopolitical attributes of state capacity made different contributions to these effects. Table 1 shows the summary of results.

Dependent variable	Predictor variable effect size	
	SC_A	SC_B
Malaria disease burden	Moderate*	None
Diarrheal disease burden	Moderate*	None
HAT disease burden	Large*	None
Leprosy incidence	None	Small†
Malaria incidence	Small†	Small†
ITN	Moderate*	None
IRS	Small	None
Water supply access	None	Small†
Improved sanitation access	None	Small†
Yellow fever vaccinations	None	Small†
Household screening activities	Small†	None
Infant mortality	None	Moderate*
Child mortality	None	Moderate*
Adult mortality	None	Small*
Malaria mortality	None	Small†
Diarrheal mortality	Small†	None
HAT mortality	Small*	Moderate*

Note. *p < 0.05; † = not significant; HAT = human African trypanosomiasis; ITN = insecticide treated nets; IRS = indoor residual spraying.

Table 1. Summary of Study Results by Variable and Effect Size

Conclusion: Findings from this study will inform policymakers, political scientists, and public and global health practitioners about key characteristics of state capacity that influence the spread of disease in state, as well as the specific characteristics of state capacity that could increase the effectiveness of prevention, intervention, and control measures. Future studies should explore the economic and sociopolitical attributes of state capacity that influence disease transmission by examining different populations or diseases, and by using different research methods.

**12.178 Help seeking behavior of mothers of children with and without measles in Shahpur block of district Kangra, Himachal Pradesh, India, 2008**S. Gupta¹, N. Gupta²¹Regional Health and Family Welfare Training Centre, Kangra, Himachal Pradesh, India, ²Kangra, Himachal Pradesh, India

Background: Based upon two measles outbreaks in highly immunized district Kangra, we conducted a qualitative comparative study to describe the help seeking behavior of mothers of children with measles and to recommend remedial measures to prevent further outbreaks.

Methods and Materials: We conducted four Focus Group Discussions; two in Shahpur case block and two in Nagrota Bagwan comparative block with 20 mothers each in group. We enrolled all 69 mothers of children with measles and equal number of mothers in comparative similarly situated non measles block-matched for age and sex. We used a pre-designed pre-tested data collection semi structured qualitative questionnaire. We compared the responses from mothers of children exposed and unexposed to selected characteristics by Focus Group Discussions and in-depth interviews.

Results: 80% of respondents from case block call measles as Dharassali; 95% mothers have bodily experience of measles. 68% respondents under Shahpur block attribute measles to the curse of goddess, 55% hold contagion as the cause for illness. For *treatment (help) seeking behavior* of mothers, 68% from case block go for faith healers followed by 12% by village elders/neighbors/friends/relatives while 59% from comparative block opt for doctors. Nutritional care is given in the form of restricted diet in case area. As follow up practices in the post recovery phase from illness, 58% respondents from Shahpur block invoke the blessings of the *goddess Sheetla* while 68% of mothers from Nagrota Bagwan block attend the medical clinic.

Conclusion: Faith healing is the principal help seeking behaviour in measles in poor hills. Aggressive IEC activities should be targeted for economic and social behavioral change and improving access to health care facility through provision of mobile services.

12.179 Social and behavioural research on Avian Influenza in Solok, IndonesiaS. Kosen¹, R. Prasodjo², T. Respati³¹ National Institute of Health Research & Development, Jakarta, Indonesia, ²National Institute of Health Research & Development, Jakarta, Indonesia, ³Universitas Islam Bandung, Bandung, Indonesia

Background: The objective of this study is to find alternative ways of implementing AI prevention and control program by using behavioural modification and community participation approaches in reducing the occurrence of Avian Influenza at community levels.

Methods and Materials: This study is the first phases of two. Data collection method applied is participatory observation in the field; in-depth interviews; group discussion and collection of secondary data. In-depth interview was held to determine underlying factors of AI related behaviour, such as social, economic, cultural and psychological factors. Group discussions were done involving local community leaders and household heads that are raising chicken/poultry. The results from this study will be used as the base for the participatory action research on the second phase.

Results: The study found that poultry, especially chicken had important social and cultural value particularly in their religious and traditional ceremony. The reason behind this behaviour is that chicken is one of the most important things in their daily life. The behaviour regarding the management of poultry and its products showed several high risks conducts such as consuming raw egg yolk and eating sick chicken. Chickens or birds are also treated as pets especially by children. The community believe that when people died after eating a sick bird it was their destiny and not because of the infected bird. The use of local media to disseminate the messages regarding AI prevention and control program varied and produce different outcomes. The community value of those animals is far greater than the perceived risks of AI.

Conclusion: The awareness of AI diseases prevention and control program is very inadequate. A socially accepted AI intervention program based on the diverse ethnic values need to be define to ensure its success.

12.180 Cross-sectoral dengue fever prevention initiatives in Brazil and the participation of waste pickers in the informal trash economy

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Background: Sharp rises in dengue fever rates in Brazil recently catalyzed new civil-state trash collection partnerships aimed at reducing mosquito infestations. This medical anthropological study investigates knowledge and attitudes of waste pickers in Brazil's informal trash economy. It interrogates the social and political significance - rather than objective validity - of claims that waste pickers' contributions to environmental modification are viable alternatives to municipal sanitation and insecticide programs. The study hypothesized that waste pickers who were more politically active would not only be more likely to understand the relationship between prevalence of container discards and dengue incidence, but would also be more likely to articulate informal trash work as important to vector management and as justification for their demands for social recognition.

Methods and Materials: Ethnographic fieldwork in Rio de Janeiro in 2009 and 2010 utilized spatial maps to identify neighborhoods with a coincidence of high dengue infections and low municipal sanitation services. Surveys were administered near trash dumps and households to recruit an initial sample (N=30) of trash scavengers who worked under no institutional aegis. Respondent-driven sampling led to final key informants (N=12), stratified by no affiliation with informal organized cooperatives (n1=4), membership in an organized cooperative (n2=4), and participation in a movement of waste picker activists (n3=4). Unstructured interviews covered themes relating to knowledge of environmental risks for dengue and of involvement in public health projects. Participant-observation permitted an "experience-near" account that provided a window into cultural subtleties between groups.

Results: 83.3% of all informants demonstrated knowledge of the relationship between accumulated trash discards and infestations of *Aedes aegypti* mosquitoes. However, none of the unaffiliated study participants (n1) articulated their work in terms of dengue control. 50.0% of cooperative members (n2) volunteered the relevance of their work to dengue prevention. 75% of the politically active participants (n3) explicitly linked their work to dengue mosquito control.

Conclusion: Informal waste pickers in Brazil are a heterogeneous group whose more politically mobilized members frame their demands for recognition and autonomy as isomorphic to civil-state dengue control agendas. These findings pose implications for the effective integration of the informal trash sector into emerging civil-state dengue control programs.

12.181 Knowledge and attitude of persons living with HIV/AIDS (PLWAs) towards HIV/AIDS in IranA. Madani¹, M. Jamshidi Makiani², P. Davoodian³¹Infectious Diseases Research Center, Hormozgan University of Medical Sciences, Bandarabbas, Iran, ² Tehran University of Medical Sciences, Tehran, Iran, ³Infectious Disease Research Center, Hormozgan University of Medical Sciences, Bandarabbas, Iran

Background: As number of persons living with HIV/AIDS (PLWAs) increases, caring for them is a new rising problem. The World Health Organization encourages caring these people at home. Patients themselves also prefer to stay at home than staying in hospital. Adequate knowledge and positive attitude are important factors in providing better care for a patient. This study was conducted to assess level of knowledge and describe attitudes existing between family members of PLWAs.



Methods and Materials: A cross-sectional study was conducted on PLWAs to assess the basic level of knowledge and attitude regarding AIDS. One hundred family members of PLWAs were selected using simple random sampling. A three-part questionnaire was delivered to measure HIV/AIDS-related attitude and knowledge.

Results: Mean score of participants were 10.69 ± 2.05 of a maximum of 14 points in knowledge. Knowledge on some aspect of the disease was quite high in the study group; Mean score was 25.42 ± 6.05 from a maximum of 40 points in attitude. Female gender, higher income and education level were associated with a greater level of knowledge. Parents in comparison with other relatives and persons older than 60 usually had lower level of knowledge. Patients with higher income or education level also had more positive attitude toward patient.

Conclusion: The findings of the study suggest that the family members of patients living with AIDS have a satisfactory level of essential knowledge on HIV/AIDS. Most of them have good attitudes toward person with HIV/AIDS. However, there are some misconceptions about the routes of transmission that can be problems on the way of providing home-based care.

12.182 Cultural practices and spread of cholera in Bauchi North Eastern Nigeria—Does it matter?

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Background: Cholera is an ancient disease caused by *Vibrio cholera*. The disease is transmitted by the fecal-oral route. Spread of the disease occurs through person-to-person contact or through contaminated water and food. Epidemics occur in communities in which water is not potable and personal and community hygiene standards are low.

In Nigeria, an epidemic of cholera had occurred in 2010 when 29,115 cases including 1,191 deaths (CFR 4.1%) was reported between January and October, 2010. Bauchi state was one of the 15 states affected by the epidemic. In one of the Cholera Treatment Centre (CTC) at the Abubakar Tafawa Balewa University Teaching Hospital Bauchi, a total of 2712 cases and 47 deaths were recorded between June to August 2010

Non availability of clean water, poor education level of the population and poor sanitation were found to be the main factors that contributed towards the spread of the disease in that state. There are a number of cultural practices in that area which are potential factors in the spread of Cholera.

Eating with the sick in the same bowl, shaking the sick,, eating with hand together with patient, using the same container without washing, hugging the sick t, visiting the sick in group, nursing the sick without taking necessary precautions and protection, sitting by the patients' side, all in attempt to show care, love and encouragement to the sick. other practices include eating parents' leftover food by the children, sharing one spoon to encourage bonding between siblings, offering of water and food to visitors. these practices are very common in the area.

Conclusion: The traditional measures for the prevention of cholera mostly emphasizes on provision of clean water, proper sanitation to populations and health education on good hygiene. It is obvious that above mention cultural practices need to be addressed in order to have effective control of cholera during.

To achieve that, community and religious leaders should be involved in social mobilization campaigns in disseminating health education messages with emphasis on the ills of such cultural practices in the spread of cholera. Further study will evaluate this assetion

SESSION 13 (Early Morning Session)
Surveillance of Antibiotic Stewardship

Sunday, February 6, 2011
Room: Klimt Ballroom 2–3 • Upper Level
07:00–08:00

13.001 Surveillance of antibiotic stewardship

J. Hutchinson
Memorial University of Newfoundland, St. Johns, Canada

Background: Antimicrobial resistance is undoubtedly one of the most pressing problems facing mankind. Thousands of people actively work at improving all aspects of antimicrobial use, often in relative obscurity. Surveillance of disease structures such as ProMed are promoting worldwide communities of those involved in prevention. We believe the use of modern, internet tools to connect and support antimicrobial stewardship efforts will create a similar community.

Methods and Materials: The International Society of Chemotherapy's new Working Group on Antimicrobial Stewardship has a new project to help identify, recognize and assist anyone working toward good antimicrobial use. We utilize Drupal—an open source content management package with a large and growing community of developers.

Results: Over 30 projects in over 20 countries have been registered with increasing participation in forums.

Conclusion: Many voices with a common goal are more likely to be heard and heeded. Combining a community solving information technology problems with a community solving antimicrobial resistance problems could be very synergistic.

SESSION 14 (Parallel Session)
New Surveillance Strategies

Sunday, February 6, 2011
Room: Park Congress • Ground Level
08:30–10:30

14.001 Innovative technologies for emerging disease surveillance

C. Freifeld
Children's Hospital, Boston, MA, USA

Increased global mobility of humans, animals, plants, and goods, human incursion into animal habitats, climate change, and antimicrobial resistance all contribute to the ongoing threat of disease outbreaks. At the same time, worldwide adoption of the Internet and mobile phones has revolutionized how we share information, breaking down barriers, reducing costs and greatly increasing communication. For public health, the ability to both transmit and receive information in near real-time via email, Web sites, blogs, and mobile devices has enabled new tools and extended existing capacity for monitoring and responding to disease outbreak events.

We show how disease outbreak investigation and reporting speed has increased over the past fifteen years, due to the evolving environment of policy and technology. We also present the HealthMap online disease outbreak monitoring system, and a range of tools we have developed around the HealthMap platform to take advantage of new technologies to improve public health surveillance. These include tools such as



smart-phone applications to engage the public in surveillance practice, models of worldwide travel networks for monitoring mass gatherings, and systems adapted to resource-poor settings to extend the global reach of public health reporting.

14.002 Regional disease surveillance networks, the ProMED experience in East Africa

B. Estambale

ProMED-mail, Nairobi, Kenya

Background: Regional disease surveillance networks of the Program for Monitoring of Emerging Diseases (ProMED) are gaining prominence for being supplementary sources of information on disease outbreaks and surveillance in various parts of the world. In the African region, two networks namely the Anglophone (English-speaking) ProMED and the Francophone (French-speaking) ProMED have been established and are actively providing the necessary reports of disease outbreaks in their regions of jurisdiction to their readers.

Methods and Materials: From the outset, the two networks have had to establish their own modes of operations but heavily borrowing from the already well established networks and more specifically the main ProMED mail.

Results: Of the two African networks, the Anglophone network is the younger, having been in existence for only 18 months. Within this period, this network has had tremendous growth in terms of subscribers / readers, postings of events and outbreaks of various diseases both human and animals.

Conclusion: The various sources of obtaining information and how this is processed, the challenges encountered and how these are handled is presented and discussed.

14.003 Travel-related illnesses in Europe, EuroTravNet 2009

S. Odolini¹, P. Parola², F. Castelli¹

¹Institute for Infectious and Tropical Diseases University of Brescia, Brescia, Italy, ²Infectious Diseases and Tropical Medicine Unit, North University Hospital, Marseilles, France

Background: The objective was to investigate travel associated morbidity in European travelers in 2009 with particular attention to emerging infectious diseases with potential for introduction in Europe.

Methods and Materials: Ill travelers presenting in the period January to December 2009 to EuroTravNet Centers with a presumed travel associated condition were included. Medical records were analysed. Main Outcome Measures included diagnosis with demographic, clinical and travel related predictors of disease

Results: A total of 6392 patients were included. The most frequent area of exposure to illness was Sub-Saharan Africa. Compared to 2008 there was a marked increase in travelers exposed in North America and Western Europe. Dermatological conditions and respiratory illnesses, in particular pandemic A(H1N1) influenza, flu-like syndromes and tuberculosis, were also observed more frequently. Newly diagnosed HIV infection was the most frequent chronic diagnosis followed by asymptomatic HIV and AIDS. A significant increase in reported dengue cases in 2009 compared to 2008 was observed (n=172, 2.7% versus n= 131, 1.90%) (p=0.002). Malaria and Chikungunya cases were also reported more frequently than in the previous year, highlighting the potential risk for introduction of these diseases in Europe where competent vector are present. Chagas disease was reported less often than in 2008 along with a decrease in the number of Bolivian patients seen in Spain. The number of patients who had sought no pre-travel advice rose significantly to 26.1% in 2009 and this was especially true for VFRs.

Conclusion: EuroTravNet data are representative of travel related illness in Europe in 2009. The possible role of the travelers in the emergence of infectious diseases of public health concern, especially for respiratory and vector-borne diseases, is highlighted. Efforts are needed raise awareness among the travelling population and improve the practice of travel medicine and surveillance system for arboviruses

14.004 New approaches to public health surveillance: MUsings from US CDC

T. Kass-Hout

CDC, Washington, DC, USA

Background: The US Centers for Disease Control and Prevention (CDC) will update the International Meeting on Emerging Diseases and Surveillance (IMED) community on the latest activities for the BioSense Program redesign^{1,2} and public health syndromic surveillance (PHSS) meaningful use objective.

A pillar of current U.S. health reform efforts is promoting the effective use of health information technology to transform how health care is delivered and population health is improved. Of immediate importance for public health authorities (PHA) is getting ready for implementation of the Medicare and Medicaid Electronic Health Records (EHR) Incentive Programs ("Meaningful Use" programs)³, a major component of the Health Information Technology for Economic and Clinical Health (HITECH) Act as part of 2009 American Recovery and Reinvestment Act (Recovery Act) legislation, developed through a joint effort by the Office for Civil Rights (OCR), the Office of the National Coordinator for Health Information Technology (ONC), and the Centers for Medicare and Medicaid Services (CMS). The CDC's BioSense Program's updated vision is to contribute to nationwide and regional (i.e., multistate) situation awareness for all hazards health-related events (beyond bioterrorism) and to support national, state, and local responses to those events. By integrating local and state-level data into a cohesive "picture," BioSense will improve its utility for state and local users. This vision is consistent with the 2006 Pandemic All Hazards Preparedness Act (PAHPA), and 2007 Homeland Security Presidential Directive (HSPD-21), both of which call for regional and nationwide public health situation awareness, through an interoperable network of systems, built on existing state and local situation awareness capability. Per rule, in order to demonstrate meaningful use of their certified EHR technology, eligible hospitals must choose at least one of three objectives related to the testing of electronic reporting to public health: immunization data to an immunization registry, electronic submission of reportable (as required by state or local law) lab results (or ELR), or syndromic surveillance. Data in these areas must be submitted electronically using specific standards, which means public health must be prepared to receive these data using the same standards. However, in the absence of standards for public health syndromic surveillance (PHSS), it was deemed necessary to document PHSS business processes and define a core set of EHR requirements to support contemporary syndromic surveillance practice and provide a current-state picture for system redesign in order to provide a nationwide and regional situation awareness picture for all hazards health-related events.

Methods and Materials: In FY 2010, under the new Office of Surveillance, Epidemiology and Laboratory Services (OSELs), CDC started redesigning the BioSense Program based on input and guidance from local, state, and federal partners. The goal of the redesign is to create a new BioSense, which coordinates and links existing health monitoring surveillance systems to enable rapid and enhanced interchange of information and improvement of BioSense's utility through a user-centered approach. In year 2010, the BioSense Program supported the International Society for Disease Surveillance (ISDS) in recommending standards that support PHA efforts to make meaningful use of EHR technology during stage 1 of the Meaningful Use programs. ISDS and CDC used a community consensus-driven process to develop the recommendation. Input from a workgroup of local and state PHSS experts served as the basis for early iterations. Workgroup members represented key public health stakeholder professional organizations (e.g., Council of State and Territorial Epidemiologists (CSTE), Association of State and Territorial Health Officials (ASTHO), National Association of County and City Health Officials (NACCHO), Joint Public Health Informatics Taskforce (JPHIT)). Input from all Meaningful use stakeholders on a provisional recommendation document was collected during an open comment period. Stakeholder input then informed ISDS's final recommendation.



Results: Financial savings achieved through improved internal contract management are being provided directly to support state and local health departments (HDs) for syndromic and other public health surveillance efforts. In FY2010, the BioSense Program awarded funding to 16 states, 4 cities and Washington D.C. BioSense retains its original purpose of early event (or threat) detection and characterization but is expanding its utility for: (1) better public health situation awareness, (2) improved routine public health practice, and (3) improved health outcomes and public health. BioSense, as an all hazards and timely electronic surveillance system, will provide regional (i.e., multistate) and national views of multiple health outcomes and syndromes. The final ISDS recommendation, released on January 10, 2011, details 3 core PHSS business processes and 32 core data elements. The recommended standards: 1) define the core objectives of contemporary PHSS; 2) describe the model core workflows, inputs and outputs of PHSS; and 3) provide a holistic picture for understanding how an EHR can add value and efficiently interface with a PHA. In addition to workgroup input, 41 Meaningful Use stakeholders commented on the provisional recommendation to ISDS. Approximately 20% were on behalf of private corporations or professional associations. The majority of commentators endorsed the ISDS recommendation stating that it provides an accurate picture of the current state of PHSS. Furthermore, the core data element set was viewed as the essentials to support the core objectives of PHSS. However, the majority of commentators remarked that there are several critical issues unaddressed by the ISDS recommendation, including: 1) a redesign of the current PHSS communication model to incorporate Health Information Exchanges and facilitate the development of scalable EHR solutions; 2) a coordinated, harmonized approach for public health "Electronic Surveillance"; 3) expansion of the recommended minimum data elements list to accommodate the requirements of advanced PHSS systems; and 4) further incorporation of federal PHSS business processes and requirements. A new BioSense Redesign Collaboration Site launched on September 1, 2010 and accessible at <http://BioSenseRedesign.org>, is designed to encourage transparent information exchange among stakeholders and the BioSense Redesign team. The site allows users to: (1) provide requirements for the redesigned BioSense Program and system; (2) exchange ideas with one another and the BioSense Redesign team; and (3) follow the BioSense Redesign project as it progresses. To date, the user requirements gathering process has identified gaps in public health surveillance practices and systems that BioSense is directly addressing through the redesign, resulting in more effective and timely public health surveillance at the local, state, and national levels.

Conclusion: Adoption of clearly defined public health surveillance standards and documented processes will improve monitoring of population-based health by supporting timely, consistent, and effective transfer and sharing of data. The final ISDS recommendations will serve as a resource for EHR technology vendors, healthcare professionals and hospitals, and public health stakeholders and will help inform the redesign of the BioSense system as it expands its ED coverage in the U.S. Working collaboratively with ISDS, CSTE, ASTHO, NACCHO, JPHIT and other professional organizations, CDC will continue to examine stakeholder requirements on a routine basis. Also, we will determine HDs and the BioSense Program's limitations, assess Meaningful Use readiness, and work collaboratively with partners on how best to meet the needs and address the limitations of state and local HDs. CDC and its partners will work collaboratively to redesign the BioSense Program to meet the objectives set forth by the public health community.

References: 1) Kass-Hout, T.A., et al, BioSense Program Redesign. Ninth Annual International Society for Disease Surveillance (ISDS) Conference, Park City, UT, USA, 2010. 2) Kass-Hout, T.A. BioSense Program: Going Forward. Eighth Annual International Society for Disease Surveillance (ISDS) Conference, Miami, FL, USA, 2009. Available from: <http://syndromic.org/conference/2009/presentations/plenaries/KassHout.pdf> 3) Regulation for the Medicare and Medicaid EHR Incentive Programs and "Meaningful Use", Center for Medicare and Medicaid Services (CMS) [Internet]. July 28, 2010; Available from: <http://edocket.access.gpo.gov/2010/pdf/2010-17207.pdf> 4) ISDS Meaningful Use Recommendation [Internet]. 2010 ; Available from: <http://syndromic.org/projects/meaningful-use>.

SESSION 15 (Parallel Session)

Surveillance & Public Health (Oral Presentations)

Sunday, February 6, 2011

Room: Klimt Ballroom 2-3 • Upper Level

08:30-10:30

15.001 Information management in PREDICT: digital and field surveillance to detect emerging infectious diseases of wildlife origin and protect human and animal health

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Background: Access to accurate, comprehensive, and timely surveillance data is critical for effective prediction and response to emerging disease issues. A component of the USAID Emerging Pandemic Threats Program, PREDICT is a UC-Davis led project to build "a global early warning system to detect and reduce the impacts of emerging diseases that move between wildlife and people." Here we employ information management technologies to integrate field and digital surveillance data to improve disease emergence surveillance strategies.

Methods and Materials: Information flow begins with surveillance: standardized field surveillance data (on a variety of pathogens) are collected at the human-wildlife interface (conducted by members of the PREDICT consortium) and collated with global digital surveillance media (which is monitored for disease outbreak reports). Data are assessed for integrity, and then made available to the PREDICT modeling and epidemiology teams. The teams conduct spatial risk analyses, upon which field surveillance activities are modified and implemented. After proper notification of results to local authorities, data will be released through a public data sharing and visualization platform: <http://www.healthmap.org/predict>.



Conceptual overview of information flow in PREDICT

Results: We have collected over 30,000 samples, incorporated 3177 media digitally-detected articles into our surveillance strategy. While many of the disease articles obtained through the HealthMap/PREDICT platform have, to-date, included known zoonoses such as avian and pandemic influenza A (H1N1), anthrax, rabies, and plague, 74 disease reports were tagged as undiagnosed. It is these undiagnosed reports that warrant further investigation, and may lead to the identification of an emerging infectious disease event.



Conclusion: Our hypothesis is that this approach of integrating field and digital surveillance disciplines will result in a more effective system for detection of emerging infectious diseases than either conducted in isolation. Relying solely on one approach or the other leaves gaps in knowledge, as digital surveillance alone will miss events out of reach of the digital realm, and can lack specificity, while field surveillance alone is constrained by logistical and financial difficulties. The ability to integrate data sources can facilitate precise modeling of spatial risk, increasing its predictive ability. Overall, this information flow and data integration form the foundation of the PREDICT endeavour.

15.002 Electronic health market used to predict the spread of dengue

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Background: Case numbers of dengue are rising, and geographical distribution is widening within the U.S. and around the world. As of December 3, 2010, 421 cases of dengue have been reported among the 50 United States. In the PAHO region of the Americas, as of November 5, 2010, reported cases of dengue have increased by 68% above last year's totals. However, the accuracy and frequency of dengue morbidity and mortality reporting varies geographically, and traditional methods of disease surveillance may not accurately capture the true impact of this disease in a timely manner.

Previously, prediction markets have been used successfully to forecast future events such as outcomes of political campaigns, movie box office returns, and developments in infectious disease outbreaks (including influenza activity). We sought to determine if prediction markets could be used as an accurate tool for dengue surveillance.

Methods and Materials: Participants were recruited through the Iowa Electronic Health Market (IEhM) website, personal contacts, and through an email delivered to experts by ProMED mail. Participants received \$100 of a valueless currency with which to trade, and choices of outcomes to make predictions in 4 categories: numbers of U.S. dengue cases; states with locally acquired cases; increase in dengue incidence in the Americas; and increase in severe dengue incidence in the Americas.

Results: As of November 26, 2010, 70 active participants were trading on the dengue markets. For 3 of the 4 market categories, the consensus opinion has, thus far, accurately forecasted changes in dengue activity. For example, in the first case count market, market prices indicated on September 16 that the most likely outcome would be greater than 301 U.S. dengue cases. For this market, traders accurately predicted that the number of cases would rise above 301 more than 3 weeks before the U.S. Centers for Disease Control and Prevention (CDC) reported cases above 301 on October 8.

Conclusion: The dengue markets will close at the end of 2010, and final determinations of accuracy will be made. However, preliminary evidence indicates that markets are potentially useful tools for augmenting traditional disease surveillance by aggregating the experience and knowledge of experts.

15.003 EpiSouth Plus Project: the new challenge of the EpiSouth Network for enhancing the Control of Public Health Threats and other risks in the Mediterranean Region and Balkans

M. Dente¹, M. Bejaoui², M. Fabiani¹, V. Alfonsi¹, D. Lausevic³, G. Salamina⁴, K. Victoir⁵, H. Kalaycioglu⁶, F. Simon Soria⁷, C. Martin de Pando⁷, D. Hannoun⁸, P. Barboza⁹, F. Belghiti¹⁰, A. Leventhal¹¹, F. Riccardo¹, P. Nabeth¹², S. Declich¹

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Background: The new phase of the EpiSouth Network activities has been approved and started on 15 October 2010. Originally co-financed by EUDGSANCO and the Italian MoH, EpiSouth was established in 2006 by 9 EU Countries. It worked for the past four years in enhancing communicable disease surveillance in the Mediterranean Basin and Balkans and includes 27 (9 EU and 18 non-EU) Countries. It is therefore the biggest inter-country collaborative effort of this kind in the region.

Methods and Materials: The new phase implies a shift of the Network's activities to a wider approach. Building on the knowledge of regional gaps and needs identified during the first EpiSouth implementation in the fields of Epidemic Intelligence, VPD and Migrants, Cross Border Emerging Zoonoses and Training, the new EpiSouth Plus Project aims at contributing to the control of Public Health Threats in the region.

The new phase, called "EpiSouth Plus" is co-financed by EU EAHC/DGSANCO and EUDGAIDCO together with national PHI and MoH.

Results: Seven Work Packages, jointly co-lead by EU and non-EU countries, will ensure the following strategic objectives:

1. To support common threat detection by developing a Regional Laboratories Network based on available resources in Mediterranean and Balkans.

2. To ensure the information exchange among EpiSouth countries and with other Early Warning (EW) Systems through an interoperable EW platform in the EPIS/ECDC environment.

3. To promote common procedures in interoperable Generic Preparedness and Risk management.

4. To facilitate IHR implementation through assessments and surveys on national procedural and legislative aspects.

Conclusion: The project promotes knowledge, resource and information sharing, cross contamination and development of international trust. Strategic documents, providing a novel basis for regional policies in health threat control, will be produced and disseminated.

15.004 Comprehensive Analysis of OIE World Animal Health Data as a Means to Identify Global Disease Trends

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Background: OIE member countries' animal health reports are published by OIE. This data set is the most comprehensive of its kind and in fact the only one of near-global reach and uniform data format. Nevertheless, this important source of information has been vastly underutilized, mainly because the data are very fragmented, but also due to a potential reporting bias resulting from countries' different levels of reporting transparency and competency.

Methods and Materials: We have analysed WAHID data for the years 2006–2008 (update with 2009 data in progress at time of submission) from 176 countries on 71 livestock diseases, and transformed them into losses of livestock units (LSUs) for comparability. In total, the scope of the analysis comprises more than 2 million data points. This data set was analysed to identify, among others, the distribution of global livestock losses by country, by disease and by livestock species, as well as temporal and spatial changes of these distributions.

Results: The three diseases that have claimed the largest losses in 2006–08 in terms of livestock units are highly pathogenic avian influenza, echinococcosis and enzootic bovine leukosis.

Of all the LSUs lost to the diseases taken into account, 46% came from poultry, 38% from cattle, 10% from swine and 5% from small ruminants. Overall, 801'155 LSUs per year were reported as lost to one of the 71 diseases, thereof 53% to zoonotic and 47% to non-zoonotic diseases.

(OIE is not responsible for any inaccuracies or misinterpretation of the analysed OIE data and information.)

Conclusion: Animal health data as provided by the OIE are a valuable source of information. Once made accessible to database analysis they do not only provide extremely detailed information, but can also be used to 'draw the big picture' and inform political decision makers about global livestock disease patterns and trends.

**15.005 Cholera outbreak in Haiti, 2010—Using a gravity model to explain spatial dynamics**A. Tuite¹, J. Tien², D. J. Earn³, M. Eisenberg², D. Fisman⁴¹University of Toronto, Toronto, ON, Canada, ²Ohio State University, Columbus, OH, USA, ³McMaster University, Hamilton, ON, Canada, ⁴University of Toronto, Toronto, Canada

Background: Haiti, the poorest country in the Western Hemisphere, is currently in the midst of a cholera epidemic that was reported (as of December 7) to have killed > 2000 individuals and sickened ~100,000. The epidemic began in the Artibonite Departement but cases are now reported in all regions of the country. Surveillance data for formulation and calibration of models of this epidemic are limited, but such models can aid understanding of epidemic processes and help define optimal control strategies. We used a “gravity model” to accurately predict the sequence and timing of regional cholera epidemics in Haiti using publicly available data.

Methods and Materials: We built a compartmental transmission mathematical model that allowed for both person-to-person and water-borne transmission of cholera (via contamination of local water supplies). We included ten “patches” representing the ten Departements in Haiti, with between-patch transmission dependent on population sizes and distance between regions. Initial estimation of the basic reproductive number for cholera (R_0) was performed using relatively high-quality surveillance data from the Cap Haitien region of the country. The model was further parameterized using 2009 census data, literature-derived values, and through model calibration.

Results: The estimated R_0 was 1.9 (95% CI 1.6 to 2.2) which is consistent with previous estimates by our group. Ordering of regional cholera outbreaks, by Departement, was correctly predicted by a gravity model incorporating a distance-squared term (Spearman correlation 0.96, $P < 0.001$). Agreement between model projected onset dates for regional epidemics was excellent (Spearman correlation 0.93, $P < 0.001$). Symptomatic attack rate estimates of 20–30% resulted in model projections that agree closely with reported cumulative hospitalized case counts for Haiti, and best-fit models project that regional Haitian cholera epidemics will likely to persist through autumn 2011.

Conclusion: Notwithstanding limitations in available public health surveillance data related to the current Haitian cholera epidemic, a compartmental patch model that represents between region disease transmission according to “gravity” (population and distance) closely reproduces disease patterns reported on the island to date. This model is a useful tool for planners, policy makers, and medical personnel seeking to manage Haiti’s cholera epidemic.

15.006 A method for quantifying transmission of Stage III zoonosesJ. Pulliam¹, S. Blumberg², J. O. Lloyd-Smith²¹Fogarty International Center, National Institutes of Health, Bethesda, MD, USA, ²University of California at Los Angeles, Los Angeles, CA, USA

Background: Stage III zoonoses are infections transmitted from animals to humans and capable of limited human-to-human transmission ($R_0 < 1$). One of the most important questions for understanding the transmission dynamics of Stage III zoonoses is whether observed infections resulted from animal-to-human (primary) or human-to-human (secondary) transmission. New analytical methods are needed to quantify transmission of these pathogens in order to better assess the risk of large outbreaks and the potential risks associated with small increases in transmission.

Methods and Materials: We have developed a model that can be used to estimate transmission parameters and determine the relative likelihood that individual infections of Stage III zoonoses, such as monkeypox and Nipah viruses, were the result of animal-to-human or human-to-

human transmission. The method requires data on the symptom onset dates of cases and descriptions of the incubation and infectious period distributions. We have also developed a general simulation model for Stage III zoonoses, which can be parameterized for specific pathogens and at-risk human populations. We tested the estimation method on 10,000 simulations of monkeypox transmission. The simulations covered a 5-year period and assumed a well-mixed unvaccinated human population of 1500 individuals.

Results: On average, the estimation technique correctly assigned over 94% of the cases in a simulation to either a human or animal source. For 43% of simulations, all individual human cases were correctly attributed to primary vs. secondary transmission. Approximately 70% of cases were assigned to the correct source individual.

Conclusion: Our estimation procedure can provide useful insight into transmission dynamics of Stage III zoonoses in situations where few data are available. The method can also be supplemented with detailed contact tracing data and risk-factor information from outbreak investigations to improve the accuracy of source attribution.

15.007 Laboratory-acquired human cowpox infection in the US: case investigationA. McCollum¹, C. Austin², J. Nawrocki², J. Howland², J. Pryde³, A. Vaid³, D. Holmes¹, R. Weil⁴, Y. Li¹, K. Wilkins¹, H. Zhao¹, S. Smith¹, K. Karem¹, M. Reynolds¹, I. Damon¹¹US Centers for Disease Control and Prevention, Atlanta, GA, USA,²State Department of Public Health, Atlanta, GA, USA, ³Local PublicHealth District, Atlanta, GA, USA, ⁴Emory University, Atlanta, GA, USA

Background: Human cowpox virus infections can be severe. Infections occur rarely in Eurasia, where the virus is endemic. Neither human nor animal infection has been reported in the United States. In July 2010, an unvaccinated laboratory researcher, who worked with a non-human pathogenic poxvirus, developed a suspicious, painful, ulcerated lesion on a finger. The patient recovered, without incident, approximately three months after lesion onset. We investigated the etiology and potential sources for the infection, laboratory biosafety precautions, and strain composition.

Methods and Materials: We interviewed the patient and laboratory personnel, and conducted a laboratory biosafety assessment. Molecular diagnostic assays and DNA sequencing were employed to identify the patient’s infection and to assess the extent of environmental contamination.

Results: In October 2010, biopsy specimens were submitted to the CDC for suspect orthopoxvirus testing. A series of realtime PCR assays on the biopsy tissue tested positive for non-variola orthopoxvirus, negative for vaccinia, and positive for cowpox DNA. Further sequencing identified the strain as cowpox Brighton. The investigation revealed cowpox virus stocks in the laboratory’s freezer, but no known or intentional use of cowpox in the patient’s laboratory in the past five years. Sequencing of the patient’s isolate revealed a recombinant region consistent with recombinant cowpox strains stored in the freezer. Cowpox was detected in multiple viral stocks and two viral lines, including the viral stocks used by the patient prior to the onset of illness. Orthopoxvirus DNA was present from environmental swabs of several surfaces in the laboratory and a shared freezer room. No live virus was recovered from the swabs. There were no additional suspect cowpox cases in the patient’s family, pets, or laboratory colleagues.

Conclusion: Data suggest that the patient was likely infected by handling laboratory reagents or environmental surfaces which were contaminated with cowpox. Laboratory exposures to vaccinia virus have been documented, but, to date, there are no reports of accidental laboratory-acquired cowpox infections. Vaccination is recommended for laboratory workers with risk of exposure to orthopoxviruses, including cowpox. Prompt diagnosis and reporting of orthopoxvirus infections to appropriate public health agencies can help reinforce appropriate infection control practices.



15.009 Recurring transmission of norovirus on a passenger aircraft

C. Thornley¹, J. Rapana¹, G. Greening²

¹Auckland District Health Board, Auckland, New Zealand, ²Institute of Environmental Science and Research Ltd, Porirua, New Zealand

Background: Air travel may contribute to global spread of pandemic strains of norovirus. Outbreaks of norovirus gastroenteritis involving aircraft have been previously reported, but solely in the context of exposures during a single flight sector. In October 2009, an outbreak of norovirus gastroenteritis persisting across multiple flight sectors flown by the same aircraft was reported.

Methods and Materials: Crew supervisors were interviewed and flight logs reviewed for information about incidents involving potential contamination of the aircraft cabin. An outbreak investigation was undertaken, comprising a retrospective cohort study of cabin crew who had worked on the implicated aircraft, using a standard questionnaire. Faecal specimens were collected from symptomatic cabin crew members for microbiologic analysis, and environmental investigation of the aircraft interior was undertaken. Aircraft passengers were not investigated. Specimens were tested for norovirus RNA of genogroups I and II, and strains were characterised by genetic sequencing.

Results: A passenger had vomited in the passenger cabin of the Boeing 777-200 aircraft on the 13 October flight sector. Cases occurred among crew members who had worked on the aircraft over the subsequent 6-day period. Of 77 crew members, 63 completed questionnaires; of these, 27 crew members had developed gastroenteritis within 50 hours of their flight sectors on the aircraft, an attack rate of 43%. There was a declining trend in the proportion of crew who developed gastroenteritis following exposure to the aircraft on successive flight sectors from 13 October onward ($p < 0.001$). Crew supervisors were significantly more likely to develop gastroenteritis than other crew members. Two cases who had worked on the plane on different flight sectors were confirmed with indistinguishable Norovirus GI.6 strains. Norovirus was not identified in environmental specimens collected from the cabin interior surfaces.

Conclusion: Although contamination was not confirmed, the results suggest that norovirus exposure on the aircraft resulted in gastroenteritis among multiple groups of crew. This outbreak emphasises that aircraft contamination can lead to transmission of norovirus, and that this transmission can continue to occur multiple days following the initial contamination incident. Cleaning agents with activity against norovirus should be used following vomiting episodes on aircraft.

15.010 Demography, migration and health: mosaics of a globalized world

D. Tomianovic, K. Liske, V. Lee, M. Cetron
CDC, Atlanta, GA, USA

Background: International migration is at record levels and unlikely to slow. According to 2007 UN figures approximately 200 million persons are international migrants (IM) defined as persons who reside outside their birth country for >12 months. IM are growing in all global regions with fastest increases in Europe, Asia and North America. Migration is circular; risks are repetitive and dynamic. Foreign-born (FB) populations frequently return to birth countries to visit friends and relatives increasing their risk for communicable diseases. Health disparities (e.g. TB, NTD, VPD) between FB and native-born populations are reported worldwide. Consequently, census records which include "birth country" offer important demographic and epidemiologic indicators of health consequences and risk factors for disease emergence.

Methods and Materials: We define, map and examine demography by birth country of FB in US between 2006–2008 by using US Census American Community Survey 3-year estimates. Geographic distribution and population concentration indices, such as Hoover Index (HI) [values 0–100, where 0 equals dispersion, 100 equals concentration], were analyzed.

Results: Twelve percent (38M) of US population is FB. States with greatest proportion of FB are California (27%), New York (22%), New

Jersey (20%), Nevada (19%), and Florida (18%). Select counties have >50% FB county share and 36 have >25%. Of 105 source birth countries, 15 make-up 2/3 of FB population. Moreover, the top countries comprise the highest TB burden in US. Since 2006, >60% of new US TB case are FB. TB incidence per 100K among FB is 20, while native-born is 2. Additionally, FB populations are tightly geo-clustered with HI 80–99 in contrast to native-born of 65.

Conclusion: The dynamics of migration and mobility are evolving rapidly creating public health challenges and opportunities. This trend is reshaping societies in distinctive and important ways. FB are highly geo-clustered which has implications for disease introduction, transmission and control. Traditionally, health disparities are linked to race/ethnicity; however, FB origin may be of greater importance. We recommend expanding international census data and public health surveillance systems to capture birth country, and map movement patterns and trends of IM. These linked variables should be integrated into analysis of social determinants of health disparity.

Country	No. of FB	% of US FB Population	Hoover Index FB
Mexico	11467056	30.2%	87
China	889643	5.0%	89
Philippines	862430	4.4%	87
India	752020	4.1%	88
Vietnam	711878	2.9%	90
El Salvador	697827	2.9%	89
Venezuela	691917	2.7%	86
Cuba	668540	2.6%	94
Canada	624364	2.2%	74
Dominican Republic	762011	2.0%	86
Guatemala	710993	1.9%	85
Jamaica	622,451	1.6%	82
Germany	615,065	1.7%	88
Colombia	606,154	1.6%	90
Haiti	622,878	1.4%	86
Other	12,366,534	32.6%	---
Total of Top 15 Birth Countries	25,484,603	67.2%	---
Total US Foreign born population	37,796,167	12.4% of total US population	83
Native Born	267,388,172	87.6% of total US population	65

Top 15 source countries with largest populations in the US as percent of foreign born and Hoover Index, 2008

15.011 Understanding the multidimensional socio-economic impacts of animal diseases: a case study of PPR and HPAI

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Background: Disease impacts are often measured in financial terms. However, this approach reflects only one, albeit important, aspect of the negative consequences of animal diseases.

Methods and Materials: This paper aims to examine a diverse range of impacts animal diseases can have on the livelihoods of smallholders. It examines the role animal health plays in smallholder farming and on the way this plays out with respect to impact of diseases, and also how farmers react. It looks at two diseases, PPR and HPAI as case studies and examines the specifics of these diseases, in relation to the animal species they affect, and to the farming system they effect. The PPR case study is based on a recent investigation carried out in northern Kenya that using the household economic approach to look at livelihood impacts. The HPAI case study is based on HPAI impact assessment analysis in Egypt for the period 2007–2010.

Results: The studies show with examples, through both PPR and HPAI impact analysis, that the consequences can vary between different farming systems, and that farmers and policy makers will deal differently with the impacts.

Conclusion: The paper concludes that it is very important to understand the different impacts a disease can have, as this can impact on the way livestock owners will deal with the disease. It also illustrates the need for more alternative approaches to understanding the multidimensional aspect of impacts and to a broader dialogue with policy makers.



15.012 ProMED-mail early warnings in Africa: Descriptive summaries of 5 years of information dissemination and the development of the African regional networks

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Background: The ProMED-mail electronic outbreak reporting system began in 1994 with the purpose of communicating, on a global basis, the latest information on events relating to the emergence of diseases in people, animals and plants. ProMED-mail functions as both expert moderated e-mail lists and a website. It is free and open to all, with more than 50,000 subscribers in greater than 180 countries and maintains an emphasis on "One Medicine".

ProMED-mail has developed regional and sub-regional networks to promote reporting and sharing of information: ProMED-PORT in Portuguese, covers Brazil and Portuguese-speaking Africa; ProMED-ESP covers Latin America; ProMED-RUS covers the Newly Independent States of the former Soviet Union; PRO/MBDS in English, covers the 6 countries in Southeast Asia bordering the Mekong river.

Methods and Materials: Current review summarizes the last 6 years (November 2004 and October 2010) of postings in Africa and describes ProMED-mail progress in the recent implementation of two new regional initiatives in Africa: ProMED-FRA covering Francophone Africa and ProMED-ANG covering Anglophone Africa. Summary statistics were extracted from the Healthmap Database covering ProMED-mail postings. Only zoonotic and animal diseases were included and strictly human diseases excluded.

Results: Since November 2004, there have been 1482 posting on ProMED-mail concerning animal and zoonotic diseases. 68% of the postings cited Avian Influenza (n=389), Undiagnosed (n=150), Rift Valley Fever (n=130), Swine Flu H1N1 (n=122), Anthrax (n=111) and Ebola (100) outbreaks. The largest number of posting have occurred recently with 342 in 2009, compared to an animal and zoonotic disease postings average of 221.15 for the 4 year period between 2005 – 2008. The etiology of disease described in the posting included 1047 citing viral diseases, 172 citing bacterial diseases and 92 citing parasitic diseases. Egypt was the country of origin for the greatest number of posting (n=258), followed by Uganda (n=151), South Africa (n=132), Angola (n=102) and Nigeria (n=91).

Conclusion: A previous review in 2006, established that while coverage of events in Africa was better than some areas, Africa only accounted for 4.2% of postings worldwide. Current analysis indicates that increased numbers of posting from Africa are beginning to emerge.

15.013 Impact of a Video-based Intervention on Knowledge and Attitudes of Ebola Prevention and Care in Rural Republic of Congo, 2007–2010

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Background: Ebola is a zoonotic disease first identified in 1976 in Zaire (Democratic Republic of Congo). Human infection is characterized by fever followed by headache, malaise, muscle pain, fatigue and/or diarrhea. Mortality ranges from 50 to 80%. An educational intervention consisting of a film followed by a structured discussion was developed to improve knowledge, attitudes, and behaviors for prevention and care of people with Ebola. This intervention method has been demonstrated to improve knowledge, attitudes, and intended behaviors regarding Monkeypox in a similar setting.

Methods and Materials: The film was produced for a Congolese audience in the local language and in French. It featured doctors and affected residents from the region. In order to facilitate outreach in areas accessible only by foot, portable projection equipment was used. In 2007 the intervention was implemented in villages in the western part of the country. Over 300 individuals attended. After one year 53 individuals were selected to participate in a post intervention evaluation surveys in order to document changes in knowledge and attitudes of Ebola prevention and care.

Results: Seventeen percent of respondents knew someone who was infected with Ebola. About (32.1%) of respondents had received the InCEF Ebola education within the past year while 65.2% had received another education. A greater proportion of respondents who received InCEF education knew that humans could transmit Ebola (100% vs. 67.7%), identified at least 1 symptom of Ebola (100% vs. 41.2%), knew there is no cure for Ebola (100% vs 52.9%), and correctly identified how to handle the remains of a victim (76.5% vs. 73.5%).

Conclusion: This method of health communication which features local populations is effective in increasing knowledge of disease prevention and care as demonstrated by our previous work. This study demonstrates retention of knowledge is high one year after exposure to the intervention. Scaling up the intervention is being explored to prevent zoonotic and infectious disease outbreaks in the Congo Basin.

SESSION 16 (Plenary)

Plenary Lecture 4

Sunday, February 6, 2011

Room: Park Congress • Ground Level

11:00–11:45

16.001 The Spread of Emerging Diseases by Global Air Travel

K. Khan
 University of Toronto, Toronto, Canada

Background: New infectious diseases are emerging faster today than at any other time in human history, while many previously controlled diseases are reemerging and posing new threats to global health, security and economic prosperity. At the same time, the world is becoming increasingly interconnected via international air travel. Today, more than two billion passengers board commercial flights every year creating unprecedented opportunities for local infectious disease events to rapidly transform into international epidemics or pandemics. Integrating knowledge of global population mobility with real-time epidemic intelligence from global infectious disease surveillance systems could significantly enhance situational awareness of emerging infectious disease threats in the world.

Methods and Materials: This presentation will include a discussion of: (i) the BioDiaspora Project—a multidisciplinary collaboration dedicated to understanding the global airline transportation network as a conduit for the international spread of infectious diseases, (ii) the HealthMap Project—a real-time, web-based global infectious disease surveillance system, (iii) the conceptual integration of intelligence as it relates to infectious disease threats associated with mass gatherings, (iv) prototype models for specific mass gatherings such as the annual Hajj pilgrimage in Saudi Arabia and the Olympic Games, and (v) an evolving technological platform designed to integrate knowledge of global infectious disease activity with global population mobility in near-real-time.



Conclusion: Real-time epidemic intelligence from global infectious disease surveillance systems can be integrated with knowledge of global population mobility via commercial air travel to enhance situational awareness of infectious disease threats in the world. This integrated knowledge could be used to rapidly identify the most effective and efficient public health countermeasures to mitigate the global spread of emerging infectious disease threats. Conversely, knowledge of *anticipated* global population mobility coinciding with events known to be associated with the international spread of infectious disease (e.g. mass gatherings) could be used to heighten infectious disease surveillance in specific high-risk global geographies.

SESSION 17 (Parallel Session)

Q Fever in the Netherlands

Sunday, February 6, 2011

Room: Park Congress • Ground Level

14:30–16:00

17.001 Q fever in the Netherlands: The animal health aspects

C. Brusckhe

Ministry of Economic Affairs, Agriculture and Innovation, The Hague, Netherlands

Up to 2007 some 20 people became infected yearly with Q fever, a zoonotic disease. Suddenly in 2007 170 people fell ill and in 2008 there were 1000 cases. In 2009 there were more than 2300 known cases of people becoming infected. Experts believed that there was a relationship between Q fever abortions on milking goat and milking sheep farms and the sharp increase in the numbers of human infections.

In the Netherlands several measures were taken between June 2008 and December 2009 to control Q-fever in animals. Measures were directed in particular at the dairy goat and sheep sector, but measures were also taken for small ruminants that come into close contact with the general public. Q fever in sheep and goats was made notifiable in June 2008. Hygiene measures, transport restrictions and restrictions for visitors were implemented. Vaccination with a non-licensed vaccine was performed in a restricted area in 2008 (voluntary) and 2009 (compulsory). In October 2009 monitoring based on bulk milk PCR was started to detect infected farms.

Knowing that the vaccine was not fully efficacious in infected or pregnant animals and having the possibility to detect infected farms at the end of 2009, the responsible ministers took the following decisions:

1. cull all pregnant animals on infected farms
2. a nation wide breeding ban for dairy sheep and goat
3. a compulsory vaccination program for the whole country in 2010.

With these very drastic measures further contamination of the environment during the lambing season would be prevented. Breeding would be only allowed thereafter with animals coming from non-infected vaccinated farms.

In 2010 the number of human patients with Q-fever was 382. As of now the focus of the measures is to prevent another outbreak with yearly vaccination of the dairy goat and sheep population.

17.002 Q fever in the Netherlands: The public health aspects

J. Van Steenbergen¹, W. V. D. Hoek¹, D. Notermans¹, C. Wijkmans², T. Oomen¹

¹RIVM, Bilthoven, Netherlands, ²Municipal Health Service HvB, 's-Hertogenbosch, Netherlands

Background: From 2007 through 2009 The Netherlands faced a series of multiple confluent Q fever outbreaks in the southern part of the country. Q fever was specifically seen in the vicinity of dairy goat farms where abortion waves due to *Coxiella burnetii* occurred.

Methods and Materials: Seroprevalence of antibodies against *Coxiella burnetii* was tested in 2006 in a random sample of the population (ELISA phase I and II). (Notermans et al)

Hospital discharge data were used in retrospect to find previously undetected clusters in time and space (vdWijngaard et al).

Incidence of acute Q fever was calculated using notification data. Smoothing incidence lines were calculated using six digit areal codes (vdHoek et al).

A case control study was performed in 2007 (Karagiannis et al).

A sample of blood donors originating from the areas with highest incidence was tested twice in 2009 with IFA (Zaaijer et al).

A sample of sera from the pregnancy screening (e.g. HBsAg, lues) was tested for antibodies against *Coxiella burnetii*.

Results: In 2006 the seroprevalence of antibodies against *Coxiella burnetii* in The Netherlands was low (<2.7%). Before 2007 small clusters of lower respiratory tract infections went undetected. Incidence of Q fever increased from 192 in 2007, to 1000 in 2008 and over 2300 in 2009. Risk for acute Q fever was increased for males in age group 45-55 yrs, and living in proximity of infected goat farms, not living near infected sheep farms. In areas where blood donor infection rate could be ascertained, only an estimated 12% of infections are leading to microbiologically confirmed disease. Preliminary data show no serious adverse events of infection during pregnancy on pregnancy outcome.

Conclusion: The total number of reported acute Q fever cases approaches 4000. Living near infected dairy goat farms was the major risk factor. The number of chronic infections with serious complications remains unknown.

17.003 Q fever in the Netherlands: *Coxiella burnetii*, laboratory aspects

H.-J. Roest

Central Veterinary Institute of Wageningen, Lelystad, Netherlands

Background: *Coxiella burnetii* is a Gram-negative intracellular bacterium, which belongs to the family of the Coxiellaceae and the order of the Legionellales. Two phases of the bacterium can be distinguished: phase I, associated with full length lipopolysaccharide (LPS) and phase II, associated with truncated LPS. In the life cycle of *C. burnetii* two stages can be distinguished. The Large Cell Variant (LCV), which is able to multiply, and the Small Cell Variant (SCV), the spore like form in which *C. burnetii* is resistant to outside influences.

Methods and Materials: Genotyping was performed by MLVA according to Arricau et al 2006.

Results: The link between dairy goats as the source of human Q fever cases in the Netherlands has been made on the basis of epidemiological evidence. Genotyping of *C. burnetii* is a tool to further investigate the connection between source and host. Using Multiple Loci Variable Number of Tandem Repeats Analysis (MLVA), the connection between sheep and humans in a small Q fever outbreak in the Netherlands could be made. MLVA was also used to type a considerable number of goat samples from goats that were considered to be the source of the Q fever outbreak in the Netherlands. Results show that one MLVA type is predominantly present on all dairy goat farms in the epidemic area in the south of the Netherlands.

C. burnetii contaminated goat manure is considered to be a major factor in the transmission to humans. Little is known about the temperature build-up in goat manure piles and the influence of the composing process on *C. burnetii*. In a joint effort of national research institutes temperatures and numbers of *C. burnetii* in goat manure, and the decimal reduction time of *C. burnetii* under these conditions were assessed. Results of this study will be presented.

Conclusion: Results on genotyping show that one MLVA type is predominantly present on all dairy goat farms in the epidemic area in the south of the Netherlands. This MLVA type should also be found in infected humans. Research on this is ongoing. Conclusions on the results of the survival of *C. burnetii* will be given during the presentation.



SESSION 18 (Parallel Session) Climate Change and Infectious Diseases

Sunday, February 6, 2011
Room: Klimt Ballroom 2-3 • Upper Level
14:30-16:00

18.001 Plague and climate change

N. Chr. Stenseth
University of Oslo, Department of Biology, Oslo, Norway

The bacterium *Yersinia pestis* causes bubonic plague. A general review of how climate variation may affect plague dynamics is presented. The lecture summarizes a broad spectrum of studies, primarily based upon the analysis of data from Central Asia, data both on the reservoir system as well as data on the human cases. Based upon our studies, it is concluded that fleas holds a key to the understanding of how plague is transmitted from the reservoir to the human population. The findings based upon such data from the last few decades are then used to look backward (is there a climate component to the past pandemics?) as well as forward (will there be more or less climate-driven plague in the future?). Part of the presentation will include a discussion of how ecological and evolutionary dynamics interact in connection with evolution of virulence. Published as well as unpublished work will be summarized: in short, climate is concluded to have a driving force on the plague dynamics, but the nature of this does depend upon the geographic location.

18.002 Malaria, climate change and policy

D. Campbell-Lendrum
WHO, Geneva, Switzerland

Background: The effect of climate change on malaria has been a subject of intense debate in the scientific literature for at least 15 years. Most past studies have focussed on whether climate change has already contributed to changes in suitability for malaria transmission, or in actual changes in transmission, and the robustness of projections of future effects; all in the context of changing non-climatic factors.

Methods and Materials: However, very little of the debate so far relates directly to policy questions. These include "should malaria control programmes do anything differently because of climate change?", "should the international funding mechanisms for climate change adaptation be used to help support malaria control?", and "should malaria be cited as a justification for greenhouse gas mitigation measures?"

Results: The presentation will briefly review the current state of evidence on the links between climate change and malaria. It will then focus on the kinds of evidence that are most relevant to the policy questions, including not only epidemiology, but more wide-ranging risk and cost benefit assessment, and consideration of who pays for different kinds of interventions.

Conclusion: The presentation will also attempt to place malaria in the broader context of health risks from climate change, and the potential benefits of health-oriented adaptation and mitigation policy.

18.003 The emergence of Lyme disease in Canada: is there evidence for an effect of climate change?

N. Ogden
Public Health Agency of Canada, Ottawa, Canada

Background: On the basis of simulation model of the life cycle of the tick vector of Lyme disease *Ixodes scapularis*, we predicted climate change would drive northward expansion of the range of the tick and thus cause Lyme disease (LD) emergence in Canada.

Methods and Materials: Emergence of LD risk in Canada was studied using data from passive tick surveillance, active field surveillance, and phylogeographic (multilocus sequence typing: MLST) analysis of *Borrelia burgdorferi*.

Results: In active surveillance, *I. scapularis* were found at 55% of sites visited in southern Quebec, and were more likely to be found at sites with a warmer climate. *B. burgdorferi* was identified at 13 *I. scapularis*-positive sites although infection prevalence in ticks and animal hosts was low. Low infection prevalence in ticks submitted in passive surveillance after 2004, from the tick-positive regions identified in active surveillance, coincided with an exponential increase in tick submissions at this time. MLST analysis suggested recent introduction of *B. burgdorferi* from northeastern USA.

Conclusion: We conclude that these data are consistent with *I. scapularis* ticks dispersed from the USA, by migratory birds, founding populations where the climate is warmest, and that recent warming in the region could have facilitated establishment of tick populations. However, we ask to what extent does this emergence event serve as an example of climate change-driven effects on a vector-borne disease risk?

SESSION 19 (Parallel Session) Emerging Infection Prevention in the Healthcare Setting

Sunday, February 6, 2011
Room: Park Congress • Ground Level
16:30-18:00

19.001 Infection prevention and control challenges experienced in the Lujo Arenavirus outbreak in South Africa, 2008

A. Duse
NHLS & University of Witwatersrand, Johannesburg, South Africa

In September-October 2008 a nosocomial outbreak of a novel arenavirus occurred in a South African private healthcare facility. The primary case, a tour agent, was airlifted from Zambia (where she was extremely ill) to Johannesburg, South Africa, for emergency medical treatment of an unspecified infectious disease.

During the course of air evacuation of the primary case and her subsequent hospitalization in Johannesburg, 1 Paramedic, 3 Nurses and 1 Hospital Cleaner acquired an arenavirus-like infection. Four of these five healthcare workers died.

The causal agent was identified as a new virus, tentatively named 'Lujo', and genetically related to Old World arenaviruses. Key to outbreak containment was stringent Infection Prevention and Control (IP&C).

This talk focuses on the multiple duties and responsibilities of IP&C practitioners as well as the containment strategies that were employed in this outbreak. Besides high-level isolation precautions, the IP&C Team was involved in development of case definitions, contact tracing and monitoring, education, counseling and laboratory biosafety.

19.002 The changing epidemiology of *Clostridium difficile* infection

P. Polgreen
University of Iowa, Iowa, USA

Background: *Clostridium difficile* is the most common cause of nosocomial infectious diarrhea in many countries. *C. difficile* infections produce a spectrum of clinical illness, ranging from asymptomatic colonization to pseudomembranous colitis with severe diarrhea, the latter may result in toxic megacolon, colon perforation, and death. Several reports in multiple geographic regions indicate that both the incidence and the severity of *C. difficile* infections are increasing. The change in the epidemiology of *C. difficile* associated disease is thought to be related to the emergence of a new more virulent strain (BI/NAP1). Historically, prior antimicrobial use has been the major risk factor for *C. difficile* infections, and while most classes of antimicrobials have been associated with *C. difficile* infections, the risk is particularly high with certain antimicrobials



(e.g., clindamycin, cephalosporins, and fluoroquinolones). Additional risk factors for CDI have included advanced age, severe underlying disease, and extended length of hospital stays. In recent years, however, reports in many countries have described *C. difficile* cases in people without traditional risk factors, including younger people without recent exposures to antimicrobials. Together, these reports suggest that community-associated *C. difficile* infections represent an emerging infectious disease that is increasingly occurring in persons who are younger, have fewer comorbidities, and less exposure to healthcare.

19.003 Controlling transmission of glanders the veterinary health setting

U. Wernery
Central Veterinary Research Laboratory, Dubai, United Arab Emirates

Glanders is an OIE listed contagious, life-threatening disease of equids, caused by the Gram-negative bacteria *Burkholderia (B.) mallei*. Although eradicated in Western Europe, glanders remains endemic in a number of Asian, African and South American countries. It recently re-appeared in Pakistan and Brasil in 2008 and 2009, and emerged for the first time in Kuwait and Bahrain in 2010. It is now confirmed, that in Bahrain the disease has spread to the dromedary camel, causing similar clinical signs and lesions as described in equids. The isolation of *B.mallei* from both, the horse and camel poses new challenges to international trade of equids from and to countries, where camels are reared. For the control and hopefully eradication of this zoonotic disease, steps must be taken which were laid down by experts dealing with the current glanders outbreak in Bahrain, which will be explained in detail during the lecture.

The risk of spread is increased by the presence of pockets of susceptibles.

All European countries must undertake preventive actions to detect and prevent further spread. This outbreak highlights the ongoing risk for all countries and the need for continued political support for ensuring vaccination of susceptible populations, especially marginalized populations, and heightened surveillance for paralytic diseases.

20.002 The epidemiology of hospitalised adults from a 22 year whole-population study on bacteraemic Streptococcal pneumoniae community acquired pneumonia (CAP)–Darwin, Northern Territory, Australia

S. Jacups¹, S. Moberley², A. Cheng³
¹Charles Darwin University, 0909, NT, Australia, ²Melbourne University, Melbourne, Australia, ³Monash University, Melbourne, Victoria, Australia

Background: Diseases caused by *Streptococcus pneumoniae* continue to cause substantial morbidity and mortality throughout the world. This study describes the epidemiology of blood culture positive *S. pneumoniae* community-acquired pneumonia (CAP) in the Top End of the Northern Territory of Australia.

Methods and Materials: Demographic, serotype and risk factor data were collected from adults presenting to the Royal Darwin Hospital with blood culture positive *S. pneumoniae* CAP between 1987-2008. A binomial generalised linear model, was used to compare risks, weighted by population.

Results: We report a total of 204 cases, with a median age of 40 years. Males and Indigenous patients were over represented. The average overall incidence rate ratio was 10.3 for Indigenous adults compared with non-Indigenous adults over the 22 year study period. There was no statistical difference between incidence rates pre and post-23-valent pneumococcal polysaccharide vaccine (23vPPV) introduction. Serotypes in presenting cases were predominantly (84.7%) also present in the 23vPPV. The whole-population logistic regression model identified significant adjusted relative risks with 95% confidence intervals for; age 45 and older 1.6 (1.1-2.2), Indigenous status 5.9 (3.7-9.5), diabetes 2.3 (1.6-3.3), excess alcohol 4.8 (2.8-8.3), smoking 2.7 (1.9-3.7) with interaction term Indigenous + excess alcohol 3.1 (1.6-5.9), (which equates to Rate Ratio (RR) 18.5 (17.3-19.7) as predictive for bacteraemic *S. pneumoniae* CAP presentation.

Conclusion: Consumption of alcohol to excess, diabetes, age greater than 45, Indigenous status and smoking are independent risk factors for *S. pneumoniae* CAP. The national 23vPPV program appears to be under-utilised, although the presented risks have been recognised in the pneumococcal vaccine recommendations. Improved vaccination rates with 23vPPV, aimed at adolescents before substances such as alcohol and smoking are habitual, is estimated to also improve vaccine efficacy. Furthermore, an integrated Public Health approach vigorously targeting risk factors including quit smoking and substance abuse programs, nutrition education, and environmental housing projects, together with increased vaccine coverage and revaccination every 5 years, will reduce the burden of pneumococcal disease in Indigenous adults in this setting.

20.003 Cost-effectiveness of Alternative Case Finding Strategies for Prisons with High Prevalence of Multidrug-Resistant Tuberculosis

D. Winetsky¹, D. Negoescu¹, E. DeMarchis¹, O. Almukhamedova², D. Pulatov², N. Vezhnina³, B. Zhussupov³, A. Dooronbekova³, J. Goldhaber-Fiebert¹

¹Stanford University, Stanford, CA, USA, ²AIDS Foundation East-West, Dushanbe, Tajikistan, ³AIDS Foundation East-West, Almaty, Kazakhstan

Background: Prisons of the former Soviet Union (FSU) have some of the highest rates of multidrug-resistant tuberculosis (MDR-TB) ever observed, and are thought to drive rising TB levels in these countries' general populations. Effective case finding strategies in prisons may interrupt the cycle of transmission, reducing treatment costs and potentially reducing TB incidence more broadly. We projected the costs and health effects of alternative case finding strategies for prisons with high prevalence of MDR-TB.

SESSION 20 (Parallel Session)
Current Approaches to New Threats
(Oral Presentations)

Sunday, February 6, 2011
Room: Klimt Ballroom 2–3 • Upper Level
16:30–18:00

20.001 Polio in Europe: Strategies to Prevent Further Resurgence

D. Jankovic, E. Gavriliu, A. Goel, S. Deshevoi, S. Huseynov, R. Martin
WHO Regional Office for Europe, Copenhagen, Denmark

Background: Certified polio-free in 2002, the World Health Organization (WHO) European Region in 2010 experienced an outbreak due to importation of wild poliovirus (WPV) type 1.

Methods and Materials: Analysis of acute flaccid paralysis (AFP) reporting by countries to the centralized information system for infectious diseases (CISID), managed by the WHO Regional Office for Europe.

Results: As of 25 November, a total number of 476 laboratory confirmed WPV type 1 cases were reported in the Region: Tajikistan, 458 cases; the Russia, 14 cases; Turkmenistan, 3 cases; and Kazakhstan, one case. Children aged <5 years accounted for 65% of these cases. Vaccination history is unknown for 261 cases (55%) and an additional 46 cases (10%) were not fully vaccinated.

Conclusion: The outbreak in Tajikistan was due to an accumulation of susceptible persons and delays in reporting the cluster of acute flaccid paralysis cases. Further spread to other countries in the European Region remains possible.

All of the Central Asian republics and the Russia conducted supplemental immunization activities using monovalent OPV type 1 vaccine or trivalent OPV with a reported ≥95% coverage in all countries.

This outbreak highlights the need for sustained vigilance (in terms of both surveillance and vaccination coverage) even in polio-free regions and particularly among hard-to-reach populations. International travel poses a risk for WPV reintroduction from polio reservoirs for all countries.



Methods and Materials: We developed a dynamic state-transition model of TB and drug resistance, calibrated to the epidemiology of prisons in the FSU. We evaluated eight alternative case finding strategies including: self-referral, symptom screening and screening with mass miniature radiography (MMR) alone or in combination, followed by sputum smear microscopy for inmates who screen positive, either alone or in combination with sputum culture or PCR analysis. Over a ten-year time horizon, we projected costs, quality-adjusted life years (QALYs) saved, TB and MDR-TB prevalence.

Results: The strategy currently used in most FSU prisons, annual MMR screening followed by smear microscopy alone cost more and was less effective than screening with symptom questionnaires followed by smear microscopy (S1). Annual screening with both symptom questionnaires and MMR followed by smear microscopy (S2) had an incremental cost-effectiveness ratio (ICER) of \$1,286/QALY compared with S1. Annual symptom and MMR screening followed by both smear microscopy and sputum PCR analysis had an ICER of \$2,659/QALY compared with S2. These results compare favorably to the per-capita GDP of FSU countries (\$1,900–\$18,300). In sensitivity analyses, symptom screening with smear microscopy and PCR at times replaced S2 as a cost-effective strategy. The cost-effectiveness of these strategies was consistent with their capacity to reduce MDR-TB prevalence.

Conclusion: In prisons of the FSU, the current strategy of annual MMR screening should be modified to include symptom screening, which will both reduce costs and improve outcomes. The incorporation of sputum PCR analysis into case finding strategies could reduce the prevalence of MDR-TB in prisons over time. More sensitive but also resource-intensive case finding strategies may ultimately reduce costs and improve outcomes by interrupting transmission of TB and MDR-TB.

20.004 Emergence of multidrug resistant NDM-1-producing superbugs in Bangladesh

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Background: A New-Delhi Metallo beta-lactamase-1 (NDM-1) has been identified in Enterobacteriaceae in the Indian subcontinent. Our objective was to detect and characterize NDM-1 positive Enterobacteriaceae from Bangladesh.

Methods and Materials: 1789 *E. coli* and 90 *Shigella* from diarrhoeal patients and healthy controls in 2009–2010 and 1816 clinical samples isolated in October 2010 were analysed for imipenem resistance. Gram-negative strains were isolated from 403/1816 samples. 100 ESBL-producing *E. coli* isolated in 2008–2009 were also analysed. Imipenem susceptibility was determined and the presence of NDM-1 gene was assessed by PCR. NDM-1 positive isolates were characterized. Plasmid profiles were analyzed and presence of transmissible R-plasmid was determined by Southern hybridization and conjugation. All NDM-1 positive patients were contacted and interviewed using a short standard questionnaire.

Results: All *E. coli* and *Shigella* isolates from diarrhoeal patients and healthy controls were susceptible to imipenem. Among 403 Gram-negative clinical isolates, 55/403 (13.6%) were resistant to imipenem and 14/403 (3.5%) were NDM-1 positive. These 14 isolates were cultured from 12 patients with the following clinical diagnoses: UTI (n=5), RTI (n=4), wound infections (n=1), unknown (n=2). All NDM-1 positive patients had received antibiotics during the last three months, five were treated with carbapenems. All 12 patients also reported hospitalization in last 3 months. The mean age was 55 years and the male/female ratio was one to two. Among 100 ESBL producing *E. coli* and *Klebsiella* strains 4 were resistant to imipenem, of which 3 were NDM-1 positive. Out of 17 NDM-1 positive strains 10 were *Klebsiella pneumoniae*, 2 *E. coli*, 3 *Acinetobacter baumannii*, 1 *Providencia rettgeri*, and 1 *Citrobacter freundii*. All NDM-1 positive isolates were resistant to multiple antibiotics, including aminoglycosides, fluoroquinolones, cephalosporins, and carbapenems. The only antimicrobials that were effective in vitro were tigecycline and colistin. ESBL genes were detected, including blaTEM, blaSHV,

blaOXA and blaCTX-M. Many strains contained 2-8 plasmids. Plasmid profiles were diverse. Hybridization experiments located this gene in an approximately 30 MDa plasmid in 3 *Klebsiella* strains, which was also confirmed by conjugation.

Conclusion: This is the first systematic study reporting the presence of NDM-1 gene in Enterobacteriaceae in Bangladesh.

20.005 Novel multiplex polymerase chain reaction primer and probe design tools applied to rapid diagnosis and characterization of viruses and bacteria

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Background: Viral species detection can be difficult given the variability of RNA viral genomes. Substantial investment is required to design species specific signatures. Many published PCR-based signatures are not robust, and in a computational analysis of dozens of published signatures, over 60% of the viral signatures analyzed failed to detect all desired targets based on available sequences. Given the exponential increase in sequence data available with advances in sequencing technology, signature design software must scale up to keep pace.

In previous work, many degenerate primer design software packages, all requiring an multiple sequence alignments as input, were tested. Most of these failed to completely detect the viruses tested. By considering sets of k-mers (oligos of length k) shared by multiple sequences, and allowing for a small number of mismatches, one can bypass multiple sequence alignments. The mismatches are converted to degenerate bases in a primer or probe.

We have developed an automated primer design system that incorporates degenerate bases and we have demonstrated the utility of this system for the highly sensitive and specific detection of all strains of Rift Valley Fever Virus tested.

Methods and Materials: Using our unique new software, primer/probe triplets with both conserved and genotyping probes were predicted for each (L,M,S) segment of Rift Valley fever virus. These were tested in the lab against over 100 different background templates as well as other bunyaviruses as near-neighbor targets first in a quantitative RT-PCR format and then in an end-point RT-PCR format followed by hybridization to bead-conjugated probes.

Results: The assays (both qRT-PCR and end-point RT-PCR) developed demonstrated sensitivities as good as assays using the same chemistry but with no degeneracies incorporated. Additionally, the assays demonstrated absolute selectivity when tested against over 100 different background and near-neighbor templates.

Conclusion: This system is of great utility to development of qRT-PCR assays that can quickly determine the presence of any of a divergent pool of targets. The amplicons thus produced can then be hybridized to strain-specific probes able to further characterize the agents in the sample. The total time from sample to detection and strain differentiation is less than 5 hours.

20.006 Impact of vaccination on the genetic evolution of H5N1 viruses in Egypt

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Background: Since 2006 H5N1 HPAI viruses belonging to clade 2.2.1 have been extensively circulating in poultry population in Egypt. In order to control the disease in poultry and reduce the risk for human health, stamping out and vaccination have been applied on large-scale. Nevertheless, the virus became endemic in this country.

To provide new insights into the epidemiology of this virus, we investigated the evolutionary and population dynamics of the HA gene



of H5N1 circulating in Egypt between 2006 and 2010. We explored the potential effect of vaccination on virus evolution, comparing the evolutionary rates of H5N1 viruses isolated from countries where vaccination was adopted or not adopted.

Methods and Materials: The HA gene of 313 H5N1 viruses from Egypt, 169 from Indonesia, 87 from Turkey and 106 from Nigeria were analyzed. Rates of nucleotide substitution per site and per year were estimated using the Bayesian MCMC approach. Positive selected sites were identified using Datamonkey web interface of the HY-PHY package.

Results: Topology of the phylogenetic tree obtained for the HA gene revealed that Egyptian H5N1 viruses evolved into distinct genetic clades with different evolutionary and population dynamics.

The mean evolutionary rates calculated for the HA gene of H5N1 isolated from Egypt and Indonesia, two countries where vaccination is applied, were higher compared to the mean evolutionary rates obtained for H5N1 viruses circulating among non-vaccinated poultry populations from Nigeria and Turkey. Moreover, clear differences in the codon based selection profiles were observed between viruses from non-vaccinated (0 or 2 positive selected sites) and vaccinated countries (8 or 6 positive selected sites, most of them located at the antigenic sites).

Conclusion: Our results suggest that vaccines and vaccination practices may impact the evolutionary rate and the occurrence of mutations in H5N1 viruses circulating in poultry. This should be taken into account when considering vaccination as a tool for controlling this infection. Proper vaccine strain selection, application of good manufactured vaccines, implementation of rigorous vaccination practices and monitoring of field vaccination coverage and vaccine efficacy must all be seriously considered to reduce the risk of vaccine failures and major antigenic drift.

20.007 Using surveillance data to estimate influenza vaccine effectiveness in Spain during seven seasons (2002–2009)

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Background: The Spanish Influenza Sentinel Surveillance System (SISSS) aims at providing timely epidemiological and virological information on influenza activity. During the influenza season (from epidemiological week 40 to week 20 of the following year), sentinel physicians collect basic information, take swabs and notify influenza like illness (ILI) patients to the SISSS. Starting the season 2002–2003, an electronic database was used for data collection. We aimed to estimate the seasonal influenza vaccine effectiveness (IVE) against laboratory confirmed influenza using data available in the SISSS, to explore the feasibility to generate timely IVE estimates each season.

Methods and Materials: We used the test-negative case control study design. All swabbed ILI patients reported to the SISSS during seven influenza seasons (2002–2009) were included in the study. Cases were ILI laboratory-confirmed for influenza A or B. Controls were ILI testing negative for any type of influenza. Primary analysis included all cases. Restricted analysis was performed for <65 year old as well as to the epidemic period of each season. Data on age, sex, vaccination status and laboratory results was available for all seasons. We used logistic regression to calculate adjusted odds ratios (OR) and computed IVE as $(1-OR)*100$.

Results: We excluded from the analysis of each season the missing data on laboratory results (range: 16–187) and vaccination status (range: 4–60). The number of swabbed patients with laboratory results available increased over seasons ranging between 567 in the season 2002–2003 to 2182 in the season 2008–2009. The adjusted IVE for age and month of swabbing varied by season ranging between 27% (-16; 54) in the season 2004–2005 and 58% (23; 77) in the season 2005–2006. In the restricted analysis (<65 years or epidemic period), the adjusted IVE did not differ significantly than the primary analysis.

Conclusion: The SISSS allowed estimating IVE each season. Different IVE values were obtained adjusting for age and month of swabbing depending on circulating strain. The IVE might be underestimated due to lack of collecting important confounding factors. To strengthen the surveillance system, systematic swabbing of ILI patients was introduced starting the season 2009–2010. Consequently, estimating IVE will improve and will be routinely included among the SISSS objectives.

20.008 Timing, Progression and Community impact of 2009 Influenza Pandemic: A comparison with historical seasons in countries of WHO/European Region

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Background: The world has recently experienced the first influenza pandemic of the 21st century that lasted 14 months from June 2009 to August 2011. This study aimed to describe and compare the timing, geographic spread and community impact of the winter wave of influenza pandemic A(H1N1) 2009 to historical influenza seasons in countries of the WHO/European region.

Methods and Materials: We assessed the timing of pandemic by comparing the median peak of influenza activity in countries of the region during the last seven influenza seasons. The peaks of influenza activity were selected by two independent researchers using predefined rules. The geographic spread was assessed by correlating the peak week of influenza activity in included countries against the longitude and latitude of the central point in each country. To assess the community impact of pandemic influenza, we constructed linear regression models to compare the total and age-specific outpatient consultation rates associated with influenza-like-illness (ILI) or acute respiratory infection (ARI) reported by the countries around the peak influenza activity in the pandemic season to those observed in the previous six influenza seasons.

Results: We found that the winter wave of the pandemic arrived, on average 11.5 weeks (95%CI: 6.2; 16.8) earlier compared to the historical seasons. The analysis of geographic spread revealed a moderate west-east spread of the pandemic virus in Western Europe ($R^2=0.20$, $p<0.05$). Comparison of ILI or ARI rates in 30 countries showed that the total rates were significantly higher than historical trends only in 10 countries. However, the age-specific analysis revealed significantly increased consultation rates in 0-4 and especially in 5-14 age groups in 14 out of 22 countries reported age-specific data.

Conclusion: Using routine influenza surveillance data, we found that pandemic influenza had several differential features compared to historical seasons in the Region. It arrived much earlier, caused significantly higher number of outpatient consultations in children in most countries and followed west to east spread that was not previously observed for A(H1N1) influenza virus. Establishment of parallel hospital-based and mortality surveillance systems in the countries of the Region is ongoing to enable monitoring of similar trends in cases with severe influenza.

20.009 A strategy on antimicrobial resistance for WHO regional office for Europe

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Background: The Global Strategy for Containment of Antimicrobial Resistance has been published by WHO in 2001 and addresses the need to strengthen surveillance and response to antimicrobial resistance. Since then several WHO regions have implemented regional strategies that focus on the actual implementation by member states. In WHO Regional Office for Europe, including 53 member states, through different surveillance networks such as EARS/NET and ESAC the implementation of appropriate surveillance and response system is well under way in 27



countries of the European Union, Norway and Iceland. Several non EU countries have been included in these surveillance networks, which are now incorporated into the European Centre for Disease Prevention and Control, ECDC. For the European Region as a whole the challenge is to implement the global strategy in all 53 member states taking into account the current capacity of health systems in the countries in Eastern and South Eastern Europe.

Methods and Materials: Review of WHO background documents and resolutions to the World Health Assembly as well as an analysis of health systems in Eastern and Southern Europe will be made

Results: In this presentation an overview will be given on a 7 point strategic plan for the WHO European Region, which will address all areas of national stakeholders as well as a review of the complexity of national health systems which may play a role during implementation. A specific note will be made on the increasing problem of MDR and XDR Tuberculosis, with an estimated 80.000 cases each year in the European Region. In addition a communication strategy to increase awareness on antimicrobial resistance will be presented and the World Health Day on the 7th of April 2011 is one of the milestones in this process.

Conclusion: A regional wide approach is needed and current standards and methods all ready in use in some of the member states, should allow for harmonized regional surveillance, monitoring and response systems.

SESSION 21 (Poster Presentations II)

Sunday, February 6, 2011 • 11:45–14:00

Room Bruckner/Mahler/Brahms / Upper Level:

- 21.001 – 21.053 Infections of public health significance
- 21.054 – 21.066 Innovations in diagnostic tests for emerging diseases
- 21.067 – 21.096 New approaches to outbreak surveillance and monitoring
- 21.097 – 21.113 Outbreak response and control
- 21.114 – 21.126 Public Communication of outbreaks and emerging diseases

Klimt Ballroom I / Upper Level:

- 21.127 – 21.139 Vaccines and emergence of vaccine preventable diseases
- 21.140 – 21.187 Vectorborne diseases

21.001 Clinical profile of tuberculosis in chronic kidney disease

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Background: Tuberculosis (TB) is one of the major causes of mortality across the world and India accounts for nearly one third of the global burden of TB.

Because of the immunosuppressive effect of Chronic Kidney Disease (CKD), these patients are at high risk of developing TB. There is limited information on the magnitude of the problem of TB in CKD.

Diagnosis of tuberculosis in uremic patients remains difficult. Uremic patients can have high ESR and Tuberculin Skin Test (TST) may be negative due to impaired cellular immunity. Diagnostic value of Adenosine deaminase (ADA) activity is also unreliable. The utility of other diagnostic tests like IGRA's in the setting of immunosuppression are not well studied

Aim of the study was to find out the incidence, clinical profile and contributing factors of TB in CKD.

Methods and Materials: This was an observational study where patients were followed up during study period from August 2008 to July 2009.

Results: Of 572 patients with CKD, 32 had TB and incidence of tuberculosis in CKD was 5.6%. This was much higher compared to the TB incidence of 0.4% in general population.

Fever was the commonest presenting complaint followed by weight loss and night sweats. Risk factors for tuberculosis were malnutrition, use of immunosuppressants, contact with tuberculosis, diabetes mellitus, smoking and alcoholism.

Extra pulmonary tuberculosis was more common form (75%), of which CNS tuberculosis was the commonest, followed by tuberculous pleural effusion, lymphadenitis, spine, genitourinary, disseminated, pericarditis, ascites and retroperitoneal abscess. Sputum AFB was negative in 96.9%, TST negative in 75% and ADA negative in 83.3%. Tuberculosis was confirmed in 31.3%. In the rest, diagnosis was based on radiological findings, fluid analysis and response to anti-tuberculous treatment, supported by the clinical picture.

62.5% were cured of the disease. 18.75% died during treatment. Mortality was maximum in disseminated tuberculosis followed by CNS tuberculosis.

Conclusion: TB is a challenge to CKD particularly in endemic regions. The presentation of Tuberculosis in uremic patients is often quite unusual and insidious and their prompt diagnosis is critical for better patient outcome. It requires a high index of suspicion in order to diagnose tuberculosis in CKD.

20.010 Evaluation of the 2009–2010 Oral Fox Vaccination (OFV) campaigns in North-Eastern Italy

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Background: Between 2008 and 2010 rabies re-emerged and rapidly spread in wild foxes in North-Eastern Italy. To control the spread of infection and to minimize the risk of human exposure, two emergency OFV campaigns were carried out by aerial distribution from December 2009 to June 2010. The results of the monitoring activity implemented to evaluate the efficacy of the OFV campaigns are presented herein.

Methods and Materials: Taking into account the limited resistance of the vaccine virus to the freeze-thaw cycle, a suitable bait drop area had to be identified on the basis of the ground freezing conditions. The OFV baits were distributed, in the winter campaign below 1000 m asl. and, in the spring campaign below 2300 m asl. The territorial coverage of each OFV campaign was evaluated by means of a GIS-based system.

To evaluate the effectiveness of each OFV campaign the monitoring activity started 30 days after the end of the field operations and lasted on average for one month.

A fox was considered protected if the fluorescent antibody virus neutralization test detected an antibody titre ≥ 0.5 IU/ml.

Results: Thematic maps illustrating the density of baits, expressed in number of baits per sq km, were produced, in order to identify the geographical areas with a lower bait density than the established threshold value. In these areas a complimentary manual distribution of baits was implemented. To monitor the efficacy of winter vaccination a total of 203 foxes were sampled. Vaccination coverage was estimated to be 77% (C.I. 95%: 69.4–81.6), while in the second campaign 554 foxes were tested with a protection level of 69% (C.I. 95%, 67.7–75.5). The foxes tested were those that had been found dead or those killed by hunters in the vaccination area.

Conclusion: The territorial coverage achieved by OFV was adequate and the GIS-based system was functional in providing information to promptly implement corrective measures. The immune coverage of OFV campaigns was satisfactory despite the climatic constraints which in winter forced large territorial areas of 1000 m asl to remain uncovered. Nonetheless OFV was successful in containing the disease and in avoiding further westward spread to unaffected neighbouring regions.

**21.002 Design and evaluation of Taq Man Real Time PCR for molecular diagnosis of typhoid fever**

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Background: Typhoid caused by *Salmonella enterica* serovar Typhi remains a major health concern worldwide but current diagnostic tests are inadequate. Classic identification methods are usually time consuming and don't have sufficient sensitivity. PCR-based detection assays have become prevalent in the last decade because they are specific, extremely sensitive, rapid, and relatively inexpensive. Most of studies confirmed that real-time PCR was a very sensitive method of detection from clinical samples. Our aim in this study is to develop and domesticate Taq Man Real-time PCR technique for rapid identification of this organism.

Methods and Materials: The Primer Express software (Version 2.0, Applied Biosystems) was used for all the oligonucleotide primers and the fluorescent dye-labelled probes designed in this study Primers were designed based on *fliC-d* and inter action of primers was analyzed with the Gene Runner. All experiments were based on real-time PCR assays using *Taqman* technology. For sensitivity and limit of detection (LOD) in this study, PCR products were cloned in the pTZ57R/T vector. The specificity of this assay was evaluated in the presence of contaminating DNA from a variety of common bacteria. In addition, limit of detection were determined in Real-time method using standard curve. Finally, the cloned fragment was sequenced.

Results: The results of Taq Man Real-time PCR were assessed. The high specificity of the test (100%) was also realized in the proficiency test. The detection range was determined by using standard curve and math means less than 2 copies in a 10 micro liter Real-time PCR reaction. The Positive Control Construct was confirmed by sequencing.

Conclusion: We have developed rapid, species-specific PCR-based assays that can be accomplished in less than 30 Min (using a ABI 7500 Fast) when killed or extracted DNA samples were used. The present real-time PCR assays for specific detection of *Salmonella enterica* are suited for routine diagnosis, which renders them important tools for the recognition of outbreaks. Generally speaking, the successful use of real-time PCR assays in a routine diagnostic laboratory requires the implementation of diagnostic quality assurance program, which should include special PCR training, workshops and proficiency tests on a regular basis.

21.003 Demographic trends among Mycobacterium tuberculosis cases in an aging population with medium disease burden in Taiwan

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Background: To characterize the epidemiological and demographic trends among the TB cases for assessment the disease burden in Taiwan.

Methods and Materials: Data of 104,887 Taiwanese TB cases and 2,729 non-Taiwanese TB cases during recent 7 years obtained from dataware house derived of the national surveillance system of the Taiwan Centers for Disease Control was analyzed.

Results: For a decade the annual incidence of tuberculosis (TB) cases in Taiwan has been estimated as a crude values. Here, for the first time, besides estimated it as the crude values as ranging from 72 to 61.8 per 105 per year, we present the annual incidence of TB cases adjusted to the standard population in Taiwan as ranging from 65 to 46 per 105 per year during recently past 7 years. Under an ongoing of aging population, the 70.24% of Taiwanese TB cases was aged over 50, with age-specific incidence rate of 36–225 per 105 per year in female and 91.8–583 per 105 per year in male. The majority of elderly cases were reactivated from putatively early infection. In contrast, 68.62% of non-Taiwanese TB cases were in females aged 20–39. Though the proportion of annual number of Taiwanese vs. foreign TB cases exhibiting big disparity (14983: 389), partially remarked association between annual numbers of foreign cases and Taiwanese cases was observed in 54.5% (12/22) of 22 single cities/counties with $R=0.3-0.74$ ($n=7$) during recent 7 years.

Conclusion: For description the disease burden with the dominant of elderly TB cases based on an aging population, it is suggested to report the TB incidence by adjusted estimates while the standard population data is available. Keeping awareness of the potential risk of disease dissemination among vulnerable individual e.g. immigrant brides and their spouses is hypothesized.

21.004 Monitoring of cytomegalovirus quantity and antigenemia following stem cell transplantation with a focus on plasma and PMN results

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Background: Before the introduction of prophylactic or preemptive therapy against Cytomegalovirus (CMV), the associated disease has been major causes of death follow allogeneic hematopoietic stem cell transplantation (AHSCT), but now the virus remains as an important factor for morbidity and long-term outcome after AHSCT. The aim of this study was to investigate the role of PMN and plasma real time quantitative polymerase chain reaction (RQ-PCR) in the diagnosis and treatment of the recipients CMV infection after AHSCT.

Methods and Materials: 450 blood specimens serially collected from 49 AHSCT recipients within 7-120 days after transplantation. DNA extractions were performed using QIAamp DNA blood mini kit, viral loads were quantified with a previously described double primer TaqMan prob Real-Time PCR and antigenemia was done by CMV Brite turbo kit.

Results: The positive rate of RQ-PCR based on PMN was significantly higher than that based on plasma (53.2% vs. 34.5%, $p = 0.002$). Of the 43 patients with serial samples, 26 were positive for HCMV DNA in PMN while 19 were positive in plasma. Moreover, the viral load detected by PMN DNA was higher than that using plasma DNA for each patient.

Conclusion: Detection of CMV DNA in plasma by real time PCR appears to be effective for the surveillance of CMV infection after HSCT, but PMN RQ-PCR results have more potency to diagnosis and prediction of high risk people who may develop CMV disease.

21.005 Uncommon syndrome secondary to sepsis with an uncommon pathogen

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Background: Macrophage Activation Syndrome (MAS) is a severe form of Systemic Inflammatory Response Syndrome (SIRS) resulting in multiorgan dysfunction. The pathognomonic feature is cytokine dysfunction, causing active hemo-phagocytosis by normally appearing macrophages. MAS is commonly seen secondary to rheumatologic diseases especially systemic juvenile arthritis but is also rarely associated with infections, autoimmune disorders or malignancies. The infections associated include viral, bacterial, parasitic and fungal although any infection can stimulate the inflammatory system resulting in MAS.

Methods and Materials: We evaluated a young chronic alcoholic, who had a history of recent hospital admission, with features of SIRS (unrelenting fever, hepatosplenomegaly and generalized lymphadenopathy) for the presence of MAS. Routine and special investigations were done. Lymphnode biopsy, bone marrow study and flow cytometry were done for confirmation.

Results: Investigations revealed pancytopenia with a declining hemoglobin level, total leucocyte count, platelet count and ESR. LFT was abnormal with evidence of coagulopathy. S Ferritin was markedly elevated (18,500 microg/dl). Peripheral smear showed leucopenia with thrombocytopenia. Hypertriglyceridemia and hypofibrinogenemia was present. Lymph node biopsy and bone marrow study showed extensive necrosis with macrophages showing hemophagocytosis. ANA and Rheumatoid factor were negative. Flow cytometry showed decreased NK cell activity. Bone marrow and blood culture revealed aerobic gram



negative bacterium *Acinetobacter baumannii*. The patient fulfilled the diagnostic criteria of MAS and was successfully treated with steroids and immunosuppressants.

Conclusion: MAS is not an uncommon syndrome but not often suspected clinically. It is usually associated with a high mortality mainly due to delay in diagnosis. Treatment should be initiated immediately when the diagnosis of MAS is confirmed since delay in therapy may lead to irreversible multi-organ failure. Steroids and immunosuppressants are the mainstay of treatment.

Acinetobacter is an opportunistic gram-negative coccobacilli that is strictly aerobic and of relatively low pathogenicity. *Acinetobacter* infections are uncommon and occur almost exclusively in hospitalized patients and is associated with nosocomial pneumonias, bacteremias, and wound infections. However, the recent emergence of community-acquired *Acinetobacter* infections has demonstrated that this organism can be highly virulent with a propensity to cause invasive disease in non-critically ill patients. This is the world's first reported case of MAS secondary to *Acinetobacter* infection.

21.006 Dog bite, recognized as a public health concern in Addis Ababa, Ethiopia

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Background: Animal bites represent the most important public health issue related to dogs and cats because of the risk of rabies transmission, associated physical and psychological trauma and wound infection by different microorganisms.

The study was aimed at estimating the epidemiology of animal bite to human beings in Addis Ababa.

Methods and Materials: A retrospective study was conducted in patients who were bitten and scratched by animals. Data about age, gender, kind of animals, site of bite, exposed body part of patients recorded in case book at the Zoonoses Diseases Research Laboratory of Ethiopian Health and Nutrition Research Institute were analyzed. SPSS version 11.5 was used for analysis.

Results: 1299 cases of human exposure to animal bite have been reported. The mean annual animal bite was 2.44 ± 1.33 . Dog, cat, other animals (Donkeys, Horses, Hyena, and Cows) and monkeys were found the most common animal species contributing bite. The majority of bites 699 (57.06%) were made by stray dogs. Median ages of all patients exposed to animals were 24.64 years ranging from 1 to 90 years old. Animal bites in ages ranging from 5-15 and 16-25 years old were found higher (50.11%) than other age groups. The ratio of male to female animal bites was found 3:1. The animal bite made by dogs was higher (55.6%) on feet followed by hands (26.45%) then 7.51% was multiple bite, 5.71% at other body parts and 4.73% was above neck and around back.

Conclusion: There is higher incidence of animal bite in Addis Ababa with majority of bites are by dogs with high rate by stray dogs proceeded by cats, horses, donkeys and least by monkeys. Such problems necessitate a preventable public education about responsible pet ownership, and regulations regarding animal control. Young adults and children should be taught to refrain from behaviors likely to provoke bites and to follow suggestions for the prevention of canine aggression.

21.007 Neurobrucellosis in children, a report of 2 cases and a review of the literature

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Background: To report on two cases of neurobrucellosis with different presentations.

Methods and Materials: Retrospective report of the data on 2 cases of neurobrucellosis: the first case presented with acute meningo-encephalitis and the second case presented with acute meningitis.

Results: Both cases had indolent fever for more than a month and a strong history of contact with animals or animal products. Both cases were diagnosed by the serum agglutination test and cerebrospinal fluid

Brucella culture. Both cases were treated for 6 months with combination therapy of anti-*Brucella* drugs with excellent outcome.

Conclusion: The description of both cases and a brief review of the current pediatric literature are provided to familiarize pediatricians with the relatively rare presentations for this common worldwide disease.

21.008 Two sequential measles outbreak investigations in highly immunized hilly areas of district Kangra, Himachal Pradesh, India, 2007

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Background: We investigated two sequential outbreaks of measles to confirm diagnosis and recommend for prevention and control.

Methods and Materials: We defined a case of measles as occurrence of fever with rash in a child aged six months to 17 years during 3rd September to 23rd November, 2006. Having line listed cases we collected information on age, sex, residence, date of onset, symptoms, traveling, treatment history and vaccination status. We described the outbreak by time, place and person. We estimated vaccine coverages and vaccine efficacies in the affected villages. We confirmed diagnosis clinically, serologically and through genotyping of the virus.

Results: We identified 69 case patients. Overall attack rates ranged between 4.2% and 6%. Age specific attack rate ranged between 1.7% to 17.3%. All cases were between 6 to 17 years; highest in 11-17 years. No death or complications were reported. The epidemic curve was suggestive of typical propagated pattern. The 1st outbreak imported virus after an inter school game competition (Relative risk: 6.44%; 95% confidence interval: 3.81-10.91) followed by 2nd outbreak people exchanged foods in the festival in one infected village of 1st outbreak (Relative risk: 5.3; 95% confidence interval: 1.90-14.77; $P < 0.001$). The calculated immunization coverage (93%) coincided nearly with administrative claims. We estimated vaccine efficacies as 85% and 81% in 1st and 2nd outbreaks. 11/16 case-patients for measles IgM antibodies and 2/5 nasopharyngeal swabs were tested positive by PCR and D4 measles strain genotyped. Vitamin A supplementations were only in 4/7 villages.

Conclusion: Measles outbreaks were confirmed in high immunization coverage areas. We recommended second dose opportunity for measles and vitamin A supplementation to all cases in affected areas.

21.009 Inhibition performed by a synthetic microbicidal peptide on the replication of Influenza virus

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Background: Influenza A viruses are seasonal or pandemic infectious agents. The objective of the present study was to assess the "in vitro" inhibitory activity against influenza A virus of an antibody (Ab)-derived killer decapeptide (SKP). SKP represents the CDR of the variable region of an antibody which has microbicidal activity against pathogenic eukaryotic as well as prokaryotic microorganisms.

Methods and Materials: Confluent monolayers of LLC-MK2 cells infected with Ulster 73 virus were treated with different amounts of synthetic killer peptide (SKP). Negative internal control was represented by a synthetic scramble peptide (SP).

After 72 hours, supernatants were assayed by HA titration: 10,20,40,60,70,80 microgs/ml were the amounts of SKP added to the maintenance medium. To verify the proper biological role of virus-coded haemagglutinin, experiments of haemadsorption of untreated v/s SKP-treated infected LLC-MK2 cells were performed.

SKP at 80 µgs/ml was also able to block the multiplication of a type A neurovirulent human strain, NWS/33 virus.

14-C-mannose and 35-S-methionine pulse-labelling experiments of LLC-MK2 cells infected by Ulster 73 virus in presence of SKP from the beginning of the infection, were done according to standard procedure.



Results: SKP was able to suppress virus replication in a dose-dependent fashion, in particular 80 microgs/ml was the concentration completely inhibiting virus growth. No inhibition was performed by SP. Similar results were obtained in other cellular types such as MDCK and AGMK 37RC.

Haemadsorption assays on monolayers of untreated v/s treated infected LLC-MK2 cells were done at 72 hours p.i. Significant differences between untreated versus treated infected cells were observed. The haemadsorption values indicate a great reduction of virus-coded haemagglutinin molecules on the plasma membrane of infected cells treated with 80µgs/ml of SKP. For comparison, results referring to MDCK (Madin Darby Canine Kidney) and AGMK-37RC (African Green Monkey Kidney) treated with the same amount showed such the inhibitory effect.

¹⁴C-mannose, as well as ³⁵S-methionine, pulse-labelling experiments of SKP-treated LLC-MK2 cells infected by Ulster 73 virus, showed a marked reduction both of glycosylation as well as the overall synthesis of haemagglutinin HA suggesting a possible double interfering mechanism performed by SKP.

Conclusion: The restriction of viral multiplication in different cells and the interfering action on HA glycosylation other than synthesis of viral HA seem results of interest. Our suggestion is an incorrect insertion of HA into plasma membrane

21.010 Leprosy presenting as Immune Reconstitution Inflammatory Syndrome (IRIS) in patients on Highly Active Anti-Retroviral Treatment (HAART)—A case series study from a tertiary care centre in Kerala, South India

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Background: "Immune Reconstitution Inflammatory Syndrome" (IRIS) is a unique syndrome which comprises of a collection of inflammatory disorders, associated with paradoxical worsening of preexisting infectious processes either previously diagnosed and treated or subclinical and later unmasked following the initiation of highly active antiretroviral therapy (HAART), in HIV-infected individuals. IRIS is usually associated with a low pretreatment CD4 count (often less than 100 cells/microL). Although the most frequently reported associated infections with IRIS are localized herpes zoster, M. tuberculosis, M. avium complex, cytomegalovirus, and Cryptococcus, rarely leprosy can also present in a similar fashion with some studies reporting an incidence of 3 per 1000 HIV cases.

Aim of the Study: Was to find out the incidence and clinical profile of Leprosy presenting as IRIS, in HIV patients on HAART.

Methods and Materials: It was a prospective study where we evaluated patients with HIV started on HAART for evidence of Leprosy, from May 2007 to June 2010.

Results: 743 patients were started on HAART during the study period and 4 patients were diagnosed to have Leprosy (Incidence was 5.38/1000 HAART patients). Of these, 3 patients had Borderline Tuberculoid and one had Borderline Lepromatous with type 1 lepra reaction. The pretreatment CD 4 counts were 25, 40, 50 and 75 cells/microL (mean-47.5 ± 21) and CD4 count at the time of disease detection was 198, 159, 245 and 230 respectively. All patients presented within 8 weeks of starting HAART. The clinical features were hypo pigmented lesions, erythematous tender plaques and foot drop. Skin biopsy of these patients showed granulomatous inflammation. These patients met the diagnostic criteria of IRIS and were successfully treated with Multi Drug Treatment (MDT) along with continuation of HAART.

Conclusion: IRIS presenting as Leprosy is quite unusual. In patients on HAART, who develop acute onset erythematous plaques or paralysis, Leprosy should be ruled out especially in endemic areas. Successful treatment depends on alleviation of patient's symptoms without compromising HAART.

21.011 A case control study for the identification of risk factors associated with HCV infection in a tertiary care hospital of Pakistan

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Background: Hepatitis C Virus prevalence and mode of transmission differ over time and vary among different countries. Pakistan carries one of the world's highest burdens of chronic hepatitis and mortality due to liver failure and hepatocellular carcinomas. However, currently at national level, exact estimates of the prevalence of and risk factors for hepatitis B and hepatitis C are not available. We report the risk factors involved in the spread of HCV in Pakistan. An epidemiological monitoring programme is direly required to aid the effectiveness of preventive measures.

Methods and Materials: A case control study comprising 50 cases and 100 controls was conducted during May to August, 2010. Informed consent was taken from all of the participants. Fifty cases and hundred controls were interviewed using pre-tested and specially designed questionnaire. Data was analyzed by using SPSS version 16.0 to measure the strength of association of various known and unidentified risk factors with HCV transmission. Cases were positive for anti-HCV antibodies confirmed by ELISA method and controls were negative for anti-HCV antibodies. All participants were resident of same area (Lahore) and 16–70 year age. Not a single participant was missed.

Results: History of clinical symptoms (OR 7.39), History of sharing of straw (OR 4.321), History of blood transfusion (OR 3.6), History of alcohol consumption (OR 2.67), History of previous surgery (OR 2.42), History of body (including Ear/Nose) piercing/tattooing (OR 2.25), History of sharing of crack pipe (OR 2.23), History of sharing tooth brush (OR 2.11), History of sharing comb (OR 2.06) were significant risk factors associated for acquiring HCV infection.

Conclusion: In conclusion, history of presence of acute hepatitis like symptoms prior to illness, sharing of straw, blood transfusion, sharing of straw, crack pipes, tooth brush, comb, history of alcohol consumption, surgical procedures and blood transfusion remains most important vehicles for spread of the HCV in Pakistan. There is a dire need of awareness and effective surveillance and monitoring program at national level to reduce and ultimately control the HCV infection.

21.012 A triple approach of an outbreak of conjunctivitis in a nursing home for psycho geriatric patients in the Rotterdam-Rijnmond area in the Netherlands

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Background: The Department of infectious Disease Control of the Municipal Health Services of Rotterdam-Rijnmond area supports and gives advice to Health Care institutions such as 110 nursing homes.

At the end of March 2010, the elder care physician reported several cases of conjunctivitis with watery or pussy discharge among psycho geriatric residents. It appeared at a newly built home, and since its construction the atmospheric humidity had been too low. The epidemic spread towards all of the four accommodation units. The residents of each accommodation unit are in a different stage of their cognitive decline.

Methods and Materials: Retrospective cohort study of 96 residents and its staff is performed of all cases during the period from March 2010–June 2010 using the health records and laboratory results. A case was defined as having at least once redness of the eye and watery and/or pussy discharge. Microbiologic investigation was performed to confirm the causative pathogen.



After creating an Outbreak Management Team, actions were taken. 1) Interrupt transmission: use of 80% alcohol hand gel, minimizing exchange between caregivers and close all wards. In spite of these efforts still more residents and staff were infected. 2) Control source of pathogen: preventative treatment with Povidone-Iodine drops. 3) Control host response to exposure: Humidity control was introduced.

An Epidemic Curve out of all cases is made.

Results: 42 residents and 17 staff developed conjunctivitis. Cultures from 6 residents and staff were taken typed as Adenovirus (Type 8).

Each accommodation unit managed its outbreak differently. This will be shown in the epicurve. This epicurve shows the difference in transmission time in these units. To suffer conjunctivitis set difference per unit in weekranks from 4 to 10 weeks. The epidemic of Conjunctivitis with an Attack Rate of 44% for the and 8 % for staff subsided because of the triple intervention of strict hygienic measures, preventative treatment with Povidone-Iodine 0,3% eye drops and humidity control.

Conclusion: In 2010 the first outbreak of Conjunctivitis in a nursing home in the Netherlands has been reported. Units of residents with more demential symptoms get more support by higher qualified staff and use more hygienic (personal and domestic) measures. This study recommends nursing homes to facilitate training programmes in hand hygiene for all staff.

21.013 Small molecule inhibitors of dengue virus replication are active in vivo

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Background: Dengue virus causes an estimated 50–100 million infections and 22,000 deaths per year globally. As this flu-like mosquito-borne illness can progress to more deadly forms - dengue hemorrhagic fever and dengue shock syndrome - an antiviral drug administered early during dengue virus infection that inhibits viral replication and prevents high viral load associated with more severe forms would be attractive. The goal of SIGA's dengue program is to develop an orally administered small molecule therapeutic for the treatment/prevention of dengue.

Methods and Materials: A sensitive and specific high throughput screening (HTS) assay has been developed to evaluate compounds from the SIGA chemical library for inhibitory activity against dengue-2 (DENV-2) virus replication. Chemically tractable hits are tested for potency and specificity and analogs are identified through substructure searches of in-house and commercial compound libraries. These compounds are acquired and tested for activity to identify quality hits. Quality hits are characterized for spectrum of activity, mechanism of action (MOA), preliminary absorption, distribution, metabolism, and excretion (ADME) properties, preliminary pharmacokinetic (PK) profiles and tolerability. Based on this characterization a lead series is identified that has an optimal biological profile. Chemical analogs of selected quality hits from the lead series are synthesized to improve the properties of the compounds, leading to the nomination of a preclinical candidate.

Results: Novel small molecule inhibitors have been identified that are potent and selective, with inhibitory activity against all four serotypes of dengue virus *in vitro*. These compounds have structures that possess chemically stable functionalities and have potential drug-like qualities. Lead series have been identified and are being defined by spectrum of activity, MOA, ADME profiles, and PK evaluations. Two of these series have shown proof-of-concept efficacy in a murine model of disease. Approximately 200 analogs of each series have been screened to generate preliminary structure activity relationships.

Conclusion: The identification and characterization of dengue virus inhibitors represents a compelling start toward our goal. We have identified potent lead compounds that are active against all four serotypes of dengue virus, have no known associated toxicity, and have desirable drug-like characteristics. We are currently optimizing these compounds to improve potency, ADME, and PK properties.

21.014 Wetland drainage (habitat modification) for Mosquito control in the Ilparpa Swamp, Northern Territory, Australia

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Background: Habitat modification is an established method of effective long-term mosquito management, particularly in salt-marsh environments. It is especially pertinent when mosquitoes are known vectors of life threatening disease and their breeding habitat is in close proximity to residential areas. The Ilparpa Swamp is located less than 10 km from Alice Springs, Northern Territory. Wet season rainfall, often followed by effluent discharges to the swamp from the adjacent sewage treatment plant, create ideal breeding sites for the common banded mosquito *Culex annulirostris* (Skuse), a major vector of Murray Valley encephalitis (MVEV) and Kunjin (KUNV) viruses.

Methods and Materials: Subsequent to increases in notifications of MVEV disease cases in 2000 and 2001, lead to the establishment of a drainage system in Ilparpa Swamp in early 2002. Using statistical modelling, we evaluate the drainage intervention effects.

Results: Results indicate a significant reduction in mosquito numbers following habitat modification, which remains low. There have been no seroconversions in sentinel chickens to MVEV or KUNV and no human infections from these viruses in the Alice Springs urban region since the drains were completed.

Conclusion: Habitat modification has successfully reduced mosquito numbers and minimized the risk for mosquito-borne disease to residents in Alice Springs urban and surrounding areas, previously undocumented in Australia.

21.015 Prognostication of thrombocytopenia development in patients with chronic hepatitis C

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Background: Risk factors for thrombocytopenia development in chronic hepatitis C are not well understood. Their study may help to predict the risk of thrombocytopenia and timely start preventive measures.

Methods and Materials: In 138 patients with chronic hepatitis C without splenomegaly it was estimated activity of ALT, quantitative PCR RNA HCV, genotyping of the virus, platelets antibodies and antibodies to *Helicobacter pylori*.

In selected cohort all patients were divided in 2 groups: with thrombocytopenia (60.9% of patients) and normal platelets level (39.1% of patients).

Results: In patients with thrombocytopenia 1th genotype was detected in 50,0 ± 5,4%. It was significantly higher than occurrence of 2th (22,6 ± 4,5%) and 3th (27,3 ± 4,8%) genotypes. In the group of patients without thrombocytopenia 1th and 3th genotype had the equal frequency - 44,4 ± 6,7% and 40,0 ± 6,6%, and 2nd genotype was recorded only in 15,5 ± 4,9%.

In patients with low platelets level viral load higher than 200 000 ME/ml was recorded more frequently than in other group: 42,8 ± 5,4% versus 17,8 ± 5,2, (p < 0, 01). Viral load from 20000 to 100000 ME/ml was prevalent in patients without thrombocytopenia - 37,8 ± 6,6% versus 15,4 ± 3,9, (p < 0,01).

Increased ALT activity in patients with thrombocytopenia was more frequent than in the other group - 29,8 ± 5,0% versus 14,8 ± 4,8% (p < 0,05).

Antibodies to *Helicobacter pylori* in patients with thrombocytopenia were observed in 61,9 ± 5,3%, in patients without thrombocytopenia in 31,5 ± 6,3%. Platelet-associated antibodies combined with thrombocytopenia were recorded in 64,2 ± 5,2% of cases, in patients without thrombocytopenia in 22,2 ± 5,6% of cases (p < 0,05).

Second stage of fibrosis is recorded more frequently in patients with low platelets level, 0 and 1th stages of fibrosis were predominate in patients without thrombocytopenia.



Conclusion: Thrombocytopenia is registered in more than half of cases with chronic hepatitis C without splenomegaly. The risk factors for its development are replicative form of disease, 1th genotype of virus, 2th stage of fibrosis, viral load of more than 200000 ME/mL, elevated ALT, *Helicobacter pylori* associated diseases, platelet-associated antibodies.

21.016 Herpes simplex virus 1 & 2 are common causes of viral meningoencephalitis in Peru

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Background: Meningoencephalitis is a significant public health problem throughout the world, however few studies have defined the etiologies outside North America and Europe. Despite advances in technology, most laboratories identify a pathogen in less than half of patients with meningoencephalitis. The objective of this study was to determine the viral etiologies of meningoencephalitis in Peru.

Methods and Materials: We conducted hospital-based surveillance at 5 hospitals in 3 geographically distinct Peruvian cities (coast, highlands, and jungle). Information about symptoms and medical history was collected from patients 2 months and older with suspected viral meningoencephalitis; serum, CSF, and nasopharyngeal swabs were collected as part of standard of care. Follow-up visits were conducted 15 days after acute presentation. Samples were tested for HSV-1/2, HIV, and 18 other viruses including dengue, West Nile, yellow fever, and Venezuelan equine encephalitis. HSV meningoencephalitis was defined as confirmed (HSV detected by PCR in CSF) or probable (HSV detected in serum or IgG seroconversion).

Results: 113 subjects were enrolled in the study. 53 subjects (46.9%) were male; average age was 26.1 years (range 2 months - 76 yrs). Four patients (3.5%) died; 4 were co-infected with HIV. 31 subjects (27.4%) were infected with herpes simplex virus (19 confirmed, 12 probable). Of these 31 cases, 21 (67.7%) had HSV-1, 8 (25.8%) had HSV-2, and 2 (6.5%) did not have HSV typed. PCR and ELISA testing for other viral etiologies were negative in all subjects.

Conclusion: This is the first report on the etiology of community-acquired meningoencephalitis in Peru. Not surprisingly, HSV infection was the most common pathogen identified. Unexpectedly, 25% of all herpes encephalitis cases were caused by HSV-2, a rate much higher than reported in other parts of the world. HSV-2 is primarily acquired via sexual transmission or vertically from mother to child. Central nervous system infection beyond the neonatal period is uncommon, but up to 28% of women develop symptoms of meningitis during initial genital infection. Further research will be needed to investigate the high prevalence of HSV-2, characterize HSV-2 meningoencephalitis, and determine risk factors for infection.

21.017 An outbreak of pulmonary leptospirosis in Honduras

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Background: Leptospirosis is uncommon in Honduras. Clinical manifestations vary from minimal to icteric-hemorrhagic forms potentially fatal. Pulmonary Leptospirosis is extremely rare in our country. We report a clinical and laboratory data of 5 cases that occurred in a short time period in the same geographical region.

Methods and Materials: During October of the present year, 5 patients with acute respiratory failure were hospitalized in the Hospital-Escuela in Tegucigalpa. All of them, coming from the south region of Honduras, near the borderline with Nicaragua. In all the cases an immunochromatographic test assay for leptospirosis was performed. Patient's records were reviewed for the clinical characterization. Complementary data was obtained from chest radiography and in some cases from autopsy.

Results: This severe and unusual disease was observed in 5 patients, 4 men and 1 woman, with an average age of 29 years (+ - 9.6 years). Four of them came from the southern region of Honduras. All the cases were confirmed by serum detection of leptospira IgM antibodies. Fever and dysnea were present in 100%, cough in 80%, and pleuritic and lumbar pain in 60% of the cases. Only 2 out of 5 cases presented with hemoptysis. None presented renal failure or significant jaundice. All the cases required mechanical ventilation. Three patients died. Postmortem histopathology studies did show spirochetes in renal tubules.

Conclusion: More males were observed with this infection, the majority were located in the same geographic region. Despite the extreme gravity of the cases, none developed Weil's typical disease, but all were presented with respiratory failure. The survivors were the two last patients, because high suspicion index that allowed specific antibiotic treatment and early ventilatory support. Pulmonary leptospirosis should be considered as an emerging disease in Honduras, which requires further epidemiological surveillance and early medical attention.

21.018 Aerial dissemination of *Clostridium difficile* spores inside and outside a pig farm

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Background: *Clostridium difficile* PCR ribotype 078 is the dominant ribotype in pigs and is the third most common found ribotype in humans with *C. difficile* infection. Pigs may be a reservoir for human infection with this ribotype, however zoonotic transmission routes have not been established.

A pilot study was conducted at a farrow-to-finish farm, known to have a high prevalence of *C. difficile* 078, to determine whether airborne dissemination of spores inside and outside the farm could play a role in transmission of *C. difficile*.

Methods and Materials: Air samples were taken using a MB1 Microbio Air Sampler (Parrett Technical Developments) over a period of 4 weeks. A continuous airflow of 100L/min air was directed upon *C. difficile* agar plates (BioMérieux) for 5 minutes. Samples were taken in the wards, ventilation system and outside the farm. All plates were anaerobically incubated for 48 hours at 37°C. Suspected colonies of *C. difficile* were transported to the Leiden University Medical Centre where additional identification tests and PCR ribotyping were performed.

Results: Preliminary results reveal that the highest numbers of spores can be found at the farrowing ward with piglets of 1-2 weeks old, while the numbers of spores decrease until weaning age of the piglets is reached. No spores were detected at the weaned pig wards, however at the boar ward and sow ward spores were present.

Movement of weaned pigs from the farrowing ward to the weaned pigs ward led to a 15-fold increase in the number of spores compared to the sample taken directly before at the same location. Spores were present in the air directly outside the ventilation exits and at 20 meters distant of these exits, however, at a distance of 40 and 80 meters no spores were found.

Conclusion: These preliminary results indicate that *C. difficile* spores are disseminated outside the pig farm by ventilation. However, it is unclear how these spores are diffused once in the outside air and what role this dissemination plays in the possible zoonotic transmission. Further research is needed to determine the significance of the aerial dissemination of *C. difficile* spores in the outside environment.

21.019 Excess early mortality in patients starting antiretroviral therapy in Georgia

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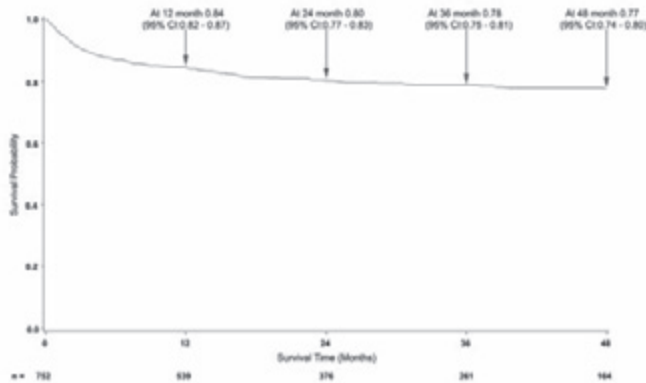
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Background: Introduction of antiretroviral therapy (ART) in mid 1990s resulted in dramatic reduction in HIV-related morbidity and mortality. ART is actively being rolled-out in developing countries. Since 2004 Georgia achieved universal access to free antiretroviral therapy (ART). The objective of this study was to evaluate outcomes of Georgian ART program.

Methods and Materials: A retrospective cohort study was conducted to evaluate the outcomes of Georgia's ART program. The study included 752 adult patients enrolled in the ART program from 2004 through 2009. Data were obtained from the National HIV/AIDS electronic database, operated by IDACIRC. Information on demographic, epidemiological, clinical and laboratory data were extracted from the database. Kaplan-Meier product-limit estimator method was used to assess probability of survival. Predictors of mortality were evaluated in multivariate Cox proportional hazards model.

Results: Of 752 adult patients, 76% were men and nearly 60% were injection drug users (IDU). The median age was 37. 59% of patients had a history of an AIDS-defining illness and 53% were co-infected with HCV. The median baseline CD4 cell count was 141 cells/mm³ and with approximately one third of patients having a CD4 cell count less than 100 cells/mm³. Median viral load was 5.4 log₁₀ copies/ml. During follow-up 152 (20%) patients died, with the majority of deaths occurring within 12 months of ART initiation. In multivariate analysis the following baseline factors were associated with death: male gender (Hazard ratio [HR] 1.96, 95% CI 1.19 – 3.24), CD4 cell count <100 cells/mm³ (HR 2.06, 95% CI 1.48 – 2.87), history of an AIDS-defining illness (HR 2.01, 95% CI 1.36 – 2.96), cirrhosis (HR 1.95, 95% CI 1.36 – 2.81). The leading causes of death were tuberculosis (22%) and end-stage liver disease (19%)



Kaplan-Meier Probability of Survival

Conclusion: Mortality was associated with advanced immunodeficiency or the presence of incurable disease at baseline indicating contribution of late HIV diagnosis. Mortality among HIV patients could be substantially reduced by improving earlier diagnosis and initiation of care. Efforts should be made to address intersecting HIV/TB and HIV/HCV epidemics.

Results: In total 307 individuals from 9 villages were included. WNF IgG positivity was detected in 77 individuals (25%) by ELISA, and 73 out of 77 ELISA positive samples were confirmed by IFA. Overall WNF IgG positivity was 24% by IFA. The titration of the sera was found to be > 1/200 in 57 individuals (78%). The avidity test was found to be <40% in only one of the seropositive individuals. None of the individuals had the history of encephalitis, but the history of fever, headache and flu-like illness were more common among the WNFV positive individuals. In univariate analysis, WNFV seropositivity was found to be significantly associated with age >50, high risk occupations for exposure to the mosquitoes, and the history of malaria. In multivariate analysis, age >50 (OR: 4.3, CI: 2.37-7.93) high risk occupations for exposure to the mosquitoes (OR: 1.9, CI: 1.06-3.62), living in better conditions (OR: 0.6, CI: 0.13-2.99) and the history of malaria (OR 2.1, CI 1.23-3.85) were found to be associated with WNFV seropositivity.

Conclusion: High WNFV seropositivity (24%) was detected in Mesopotamia region of Turkey. According to avidity test, all the individuals except one acquired the infection in the past. The physicians in the region should be aware of the risk of WNFV infection, and should be alert to detect the clinical cases. An active health education program should be implemented to raise awareness about the disease in the region.

21.021 **Detection of Clostridium difficile toxins in stools of patients reporting in a tertiary care hospital of North India**

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Background: *Clostridium difficile* associated diarrhea (CDAD) has received medical limelight due to the rising morbidity and mortality. It is the major cause of nosocomial and community related antibiotic associated diarrhea, colitis and pseudomembranous colitis. *C. difficile* produces two potent toxins A and B, responsible for the pathogenesis of the disease. We prospectively studied the clinical and demographic profile of patients suspected to have CDAD.

Methods and Materials: One thousand and sixty five fecal specimens from hospitalized patients or those reporting to the hospital for various ailments and suspected to have a *C. difficile* etiology were investigated for *C. difficile* toxins using commercial enzyme linked immunosorbent assay. The clinical and demographic details of the patients were also recorded in pre-printed performa.

Results: The patient population from whom stool samples were received comprised of 679 males and 386 females. The age range of the patients was 18 days to 87 years. Among these, 853 were on antibiotics, 351 had abdominal pain, and 412 had fever. During the time of testing, 352 passed watery stool, 495 semi-solid and 218 solid stool. Additionally, blood was present in the stool of 221 patients. *C. difficile* toxins were detected in the stools of 170 (15.9%) patients, among whom 12 were below 2 years and 15 above 65 years. Detection of *C. difficile* toxins correlated well with the clinical features and medical history of the patients.

Conclusion: *C. difficile* infection is prevalent among the patients attending our tertiary care hospital. Detection of *C. difficile* toxins is a valuable asset for laboratory diagnosis of CDAD, correlating well with the clinical features of the patients.

21.022 **Prevalence of Hepatitis B and C among HIV Positive Patients in Georgia and It's Associated Risk Factors**

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Background: HIV is one of the most serious health care problems in the world. Base on World Health Organization (WHO) at the end of 2007 approximately 33.2 mln people are infected with HIV. The aim of the study was to determine the prevalence of Hepatitis B and C co-infection among HIV positive patients, to identify most relevant risk factors of co-infection and develop preventive interventions.

21.020 **Emerging West Nile Fever Infection in Mesopotomia region of Turkey**

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Background: West Nile Fever (WNF) is now a global threat, but its epidemiology is not well known in Turkey. We aimed to describe the serological prevalence in a region where the WNF was studied 35 years ago, and suspected cases were reported previously.

Methods and Materials: A serosurvey was conducted based on suspected cases in April 2009 in Mesopotomia region of Turkey. The study population was from the villages, which were located throughout the Zergan river. All the sera were tested by ELISA (Euroimmune™), and the positive samples were tested by IFA (Euroimmune™) for confirmation. The avidity testing and titration of the seropositive samples were performed.



Methods and Materials: Study participants were recruited from Tbilisi IDACIRC Voluntary Counseling and Testing (VCT) unit. HIV positive diagnoses was based on detection of HIV antibodies by ELISA method (Vironostica HIV Uni-Form II Ag/Ab, bioMerieux, Netherlands) and confirmed by Western Blot method using HIV BLOT 2.2 Western Blot Assay. By research protocol, patients, 18 years and older and were identified as HIV positives, were asked participate in the study.

Results: Prevalence of Hepatitis C among HIV positive patients is high. Almost half (48.57%) HIV positive patients are co-infected with Hepatitis C. Men were more likely to be co-infected with Hepatitis C compare women (60.80% and 18% accordingly). Major risk factor of male co-infection was related to drug use, needle and injection equipment sharing. Prevalence of Hepatitis C among injecting drug users was (73.40%). Drug users had 3.25 times more risk (PR 3.25; 95%CI; CL – 1.89-5.26; $p < 0.01$) to be infected with Hepatitis C compare non IDUs. Prevalence of being infected with Hepatitis B (Anti-HBc) among HIV positives was 43.42% (76/175) and the prevalence of Chronic Hepatitis B (HBsAg positive) was 6.86% (12/175). Prevalence rate of HBsAg among IDUs was 8.51% and among non IDU participants 5.26%.

Triple infection (HIV, Hepatitis C and chronic form of Hepatitis B-HBsAg) was determined among 9 patients (5.14%). Infections were significantly associated with injection drug use (88.88%) and mostly were related to share of needles/syringes and other injecting medical equipment.

Conclusion: High risk behavior among HIV positive participants mostly related to drug use and unprotected sex with non regular partners. Other risk factors for Hepatitis transmission were associated with invasive medical manipulations, blood transfusion, surgery, abortions and etc.

21.023 High seroprevalence, norms, social network and HIV related behaviours among injection drug users (IDUs) in Faisalabad, Pakistan

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Background: To estimate the seroprevalence and knowledge of HIV infection and to determine the high risk behaviours among Injection Drug Users in Faisalabad, Pakistan.

Methods and Materials: In year 2009, specific demographic and behavioural characteristics of 80 male Injection Drug Users from 8 drug user sites of the city were determined. A pretested structured questionnaire was used for this purpose. Anti-HIV antibodies were detected by 3rd generation ELISA method.

Results: A total of 9 (11.25%) out of 80 IDUs were HIV seropositive. Data analysis revealed that 67% of IDUs had knowledge about the disease, its modes of transmission and preventive measures. HIV risk injection behaviours included: group injecting (92.5%) and sharing of syringes and needles (61.25%) which were significantly associated with seropositivity of HIV infection. Various risky sexual practices included contact with Commercial Sex Workers (11.1%), homosexuality (22.2%). Use of condom during sex was low (16.25%). There were also reports of trading sex for drugs or money.

Conclusion: The HIV disease burden is extremely high and can play a significant role in transmitting the infection to other vulnerable groups. Extremely High HIV disease burden and risk practices among IDUs signal the potential for future transmission of infection to general public as well as to other vulnerable groups across Pakistan. We recommend HIV prevention programs encompassing health education and health promotion strategies based on harm reduction techniques be used for injection drug users.

21.024 Prevalence and risk factors for human hydatidosis and canine echinococcosis in rural areas of the Limarí province, Chile

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Background: Hydatidosis is a zoonotic parasitic disease of worldwide distribution, transmitted by *Echinococcus granulosus* (Eg). In the life cycle of this parasite, the final guests are mostly dogs, which excrete eggs into the environment through its feces. The herbivores are intermediate hosts and get infected by feeding on contaminated vegetation. They develop a larval stage in various organs, which is called cyst hydatidosis. Humans become infected when contacted by accident with the eggs excreted by dogs. Although hydatidosis is hyperendemic in Chile no studies have been carried out to determine risk factors for both hydatidosis in humans and echinococcosis in dogs at the household level. This study determines the prevalence and risk factors for hydatidosis and echinococcosis in rural areas of the Limarí province in northern Chile.

Methods and Materials: From August to November 2009 a cross-sectional study was conducted using a stratified sampling design depending on the number of villages in each of the five districts of the province, using the software WinEpiScope for sample size calculation. In each selected village a maximum of 10 households were sampled where a questionnaire was applied for assessing risk factors. Blood and faecal samples of an adult and a dog were taken at the household. To assess seropositivity to Eg in humans a commercial Elisa followed by a Western-blot test were applied. To determine copropositivity in dogs a coproantigen Elisa test was carried out. Logistic regressions were used to assess risk factors for human seropositivity and dog copropositivity to Eg.

Results: Overall 393 questionnaires were carried out and 403 blood and 393 fecal samples taken. A prevalence of 2.5% of human hydatidosis was found, and the only risk factor was the high contact with dogs. The prevalence of echinococcosis was 22% and higher probabilities of detecting Eg coproantigens were found in non-breed dogs that were feed with uncooked meat from animals slaughtered at home.

Conclusion: Hydatidosis is highly prevalent (2.5% in humans and 22% in dogs) in Limarí province. A reduction of human-dogs contacts is suggested for reducing disease prevalence.

21.025 Molecular epidemiological tracing of HIV-1 cases in Georgia

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Background: Injection drug use (IDU) still remains the main mode of HIV-1 transmission in Georgia accounting for 58% of total reported HIV cases but the incidence of sexual transmission of HIV-1 increases steadily over time. Less than 19% of total HIV/AIDS patients diagnosed in 2000 were infected heterosexually. By 2010 this amount increased up to 36%. IDUs can potentially serve as a bridge between a high-risk group and a lower-risk population, such as heterosexually active adults that constitute the second HIV-infected group in Georgia. The objective of this study was to investigate molecular epidemiology of HIV-1 transmission events between heterosexual couples.

Methods and Materials: The study included 30 HIV-1 positive persons representing 15 epidemiologically linked transmission events. Viral RNA was extracted from plasma samples using the QIAamp Viral RNA kit.



Sequence data was obtained from *pol* region using TruGene HIV-1 Genotyping Kit. Reference sequences were obtained from the Los Alamos National Laboratory HIV Sequence Database (<http://hiv-web.lanl.gov>). Multiple alignments were created with CLUSTAL W program. Phylogenetic relationships were assessed using Neighbor Joining method with Kimura two-parameter and reliability estimated from 1000 bootstrap replicates.

Results: Of 15 transmission pairs, HIV infection among all women was attributed to heterosexual transmission from their partners. Nine (60%) males were infected through IDU. Sequences isolated from 11 pairs were subtype A, three couples were infected with subtype B and one couple with subtype G viruses. Phylogenetic analysis confirmed the existing epidemiological link in 11 pairs (figure). Sequences from 10 couples (P1-P3, P5-P11) segregated together with bootstrap values ranging from 73% to 100%.

Conclusion: The molecular analysis helped us to establish linkage between transmission pairs. Given that the HIV epidemic growth in Georgia is relatively slow and prevalence of HIV infection is still low (0.05%) identifying and management of target groups for prevention intervention will be the key strategy for holding back the HIV epidemic in our country.

21.026 Influence of mother HIV and/or syphilis infection on the outcome of newborns

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Background: Sexually transmitted diseases (STDs) during pregnancy pose a major risk to the fetus due to vertical transmission. Congenital disease still represents a significant public health problem worldwide, particularly in developing countries.

Methods and Materials: A retrospective investigation was performed comprising all pregnant women with HIV and/or syphilis infections admitted at the central hospital of two Western Cities of Venezuela, during January 2007–September 2010; pregnant women without STDs served as control group. Epidemiological characteristics were reported, anthropometrical variables in newborns were considered. Statistical significance was defined as $p < 0.05$. Statistical analyses were performed on SPSS v.17®.

Results: 76 pregnant HIV patients and 77 patients with syphilis infection were identified, three of them being coinfected. 87 pregnant women without STD served as controls. Mean age of infected mothers (HIV/syphilis) was 26 years (range 14–42 yrs) with a mean of 3 pregnancies (range 1–12). In the control group, pregnancies of 38±1 weeks were observed; newborns had a mean birth weight of 3,220±524 and a mean height of 51±3cm. In HIV infected patients, mean gestation was 36 weeks (range 26–41 weeks). Mean birth weight of newborns was 2,829±686 g (range 510–3,900 g); 22,6% were low birth weight newborns; mean birth height was 49±4 cm (range 30–56). In syphilis infected patients, mean gestation was 37 weeks (range 22–41 weeks). Mean birth weight of newborns was 3,159±649 g (range 700–4,240 g); 11,5% were low birth weight newborns, mean birth height was 51±4 cm (range 33–59 cm).

Maternal VDRL titers were strongly associated with birth weight; higher mother VDRL titers correlated with lower birth weight. Cephalic, thoracic and abdominal circumference did not show considerable differences between groups.

Conclusion: STDs cause considerable morbidity in women during the gestational period. Congenital and perinatal infection of the newborn, miscarriage and low birth weight have been described. In this study, both HIV and syphilis infections resulted in lower birth weight, particularly in newborns from HIV infected patients. Treatment of the etiologic agent is considered effective for prevention of vertical transmission and is recommended for STDs.

21.027 Super early viral response and IL 28 B genotype as the strong predictor for SVR for HCV Genotype 1 patients

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Background: Single nucleotide polymorphism (rs12979860) near IL28B gene has been reported as a strong predictor for more favorable response to interferon therapy. We investigated the roles of polymorphisms rs12979860 on the super early virologic response among genotype 1 patients on interferon and ribavirin therapy.

Methods and Materials: SNP rs12979860 and its role on rapid viral load decline and SVR rates was studied among 102 chronic hepatitis C patients infected with HCV genotype 1 and moderate (F2-F3) liver fibrosis. HCV RNA was measured by real time PCR with the detection limit of 25 lu/ml. HCV viral load was measured at baseline, 3, 24 and 72 hours after initial interferon injection and at 1, 2, 4, and 12 weeks accordingly. Liver fibrosis was evaluated by transient elastography. IL28B genotyping was performed with the ABI SNP genotyping kit.

Results: SNP rs12979860 genotypes distribution was as follows C/C (39%), C/T (40%), T/T (22 %). SVR rates among different C/C, C/T and T/T genotypes were 70%, 35% and 22% respectively. The mean baseline viral load among C/C group (105 lu/ml) was found to be lower than among C/T (>106) or T/T (>106) group. Furthermore, rapid viral decline at week one after initial interferon injection was strongly associated with C/C allele and therefore, high SVR rates versus C/T and T/T groups.

Conclusion: Determination of IL 28 B genotypes along with super early viral decline at week one can be the earliest prognostic marker for SVR for this difficult-to-treat population.

21.028 Is there a need to do West Nile surveillance in Asia?

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Background: In New York City in 1999, mysterious deaths of crows preceded an unprecedented West Nile Virus (WNV) outbreak and resulted in a huge economic burden. Since 1999, WNV has swept across USA and most recently to its northern neighbours. Outside of the Americas, recent outbreaks of WNV have been reported in Romania, Israel, Italy and Spain. As migratory birds are known to be important in the movement of WNV, a strong WNV surveillance network has been set up in Europe and USA to look at these groups of birds.

With Europe and USA being the forefronters in WNV research, very little is known about WNV in Asia.

Methods and Materials: A comprehensive literature search on WNV and Asia were performed.

Results: Amongst the Asian countries, WNV was only reported in India and an isolate (KUNMP502-66) of Kunjin virus (KUN) from Sarawak, Malaysia in *Culex Pseudovishnui* in 1966. KUN is otherwise geographically distinct to Australia. As many of the *Culex* species incriminated in WNV transmission are well distributed in many parts of Asia, there is a pressing need to find out the prevalence, if any, of WNV in Asia.

Conclusion: Judging from the dearth of information regarding WNV in Asia, there appears to be a lack of concern in WNV in this region. Can this apathy be interpreted as confidence that the virus is absent, or is it because the presence of other flaviviruses overwhelmed all efforts and overshadowed any desire to look for WNV? Japanese Encephalitis virus (JEV) and Dengue virus (DENV) are endemic in this region and diagnostically serologically cross reactive. Singapore lies on the East Asian/Australasian flyway, and serves as a major pit stop for migratory birds. This could be a risk area, and there is an urgent need for a



surveillance system to be in place for WNV monitoring in birds, as well vectors. However, data collected from just one country is not sufficient to elucidate the presence and distribution of WNV in Asia. Countries that have existing avian influenza surveillance programmes can use the same system for WNV surveillance and perhaps a regional surveillance programme can be set up for such purposes

21.029 Retrospective analysis of suspected rabies cases reported in Dodoma Region, Tanzania

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Background: In humans, rabies is almost invariably fatal once clinical signs occur. Rabies vaccine has an high efficacy when correctly and completely administered. The aim of the study is to determine the incidence of humans being bitten by rabies-suspected animals and the victims' adherence to post-exposure prophylaxis (PEP) in the Dodoma Region.

Methods and Materials: Data were collected from the regional records of animal bites in the period 2008-09. Adherence to PEP was calculated in terms of doses received and rabies awareness in terms of time between the bite and hospital attendance.

Results: A total of 3629 bite injuries were reported at the Regional Health Officer. Of these, 2626 (72.3%) were from suspected rabid animals. People <18 years old constituted the 61.7% of the total number of cases and <5 years old were involved in the 20% of cases. Dogs were the highest proportion of suspected animals (96.1%). As expected the majority of the victims (74.6%) were from rural areas with a annual incidence of 50 cases per 100.000. The majority (88.2%) of the cases seek medical care in a week after the bite. To all suspected cases was offered the human diploid-cell vaccine (H DCV). Only the 42.6% completed the vaccine schedule with an increase in the compliance in 2009 compared with 2008 (p<.01) and with no difference in between rural and urban areas. The 7.2 % of the total cases didn't receive any vaccine dose. No rabies cases were reported.

Conclusion: The demographic results are in accordance with the epidemiology of rabies. There was not much delay in seeking medical care proving a good awareness and education of the population. Conversely, the compliance to the vaccination is still low (42.6%) even if there was an increase in 2009. The lack of compliance is mostly related to the lack of counseling and to the unavailability of the vaccine and to the costs of transportation to return for the scheduled doses. Animal and human vaccine coverage has to be always followed by a proper education and awareness campaign of the covered population.

21.030 Pathogen inactivation of blood components for prevention of transfusion-transmitted emerging infectious diseases: The INTERCEPT blood system

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Background: Pathogens continuously emerge and reemerge around the world, impacting transfusion safety as local blood donor populations are exposed to each agent. Conventional measures to assure blood safety, such as donor deferrals and testing, are reactive strategies that depend on lengthy studies to identify the pathogen and to develop and validate appropriately sensitive and specific assays. Pathogen inactivation offers a proactive approach to help protect transfusion recipients from emerging pathogens, and has been successfully applied to safeguard plasma-derived proteins for many years. The INTERCEPT Blood System for platelets and plasma utilizes amotosalen HCl and UVA light to crosslink DNA and RNA, inactivating blood-borne pathogens. Over 600,000 treated units have been safely transfused in Europe, CIS and the Middle East,

and the system is used by over 60 blood centers in 15 countries. A similar treatment system for red blood cells is under development.

Previous studies have shown inactivation of high levels of a broad spectrum of pathogens, including those for which blood is already routinely tested: HIV-1/2, HBV, HCV, HTLV-I/II, CMV and *Treponema pallidum*. This study evaluates the efficacy of the INTERCEPT system against a number of emerging pathogens in platelets and plasma.

Methods and Materials: Platelet and plasma units were inoculated to a final concentration of ~106 organisms/mL whenever possible, and treated with 150 µM amotosalen and 3.0 J/cm² UVA. Samples were taken before illumination to determine the input titer and after illumination to detect residual viable organism. These samples were tested for viable organisms using cell culture or animal infectivity. Inactivation was expressed as log-reduction.

Results: High titers of emerging viruses (chikungunya, West Nile, H5N1 influenza, SARS, vaccinia, lymphocytic choriomeningitis and XMRV/MLV-related viruses), parasites (*Plasmodium*, *Trypanosoma*, *Babesia* and *Leishmania*) and *Borrelia* were inactivated to or below the limit of detection by treatment with the INTERCEPT process in platelets and/or plasma.

Organism	Platelets (Log ₁₀ Reduction)	Plasma (Log ₁₀ Reduction)
Chikungunya virus	>6.4	≥7.6
West Nile virus	>6.0	≥6.8
H5N1 influenza	>5.9	>5.7
SARS Co-V	>6.2	≥5.5
Vaccinia	>5.2	-
Lymphocytic choriomeningitis	-	>5.6
XMRV/MLV-related viruses	>4.0	-
<i>Plasmodium</i>	≥6.0	≥6.9
<i>Trypanosoma</i>	>5.3	>5.0
<i>Babesia</i>	>5.3	>5.3
<i>Leishmania mexicana</i>	>5.0	-
<i>Borrelia</i>	>6.8	>10.6

"-" = not tested

Table 1. Loss of infectivity following INTERCEPT treatment.

Conclusion: The ability to prevent infectivity of these emerging and reemerging pathogens in platelets and plasma makes the INTERCEPT Blood System a potentially safe and effective defense strategy against current and future pathogens in the blood supply.

21.031 Assessment of liver fibrosis/cirrhosis using Fibroscan and FibroTest/FibroMax in patients with chronic HBV and HCV infection in Georgia

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Background: Prevalence of hepatitis B and C infections among healthy general population in Georgia is alarming and equals to 6.7% and 11.4 % respectively. High rates of these infections lead to the end stage liver disease and increased liver related mortality. Therefore, it's of interest to study the role of non invasive liver fibrosis tests versus liver biopsy.

Among various non-invasive tools transient elastometry using FibroScan and FibroTest/FibroMax are believed to be the most reliable methods for assessment of liver fibrosis as well as they are easy to perform and therefore allow regular follow-up of the course of liver fibrosis.



Methods and Materials: The aim of the study was to evaluate liver fibrosis/cirrhosis using transient elastometry and FibroTest/FibroMax in patients with chronic HCV and HBV infection to compare the results of Fibroscan and FibroTest/Max.

Overall 504 patients infected with chronic HCV (373) and HBV (131) infections were included in the study. After confirmation of HCV and HBV infections, viral load test was performed. Transient elastometry and FibroTest/Max were performed at one and the same day to assess liver fibrosis stage.

Results: Among patients with chronic HCV or HBV infection fibrosis stages measured by Fibroscan and Fibrotest/FibroMax were concordant in 253 (67.8%) and 88 (67.1%) cases, respectively. Discordance in one degree of fibrosis stage was found in 69 (18.5%) patients with chronic HCV infection and in 29 (22.1%) patients with chronic HBV infection. Discordance in more than one degree of fibrosis stage was found in 51 (13.6%) and 14 (10.7%) cases, respectively.

Discordances were seen in those with elevated ALT and AST (4-5 times of the upper limit of the norm), in obese patients (BMI>25) and in those with Steatosis (S3-S4), as well as in cases of extrahepatic cholestasis or chronic hemolysis.

Conclusion: The high rates of concordant results among chronic HCV and HBV infected patients when using Fibroscan and Fibrotest/FibroMax justifies the high sensitivity and specificity of these methods and therefore liver biopsy can be avoided in this group of patients

21.032 Performance of four rapid diagnostic tests for the diagnosis of falciparum and non-falciparum malaria in endemic areas of Gondar region, Northern Ethiopia

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Background: Malaria remains a major public health problem in Ethiopia, despite decades of a sustained national control program. One of the major obstacles to this control program is the lack of accurate and rapid diagnostic service in most resource poor settings where malaria is endemic. Very recently, efforts have been made to develop and implement various formats of malaria RDTs.

Methods and Materials: In view of this, the performance of the OptiMAL-IT, Paracheck-Pf, CareStart™ malaria pLDH 4 line test (CareStart 4 line) and CareStart™ malaria pLDH/HRP II combo test (CareStart 3 line) were investigated in comparison with microscopic examination of thick and thin blood film in malaria endemic areas of Gondar region. In order to evaluate these assays, the sensitivity, specificity, PPV and NPV values of each RDT were calculated taking microscopy results as the gold standard in a total of 588 febrile patients.

Results: Paracheck-Pf was the most sensitive (100%) assay for the diagnosis of *P. falciparum* in comparison with OptiMAL-IT (98.1%), CareStart 4 line (98.1%) and CareStart 3 line (96.2%). However, OptiMAL-IT was the most specific (99.1%) as compared to Paracheck-Pf (97.9%), CareStart 3 line (96.4%) and CareStart 4 line (93.8%) for falciparum malaria diagnosis. For the diagnosis of *P. vivax*, both CareStart™ assays had better sensitivity (94.4% for CareStart 4 line and 94.2% for CareStart 3 line) as compared to OptiMAL-IT 88.2%. But OptiMAL-IT gave the higher specificity (99.8%) than CareStart 4 line (98.1%) and CareStart 3 line (97.9%).

Conclusion: Although microscopy remains the gold standard for malaria diagnosis, OptiMAL-IT, Paracheck-Pf, CareStart 3 line and CareStart 4 line may prove a useful screening for malaria control in Ethiopia where microscopic examination is not in place. Finally, further studies on RDT performance is recommended to be undertaken in multisite study fields, in monitoring drug therapy and with respect to molecular analysis.

21.033 Prognostic value of IL28B for spontaneous clearance from HCV infection

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Background: The aim of the study was to assess the prognostic value of host genetic factor IL28B by identifying the most favorable genotypes for spontaneous clearance from HCV infection among HCV mono-infected and HIV/HCV co-infected patients.

Methods and Materials: We retrospectively analyzed 129 acute HCV infected patients who spontaneously cleared HCV virus. Patients age varied from 25–45. Among them 39 were female and 90 male.

Among total 129 patients, 65 were with HCV mono and 59 HCV/HIV co-infected. All patients were anti-HCV (+) positive, HCV RNA (-) negative and HCV treatment naive.

We studied the prevalence of IL28B genotypes namely (single nucleotide polymorphism rs12979860) and their correlation with HCV disease recovery.

Anti-HCV antibodies were detected by ELISA method, HCV RNA - by real time PCR (COBAS TaqMan) and IL28B genotyping by the ABI SNP genotyping assay. HIV infection was confirmed by Western Blot method.

Results: The distribution of IL28B genotypes among 65 HCV mono-infected patients who cleared HCV virus were C/C-39, C/T- 17 and T/T-9 patients respectively. Spontaneous clearance of HCV virus was observed among 60%, 26% and 14% in patients with C/C, C/T and T/T genotypes respectively.

The distribution of IL28B genotypes among 59 HCV mono-infected patients who cleared HCV virus were C/C-34, C/T-18 and T/T-7 patients respectively. The scenario of spontaneous clearance of HCV virus was similar to the mono infected group namely 58%, 30% and 12% respectively.

Conclusion: IL28B is significant prognostic host genetic factor for patient with HCV infection. IL28B C/C genotype is a favorable genotype and is strongly associated with HCV spontaneous clearance from HCV infection among both HCV mono-infected and HIV/HCV co-infected patients.

21.034 Correlation between the result of leishmanin skin test and clinical forms of cutaneous leishmaniasis and species of parasite

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Background: Cutaneous Leishmaniasis (CL) is a common parasitic skin disease which is endemic in many parts of Iran, including Khorasan. Both Anthroponotic Cutaneous Leishmaniasis (ACL) & Zoonotic Cutaneous Leishmaniasis (ZCL) have been reported from Mashhad. Leishmanin Skin Test (LST) is used for clinical diagnosis of previous infection due to *Leishmania tropica*, *Leishmania major*. The aim of this study is to determine the correlation between the result of LST with the clinical form of CL lesion and species of causative agent in patients referred to the Parasitology laboratory, Imam Reza hospital during 2007-2008.

Methods and Materials: This study was under taken over a 12 month period. Following confirmation of diagnosis of CL in 50 patients who obtained positive result by direct smear test, their demographic, clinical and laboratory information were recorded. LST was performed for each patient. PCR (polymerase chain reaction) was used to determine the species of parasite. The result of LST read after 24, 48 and 72 hours. The collected data were statistically analyzed using SPSS version 17.5.



Results: Among 50 persons with CL, 60% were females, 40% were male. *Leishmania major* was isolated from 50% of females and 50% of males. *Leishmania tropica* isolated from the lesion of 66.7% and 33.3% of females and males respectively. Most of the patients were between 10-30 years old. 48% had dry ulcers and 46% had moist suppurative ulcers. The result of LST was positive in 30% & 12% of dry ulcers and moist ulcers respectively. Also the result of LST was positive in 19 patients that 15 individuals (30%) had ACL and 4 patients (8%) had ZCL.

Conclusion: There was a significant relationship between the clinical form of CL lesion and causative agent with the result of the LST; but no significant relationship was observed between causative agent and clinical form.

21.035 Unexpectedly high incidence of HTLV1 infection and atypical HPV genotypes detected in cervical smears from HIV positive and negative Kenyan women

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Background: Infection with the oncogenic retrovirus HTLV1 is endemic in some countries where it has been linked to a variety of pathologies. The incidence of this agent in Sub Saharan Africa and its ability to synergise with other common sexually transmitted viruses to induce disease is not known. In order to address this issue we have investigated the prevalence and potential association of HIV infection with HTLV1 and HPV in Kenyan women.

Methods and Materials: Liquid based cytology (LBC) samples were collected from HIV+ve (n = 113, 50% on HAART) and HIV-ve (n = 111) women attending Kenyatta National Hospital. This material was used to analyse; Pap stain cytology; HTLV1 DNA and RNA by TaqMan and endpoint PCR and PapilloCheck™ HPV genotyping.

Results: 31.0% of HIV +ve patients were HTLV1+ve; whereas this was only found in 11.7% of HIV -ve subjects (p=0.0001). Significantly, 43% of the HIV/HTLV1 +ve's expressed detectable HTLV1 mRNA as compared to 15% of the HIV-ve/HTLV1+ve samples (OR (95% CI) = 4.125). 30.0% of HIV +ve women had abnormal cervical cytology as compared to 6.3% in HIV -ves (p value= 0.01). However, there was no association between HTLV1 infection and abnormal cytology (p = 0.83). 55% of women were HPV+ve with the commonest types being 56 (19.0%)> 52 (16.5%)> 58 (14.9%)> 16 (12.4%)> 35 (10.7%)> 33 (9.9%)> 45 (3.3%)> 18 (2.5%)

Conclusion: The finding of 31% positive for HTLV1 DNA in HIV positive women is the highest rate of HTLV1 infection ever reported in an African country. In addition the positive association between detection of HTLV1 mRNA and HIV is novel. Given that HTLV1 is an established cause of diseases with fatal or disabling consequences, the apparent synergy with HIV is likely to have far-reaching public health implications. Moreover, the relative abundance of the different HPV genotypes detected was radically different from those found in other areas of the world. Since the current HPV vaccines are based on the latter, these observations could have fundamental implications for the implementation of such vaccines in African populations

21.036 Prevalence of tuberculosis in slaughter camels (*Camelus dromedaries*) based on lateral-flow technology (Camelid TB-STAT PAK™)

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Background: Tuberculosis (TB) in camels has been documented since the 19th century (Lingard, 1905; Leese, 1908; Littlewood, 1989). Diagnosis of TB in camels faces many difficulties (Wernery and Kaaden, 1995), with none of the standered available tests being able to detect the disease with some certainty. The intradermal tuberculin test, which

is the traditional diagnostic tool in cattle, appears to produce too high a non-specific reaction in camels. Schillinger (1987) reported false-positive result of the skin test in 10-20% of Australian camels. This form of diagnosis, (Lateral-flow technology) though not confirmatory, is still better than tuberculin test that has been found to be not as reliable in camels as it is in cattle (Wernery, et al., 2007). In Nigeria and indeed Africa, camels are increasingly gaining economic importance, especially in the northern part of Nigeria due to their increasing value as a source of meat, milk, hide and as draught animals (Abdullahi, 2006).

Methods and Materials: Five hundred clotted blood samples were centrifuged at 704 x g for 5-10 minutes. The resultant sera was transferred into clean labelled serum sample bottles and processed as described by the manufacturers.

Results: A total of 500 camels, consisting of 188 males and 312 females were tested for *Mycobacterium* infection. One hundred and thirteen (113) were positive with a prevalence rate of 22.6%. Forty five were males with a prevalence rate of 23.9 while 68 were females with a prevalence rate of 21.8%. (Table 1) The chi-square (x²) test was not statistically significant (P>0.05).

Conclusion: From this study, 22.6% prevalence rate of a sample of 500 slaughtered camels in Sahel part of northern Nigeria were found to be infected with TB. Transmission of this agent among other domesticated species is believed to be the most likely source of the infection since camels are traditionally herded together with other species of animals

21.037 Haiti in the time of cholera

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Background: *Vibrio cholerae* appeared on Hispanola for the first time in over 50 years following recent flooding. Bacterial genetic studies isolated the organism in river water. The nature of the diarrheal disease allows itself to spread in the environment. Cholera presents an ongoing public health threat due poor water and sewage systems and inaccurate biosurveillance.

Historically, Haitian media has not been a consistent source regarding domestic health events. This was particularly disrupted by the earthquake in January 2010. Two weeks after the earthquake, the MSP, PAHO and the CDC established a National Sentinel Site Surveillance system connecting 51 health centers in Haiti's 10 departments. The system was created to track the emergence of infectious diseases and injury.

Methods and Materials: The data is a compilation of open-source information, graphs and timelines, medical journals and epidemiological records.

Inconsistent generalizations of case count updates and healthcare capacity were placed on maps of Haiti.

Results: Since the earthquake, biosurveillance in Haiti has been the domain of international media led by the Dominican Republic, PAHO, the United Nations and other foreign agencies with a local presence. As a result, MSF quickly detected the index case on 20 October in the lower Artibonite region and immediately notified the MOH of the suspected outbreak. Cholera was confirmed within 48 hours through laboratory analysis.

Conclusion: Despite the early detection of the first human cases, the failure to initiate analysis of environmental reservoirs in crucial post natural disaster conditions and delayed implementation of a consistent reporting structure for timely cholera outbreak surveillance provided man-made opportunities for an epidemic. Conditions were exacerbated by Hurricane Tomas which touched ground in November 2010.

The appearance of cholera after decades of little disease activity should still be limited to a CFR of 1%. Recent events, including the devastating outbreak in Zimbabwe in 2008-2009 had CFRs as high as 50% due to crippled infrastructure, poor case management and inaccurate disease tracking. At the onset of the outbreak, Haiti's CFR reached 9%—an unacceptably high figure. The death toll is expected to increase due to the number of internally displaced people left homeless after the earthquake.

**21.038 HBV, HCV in the street children**

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Background: There are approximately one hundred million children spending their life in streets. Many countries are suffering from an individual relation the issue of street children despite possessing common properties, and by controlling this phenomenon each country will get in specific picture.

Methods and Materials: 203 street children were studied. These children were clinically examined by pediatrician and requested to answer the questionnaire (asking about their gender; age; birth place; educational status; the origin of the family; sleeping place; occupation, income and social security of parents; number of siblings; reasons for being in streets; period of living in the streets; street friends; means of earning money; substance use. In order to determine the existence of *Hepatitis B Virus* (HBV) and *Hepatitis C Virus* (HCV) infections, ELISA, PCR and RT-PCR methods were performed on serum samples.

Results: Among 203 street children studied in this research, 196 children were boys and 7 children were girls. 6 cases (3%) were HBsAg positive, 54 cases were HBs-Ab positive (26.6%) and 16 cases were HBe-Ab positive (8%). 7 cases (3.5%) were HCV Ab positive. All of the positive cases were boys. There were 3 Iranian and 3 Afghanian kids among HBsAg positive cases. In HCV Ab positive cases there were 5 Iranian and 1 Afghanian kids. 3 children did not have family, 6 children did not smoke and one of them was addicted to crack and had tattoo on his body. The average age of this group in three cases was 14+ and in four cases 14 < years. 4 cases were HBV PCR positive and 6 cases were HCV-RT-PCR positive. According to this results, additional laboratory examination for screening of acquired infectious disease such as *Hepatitis* seem to be necessary.

Conclusion: Although in this type of infection clinical symptom may appear a few months after exposure to the virus, it can be transmissible in this latent period.

21.039 Risk of complications and progression to death from diarrhea due to *C. difficile* infection compared with non-*C. difficile* diarrheaH.-W. Kuo¹, D. Schmid¹, C. Wenisch², F. Allerberger³¹Austrian Agency for Health and Food Safety, AGES, Vienna, Austria,Vienna, Austria, ²Kaiser-Franz-Josef-Spital Vienna, Vienna, Austria,³AGES, Vienna, Austria

Background: In the absence of an Austrian-wide surveillance system of *C. difficile* infection (CDI) the impact of this disease on the mortality of hospitalized patients in Austria is unknown. Therefore a hospital-based study was conducted to measure the risk of complications and of death from diarrhea due to CDI compared to diarrhea due to pathogens other than *C. difficile* (CD).

Methods and Materials: A prospective hospital-based cohort study was performed in a 1000-bed hospital in Vienna. Hospitalized patients with infectious diarrhea were consecutively included and assigned to the two comparison groups according to the results of laboratory testing of the stool samples. The study population included 90 CDI-diarrhea patients and 180 Non-CDI-diarrhea patients. The two groups were compared with regard to complications (including recurrent diarrhea, pseudomembranous colitis, colon perforation, toxic megacolon, pancolitis, septicemia, surgical intervention) and 30-day mortality. Data on patient characteristics and outcome were collected by reviewing medical charts and telephone interviews. The difference in age and duration of diarrhea was tested by using t-test. The crude relative risk (RR) of complications and 30-day mortality were calculated by using Chi-square test. A stratified analysis and a poisson regression model were applied to adjust the relative and attributable risk of complication and death for co-morbidity.

Results: Duration of diarrhea was longer in CDI study subjects compared to non-CDI study subjects (12.5 vs. 5.5 days; $p < 0.0001$). The risk of recurrent diarrhea was 7.5 times higher in CDI study subjects (95% CI: 2.56-21.9). There was no difference in the risk of other complications

found. The CDI study subjects were 2.5 (95% CI: 1.22-5.119) times more likely to die within 30 days after diarrhea onset (15/90; 16.9%) compared to Non-CDI study subjects (12/180; 6.9%). The stratified analysis by co-morbidity revealed among study subjects with moderate/severe co-morbidity a mortality fraction due to CDI of 62.8% (95%CI: 14.5%-83.8%).

Conclusion: Excluding CDI in hospitalized diarrhea patients with moderate/severe co-morbidity will prevent 62.8% of deaths in this patient group. Our findings underline the importance of applying evidence based measures to control the spread of *C. difficile* in health-care facilities.

21.040 Evaluation of neonatal tetanus surveillance system in Baluchistan, Pakistan, 2009A. Akbar mengal¹, M. A. Ali²¹Feltp-Pakistan, Balochistan, Balochistan, Pakistan, ²Feltp-Pakistan, Quetta, Balochistan, Pakistan

Background: Neonatal Tetanus (NNT), caused by a potent neurotoxin producing bacteria *Clostridium tetani*, poses substantial public health threat across the globe. With global mortality of approximately 6.7/1000 live births, the disease caused estimated 59,000 newborn deaths in 2008. The disease is targeted for elimination but despite 92% reduction since 1980s; 40 countries are yet to achieve this status. Pakistan reported 518 cases (65%) out of 797 NNT cases occurring in WHO Eastern Mediterranean Region (EMRO) during 2005. Under reporting however, is a major issue especially in province of Baluchistan with Infant Mortality of 130/1,000. We evaluated NNT surveillance done by Health Management & Information System (HMIS) and District Health Information System (DHIS) to recommend improvements.

Methods and Materials: The CDC's updated guidelines for evaluating public health surveillance system were used as tool. Data was collected through systematic literature review and focused interviews with key stakeholders. System was devised and graded as poor, average and good on system attributes.

Results: Despite average simplicity, acceptability and stability, both HMIS and DHIS had poor sensitivity (4.6%), flexibility, timeliness and representativeness. None was capable of detecting outbreaks. Collecting information on 118 indicators, HMIS had poor data quality. Predictive value was hard to assess as both systems used syndromic case definition without laboratory component. DHIS was launched recently in some districts and had experience limitations

Conclusion: Both HMIS and DHIS had serious limitations and did not meet the epidemiological needs of NNT surveillance and elimination. Considering public health significance of the illness, a disease specific and active surveillance system is proposed to improve case detection and evidence based decision making.

21.041 Incidence of cerebral edema in CNS infections among adults in Tirana population in AlbaniaA. Ndreu¹, E. Puca², E. Mingomataj³, G. Stroni², D. Kraja², I. Akshia⁴¹Intensive Care Unit, Service of Infective Diseases, University HospitalCenter, Tirana, Albania, ²Service of Infective Diseases, UniversityHospital Center, Tirana, Albania, ³Service of Immunology, UniversityHospital Center, Tirana, Albania, ⁴Statistics Department, University

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Background: Cerebral edema (CE) is the increase of intracranial pressure as a consequence of cerebral cellular hyperhydration during infections of central nervous system (CNS).

Objective: The study objective is the description of epidemiologic characteristics of diagnostic issues related to CE during infections of CNS in adults, and calculation of CE incidence in Tirana population in Albania.

Methods and Materials: This was a retrospective study of 58 patients (58% male and 42% female), hospitalized in 2005 in UHC after CE development and/or conscience alteration during CNS infections. Additional criteria were the age above 15 years old, and the residence needed to be in Tirana. Based also on Tirana population during 2005 (597040 people or 19.09% of Albania population), it was calculated the incidence of CNS infection-related CE.



Results: Medium age was 43.8 years old with $17.0 \pm$ SD. The most prevalent diagnosis among infections of CNS was bacterial meningitis 42 patients (72%), meningo-encephalitis 13 patients (22%), cerebral abscess 2 patients (4%), and meningitis after non-bacterial infections 1 patient (2%). The incidence of CNS infection-induced CE among adults in Tirana population was 5.9 cases on 100000 peoples, whereas the rate of CE after bacterial meningitis (as the most prevalent diagnosis) was 3.6 cases in 100000 people.

Conclusion: These data suggest that incidence rate of CE during CNS infections, and especially during bacterial meningitis among/ in Tirana adult population was comparable to the worldwide known average data. CE is more prevalent in bacterial meningitis than in other CNS infections.

21.042 Persistence of the influenza A(H1N1) pandemic virus in water and on non-porous surface

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Background: Influenza A virus survival in different environmental conditions is a key element for the implementation of hygiene and personal protection measures by health authorities. As it is dependent on virus isolates even within the same subtype, we studied the survival of the H1N1 pandemic (H1N1pdm) virus emerging in 2009 and the seasonal A/New Caledonia/20/99 (H1N1) virus strain, in water and on non porous surface.

Methods and Materials: Both viruses were subjected to various environmental parameters over time and tested for infectivity using a microtitre endpoint titration. Viruses were put in water at different temperatures and with different salinity levels, for at least 400 days. Watch glasses were used to mimic smooth surfaces. And genomic RNA concentration was also determined to evaluate the integrity of the viral genome.

Results: In water, at low and medium salinity levels and 4°C, H1N1pdm virus survived at least 200 days. The A/NewCaledonia/20/99 virus strain survived no more than 40 days at 35 parts per thousand (ppt) of salt suggesting that H1N1pdm strain is more stable than seasonal H1N1 virus in liquid environment. Increasing temperature and salinity had a strong negative effect on the survival of both viruses which remained infectious no more than 2 days at 35°C and 270 ppt of salt. On smooth nonporous surface, the H1N1pdm virus retained its infectivity for at least 6 days at 35°C and up to 66 days at 4°C.

Conclusion: The H1N1 viruses have thus the ability to persist in water and on glass surface for extended periods of time, even at 35°C. Additional experiments also suggest that external viral structures in direct contact with the environment are involved in this virus loss of infectivity.

21.043 Diversity of Rotavirus Strains in Diarrhea Children in Lagos, Nigeria

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Background: Group A rotavirus has been recognized as the major etiologic agent of severe diarrhea in children less than five years of age worldwide. A pentavalent vaccine (RotaTeq) has demonstrated very good safety trials in Latin America against the globally predominant serotypes G1-G4. However, the emergence of new genotypes that are not cross protective, together with possible reassortment of co-circulating strains of different genotypes, have made it crucial to conduct rotavirus surveillance in countries before, during and after vaccine introduction. A hospital based cross sectional study was conducted in Lagos, Nigeria to determine the genetic diversity of rotavirus, to ascertain if there are some unusual or new strains present which may not be covered by the existing vaccines prior to its introduction.

Methods and Materials: From August 2006 to June 2008, three hundred and two (302) faecal samples were obtained from diarrheic children on admission in four hospitals in Lagos, Nigeria. Stools were examined for presence of group A rotavirus antigen by monoclonal antibody enzyme immunoassay (EIA), while genotyping was by multiplex semi-nested RT-PCR.

Results: On the overall, 26% of samples yielded 6 rotavirus serotypes (G1, G2, G3, G4, G9, and G12). Serotypes G1 and G2 were the most prevalent (31%), followed by G3 (9%), G4 (5%) and G12 (2%). Mixed infections (G1+G2) and (G1+G3) were also detected.

Conclusion: This is the first report of G12 serotype in Nigeria. The genetic diversity of rotavirus strains in Nigeria implies that the existing vaccines may not be cross-protective.

21.044 Association of Neonatal Sepsis with Maternal Premature Rupture of the Membranes (PROM) in Our Area Since 2010

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Background: Preterm premature rupture of the membranes (PPROM) is one of the most common complications of the pregnancy. PPRM increases the risks of certain pregnancy complications, including: early sepsis in the neonate, infection in the uterus or baby. The aim of this prospective study was to determine the incidence of neonatal sepsis with maternal PROM and to determine the duration of PROM most likely associated with neonatal sepsis.

Methods and Materials: The study included 297 newborns that were born after PROM since 2010 and some of them hospitalized in the neonatology ward of Mousavi teaching hospital of Zanjan University of Medical Sciences. Neonatal data included wbc count, platelet count, blood culture, clinical signs of sepsis, use of antibiotics, the latency period, gestational age and 5-minute APGAR score. The influences of selected variables on the development of sepsis were analyzed.

Results: From total 148 cases of clinically sepsis diagnosis which have been performed during 2010, fifty-seven of neonates were immediately hospitalized at first day of their lives. Fifty percent (24 Cases) were related with their mothers' PROM delivery. Prolonged PROM (>36 hours) were detected in 21 cases. Fourteen and 10 of the neonates were female and male respectively.

Conclusion: The presence of membrane rupture before delivery was not associated with increased neonatal mortality in any gestational age group. The effects of a prolonged latency period were not consistent across gestational ages. Clinical neonatal sepsis was associated with time from PROM to delivery over 32 hours, caesarean section, parous women and gestational age between 34 and 36 weeks. Sepsis rates did not differ between those with recent or prolonged preterm PROM at any gestational age. Therefore antibiotics regimen should be considered for newborns with maternal PROM delivery as important predisposing factor to early neonatal sepsis.

21.045 Relationships of 7th pandemic *Vibrio cholerae* using genome wide single nucleotide polymorphisms and multilocus variable number tandem repeat analysis

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Background: *Vibrio cholerae* causes cholera which affects mainly developing regions which lack clean water supplies. To date, there have been seven pandemics. The current 7th cholera pandemic started in Indonesia in 1961 and spread to Africa in 1970 and Latin America in 1991.



Resolving the genetic relationships of the pandemic isolates is important in understanding the origins and development of the pandemic clone.

Methods and Materials: In this study, we used two molecular markers: genome-wide single nucleotide polymorphisms (SNPs) derived from published *V. cholerae* genomes, and Variable Number Tandem Repeats (VNTR), to type a collection of 71 pre-7th and 7th pandemic *V. cholerae* isolates.

Results: Typing of 30 SNPs resolved isolates into 11 SNP profiles which were separated into 6 phylogenetic groups. The SNP results show that Latin American isolates are much more closely related to African isolates than to Asian isolates, which is in contrast to the existing theory that cholera spread to Latin America from Asia. Multilocus VNTR analysis (MLVA) of 6 VNTR loci divided 63 isolates into 58 MLVA profiles. Complete VNTR data was unable to be obtained from 8 isolates. MLVA demonstrated higher discriminatory power than SNP typing. However the relationships derived from MLVA data is incongruent with SNP data.

Conclusion: The genome wide SNPs used in this study has shown that SNP typing is useful for determining the evolutionary relationships of a range of 7th pandemic *V. cholerae* isolates. Phylogenetic analysis of SNP profiles shows a stepwise evolution of the 7th pandemic and correlate closely with epidemiological data.

SNP typing shows that the Latin American isolates have identical SNP profiles to isolates from Africa, suggesting that Africa may be the origin of the 1991 outbreak rather than Asia. VNTRs were most useful in drawing relationships between closely related isolates such as those from the O139 Bengal group but were too variable to be used to draw conclusive relationships for this set of 7th pandemic isolates when compared to SNPs. We conclude that a combination of SNP and VNTR typing offer the best resolution to establish the evolutionary relationships and will be highly valuable for local and global surveillance of *V. cholerae*.

21.047 Molecular epidemiology hepatitis C in Belarus, prevalens of 1b and 3a genotypes

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Background: In territory of Belarus dominate 1b (53,8%) and 3a (28,8%) genotypes of a hepatitis C virus which approximately meet identical frequency in all regions of the country.

Methods and Materials: EIA, RT-PCR, sequencing (SeqScape, BioEdit, MEGA 4.1 software)

Results: In territory of Byelorussia in population of HCV-infected patients and among HCV+HIV-co-infected patients 1b (53,0 %) and 3a (27,1 %) genotypes are dominated. During too time in Grodno and the Grodno region 1a a genotype (40 %) is dominated. The distribution of HCV genotypes in Belarus corresponds to the data about prevalence of these genotypes in the western Europe, Russia, Estonia and Georgia. At the same time, it is necessary to notice that frequency of revealing 1b a genotype in Russia in 1997 was in 4 times above, than 3a a genotype. The similar data is received in Minsk and Vitebsk regions, where frequency of revealing HCV 1b a genotype in comparison with 3a genotype above in 2,8-3,7 times, than in other regions of the country. In group of patients with HCV a monoinfection dominate 1b (55.8 %) and 3a (26.6 %) virus genotypes. The similar picture is observed and in group HCV+HIV co-infection: 1b the genotype is revealed in 13 cases (40,6 %), 3a in 10 (31,3 %), 1a genotype is found out at 8 patients (25,0%). 2a HCV genotype is revealed only in 1 (3,1 %) of 32 investigated samples. In 2 cases of HCV+BFBco-infection have been revealed 1b and 2a genotypes. The average p-distances in groups of various HCV genotypes were 0,07, 0,06 and 0,06 for 1b, 1a and 3a genotypes, accordingly, that testifies about circulation same HCV isolates in the territory of republic throughout a long time.

The phylogenetic analysis of core/E1 HCV region, received in our researches and the data from GeneBank have shown that they don't form a new evolutionary branch and don't differ considerably from group of the genotypes circulating in other geographical regions.

Conclusion: The obtained data testifies to a real-life problem of hepatitis C in republic which is not only medical, but a social problem.

21.048 Prevalence of syphilis (STD) in healthy blood donors of Lahore, Pakistan

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Background: The widespread of sexually transmitted diseases has become the major public health concern in developing countries. Although syphilis transmission may occur through blood transfusion but there is insufficient information on syphilis in blood donors in Pakistan.

Methods and Materials: We determined the seroprevalence of syphilis among voluntary healthy blood donors in Lahore, Pakistan. The study was a hospital based cross sectional carried out at the blood bank of a private hospital, Lahore, Pakistan from August, 2010 to November, 2010. Seven hundred and seventy five voluntary blood donors were consecutively recruited and tested for syphilis using Architect Syphilis Chemiluminescence Assay (CLIA) for antibodies to *Treponema pallidum*. Written informed consent with biodata was taken from all the patients. All syphilis reactive patients were informed about results and referred to surveillance center.

Results: Out of the 775 voluntary blood donors screened, 757 donors (97.6%) were male while 18 (2.4%) were female. The mean age was 30 years. Only the male donors had syphilis. 11 donors (1.41%) were positive for syphilis. The situation could be worsen but sero-positivity among donors is attributed to pre-donation counselling in donor selection.

Conclusion: In conclusion, the seroprevalence of syphilis demands awareness of general population, strict screening among voluntary blood donors and STD's prevention programme at national level in Pakistan.

21.046 Impact and incidence of sputum smear positive tuberculosis on children in the era of ART attending Kanombe Military Hospital between January 2009–June 2010

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Background: Tuberculosis (TB) infection has markedly increased in the HIV era and TB is the most common opportunistic infection in HIV patients. However with ART the impact of TB is expected to be reduced.

Methods and Materials: We conducted a retrospective cohort study utilizing records of all patients on TB treatment at Kanombe Military Hospital in Kigali, Rwanda from January 2009 to June 2010. We abstracted demographic data, sputum acid fast bacilli (AFB) stain, and HIV serostatus. Data were analysed using STATA version 10.

Results: 452 TB patient records on treatment were reviewed male: female ratio was 2:1, median age 29 years (age range: 0.125 to 99 years). Pediatric TB (aged ≤18 years) accounted for 19.5% (88/452) with median age of 5.25 years (IQR: 1.2-12.5 years). Pediatric HIV/TB coinfection was 13/88 (14.8%) and 4.6% (4/88) who were sputum positive were adolescents.

Overall incidence of smear-positive PTB was 138/452 (30.5%) with HIV coinfection 30.9 % (44/138). Smear positive PTB was 108/266 (40.6%) and 30/186 (16.1%) in 2009 and 2010 respectively with an odds ratio (OR) of 0.28 (CI: 0.2-0.4) and p value of <0.001 while the HIV incidence was 98/266 (36.8%) in 2009 and 54/186 (29%) in 2010 OR: 0.7 (CI: 0.5-1.1) and p value of 0.22.

Risk factors for sputum smear positive TB were: being 8 -18 years, >18-25 years and >25-35 years OR: 0.125 (CI: 0.04-0.36), OR: 2.3 (CI: 1.32-4.0) and OR: 1.7 (CI 1.0-2.9) respectively with a p-values of <0.001, 0.003 and 0.035 respectively

Conclusion: In resource limited areas pediatric TB continues to be high against a background of high burden of smear positive PTB/HIV coinfecting adolescents and young adults. However there is evidence from this data indicating that with excellent ART implementation TB can be prevented and reduced over time. Therefore there is need for strengthening ART programs as a strategy of TB prevention and for prospective studies to assess the impact of ART on TB in the resource limited settings.



21.049 **Prevalence of HBV,HCV and HIV in healthy volunteer blood donors of Lahore, Pakistan**

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Background: The widespread of transfusion related infections has become the major public health concern in developing countries. Blood transfusion had remained the major risk factor and important mode of transmission of infections to recipients. The objective of the study was to assess the prevalence of transmissible infections through transfusion in healthy blood donors of Lahore, Pakistan. There is insufficient information on prevalence of HBV,HCV and HIV in blood donors of Pakistan.

Methods and Materials: We determined the seroprevalence of Hepatitis B virus (HBV), Hepatitis C virus (HCV) and Human immunodeficiency Virus (HIV) among voluntary healthy blood donors in Lahore, Pakistan. The study was hospital based, cross sectional, carried out at the blood bank of a trust hospital in Lahore, Pakistan from August, 2010 to November, 2010. Seven hundred and seventy five voluntary blood donors were consecutively recruited and tested for HBV,HCV and HIV using Architect Chemiluminescence Assay. Written informed consent with biodata was taken from all the blood donors. All reactive patients were informed about results and referred to surveillance center.

Results: Out of the 775 screened blood donors, an overall seropositivity of 6.19% (48/775) was observed. Male donors were 757 (97.6%) while 18 (2.4%) were females. The mean age was found 30 years. Among 775 blood donors, 3.74% (29) had anti-HCV, HBsAg was positive in 0.90% (7) while Seroprevalence of anti-HIV was 0.12% (1). Co-infection of HBV & HIV was found only in one male donor.

Conclusion: In conclusion, seroprevalence indicate that situation could be more worst if strict screening policies are not adopted at public as well as private blood banks. Prevention and control programmes need to be more active in this country.

21.050 **Amyotrophic lateral sclerosis: A case control study on infectious agents as etiologic factors**

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Background: Amyotrophic Lateral Sclerosis is a neurodegenerative disease of unknown etiology. An etiologic role for infectious agents, such as virus and bacteria, and a pathogenesis as a late sequela of the primary infection were suspected but never sufficiently demonstrated. Here we presents our results from a survey performed in Emilia Romagna Region through a case-control study model, focused on infectious disease history of patients with a confirmed diagnosis of ALS disease.

Methods and Materials: Twenty-one cases (El-Escorial criteria confirmed) and 36 controls matched for age, residence, and work history at diagnosis were enlisted. Patients and controls were questioned about their infectious diseases history, focusing on viral (mumps, measles, rubella, varicella, viral hepatitis A/B/C, herpes virus) and some bacteria (scarlet fever, tuberculosis) infections. When possible, patients records and serologic data were retrieved (80% of cases and controls) for a more accurate diagnosis. All variables were evaluated as dichotomous ones and the data processed through Fisher's test and calculation of respective Odds Ratio for the diagnosis of ALS. A multivariate model was the performed in Binary Logistic Regression and by considering all variables at the moment associated with ALS diagnosis (i.e. age at diagnosis, previous exposures to chemicals, smoke, head trauma).

Results: Patients with El-Escorial confirmed ALS referred more frequently a diagnosis of measles (OR=1.44), rubella (OR=1.49) and herpes zoster infections (OR=2.50). On the other hand, no one of enlisted viral or bacterial diseases reached the significance level (in all cases, p

value at Fisher's test >0.05). Also at multivariate analysis an association between the evaluated infectious diseases and ALS was unconfirmed.

Conclusion: Despite the efforts, the etiology of ALS remains elusive. At the moment, an association of congenital (i.e. anomalies in xenobiotics detoxification enzymes) and environmental (e.g. trauma, exposure to reactive heavy metals and organic compounds such as solvents and pesticides) factors appears as suggestive. On the other hand, a possible role for infectious agents was previously suggested by some clusters, but never clearly confirmed. Our study was apparently negative, but its main limitations (relatively small number of cases, retrospective design) force our results as substantially not resolute.

21.051 **Risk factors in patients with chronic hepatitis C from Timis Country, Romania**

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Background: Chronic hepatitis C is a major health concern. We proposed ourselves to study the risk factors in a group of adults patients with chronic hepatitis C from Timis Country, Romania.

Methods and Materials: The study included a group of 62 patients, with chronic hepatitis C in different evolutive stages, hospitalized in the Department of Infectious Diseases Timisoara in 2008. The positive diagnosis was established based on the subjective data (asthenia, nausea, jaundice, hepatalgia, fatigue, anxiety) associated with the results of the clinical examination, the results of the biological samples (blood cell identification, erythrocyte sedimentation rate, glicemia, amylasemia, amylasuria, ALT, Bd, Bt, gamma-GT, HBs Ag, VHC Ab, cholesterol, triglyceride, summary urine exam, electrophoresis etc) and paraclinics investigations (abdominal ultrasound, liver biopsy). The study of the risk factors included the discovery of the blood transfusions in personal history, injectable treatments, stomatological treatments, surgeries, abuse of iv drugs, tattoos, body piercing, familial hepatodiseases. Liver biopsy samples were graded for histological activity and fibrosis according to the Metavir scoring system. The anamnestic data were preserved in the individual file, according to the study protocol and processed with the help of a computer, using the Epi Info program. The determination of VHC-Ab was done with the help of Murex kits, third generation in our laboratory.

Results: From group of the study, 45 patients have effectuated blood transfusions (72.58%), 53 have effectuated injectable treatments (85.48%), 56 have followed stomatological treatments (90.32%), 34 had different surgeries in history (54.83%), 16 had body piercings (25.80%), 44 with familial liver diseases (70.96%), 8 with tattoos (12.90%) and only 2 (3.22%) patient with iv. drugs abuse. The statistic process of the studied risk factors confirms the parenteral transmission of the HCV. Histological activity (A) and fibrosis (F) determined by Metavir score was: A1 in 30/62 (48.38%) patients; A2 in 20/62 (32.25%) patients, A3 in 12/62 (19.35%) of cases, F0-F1 in 42/62 (67.74%) patients and F2-F3 in 20/62 (32.25%) patients.

Conclusion: Knowing the risk factors at patients with chronic hepatitis C from a geographic zone represents the previous stage for the initiation of the preventing measures which can reduce the incidence of this illness.

21.052 **Mycobacterium tuberculosis infection and associated risk factors including HIV co-infection among the prison inmates in a jail of Pakistan**

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Background: Prison areas provide excellent environment for transmission of *Mycobacterium tuberculosis* (MTB) among individuals during their imprisonment. Factors like stress, overcrowding, poor



ventilation, sharing of utensils, unhygienic conditions and substandard quality food consumption contributes towards low immunity thus prisoners become vulnerable to acquire infections like tuberculosis (TB). Human immunodeficiency virus (HIV) infection is a strong risk factor for the progression of tuberculosis. Coinfection of TB and HIV shorten the lifespan of infected persons. Hence these infections are major global health issues. This study was designed to assess the prevalence of TB and associated risk factors including HIV coinfection among the prison inmates in a jail of Lahore Pakistan.

Methods and Materials: In a cross-sectional study, pre-evaluated questionnaires were filled by trained team members. After taking the history and pre-test counselling, blood samples of prisoners were drawn and processed for routine testing and for the detection of TB and HIV antibodies by ELISA method. X-ray chest were examined by chest physician.

Results: Of the 1702 prisoners, a total of 102 (5.99%) individuals were found positive for MTB-IgM, 37 (2.17%) for anti HIV and 7 (0.41%) were found reactive for both TB and HIV coinfection. A strong association was found among TB cases and risk factors.

Conclusion: It is concluded that there is non-existence or poor implementation of TB and HIV prevention and control program in jail premises.

These are the recommendations that there is a dire need of awareness program for prevention and control of TB/HIV, to develop the strategies for minimization of morbidity and mortality, regular monitoring for TB and HIV cases, isolation policy of TB cases, vaccination for prisoners/other jail staff and educational activity for personal hygiene at individual level.

21.053 Zoonotic aspects of *Coxiella burnetii* antibody positivity between dairy cattle herds and their farmers

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Background: Q fever is a zoonotic disease caused by *Coxiella burnetii*. The study aim was to elucidate relationships of *C. burnetii* seropositivity between farmers and their herds.

Methods and Materials: This is an observational cross-sectional study of 100 randomly selected herds and their 163 farmers. A bulk tank milk sample from each herd was examined using the CHEKIT Q-Fever antibody ELISA Test Kit (IDEXX) and estimated as the S/P value. One blood sample from each farmer was tested for IgG phase 1 and 2, and IgM phase 1 and 2 and estimated as titre values using IFA (Focus Diagnostics, Cypress, CA, USA).

Results: There was a prevalence of 59% antibody positive herds, 11% antibody intermediate herds and 30% antibody negative herds. Over all prevalence of seropositive farmers was 3% representing 5% of the herds. Detailed prevalences of farmer test results were IgG phase 1: 10% intermediate and 4% positive; IgG phase 2: 20% intermediate and 2% positive; IgM phase 1: 5% intermediate and 3% positive; and IgM phase 2: 11% intermediate and 0% positive.

Prevalences of positive farmers in positive, intermediate and negative herds were 5%, 9% and 3% respectively. Thus, the relative risk of farmers being *C. burnetii* antibody positive was 1.5 in positive herds and 2.7 in intermediate herds when compared to negative herds.

Associations between herd sp-values and IgG phase 1 ($p < 0.07$) and IgM phase 1 ($p < 0.03$) are slightly positive and significant. Associations between herd sp-values and farmer IgG phase 2 and IgM phase 2 levels were not significant.

Conclusion: It is concluded that despite a high prevalence of test positive dairy cattle herds there is a very low prevalence of test positive farmers using conservative cut off values. When including intermediate results the prevalences are higher. However, although not significant, farmers of test intermediate herds seem to be at increased risk. This may indicate an active infection in these herds.

21.054 Development of simple, rapid and very sensitive molecular detection method for laboratories and field applications

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Background: Recently we have developed very simple, rapid, sensitive, specific and cheap molecular amplification method for detection and identification of infectious diseases and other molecular and gene detection applications in Medicine, agriculture and Veterinary medicine

Methods and Materials: This, rapid, and sensitive technique called loop-mediated isothermal amplification (LAMP). The LAMP reaction can be conducted under isothermal conditions in very simple water bath without the need of PCR machine by using only one type of enzyme and four primers recognizing six distinct regions. In this study we used 7 different strains of salmonella to compare the PCR and LAMP method. Conventional PCR method for detection of Salmonella with standard thermocycler takes 3 hrs but with LAMP method we are able to amplify and detect the salmonella in very simple thermal block made in IRAN.

Results: After optimization of the process it was possible to rapidly detect and identify *Salmonella typhi* bacteria within 90 minutes. With no need to post electrophoresis or gel documentation instruments

Conclusion: This method is also 10 times more sensitive comparing to the PCR. And the result can be detected by turbidity of positive tubes comparing to transparent negative tubes.

21.055 A specific serum IgA antibody discriminates pneumonia from colonization state in patients with *Pseudomonas aeruginosa* in sputum culture

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Background: We attempted to develop a new specific antibody detection method for discriminating infection state from colonization state in hospitalized immunocompromised patients with positive sputum cultures for *Pseudomonas aeruginosa*.

Methods and Materials: Serum samples from 65 patients with *P. aeruginosa* in sputum culture (total PA patients), including 24 patients with *P. aeruginosa*-related pulmonary infections (PA infection group) and 21 patients without pulmonary infections (PA colonization group), as well as samples from 20 patients positive for other bacteria in blood culture (non-PA infection group) and 38 healthy controls were examined and compared for IgG and IgA anti-*P. aeruginosa* antibodies by a newly developed enzyme-linked immunosorbent assay (ELISA).

Results: Both IgG and IgA antibody ELISA showed satisfactory reproducibility with low coefficient of variation (CV) percent, and a western blotting analysis showed two protein bands as the corresponding antigen common to both antibodies. The serum levels of both antibodies in total PA patients were higher than those in the healthy controls with high significance ($p < 0.0001$). The PA infection group showed significantly higher mean levels of both IgG and IgA class antibodies than the PA colonization group, non-PA infection group and healthy controls (each, $p < 0.0001$). In receiver operating characteristic (ROC) curve analysis to differentiate between PA infections group and PA colonization group, the area under curve (AUC) of the IgA antibody (0.848) was significantly larger than the AUC of the IgG antibody (0.677) ($p = 0.019$). At the optimal IgA antibody cutoff value for differentiation between the two groups (1.37 units/mL), the sensitivity and the specificity of IgA anti-*P. aeruginosa* ELISA were 83.3% and 85.7%, respectively.

Conclusion: These findings suggest that IgA antibody ELISA, rather than IgG antibody ELISA, may be useful for differentiating *P. aeruginosa*-related pneumonia from the latent colonization in immunocompromised patients with positive sputum cultures.

**21.056 Newly sensitive competitive ELISA using monoclonal antibody against NS1 of West Nile Virus NY99 strain**J. Hirota¹, K. Morita², S. Shimizu¹¹National Agriculture and Food Research Organization, National Institute of Animal Health, Japan, Tsukuba, Japan, ²Nagasaki University, Nagasaki, Japan

Background: Epitope Blocking ELISA (B-ELISA) or Competitive ELISA (C-ELISA) is useful for serodiagnosis in the case that cross reaction was observed. However, lower diluted sera, 5 to 10 times dilution, is needed to perform B-ELISA against flaviviruses. So, it needs comparatively large volume of sera. But especially in small birds, it is difficult to collect large volume of blood. Thus, the small amounts of sample sera have been one of the limitations in sero-surveillance in small animals.

Methods and Materials: Monoclonal antibody (mAb): MAbs were obtained by the usual method using purified WNV (NY99 strain) as immunization antigen.

Serum samples: Purified West Nile virus (WNV) (NY99, g2266, Eg101, Kunjin MRM61C strain), Japanese encephalitis virus (JEV) (Nakayama NIH, JaNAr0102 strain), Murray Valley encephalitis virus (MVE1-51 strain) or St. Louis encephalitis Virus (SLE) (Parton strain) immunized chicken sera were used to check the cross-reactivity in C-ELISA. And WNV (NY99 strain) infected serial sera were used to check the sero-conversion in C-ELISA.

Results: Anti-WNV mAb, SHW-7A11, was developed. It has reacted with NS1 in western blot analysis. In indirect ELISA, SHW-7A11 strongly reacted with WNV NY99 strain, and it moderately reacted with Kunjin strain and Eg101 strain. SHW-7A11 based two C-ELISAs were constructed for 10 or 100 times diluted serum samples. They were named C-ELISA10 and C-ELISA100 respectively. Anti-WNV NY99 strain antibodies and anti-WNV Kunjin strain antibodies could be detected in both C-ELISAs. Anti-JEV antibodies and anti-SLE antibodies did not highly cross-reacted in both C-ELISAs. In C-ELISA10 using the cutoff value of SLE, all of WNV infected chickens turned positive at 21 dpi. In C-ELISA100 using the cutoff value of SLE, six of nine infected chickens turned positive at 10 dpi, and all of infected chickens turned positive at 21 dpi.

Conclusion: We developed new mAb against WNV NY99 strain, SHW-7A11. The C-ELISAs using SHW-7A11 could detect antibodies against WNV NY99 strain. Our developed C-ELISA can detect WNV infection using 100 times diluted sera, therefore, this C-ELISA would be valuable for WNV sero-surveillance of small animals.

21.057 Simultaneous detection and differentiation of influenza A virus and Newcastle Disease Virus by real-time PCRD. Nidzworski¹, E. Wasilewska¹, B. Gromadzka¹, K. Śmietanka², Z. Minta², B. Szweczyk¹¹University of Gdansk, Gdansk, Poland, ²The National Veterinary Research Institute, Puławy, Poland

Background: Enveloped, single stranded, negative-sense RNA viruses as Newcastle disease Virus (NDV), a member of the *Paramyxoviridae* family (order *Mononegavirales*) and influenza A virus (IAV), a member of the *Orthomyxoviridae* family, are avian pathogens and may cause serious economical problems in poultry farming. Similar symptoms were described for both NDV and IAV and ranging from sub-clinical infections to severe disease, with loss in egg production, acute respiratory syndrome and high mortality. Symptoms can not be distinguished by standard veterinary procedures and they are evident only on post mortem examination. The regular outbreaks indicate that rapid and simultaneous test for detection and differentiation between these viruses are needed.

Methods and Materials: Rapid diagnostic method based on TaqMan probe real-time PCR analysis was developed to detect and differentiate between Newcastle disease and influenza viruses. The degenerated primers based on the conserved fragments of the genomes were designed to detect all NDV and IAV strains. Also, two probes containing reporter dyes with different emission spectra (530 nm for IAV and 560 nm for NDV) were designed.

Results: Several strains of Newcastle disease virus and influenza A virus were examined. In 40 cycle-reaction within 45 minutes it was possible to detect and distinguish both viruses using 560 nm and 530 nm probes. The detection limit of real-time PCR was 102 plasmid copies of NDV and 103 plasmid copies of IV per reaction.

Conclusion: The results obtained in this study show the applicability of TaqMan real-time PCR analysis in laboratory practice for diagnostic and screening tests for the identification and differentiation of Newcastle disease virus and influenza A virus in birds.

21.058 Searching online books of infectious diseases: A new way to load decision-support software with the most up-to-date information

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Background: Electronic books of medicine are now available on the Internet for text searching. These books provide a new way to collect the clinical findings for each infectious disease, which can then be stored in a database designed for useful queries.

Methods and Materials: Microsoft Access was used to create a relational database of infectious diseases for decision support. The database profiles 275 communicable diseases, and each disease is linked to one or more findings. There are 119 findings (signs and symptoms). Each finding was used as a search term in three available online books: Principles and Practice of Infectious Diseases (PPID), Infectious Diseases (Cohen), and Control of Communicable Diseases Manual (CCDM).

Results: The results of the online searches were used to check and revise the findings linked to each disease. Most of the findings were used without modification, but some were changed to terms that retrieved more results. For example, "pus in stool" was changed to "fecal leukocytes." Several findings were deleted from the database because they lacked specificity. For example, the finding "kidney function test, abnormal" was dropped, but "acute renal failure" was retained. A search in PPID retrieved 158 hits for "abdominal pain" and 105 hits for "eosinophilia." CCDM found 26 hits for "abdominal pain" and 17 hits for "eosinophilia." Comparing the database before and after the retrievals from online searching, the number of diseases linked to findings increased from 115 to 128 for "abdominal pain" and from 36 to 40 for "eosinophilia." The number of diseases linked to both findings increased from 27 to 31.

Conclusion: Searching online books of infectious diseases is a new way to load the current state of knowledge into a relational database for decision-support. Each query of such a database produces a set of all infectious diseases that match one or more of the search criteria entered. Each search criteria is essentially an index that is useful for building a list of differential diagnoses. Improving the sensitivity and specificity of these indexes will increase the likelihood that this decision-support tool can help the clinician to make the correct diagnosis.

21.059 Detection and quantification of avian hepatitis E virus from clinical samples by a new TaqMan real-time RT-PCR including an internal controlS. Troxler, A. Marek, I. Prokofieva, I. Bilic, M. Hess
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Background: The genomic organization of avian HEV is consistent with mammalian HEV, but the length of avian HEV genomes is about 600 bp shorter and they share only 50 to 60 % sequence identity. Avian HEV has been reported in Northern America, Australia and several European countries and sequence analysis revealed at least three different genotypes. Due to this heterogeneity and lack of knowledge about prevalence and pathogenicity of avian HEV, a universal, reliable and fast diagnostic method is needed. Therefore, a duplex TaqMan real-time RT-PCR including a heterologous internal control RNA for detection and quantification of avian HEV from clinical samples of different geographical origin was developed.

Methods and Materials: Based on sequence analysis of clinical samples from Europe and Australia, primers and TaqMan probes were



designed, which anneal within the relatively conserved ORF3 of avian HEV. Dilution series of *in vitro* transcribed RNA were used as standard for quantification. *In vitro* transcripts from the AcGFP gene were used as heterologous internal control RNA for both RNA isolation and real-time RT-PCR. Sensitivity of the new method was compared to conventional RT-PCR and its specificity was shown on samples positive for mammalian HEVs, different viral avian pathogens and non-infected tissues. The new real-time RT-PCR was applied to field samples, which consisted of various sample types and genotypes.

Results: The standard curve based on tenfold dilution series of *in vitro* transcribed avian HEV RNA achieved a range over ten orders of magnitude, having an efficiency of 1.04 and a regression square of 0.996. A minimum of 3.6×10^3 copies of HEV RNA per reaction were measured and internal control RNA was detected reliably and accurately. By diluting a sample, the same sensitivity was observed as in conventional RT-PCR. The new method was shown to be highly specific and detected all clinical samples tested, an advantage in comparison to conventional RT-PCR applying primers which anneal within ORF1 and ORF2.

Conclusion: The firstly developed fast and reliable duplex TaqMan real-time RT-PCR for universal detection and quantification of avian HEV is highly suited for various clinical sample material with use in research as well as in routine laboratory diagnostics.

21.061

Diagnosis of Mediterranean visceral leishmaniasis by detection of Leishmania antibodies and Leishmania DNA in oral fluid samples

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Background: Current methods for visceral leishmaniasis (VL) diagnosis require invasive sampling procedures such as visceral aspiration and blood drawing. The development of diagnostic tests using other biological fluids, more available and easy to collect would be more simple and practical for VL diagnosis especial under field conditions. The aim of this study was to assess diagnostic performances of saliva-based assays in VL diagnosis.

Methods and Materials: Oral fluid and blood samples from 37 VL cases and 40 healthy controls were analyzed by rK39 Enzyme Linked Immuno Sorbent assay (rK39 ELISA) and quantitative real-time PCR (qPCR) to detect and to quantify respectively specific *Leishmania* antibodies and *Leishmania* DNA.

Results: ROC curve analysis showed that indirect biotine-streptavidine ELISA test using saliva samples had an excellent ability to discriminate between VL cases and healthy controls. The sensitivity of antibodies detection was 100% in both sera and saliva whereas the specificity of antibodies detection was 95% in sera and 97,5% in saliva. A significant positive correlation was found between antibody levels measured in sera and saliva, ($p=0.655$, $p=0.01$).

ROC curves analysis demonstrated that qPCR assays performed on DNA extracted from oral fluid cells could discriminate between VL cases and healthy controls. It was not the case while using DNA extracted from oral fluid supernatant. DNA detection in salivary cells was equivalent to blood in accuracy with a sensitivity of 94.6% and a specificity of 90%. The median parasitic load estimated in blood was higher than that estimated in oral fluid cells (133 parasites/ml, IR: 10-1048 *versus* 2.9 parasites/sample, IR: 0.34-80). However, parasitic load didn't show a significant linear relationship between counts assessed from the 2 biological samples ($p=0.31$, $p=0.06$).

Conclusion: Saliva revealed a promising sampling for VL diagnosis. It allows the detection of specific anti-*Leishmania* antibodies and parasite DNA with equivalent results to blood sampling. Less invasive, this approach could be relevant for clinical use.

21.062

Proventricular dilatation disease in psittacines may be caused by mixed infections with different genotypes of avian bornaviruses

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Background: Proventricular dilatation disease (PDD) is a fatal, progressive neuropathic disorder of psittacine birds which is caused by a single stranded RNA virus, the avian bornavirus (ABV). The disease pattern includes lymphoplasmacytic inflammation of the central, peripheral and autonomic nervous system. Seven avian bornavirus genotypes have been characterized during the last years. Previous studies attributed mono-infections with a single genotype of ABV to PDD cases. However, after a recent survey discovered one case of double infection with two different ABV genotypes we decided to look more systematically for mixed infections. Aim of the investigation was to generate sequences of a part of the matrix protein gene and to evaluate whether sequences of more than one ABV genotype were present.

Methods and Materials: From paraffin-wax embedded brain samples of 21 psittacine birds RNA was extracted, followed by an RT-PCR with primer pairs generating a partial sequence of the matrix-protein. Afterwards a cloning procedure was performed and 10 randomly selected clones per case were further investigated. The clones were sequenced in order to elucidate whether sequences characteristic for one or more than one genotype were present.

21.060

Continuous improvement of a novel real-time PCR for detection and quantification of DNA from pathogenic leptospires

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Background: Leptospirosis is considered an important zoonosis as well as an emerging infectious disease of both, humans and animals. Livestock may be infected through contact with infectious urine shed by reservoir animals. Importantly, *Leptospira*-infected animals may proceed to an asymptomatic carrier state, thus providing a source of infection for humans. In order to establish a sensitive and specific method for direct demonstration of leptospiral DNA in clinical samples, we developed and validated a novel real-time PCR (qPCR), targeting the *lipL32* gene that is only present in pathogenic leptospires.

Methods and Materials: The *lipL32* gene was chosen as target region for assay design. Analytical sensitivity and qPCR kinetics were evaluated by amplifying serially diluted plasmid DNA, obtained by cloning the *lipL32* gene into a commercial vector. Analytical specificity was assessed by testing a variety of pathogenic and non-pathogenic *Leptospiraceae*, as well as other common infectious agents of livestock. Clinical samples from several animal species, such as pigs, cattle and rats were used to further validate the assay.

Results: The novel *lipL32* qPCR assay showed high sensitivity (50 copies/reaction), linear amplification within at least 5 orders of magnitude and acceptable qPCR kinetics ($R^2 > 0.99$; qPCR efficiency = 93 %). The assay was capable of detecting all pathogenic leptospires tested ($n = 13$), while no positive signal was observed with any non-pathogenic member of the *Leptospiraceae*, nor with any of the other infectious agents tested. Leptospiral DNA was detected in several clinical samples of domestic animal origin. No positive signal was, however, detected in a suspected case of leptospirosis among cattle, although infection was clearly demonstrated by immunofluorescence microscopy and serology. Sequencing determined the presence of two mismatches in the reverse primer, suggesting this as the most likely cause for assay failure and providing a basis for improvement of the assay.

Conclusion: Despite excellent technical performance of the test and although all culture grown *Leptospira* strains, belonging to a variety of pathogenic *Leptospira* species, were correctly identified by the novel *lipL32* qPCR assay, testing of clinical samples revealed the necessity for assay improvement. This example underlines the importance of using clinical material for validation of qPCR assays.



Results: Investigated birds were either affected with ABV 2 or 4, which are the predominant genotypes in Europe. Three cases showed mixed infections: two with ABV 2 and ABV 4, and one with ABV 2 and the more rarely found ABV 6. Disease severity and lesion profile was not different from cases of mono-infections.

Conclusion: This study clearly demonstrated that the molecular cloning method is a useful tool for distinguishing between single and multiple infection events of different ABV genotypes. However, mixed infections seem to occur only in a low percentage of PDD cases. Furthermore, mixed infections do not seem to be a prerequisite for disease development or a more severe clinical course.

21.063 Chromogenic in situ hybridization as a tool for identification of emerging protist species in tissue samples

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Background: Infections with protist species are frequent in human or veterinary medicine. In many cases the pathogenic agent cannot be easily identified in tissue samples using standard histopathological methods. Therefore, a morphologically based detection method allowing tagging of pathogenic organisms within the tissue was considered useful. In situ hybridization (ISH) is a method combining modern molecular biology techniques with commonly used state-of-the-art pathologic methods. ISH was shown to be a specific and reliable tool for detecting different protists.

Methods and Materials: Fifteen oligonucleotide probes were designed, all targeting a part of the 18S or 5.8S ribosomal RNA (rRNA) gene, which were selected due to the abundant presence and high accessibility of rRNA within the cytoplasm. The probes were labelled with digoxigenin. Probe detection was carried out using an anti-digoxigenin antibody followed by an enzymatic color reaction. To ensure probe specificity and rule out cross-reactivity each probe was rigorously tested on a large variety of commonly found pathogenic protozoa, bacteria, viruses and fungi.

Results: Successful design and application of probes specific for a large variety of different protists (*Giardia duodenalis*, all relevant members of the order Trichomonadida (*Tritrichomonas foetus*, *Tritrichomonas augusta*, *Histomonas meleagridis*, *Tetratrichomonas gallinarum*, *Trichomonas gallinae*, *Pentatrichomonas hominis*, *Monocercomonas colubriformis*, *Hypertrichomonas acosta*, *Trichomitus batrachorum*), all members of the family Tritrichomonadidae, *Pentatrichomonas hominis*, *Tetratrichomonas gallinarum*, *Trichomonas gallinae*, *Histomonas meleagridis*, *Leishmania* spp., *Entamoeba* sp., *Entamoeba invadens*, *Cryptosporidium* sp., *Plasmodium* sp., *Encephalitozoon cuniculi*, *Pneumocystis* sp. *Prototheca* sp.) could be shown. None of the probes showed cross-reactivity with other tested pathogens.

Conclusion: ISH was shown to be a useful tool to specifically detect various protists within tissue samples.

21.064 Non-invasive dengue diagnosis: Can saliva substitute blood?

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Background: The necessity of a venous blood collection in all dengue diagnostic assays and the high cost of tests that are available for testing during the viraemic period hinder early detection of dengue cases and thus could delay cluster management. This study reports the utility of saliva in an assay that detects Dengue virus (DENV) specific immunoglobulin A (Ig A) early in the phase of a dengue infection, as well as the detection and serotyping of viral RNA in the saliva.

Methods and Materials: Using an in-house established antigen capture anti-DENV IgA (ACA) ELISA technique, we tested saliva samples collected from dengue confirmed patients. PCR and virus isolation were also performed on these saliva.

Results: The overall sensitivity within three days from fever onset was 70%. The performance is markedly better in secondary infections with 100% sensitivity reported in saliva samples from day one after fever onset. Serum and salivary IgA levels showed good correlation (Pearson's $r = 0.69$; $p < 0.001$). Specificity was found to be 97%. PCR results yielded a sensitivity of 93% within the first three days of fever and serotypes matched those detected in serum. The PCR results were confirmed by virus isolation.

Conclusion: Our findings suggest that the detection of anti-dengue IgA in saliva would be very useful in dengue endemic regions, where majority of dengue cases are secondary. The ACA-ELISA is easy to perform, and is cost effective, especially in laboratories without facilities for sophisticated equipment. In places where PCR facilities are available, saliva can also potentially replace blood as the biospecimen of choice for dengue diagnosis without compromising any downstream virus work.

21.065 Role of the protein microarray technology in the development of a rapid immunoassay for the influenza virus

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Background: Influenza is a contagious viral disease whose causative agent can rapidly mutate into new antigenic variants, causing high-rate mortality amongst humans and animals worldwide. Early diagnosis at the point-of-care (POC) is a key component of disease surveillance activity. However, available diagnostic methods are mainly laboratory-bound, and thus alternative POC-suitable tools must be developed and implemented against future pandemics. The present work, funded by the European Seventh Framework Programme for research and technological development (FP7), is a consortium based effort of 6 European partners that cooperated to develop a rapid diagnostic system for the detection and type-differentiation of the influenza virus.

Methods and Materials: Microarrays of monoclonal antibodies (mAbs) are employed to develop a sandwich-type immunoassay for the detection of recombinant influenza A, B, and Avian nucleoproteins. Viral antigens are selectively captured on the array and detected using a panel of biotin-conjugated mAbs and streptavidin-HRP reagents. The mAbs are generated by a combination of somatic cell hybridoma and microarray immunoassay technology, which allows the rapid screening of antibodies directed against a large number of viral antigens. Promising antibody candidates are produced, purified by affinity-chromatography, and then employed in the assay.

Results: The protein-microarray technology proved to be an excellent tool for the rapid screening of hundreds of hybridoma samples against different antigens. Five antibodies were selected, and two of them were successfully employed in this pilot-study. Overall the microarray immunoassay developed so far allows for detection of approximately 10 ng/ml of recombinant antigen in a total assay time of 30 minutes. Influenza A and B nucleoproteins are selectively detected, and no cross-reactivity is observed.

Conclusion: The pilot-study indicated that the developed immunoassay is a promising tool for the rapid diagnosis of influenza A and B. Current optimization is focused to improve the achieved detection limit, and to evaluate performance of the procedure using clinical samples. Finally, the optimised immunoassay will be progressively combined with a consortium-produced automated diagnostic analyser and the resulting system will be thoroughly evaluated and assessed as first-line defence against pandemic threats.

**21.066** Descriptive study of iron biomarkers in Ethiopian Visceral leishmaniasis patients**T. Ambaye**

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Background: Visceral leishmaniasis (VL) is a neglected systemic parasitic disease caused by the *Leishmania donovani complex* species. It commonly affects poor populations in the tropics and sub-tropical endemic areas, causing 500,000 morbidities and more than 50,000 deaths annually. Although anaemia is a common sequel of VL, use of iron status assessment and biomarkers is little studied.

Objective: To describe the clinical characteristics, and changes in iron status biomarkers (ferritin, sTfR, and hepcidin) at admission and during the month following commencement of anti-leishmanial treatment in newly diagnosed VL patients.

Methods and Materials: A prospective longitudinal descriptive study was conducted in newly diagnosed, HIV negative VL patients admitted to Arba Minch Hospital-Leishmaniasis Research and Treatment Centre, South-West Ethiopia, between April and May 2010.

Results: A total of 20 confirmed VL cases, 2 female and 18 male, with a median age of 18 years were enrolled. While fever was the initial presenting symptom, with mean duration of 4.4 ± 3.7 months, 6 (30%) patients had no measurable fever on admission or during follow-ups. Splenomegaly was present in all patients with 12 (60%) of them being malnourished. Pancytopenia was a common hematologic manifestation. The Mean \pm SD of haemoglobin at admission was 7.2 ± 1.99 g/dl with 9(45%) patients classified as iron deficient (ID). Ferritin was elevated at baseline, 1373.13 ± 1191.19 μ g/l, and concentrations significantly decreased following anti-leishmanial treatment. sTfR was increased in ID patients only, whereas serum hepcidin concentration was higher in non-ID (NID) patients. A significant correlation ($p < 0.05$) was observed between sTfR and haemoglobin, between hepcidin and ferritin, between ferritin and body mass index, and between sTfR and the sTfR-F index. With treatment, significant improvement was observed in both clinical and laboratory parameters.

Conclusion: sTfR-F index was a useful biomarker in differentiating ID and NID patients. Iron deficiency contributed to the development of anaemia in about half of the patients. A future study is recommended to evaluate the utility of serum sTfR and hepcidin against bone marrow staining for iron, and consideration of clinical value of iron interventions for the management of anaemia in ID VL patients.

21.067 Did advances in global surveillance and notification systems make a difference in the 2009 H1N1 pandemic?**M. Stoto**

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Background: The last decade saw substantial enhancements to global disease surveillance systems, including laboratory capacity, syndromic surveillance, and automated web-searching systems such as HealthMap, as well as notification systems such as the IHR, GPHIN, and ProMed. The 2009 H1N1 pandemic provided an opportunity to see how well these systems functioned in practice as an integrated public health surveillance system.

Methods and Materials: Formal process mapping, root cause analysis, and other Quality Improvement methods based on a systematic review of the scientific literature, websites, and news reports, supplemented with key informant interviews.

Results: Enhanced laboratory capacity in the US and Canada, including an experimental surveillance system operated by the U.S. Department of Defense in California and a trilateral agreement among the United States, Canada, and Mexico to enhance regional cooperation and information sharing, led to earlier detection and characterization of the

2009 H1N1. Improved global notification systems, including expectations that outbreaks could not be suppressed, contributed to this success. An outbreak at a New York City high school, for instance, would likely not have been recognized had it not been for a global alert. Syndromic surveillance systems, on the other hand, did not contribute to detection of the outbreak because there were too few insufficiently differentiated cases during normal flu season. Automated web-searching systems did not substantially improve outbreak detection in 2009, but at best would only have quickened the response by one or two weeks.

Conclusion: Investments in global surveillance and notification systems did make a difference in the 2009 H1N1 pandemic, enabling the earlier development and deployment of a pandemic vaccine and other local, national, and global public health responses. Not all surveillance capacity enhancements, however, translated into enhanced capabilities; syndromic surveillance and automated web-searching systems had a minimal impact. This analysis also illustrates the challenges of early detection and characterization. Characterized by intrinsic uncertainty that takes weeks to months to resolve, epidemiologic analysis of a new pathogen is rightly compared to the "fog of war." Thus, in preparing for the emergence of a new pathogen, it is important to expect and plan for uncertainty.

21.068 Origin and diffusion of tuberculosis breakdowns by *Mycobacterium caprae* in cattle herds in an officially tuberculosis free Province of Italy**G. Zanardi¹, M. B. Boniotti¹, C. Costanzi², F. Chin², A. Moresco², M. L. Pacciarini¹**¹Istituto Zooprofilattico Sperimentale della Lombardia ed Emilia Romagna, Brescia, Italy, ²Servizi Veterinari Provincia Autonoma di Trento, Trent, Italy

Background: Bovine Tuberculosis (bTB) by *Mycobacterium bovis-caprae* is an infectious disease affecting human and animal health with trade implications. We describe the pattern of a bTB infection that occurred in the officially-tuberculosis-free (OTF since 1999) province of Trento in Northern Italy. This Province (6,206 Km²) is characterized by the presence of mountains and common pastures; 45,000 heads are reared in 1,500 cattle herds.

Methods and Materials: bTB surveillance has been performed by skin test and slaughterhouse inspection.

M. caprae isolation was carried out by liquid (MGIT) and solid (Stonebrink and Lowenstein-Jensen) culture media.

Molecular typing of strains was performed by spoligotyping and variable-number tandem repeat (VNTR) typing.

Results: From 1992 to 2004 the tuberculin test has been carried out every two years; three sporadic bTB were detected. Since 2005 skin test has been performed every 4 years supported by continuous *post mortem* inspection and pre-movement test of animals from non-OTF areas.

Between 2007 and 2009, a cluster of bTB outbreaks occurred in dairy herds. The disease was detected at the slaughterhouse and confirmed by the isolation of *M. caprae*. The positive animals, born in Austria and Germany, were introduced in 2005-2006. In 2008 an annual tuberculin test was performed on every cattle herd leading to the detection of further 24 bTB outbreaks, 6 primary and 18 secondary. The epidemiological survey showed that bTB had probably been present since 2005 due to a batch of infected cattle commercialized by the largest dealer in the Province linked to other dealers' located in Austria and Germany. The spread of the infection took place in common pastures and the live animal trade. Two different molecular patterns of *M. caprae* were identified: spoligotyping SB0418 – VNTR 43534 and SB0418 – ETR 53523; both genetic profiles are present also in Austria and Germany.

Conclusion: It is important to remember that in OTF Regions up to 0.1% of herds in a year can potentially be bTB infected. A timely alert system is required for the management of introduction and spread of infection. This recrudescence of bTB points out the necessity to protect OTF areas by implementing a bTB surveillance plan based on risk assessment.

**21.069** Are we ready for new challenges in epidemic intelligence?

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Background: Due to the increased diversity of available information sources that could support detection of potential health threats, health officials are confronted with new challenges. The various existing tools for indicator- and event-based surveillance provide already support to some extent. However, there are different kinds of public health events and it is still unclear which events can be detected by current systems. We first characterize the various notions of public health events and identify potentials and limitations of existing systems with respect to the kind of events they are able to detect. From this we derive future challenges.

Methods and Materials: We characterize public health events by two criteria: their publicity and their occurrence frequency. Based on these two criteria, six different groups of events can be distinguished. An event might occur rarely (e.g., Dengue fever in Germany) or frequently (e.g. Influenza in Europe). Further, known, semi-known and unknown events can be separated, depending on the knowledge, public health officials have already on the disease. Last year, swine flu could be characterized as unknown and rare. Today, it is a rather known and rare event. The single types of events make different demands on an automatic detection system. Results and approaches of existing indicator- or event-based surveillance tools have been analysed manually with respect to detect the various types of events characterized before.

Results: Indicator-based systems such as SurvNet@RKI allow to detect events that are either known and occur either rarely or frequently. Existing event-based systems (e.g. MediSys, PULS) use various sources, but rely upon previously defined keyword lists and therefore detect known – and to a certain extent semiknown event - that occur either rarely or frequently. Previously unknown events cannot be identified by existing surveillance systems and require additional information sources to be considered and new technologies to be exploited.

Conclusion: Previously unknown events cannot be recognized by existing systems due to the technology or data they rely upon. In the future, techniques such as machine learning need to be tested for their ability to detect also such events and to have additional means to detect events of the other categories.

21.070 Pattern detection for social media-based epidemic intelligence: A user study

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Background: State-of-the-art approaches for Social Media-based Epidemic Intelligence usually use supervised learning algorithms for detecting public health events. Although supervised approaches have yielded good performance, they rely upon human effort for learning examples and engineering features to train the supervised algorithm. In contrast, the less well studied, but more generic and flexible, unsupervised approach tends to produce very complex results, which poses a significant challenge for an epidemic investigator, given the number of potential patterns. It is still unclear 1) to what extent unsupervised approaches are suited to address current problems in EI and 2) which result representations are preferred by users of such systems.

Methods and Materials: We present a novel framework that allows epidemiologists to interact with the results produced by unsupervised EI algorithms. Such algorithms require several parameters and group web documents in a predefined number of clusters. We represent the clusters as word clouds; produced either using word frequencies or using frequencies of extracted named entities. In the framework user feedback is considered to adapt the parameters and improve the algorithm automatically. The framework has been implemented and the unsupervised event detection algorithm is applied to more than 30.000 blog entries for evaluation purposes.

Results: Five epidemiologists participated in the evaluation. For detected events, they were asked to judge the word cloud representations with respect to their suitability for gathering information on public health

events. Further, users had to judge to what extent a document fits a cluster it was assigned to. As a result, the users preferred word clouds that contain more general terms instead of specific named entities such as medical conditions and locations. The automatic clustering of documents was rather clear to them.

Conclusion: The novel framework to social media-based gathering and analysis for EI allows previously unknown emerging epidemic events to be detected and presented to the domain experts in a human-centric manner. This work helped to get an improved understanding of the types of visualization and representations that are useful to domain experts in the areas of epidemiology and showed that unsupervised approaches might also become a useful for supporting in EI.

21.071 Risk map of highly pathogenic avian influenza spreading areas in poultry based on risk factors

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Background: Highly pathogenic avian influenza (HPAI) virus has caused significant economic losses in the poultry industry. Understanding how a disease spreads as a function of its risk factors, is useful to determine appropriate surveillance plans to specific areas. The objective of this study was to present an approach to spatially identify risk spread areas of HPAI in poultry based on risk factors.

Methods and Materials: The study area was Castilla-León, an autonomous region in the north of Spain, with 669 poultry industry farms (broilers, breeders, layers and hatchers) censed in this area. Four risk factors have been studied on each farm: biosecurity (biosecurity surveys), trade movements between farms (network analysis made using elaborated by the free Pajek software), farm census, and farm density (analyzed by Kernel density method). All factors have been normalized and transformed into four raster layers. Using multicriteria decision the layers have been incorporated into one map of risk of HPAI spread. The Getis-Ord test has been applied to identify significative clusters or “hot-spots” of risk. Finally, the identification of critical risk factors was made by a sensitivity analysis using MonteCarlo simulation and tornado charts (Using @risk palisade © software). The resulting regression coefficients showed the relative influence of the each risk factor in the model.

Results: The risk maps showed that the risk of spreading was mainly focused on broiler farms and in the region of Segovia (one of the nine provinces of Castilla-León). The Getis-Ord test identified 25 “hot-spots” within which the relative standard deviation is more than 10. Sensitivity analysis showed that “trade movements between farms” was the most influential risk factor in the model with a 0.36 coefficient regression. “Farm density”, “farm census” and “biosecurity” have a 0.28, 0.23 and 0.15 regression coefficients respectively.

Conclusion: This approach contributes to the identification of high spread risk areas and to the knowledge of the main risk factors of Spread of HPAI which could help improve efforts in national surveillance plans.

21.072 Serological monitoring of Newcastle disease virus in poultry, synanthropic, zoo, and wild birds in Ukraine in 2006–2009

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Background: Newcastle disease (ND) remains one of the most dangerous viral infections of poultry. In Ukraine ND is registered sporadically; separate outbreaks occur in chicken, mostly in backyard birds.

Methods and Materials: In 2006–2009 serological monitoring of poultry, synanthropic, zoo, and wild birds for the presence of ND virus (NDV) antibodies was conducted using haemagglutination inhibition test and ELISA in different regions of Ukraine. In total, 8 poultry species, 7 synanthropic, 2 zoo, and 72 wild bird species were surveyed. Chicken



were not monitored because of postvaccination antibodies (administration of ND vaccines is mandatory for chicken in Ukraine).

Results: NDV antibodies were found in 4 poultry species, 5 synanthropic, 2 zoo, and 26 wild bird species. Among monitored poultry species having been not undergone NDV vaccination, the presence of NDV antibodies was detected in: geese (0.7–2.35% in farms; 0.4–1.74% in backyards); ducks (0.5–2.1% in farms; 0.1–0.75% in backyards); turkeys (0.5% in backyards only); quails (1.48% in one farm). Among zoo birds, NDV antibodies were found in parrots and peacocks in solitary instances. Among synanthropic birds, NDV antibodies were detected in: pigeons (3.3–7.9%); sparrows (3.5–8.5%); crows (4.5–5%); magpies (3.3–5.25%); jays (4.0–7.4%). Among surveyed species of wild birds, the most representative NDV positive group was wild waterfowl, especially different species of wild ducks: depending on the species, from 3–4.5% to 23–25% (in mallards and teals); wild geese (1.2–3.8%); cormorants (up to 7%); and seagulls (2.4–4.1%). Among other wild bird species, antibodies were found in wild pigeons (2.8–24%), as well as in partridges, cranes, herons, pheasants, common ravens, owls, and hawks.

Conclusion: Obtained data shows the wide NDV circulation in above mentioned bird populations. This clearly poses the necessity of isolation of the field NDV isolates from different bird species in order to study in detail their molecular-genetic characteristics and pathogenicity for chicks.

21.074 Development of influenza epidemiology and virology surveillance in Indonesia, 2009

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Background: Influenza has become an important health issue, especially in Indonesia where many cases of Avian Influenza (AI) in human occurred, with a high case fatality rate. AI symptoms in human were ranged from typical human Influenza Like Illness (ILI) to pneumonia/ Severe Acute Respiratory Infection (SARI).

Objective: to measure the magnitude of influenza in Indonesia

Methods and Materials: (1) Development of Influenza Like Illness epidemiology and virology surveillance selected from 20 of 33 provinces and SARI surveillance in 8 location at the same city as the ILI sites. (2) Message development of ILI and risk communication training for health provider.

Results: Most of ILI and flu B cases were male, but flu A were female, ILI, flu A/B mostly found in children aged 4–14 years old. The highest number of ILI and flu B were reported from South Sulawesi, but flu A was reported from Lombok Island. ILI was high in an period of April to September, for flu A, the cases were dramatically increased in periode of July to August. Flu B cases were not as high as ILI and flu A, but it occurred in all year long with a peak in March. The cases of flu A and flu B tend to increase every year. SARI cases were mostly found in male, children age 0–4 years old with diagnose of bronchopneumonia (40%) and pneumonia (30%). the serotype of influenza virus were H3 (82%) and H5 (12%). For risk communication, it was showed that health provider have raise awareness of ILI symptoms and already encourage FLU-WISE preventive action.

Conclusion: ILI cases found in children aged 4–14 years old and SARI cases were mostly found in children age 0–4 years. ILI, flu A, flu B cases were reported from different Island. it is needed to plan influenza vaccination program for children and expand ILI and SARI surveillance at all provinces in Indonesia

21.075 Essential Requirements for Surveillance Systems for Emerging Diseases

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Background: Surveillance systems should support the ongoing systematic collection and analysis of data, resulting in relevant intelligence at an appropriate geographical and temporal scale to support risk managers in taking decisions to prevent and control an emerging disease. Two recent emerging disease events, reported colony losses in bees and the Q fever outbreak in the Netherlands, have highlighted important requirements for existing surveillance systems to ensure preparedness for emerging diseases at EU level.

Methods and Materials: For each disease event existing surveillance data for the EFTA member states were collated and reviewed. In addition questionnaires were completed by reporting organizations in these countries describing the existing surveillance systems.

Results: *Colony losses in bees:* For the 24 countries completing the surveillance network analysis tool (SNAT) a general weakness in most of the surveillance systems was identified. Key system components missing included, technical committee to develop procedures, integration with laboratory services, consistent definition of “colony losses”, protocols suitable to collect representative figures, relational data management tools and performance indicators.

The review of the existing surveillance data indicated a lack of representative data at country level and comparable data at EU level for colony losses. The major problem was the variability and validity of the epidemiological indicators reported.

21.073 Strengthening links in disease surveillance in the international setting

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Background: The International Society for Disease Surveillance (ISDS) was formed in 2005 and has a strong focus on syndromic surveillance. It has a number of subcommittees including a Global Outreach (GO) section. We aimed to determine which areas GO committee members felt GO was most likely to make an impact upon and what were the key topics for international group discussions.

Methods and Materials: A web-based survey of GO members was undertaken in January 2010. Participants were asked to rate on a 5-point scale their level of agreement to stemmed statements.

Results: 15/53 (28%) responded with all respondents completing all sections. The percentage agreeing (agree or strongly agree) with statements are presented.

Networking was identified as a key activity through which GO could bring about significant advances in disease surveillance.

47%	Advocating for national international policy on biosurveillance
73%	Identifying effective methods and technologies in biosurveillance globally
80%	Identifying biosurveillance needs globally
87%	Promoting global professional networking in biosurveillance

Innovation scored highly in areas that were identified as important for web seminars.

60%	International Health Regulations
80%	The role of major international organisations, governmental, non-governmental and private in global surveillance
87%	Significant transnational biosurveillance systems
93%	Innovative biosurveillance approaches in developing settings

Conclusion: The survey allowed engagement of committee members in setting the direction of the GO activity for 2010. Goals were further refined through group teleconferencing leading to an agreed approach for 2010. In response to the survey results members of GO organised webinars over the year, and a workshop on International Health Regulations at the ISDS 2010 Conference in December (www.syndromic.org). Where capacity for activity relies upon the voluntary engagement of a virtual group having a focused yet innovative programme of work is particularly important.



Q Fever in ruminants: The responses from 26 countries completing the questionnaire indicated that most of the MS do not carry out official monitoring or control programs. The review of available surveillance data highlighted problems of missing data, inconsistent case definitions and insufficient information to discriminate between prevalence and incidence epidemiological indicators.

Conclusion: Clear and specific case definitions should be specified for all disease events monitored by a system.

Integration with laboratory services and use of appropriate testing methods is essential, for emerging diseases negative results represent valuable information.

Consistent and robust epidemiological indicators calculated according to standard protocols for comparable populations should be defined.

Development of generic data models to facilitate data transfer and analysis at country and EU level is recommended.

Development of common performance indicators for surveillance systems would result in a robust standardised surveillance at EU level for emerging diseases.

21.076 Surveillance of arbovirus infections in the French forces: being less specific to be more efficient

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Background:

One of the issues of disease surveillance is to provide early warning from the beginning of unexpected outbreaks. The time necessary to confirm the biological diagnosis (preliminary step before epidemiological declaration) directly impacts the reactivity of the surveillance system.

Methods and Materials: In the French forces, disease surveillance is based on weekly report realized by military physicians for 64 epidemiological events of interest like diseases. For most of them a specific form is completed for each new diagnosis. Concerning arboviruses, three specific forms existed for Dengue, Chikungunya (since the 2006 outbreak in La Reunion island) and other arboviruses.

In parallel to this disease-based surveillance system, the French health service experimented a near real-time surveillance system in two overseas deployment areas (Djibouti and French Guiana). The system gather symptoms or syndromes (fever, diarrhoea etc...) and an automatic statistical analysis authorises rapid alarm in cases of unexpected incidence. This system is complementary to the weekly surveillance (alarms generally precedes clusters in weekly reports) but not yet implemented in all the overseas deployment areas.

Results: In 2006, a large outbreak of Chikungunya spread thought La Reunion island. This specific disease was not yet under surveillance which explains why the military disease surveillance system failed to early identified this problem. Six months after the peak, a retrospective cohort study among gendarmes deployed in Reunion showed a chikungunya seroprevalence of 19%. As well, the dengue outbreak in French Caraibes in 2010 was underestimated due to the lack of specific diagnosis.

The experience of both regular unexpected arbovirus outbreaks and syndromic surveillance conducted the French forces epidemiology and public health department to propose a new event to the weekly surveillance. This event is called Dengue-like syndrome. The unique form replace the three arboviruses forms and collects common symptoms to all arboviruses: fever, myalgia, headache, arthralgia, rash, gravity symptoms (bleeding, purpura, choc etc) and virological diagnosis when available. If not, the epidemiological context must be provided.

Conclusion: Facing regular arbovirus outbreaks (West Nile, Chikungunya, Dengue), the French military health service decided to enlarge surveillance to all dengue-like syndromes in order to avoid delay in epidemic alert.

21.077 VSD: A database for virus nucleotide sequence including epidemiological information

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Background: The representative databases of nucleotide sequence, GenBank, EMBL database and DNA Data Bank of Japan have contributed to collection and release of the original and authentic DNA sequence data. However, these databases provide insufficient epidemiological information regarding genotypes, serotypes, origin, isolation year and region (country) of pathogenic agents which are crucial factors for analysis of molecular epidemiology. The Korea National Institute of Health has constructed a nucleotide sequence database, Virus Sequence Database (VSD, <http://www.cdc.go.kr>) to supply epidemiological information as well as sequence data and genetic analysis tools.

Methods and Materials: The nucleotide sequence information was based on GenBank built by the National Center for Biotechnology Information, USA. The nucleotide sequence data queried from GenBank were curated by addition of epidemiological information which was searched from references. We selected RNA viruses which cause a frequent mutation of gene, highly pathogenic RNA viruses, and papillomavirus which is an agent of cancer.

Results: Databases of hantaviruses, flaviviruses, rotaviruses, enteroviruses, coronaviruses, noroviruses, human papillomaviruses, arenaviruses, ebola viruses, marburg viruses and henipavirus are now available. Among hantavirus sequence data, more than 50% were corrected or added information of the genotype, serotype and geographic origin. Genotype, originated country and host were also informed in other viruses of VSD. The VSD has features such as systemic curating scheme, supporting interfaces for rapid peer review, query generation and display fields selection, format conversion and quick link to various genetic analysis tools and Web-based administration of sequence data.

Conclusion: The VSD should provide important information for epidemiological researches as well as nucleotide sequence data.

21.078 GEMMA and ENPS—new tools for the analysis of functional protein complexes, lipoparticles and viruses

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Background: Noncovalent interactions of proteins are of great interest as they play a vital part in biology and medicine. Analysis of the formation process, stoichiometry, and molecular weight of those complexes can be very challenging as noncovalent interactions can easily be destroyed or biased when leaving specific native conditions

Methods and Materials: Differential mobility analysis (DMA) is a technique developed to classify charged aerosolized particles under ambient pressure according to their electrophoretic mobility diameter. In the recent years its working range was extended from μm down to the nm size range, or in terms of molecular mass, into the kDa to GDa molecular mass range, thus closing the gap between classic aerosol particle technology and MS. Combined with a modified nano electrospray source (nES) for nanoaerosol generation, and bipolar charging process delivering mostly singly charged ions it allows the analysis of intact biospecific protein complexes, viruses, virus-antibody and virus-receptor complexes delivering new knowledge.



Results: Here, we present new interesting applications of nES DMA technology with two types of instruments namely nES gas-phase electrophoretic mobility molecular analyzer (GEMMA) and parallel DMA (PDMA) with and without ENPS (electrostatic nanoparticle sampler). The presented applications show that differential ion mobility/GEMMA analysis is indeed suited to analyze high molecular weight noncovalent complexes, which are often in a molecular mass regime not accessible to MS with high accuracy. Furthermore, this technique is able to determine the size and size distribution of intact lipoprotein particles and subspecies in a convenient way. Additionally we demonstrate that it is possible to analyze such nanoparticles as tobacco mosaic virus (TMV) particles or candidate vaccines, and to collect a specific size fraction out of the rather polydisperse sample by means of ENPS. The TEM analysis of the sampled size fraction showed great uniformity of the collected viral particles and could actually reveal e.g. that the TMV was folded during the electrospray and droplet drying process.

Conclusion: The experimental results clearly show that singly charged nanoparticles (e.g., rod-like and spherical viruses, vaccines, lipoparticles or functional complexes) can be size characterized and collected by the GEMMA/ENPS or PDMA/ENPS system for subsequent shape/size and functional analysis.

21.079 Mobile technology for syndromic surveillance of livestock diseases in Kenya

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Background: Small-scale producers dominate livestock production in Kenya, so diseases of livestock have a direct impact on livelihoods even if they are not transmissible to humans. Despite the prevalence of livestock and close interactions between people, livestock, and wildlife, animal disease surveillance efforts in Kenya are limited and reports are slow to reach a central database. Real-time disease surveillance can be accomplished using mobile technology: mobile phone use is growing rapidly, and the technology has already been used in various sectors to transmit data from resource poor areas.

Methods and Materials: Building on existing open-source software including FrontlineSMS and the Android operating system, we piloted a community-based livestock disease surveillance system using mobile phone reporting in 10 villages in Asembo, Kenya in 2010. Reports of cattle, sheep, or goats showing particular syndromes (live birth, abortion/stillbirth, red urine, nervous signs) were submitted via SMS by designated animal health reporters and a team of animal health technicians responded to each case. Data on clinical signs were collected and submitted to a central database and diagnostic samples were sent to the KEMRI/CDC lab in Kisumu for testing.

Results: Reports were received from all participating villages throughout the study period, with an average of more than 10 reports per week. Based on the number of live births reported versus predicted, it is estimated that there was severe underreporting, with less than 1/4 of predicted events reported. However, the number of reports increased as the pilot study progressed. Throughout the pilot, we faced technological challenges due to inadequate electricity infrastructure and limited mobile network coverage.

Conclusion: Mobile phone technology can feasibly be used for real-time disease surveillance of livestock. However, although access to mobile phones is growing rapidly in Kenya, there are still challenges of implementation due to lack of electricity and network coverage in certain areas. Centralization of the SMS server in a location with consistent electricity and network coverage would help overcome these issues. Outreach, education, and diagnostic feedback are expected to encourage consistent reporting. A follow-up system is currently being implemented to build on the lessons learned in this study.

21.080 Social media and epidemiology: tweets indicate Norovirus outbreak at a university

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Background: It is not clear whether or not information from social media can enhance already established indicator-based surveillance of known infectious diseases. We examined a recent community outbreak of Norovirus at a university in Lower Saxony, Germany to determine if news articles and information posted to the websites Facebook, Twitter and blogs was faster than reporting through established indicator-based surveillance. This study was part of the Medical Ecosystem (M-Eco) project, an EU FP7 funded project, which aims to develop a new platform for information collection about health events 3.

Methods and Materials: We compared information from each day of the outbreak from local and state health authorities to information from Internet sources. We obtained news articles from an existing RSS-feed established to collect news on health and infectious disease in Lower Saxony from local online news websites. We entered outbreak-related search terms into Topsy, a search engine to analyse Twitter content, and Google to search for information from blogs or other Internet forums.

Results: An initial report from the university canteen to the local public health department occurred a day after first signs of infection, and a timely press report was formulated on August 12, 2010. Activity in all information sources followed this inquiry closely (Peak 1), and there was an increase of coverage from social media after official pathogenic test results from infected individuals were reported on Friday August 13, 2010 (Peak 2). The majority of news media, however, occurred after the weekend, on Monday August 16, which in turn also spawned more social media coverage that could be linked to the content in newspaper reports (Peak 3). A final peak occurred in social media a day later (Peak 4).

Conclusion: The first notification of this case was made by the canteen to the local health department, a report not required by established laws for indicator-based surveillance of Norovirus in Germany. News and social media followed. Social media was also used for information exchange about the event, creating more information and more noise, and potentially amplifying possible signals for monitoring purposes.

21.081 Horizon scanning—helping predict the next emerging infection

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Background: Horizon scanning is a key function carried out within Microbial Risk Assessment (MRA)—part of the Health Protection Agency (HPA)'s Emergency Response Department (ERD)—to identify emerging infectious disease issues and their possible threat to United Kingdom public health. Outputs generated from our horizon scanning are shared across the agency and communicated to other public health professionals interested in infectious diseases through monthly reports, mapping, risk assessments and scientific papers.

Methods and Materials: National and international sources are used for horizon scanning including: Promed, Health Protection Report, World Health Organisation, Emerging Health Threats, Eurosurveillance and World Organisation for Animal Health. Global disease outbreak data and issues of potential concern are scanned, inputted and stored within the Global Disease Outbreak Reporting System (GDORS) a database program developed by the HPA and this allows for bespoke interrogation and analysis and production of monthly and *ad hoc* reports such as disease profiles and risk assessments. Risks identified help steer our future work, both desk and field based.



Results: GDORS is used to automatically generate outputs such as the Monthly Global Disease Report or Geographical Information Systems disease mapping and this allows us to share information with others such as the UK multi-agency HAIRS (Human Animal Infections Risk Surveillance) Group, Government Department of Health and the Department for Environment Food and Rural Affairs (Defra). GDORS also promotes collaborative working both within the HPA and without, as it is designed for multiple users and data sharing.

Conclusion: Horizon scanning is a continual and iterative key function within ERD. It helps us to deepen our knowledge of infectious disease, share this knowledge with key stakeholders and provide advice to the public and public health professionals alike. The information archived within GDORS compliments and supports our expertise and research into infectious disease and will be used to help assess the risk of new and (re-)emerging infectious disease threats to the UK.

21.082 Surveillance and monitoring of an Influenza pandemic: a network of web-based platform

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Background: Systematic collection and analysis of epidemiological data and the timely dissemination of information are crucial during a public health crisis such as a pandemic influenza season. Influenza surveillance in most European countries is based upon Influenza-like Illness (ILI) consultations reported by GPs. During the last pandemic, the high prevalence and the high rate of consultations have raised the burden on the capacity of hospitals and health care centers to provide diagnoses and responses.

Influenzanet is a network of web-platforms used to measure ILI in the community for several European countries. The activity network intends to overcome the limitation of the state of the art surveillance systems by proposing an innovative ICT approach based on web2.0 tools.

Methods and Materials: The web-based platforms work with the Internet participation of the population to collect real-time information on the distribution of diseases through web services. The collaborative participation of users is achieved through targeted communication and recruitment. Individuals are recruited, via TV, Internet, radio. On registering, participants are requested to complete a short on-line background questionnaire containing demographical, medical and lifestyle questions. Thereafter, registered participants receive by e-mail a weekly newsletter with a link to a short symptoms questionnaire about their recent symptoms, if any and follow-up questions, including whether they sought medical assistance, whether they took any medication and changed their daily routine. The collection of data by means of the volunteers' activity allows researchers to estimate incidence of ILI, propensity to consult, delays to consultation, etc.

Results: During the last pandemic influenza, the network of Influenzanet platforms has been able to monitor ILI in the community all along the pandemic season, detecting a wider range of cases, unaffected by changes in care-seeking behavior (which varied widely from the beginning of the pandemic to the end). It was also possible to measure consultations and absenteeism rates, essential for forecasting and allocation of resources, behavioral changes, patterns of contacts with GPs, use of antivirals, uptake of vaccination.

Conclusion: In conclusion, the web-based platforms have proved to be a useful addition to the sentinel GP surveillance when the regular health system is under stress in a pandemic situation.

21.083 Identification of dynamic and consequences of an epidemic of highly pathogenic avian influenza in poultry farms using spread modelling

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Background: Highly pathogenic avian influenza (HPAI) virus has caused significant economic losses in the poultry industry. Modelling and simulation an epidemic is a key tool to understand the behaviour of a disease. The objective of this study was determined the dynamic and consequences of the spread of HPAI using stochastic and spatial simulation model. The results were usefully to determine the required surveillance efforts into specific areas.

Methods and Materials: Simulation model was performed using real poultry industry data from Castilla-León, an autonomous region in the north of Spain. The data included a total of 669 farms (broilers, breeders, layers and hatchers). InterSpread Plus (V.2.001.8©Massey University) was parameterised to simulate epidemics of HPAI. More than 50 parameters were included as input values which defined: poultry industry activity (movements between farms and to slaughter houses); poultry industry characteristics (density, census, biosecurity); resources (protection and surveillance zones, detection time) and infectivity of HPAI. *Risk of spread* value was evaluated using the mean of infected farms obtained for each farm. *Consequential values* were evaluated using the number of infected animals, the number of farms depopulated and time of depopulation. The Getis-Ord test has been applied to identify significative clusters or "hot-spots" of risk of spread value. The identification of critical parameters was made rerunning the analyses in eight scenarios changing in a 20% the inputs values.

Results: The estimated mean number of infected farms was 2.06 (SD=1.53), a 0.3% of total poultry farms. The estimated *consequential values* were 71.930 (SD=12.300) infected animals and 2.06 (SD=1.5) farms depopulated with a time of depopulation of 8-10 (days). Getis-Ord test identified 9 "hot-spots" within which the relative standard deviation was >7. The critical parameters were associated with local spread and trade movements between farms. Results were consistent with the spread of previous HPAI in other countries with similar poultry industry as Italy and Holland.

Conclusion: The results of this study contributes to the knowledge of dynamic of spread of HPAI which could help improve the surveillance and control programmes for HPAI in a national context.

21.084 Integrated disease surveillance program (IDSP): A long overdue initiative for Pakistan

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Background: Communicable diseases remain the most important health problem in Pakistan. The commonest causes of death and illness in the country are acute respiratory tract infections, diarrhea diseases, malaria, tuberculosis, vaccine preventable infections and Epidemic-prone diseases. A functional disease surveillance system is thus needed for priority setting, planning, resource mobilization and allocation, prediction and early detection of epidemics and monitoring and evaluation of intervention programs.

To respond to this need Ministry is pursuing a set of activities for developing a comprehensive disease surveillance program so as to become operational at community, health facility, district and national levels.



Methods and Materials: To start with Ministry initiated an assessment study with the support of WHO (Hq), World Bank, CDC-Atlanta and Infectious Disease Society of Pakistan to explore the existing situation of data collection, analysis, processing, its use and response for supporting both the communicable and non-communicable Disease Surveillance.

Subsequently an inter - provincial consultative process was initiated to decide about the list of priority diseases to focus under the new system and to develop a ten years National Strategic Framework on Disease Surveillance

Results: Some of main study findings are:

- A number of parallel systems existing under various programs.
- The existing programs do not cover non-communicable diseases.
- Need to bring the medical colleges and large tertiary hospitals and private sector into the reporting system.
- Surveillance must be not only for detection of epidemics but for rapid response.
- There is a need for increased use of information technology.

Conclusion: It covers both communicable and non communicable diseases and is response/ action oriented, is to integrate all existing surveillance activities of the disease control programs. A situation for pre-testing this plan occurred during October 2005 disastrous earthquake that hit the Northern province and areas of Pakistan, which led to massive mortalities and morbidities. Based upon the parameters drawn in the national plan an efficient surveillance system was experimented in affected districts and it averted a massive second wave of deaths that could have occurred due to injuries, distorted public health systems and emerging communicable diseases, like cholera, diarrhea, malaria and pneumonia.

21.085 Global Food Safety Portal: A visualisation tool to promote new research into data relations and assess trends, patterns and risk factors for foodborne pathogens

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Background: Foodborne diseases represent a major toll in terms of public health. With the recent trends in global food production, processing, distribution and preparation, there is a need for a better integration and public availability of the data collected and reported by monitoring programs in the food safety area. The objective of this web-based Portal is to integrate and display data from veterinary, food and public health monitoring programs from different countries with other possible relevant types of data (e.g. food consumption, production, or climate) to assess trends as well as to investigate associations, patterns and risk factors, through a user-friendly web interface.

Methods and Materials: A multi-relational database was constructed and, as a starting point, already publically available veterinary, food and human health data was included. The database will be updated with new categories of data as well with more recent data in the already existing explanatory categories. The portal is connected to other existing databases receiving automatic updates. An example is the WHO Global Food Network Country Databank (CDB), which collects data on *Salmonella* serovar distributions from 84 countries. All data in the portal can be visualised through an interface that allows the users to perform intuitive queries.

Results: Using some of the data in the portal (*Salmonella* prevalence, food consumption and production and general health statistics data), the user can query the data by serovar, country, region or product, having access to data from different years displayed through plots, charts and maps, and then compare, e.g. the evolution of different *Salmonella* serotypes prevalences in a country with the consumption patterns of certain food types in the same time period, but also look into demographic data that can be useful for interpreting the situation.

Conclusion: The possibility of combining different types of existing data can bring new insights into data relationships. The Food Safety Portal has the potential to become a reference tool in the food safety and foodborne disease surveillance field. The collaboration with WHO GFN assures the global perspective of the portal, which will be re-enforced with the gradual addition of new data on pathogens and their sources.

21.086 An interdisciplinary approach to Chagas surveillance: How the New Mexico Geo-Epidemiology Network addresses the challenges of a neglected disease

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Background: Chagas is a chronic parasitic condition that can reside latent in humans for decades before causing cardiac complications, often resulting in death. While Chagas has been endemic in Latin America for centuries, currently it is working its way north from Mexico into southern New Mexico, Arizona, and Texas. The recently formed New Mexico Geo-Epidemiology Research Network has initiated collaborations to investigate Chagas as an interdisciplinary program. The goals of the Network are to utilize the expertise of various biological, social, quantitative, computer, and physical sciences for effective surveillance on the vector *Triatoma dimidiata*, the parasite *Trypanosoma cruzi*, and the social epidemiology of Chagas.

Methods and Materials: Discipline-specific research often does not transcend to other research concepts, which is a barrier to surveillance solutions. To address this issue, a group of diverse researchers with a common interest in infectious disease gathered for a 3-day workshop to examine research perspectives, data analysis, and other approaches to the geography and ecology of infectious disease. The main goals were to integrate old concepts into new, effective collaborations on disease surveillance and to identify a specific regional problem that would benefit from these new approaches. Breakout groups identified knowledge gaps as a starting point for new surveillance techniques, with an initial focus on Chagas as it presents itself as a new border issue challenge.

Results: New surveillance strategies include tracking Chagas reservoir movement associated with long-term research on climate change, GIS vector and sentinel mapping, mathematical modeling, and information management. By combining research methods as a planned surveillance strategy rather than waiting for disease emergence, resources are effectively managed.

Conclusion: We believe the Geo-Epidemiology Research Network sets a positive example of how various disciplines can effectively work together prior to disease outbreak to model potential disease problems which in turn enables public health officials design effective solutions for lowering disease risk among vulnerable populations. The next step includes incorporating innovative technologies for emerging disease surveillance which should result in risk reduction for not only rural and poor populations, but also for occupational risks such as those encountered by border patrol agents.

21.087 SAGES: A suite of freely-available software tools for electronic disease surveillance in resource-limited settings

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Background: Emerging and re-emerging infectious diseases are a serious threat to global public health. The emergence of the novel 2009 influenza A (H1N1) virus and the SARS coronavirus demonstrated how rapidly pathogens can spread worldwide. This infectious disease threat,



combined with a concern over man-made biological or chemical events, spurred WHO to update their International Health Regulations (IHR) in 2005. *SAGES* aims to improve local public health surveillance and IHR compliance in resource-limited settings.

Methods and Materials: More than a decade ago, in collaboration with the US Department of Defense (DoD), the Johns Hopkins University Applied Physics Laboratory developed the *Electronic Surveillance System for the Early Notification of Community-based Epidemics* (ESSENCE). The current *SAGES* initiative leverages the experience gained in the development of ESSENCE; the analysis and visualization components of *SAGES* are built with the same functionalities in mind. Cognizant of work underway on individual surveillance systems components, e.g., collection of data by cell phones, we have focused our efforts on the integration of inexpensive, interoperable software tools that facilitate regional public health collaborations.

Results: *SAGES* tools are organized into four categories: 1) data collection, 2) analysis & visualization, 3) communications, and 4) modeling / simulation / evaluation. Within each category, *SAGES* offers a variety of tools compatible with surveillance needs and different types or levels of information technology infrastructure. In addition to the flexibility of tool selection, there is flexibility in the sense that the analysis tools do not require a fixed database format. The *SAGES* tools are modular in nature, allowing the user to select one or more tools to enhance an existing surveillance system or use the tools *en masse* for an end-to-end electronic disease surveillance capability.

Conclusion: We have combined electronic disease surveillance tools developed at the Johns Hopkins University Applied Physics Laboratory with other freely-available, interoperable software products to create *SAGES*. We believe this suite of tools will facilitate local electronic disease surveillance, regional public health collaborations, and international disease reporting. The US DoD Global Emerging Infections Surveillance and Response System welcomes inquiries on the *SAGES* tools from interested WHO-member countries.

21.088 Ecology, genetic clustering, and virulence of medically important bacterial and viral pathogens in Georgia

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Background: Georgia is a country with a significant endemic pathogen population of several especially dangerous pathogens (EDPs), and includes several class A select agents, such as *Bacillus anthracis* (the etiologic agent of anthrax), *Yersinia pestis* (the etiologic agent of plague), *Francisella tularensis* (the etiologic agent of tularemia), several hemorrhagic fevers viruses, and other medically relevant pathogens. Most of these pathogens appear in the Southern Caucuses region of the country of Georgia.

Methods and Materials: In this study, we are using several modern molecular diagnostics methods to begin surveillance and monitoring for these infectious disease agents of high public health and bioterrorism importance in the country of Georgia.

Results: Since the project's inception, two specific field expeditions have been completed and resulted in the surveying of over 300,000 hectares of land throughout Georgia and in the collection of over 5,000 samples (mosquitoes, soils, arthropod vectors, and animal and human samples). From these samples, 14 isolates of *B. anthracis* and 3 isolates of *F. tularensis* were identified. In addition, three samples tested positive for Crimean Congo Hemorrhagic Fever (CCHF) virus and four samples tested positive for tick borne encephalitis virus. Identification and confirmation of the CCHF virus positive samples represents the first human infection recorded for Georgia. Other medically relevant pathogens include several *Rickettsia* species that have been found in approximately 50% of the pooled tick specimens collected from selected regions of the country.

Conclusion: When fully implemented, this project, in collaboration with the US Department of Defense, the Defense Threat Reduction Agency and the UK's HPA, will significantly improve the surveillance capabilities and diagnostic infrastructure in Georgia, and will enable the country to properly monitor for the prevalence and distribution of EDPs.

21.089 Personalized event-based surveillance and alerting support for the assessment of risk

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Background: In a typical Event-Based Surveillance setting, a stream of web documents is continuously monitored for disease reporting. A structured representation of the disease reporting events is extracted from the raw text, and the events are then aggregated to produce signals, which are intended to represent early warnings against potential public health threats.

Methods and Materials: To public health officials, these warnings represent an overwhelming list of "one-size-fits-all" information for risk assessment. To reduce this overload, two techniques are proposed. First, filtering signals according to the user's preferences (e.g., location, disease, symptoms, etc.) helps reduce the undesired noise. Second, re-ranking the filtered signals, according to an individual's feedback and annotation, allows a user-specific, prioritized ranking of the most relevant warnings. We introduce an approach that takes into account this two-step process of: 1) filtering and 2) re-ranking the results of reporting signals. For this, Collaborative Filtering and Personalization are common techniques used to support users in dealing with the large amount of information that they face.

Results: We demonstrate the use of a multi-interest profile, which compactly allows users to define numerous criteria for filtering. Profiles can be decomposed by the system, so multiple interests can be automatically generated from the composite profile and be used to filter out undesired information. A key result is tackling the problem of equally ranked signals, by exploiting the information within the underlying document and metadata provided by the user, such as annotations and favorite items. This metadata are exploited to learn the user's interests. Moreover, by combining multiple sources (e.g., annotations, favorite items, external Web 2.0 and multimedia data) a more comprehensive computational view of the user can be built to help re-rank results according to system-learned user preferences.

Conclusion: We introduce a method to allow users to explicitly build a profile to facilitate access to personalized health events, alerts and apply the profile for personalized ranking for different users or groups to support filtering of signals and associated documents. This work is supported by the European Community's Seventh Framework Program (FP7/2007-2013) Medical Ecosystem: Personalized Event-Based Surveillance grant number ICT 247829.

21.090 Assessment of IDSR implementation at the Local Government level in Nigeria 2009

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Background: In 1998, the WHO AFRO countries endorsed the integrated disease surveillance and response (IDSR) as a strategy for disease surveillance and response. Nigeria commenced implementation in 2001. As the first line of disease surveillance and response, the Local Government Area (LGA) public health system is critical for the successful implementation of IDSR in Nigeria. We report here an assessment of the structure and functionality of IDSR at the local government level.



Methods and Materials: A cross-sectional survey using a staged sampling technique was conducted. The WHO Generic Protocol for the Assessment of National Communicable Disease Surveillance and Response Systems was adapted and administered to health officers in the selected LGAs. Data were entered and analyzed using the Epi Info software.

Results: Of the 24 LGAs assessed, 12 (50.0%) had a copy of the National IDSR Technical Guidelines and 18 (75.0%) had action thresholds for all the priority diseases displayed. In the 6 months preceding survey, 14 (58.3%) of LGAs lacked immediate notifiable disease forms and 13 (54.2%) lacked routine reporting forms. Only 46.8% (95) of the staff involved with IDSR had been trained on IDSR. Sixteen (66.7%) of the LGAs routinely carry out descriptive analysis of their IDSR data. Analysis of data by person, place and time was observed in 10 (41.7%), 13 (54.2%), and 12 (50.0%) of the LGAs, respectively. The majority of LGAs (79.2%) had not produced written reports in the preceding 1 year. Likewise, only 8 (33.3%) LGAs received feedback at least once from the higher level.

An emergency preparedness and response plan was observed in only 5 LGAs (20.8%) and a functional epidemic response team in 9 (37.5%). Of the 29 reported outbreaks within the preceding year, 25 (86.2%) were investigated. Only 7 (29.2%) of LGAs responded to their last reported outbreak within 24hrs.

Conclusion: The necessary IDSR tools and guidelines are not widely available at the local government level. IDSR implementation is not optimum in a majority of the local governments. These findings highlight the need for greater technical, material, and logistics support to surveillance activities at the LGA levels.

21.092

A Global, Web-based Food-borne Pathogen Annotated Tracking Resource Network (PATRN) System

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Background: Investigation of foodborne diseases requires the capture and analysis of many complex data types on microbial pathogens derived from multiple analytical methods, including phenotypic, genotypic, and genomic data. FDA, together with cBio, Inc., has developed a novel system, known as the Pathogen Annotated Tracking Resource Network (PATRN) system, to collect and manage such complex data types. PATRN captures isolate-specific data in a standardized, structured format and allows secure and controlled access to the data for sharing with multiple user groups.

The PATRN system consists of: a) an integrated database of expert-curated published data on foodborne pathogens, data from multiple types of experiments, and data from outbreak and surveillance activities; b) an architecture that enables users to store data in their own private, secure workspace; c) a facility for sharing private data with designated users; d) a workbench with computational tools for data analysis, and e) a live, secure website located at www.patrn.net.

Various data types, such as phenotypic and genotypic features, virulence factors and antibiotic resistance properties, GIS-based source locations, disease information, laboratory sources, and documented analytical protocols and reports are included. Being an assay- and organism-agnostic system, PATRN contains data for a variety of assays on a number of organisms. PATRN can potentiate the exchange of data with other resources used in outbreak investigations by food science regulatory groups. Beta-testing of PATRN's features and capabilities has commenced in collaboration with a cadre of five US food science regulatory laboratories. Curated and experimental data for *Escherichia coli*, *Cronobacter* spp., and *Listeria monocytogenes* is currently available and similar data for *Salmonella* spp., *Shigella* spp., and *Vibrio* spp will be added by October 2011, marking the end of the initial developmental phase of the project. In the meanwhile, we continue to build-out this system to provide a facility for users to attach raw data files linked to specific isolates and to aggregate isolate-specific information from a variety of sources.

Conclusion: PATRN aims to become a useful resource tool for the food safety community.

21.093

The medical ecosystem [M-Eco] project: Personalized event-based surveillance

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Background: Only the early detection of disease activity, followed by a rapid response, can reduce the impact of epidemics. It is the goal of the M-Eco project to complement traditional systems with additional approaches for the early detection of emerging threats. M-Eco addresses limitations of current systems for Epidemic Intelligence by more sophisticated event-detection technologies.

Existing State-of-the-art approaches that are based on supervised learning algorithms suffer from high initial and sustainability costs (i.e., manually labeling examples to train and update a classifier which detects disease reporting activity in social media). Given the dynamic nature of incoming documents (i.e. their the volume, variety, rate) any training set built using the blog documents can become easily outdated.

21.091

Using spatio-temporal modeling to predict exposure to ticks at a fine-scale and recommendations on the prevention and monitoring of Lyme borreliosis

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Background: Reducing exposure to ticks is currently *the most effective method of prevention* of Lyme borreliosis, which appears to pose a new public health problem in heavily urbanized areas. Therefore, the analysis of contacts between the routes that people adopt in forests (where ticks live) and the spaces and environments considered to be of risk (the most suitable habitat for ticks) constitutes a privileged avenue of study. So there is a need to study these spatial dynamics (and to model this contact), as well as to study ways in which it is possible to minimize risk via the landscape and design.

Methods and Materials: Two databases were created, one related to ticks that can transmit the infection and the other to trajectories of forest users. The first was fed by samples collected by the CNR of *Borrelia* (Pasteur Institute) in the forest of Sénart (France) during the years 2008 and 2009. The second gathered descriptive data on volume, variation and characteristics of human flow through the forest area (on the same period). This was done by surveying the population visiting the study zone.

Results: All the data have been entered into a GIS database. A characterization by geosimulation of the busiest portions of routes in relation to data on tick populations densities and distribution (and, in fact, a characterization of individual vulnerabilities on the type of socio-demographic profile associated with these portions) has then been conducted and has enable us to model human exposure to ticks according to the locations visited by users.

Conclusion: Various actions related to forest management will be discussed with the forest officers such as, for example, the closing off of certain areas at certain times of the year, the relocation or closure of some trails, or the changing of points of attractions for users in the forest. These proposals are part of a broad effort at prevention and health monitoring actions at different scales. So this paper deals with the issue of society's vulnerability in relation to environmental health risks and looks particularly at how to manage the public's use of forests in the context of an emerging health risk.



To overcome the high initial and sustainability costs associated with a supervised event detection, we rely upon the automatic labeling of training examples. Based on the underlying properties of the outbreak reports, we automatically label the sentences in the auxiliary data as positive or negative and use them for training a binary classifier.

We address the problems associated with the noisy and dynamic nature of blogs by exploiting the language in moderated sources, as a type of 'interlingua', which constrains the pattern a disease-reporting sentence can have within a dynamic source. Our experiments show that with no feature engineering and automatically labeled training data, we achieve an overall precision of 92% an accuracy of 78.20%.

Conclusion: The project work is highly user-driven, involving potential end users (e.g., epidemiologists working in health organizations) right from the beginning in requirement gathering, scenario specification and system evaluation. To find out whether Web 2.0 data is able to provide a valuable source of information for Epidemic Intelligence, the M-Eco Portal will be evaluated by different user groups. This includes health organizations at the State level: Niedersächsisches Landesgesundheitsamt; the National level: Robert Koch-Institut, Health Protection Agency, Institut de Veille Sanitaire; the International level: World Health Organization; European Centre for Disease Prevention and Control.

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21.094 Using an ecohealth approach to livestock production: community surveillance of newly emerging infectious diseases (nEIDs)

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Background: Traditional backyard poultry production in Vietnam exposes farmers to high risks of production losses as well as human health threats relating to of newly emerging infectious diseases (nEIDs) such as highly pathogenic avian influenza (HPAI). Possible culling and production losses result in loss of livelihoods, worsens rural poverty, and makes compliance in nEIDs surveillance programs less likely. Backyard poultry is the most common form of livestock in Vietnam with 80% of small scale farmers own some form of livestock. However, farmers lack management skills that can encourage engagement in nEIDs surveillance. Furthermore, surveillance programs have not targeted backyard livestock production (IMCAPI Hanoi, 2009). Attention has been focused on training, laboratory, and diagnostic systems for surveillance, rather than community level risks. It is important to partner with commune stakeholders (rural farmers, para-veterinarians, and community health workers) to encourage active surveillance, vaccination, and response (Hall and Ba, 2009). Training community stakeholders in an ecohealth approach to livestock production is needed to enhance capacity and facilitate behavior change toward proactive and responsible participation in nEIDs community surveillance.

Methods and Materials: The methods used for transfer of ecohealth knowledge include development and delivery of an ecohealth training course, participatory surveillance, and improved livestock production. Further training course relating to ecohealth approach in livestock production with focus on nEIDs community surveillance will be organized for local training-of- trainers (ToT) and commune stakeholders.

Results: Human resource development in ecohealth has been initially established in Vietnam through training and networking. As part of the South East Asia ecohealth network, nine Vietnamese persons were trained in ecohealth, and have started engaging in this area through development of research initiatives. Focus has been on ecohealth research addressing the reduction of risks of nEIDs through restructuring of sustainable small scale livestock production. Ecohealth messages and recommendation have reached various ministries; for example, through the report and dissemination workshop of the Midterm Evaluation of the UN- Government Program.

Conclusion: An ecohealth approach in livestock production can significantly and sustainably improve capacity in nEIDs commune surveillance, reduce precipitating factors of nEIDs, and improve health.

21.095 Using Craigslist messages for syphilis surveillance

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Background: This paper describes a novel method of conducting large scale syphilis surveillance by examining anonymous Craigslist posts by men who have sex with men (MSM).

A 2010 study by the Centers for Disease Control (CDC) shows a 39% increase in syphilis cases from 2006-2009. The majority of this increase is amongst the MSM community, specifically young black men. The anonymity and relative ease of finding partners on the Internet has facilitated a culture of casual sexual encounters encompassing a variety of unsafe sexual practices, e.g., anonymous partners, illegal drug use, unprotected sex, group sex, etc. These anonymous sexual encounters make it more difficult for public health officials to notify exposed partners.

Craigslist is a website specializing in online classifieds and contains a large community of casual sex participants. Our hypothesis is that a community's rate of risky behavior (i.e., unprotected sex) requests can be correlated to syphilis rates.

Methods and Materials: Daily Craigslist RSS feeds were collected for 416 sites around the United States (54,450,547 individual posts as of September 1st, 2010). 2,377,449 posts can be identified as MSM-specific and geocoded to counties in California. Messages were searched for keyword content to identify explicit requests for unprotected sex.

We used a weighted least squares, log-log regression model on panel data comprising 56 California counties over 5 quarterly time periods (Q3 2009 - Q3 2010). Our dependant variable was syphilis incidence rates and our independent variable was the rate of unprotected sex requests.

Results: Messages requesting unprotected sex were positively correlated with syphilis rates. A 1% increase in unprotected sex requests results in a 0.47% increase in syphilis rates, statistically significant at 1% level (coeff. 0.47; p-value < 0.001). These results suggest that we can use the changes in the rate of messages requesting unprotected sex to predict the changes in syphilis rates.

Conclusion: Craigslist messages contain useful information for disease surveillance. Keyword-based message classification techniques show that the rate of unprotected sex requests in MSM-specific messages can function as proxy for syphilis rates in California at the county level.

21.096 Samos: A community-driven open-access prediction market system

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Background: Prediction markets are a type of futures market in which users trade shares that pay off if the event to which they are connected occurs. They are used to aggregate knowledge on a large scale, since the prices of the various contracts can be interpreted as probabilities of their events. Since 2006, our group has been using prediction markets and testing their utility in predicting the spread and impact of diseases, including seasonal influenza, syphilis, and others on a market called the Iowa Electronic Health Markets (IEHM), found at <http://iehm.uiowa.edu>.

We are now moving into a new phase of development that will allow the community of users to submit proposals for new prediction markets which will then be approved by site editors and referees. We call the new system Samos.

Methods and Materials: Samos consists of the prediction market engine already in use coupled with a new proposal management system (Proposals) currently in development. Proposals provide a workflow for the submission, construction, and approval of prediction markets that is modeled after the workflow for the submission and approval of journal articles. This workflow is designed to ensure that submitted proposals conform with prediction market principles and are interesting and timely from a public health perspective. It includes an abstract, mock-up, and final write-up stage.



Results: We have developed a platform for eliciting ideas for prediction markets from a user community, transforming these ideas into contracts suitable for prediction markets, and encouraging collaboration among users.

Conclusion: Samos will soon be publicly available. We will run a live demo at the conference based on participants' suggestions; participants will be able to use the system to make predictions about emerging infectious disease related events at the meeting.

21.097 **Methodological supplies of African swine fever monitoring and preparedness in Ukraine by NSC 'IECVM'**

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Background: The European Union ASF Programs have badly low attention to treats of ASF traffic in EU through Ukraine. It is because the natural conditions in Ukraine soon become (as World Climate Changes will come) very similar to country with ASF' endemically distribution. Moreover, the Post-Chernobyl' polluted zone in Ukraine may be play as "bottle neck" for ASF agent biodiversity, like to Teschen Disease or other infectious agents. There we summarized NSC "IECVM" initiatives covering Ukrainian ASF' preparedness.

Methods and Materials: EU ASF Reference Laboratory (EU-ASF-RL) SOP on ELISA, IB and PCR for ASF diagnosis. Were used Protein A-HRP, batch 32400; ASF Ag, batch 351; ASF serum (limit), batch C14; ASF serum (positive), batch C87; ASF serum (negative), batch C48; ASF IB strips (all diagnostic manufactured in EU-ASF-RL); 96-wells plates, o-dianizidine and appropriate devices of Ukrainian origin were included in the study also. In another projects were used wild boar repellent Repellowit (Bio-Technik/Chemie WITASEK) for wildlife regulation and ticks extracts for pigs immunization.

Results: The conception of the traps to bloodless killing of migrating boars with use of repellents to form of trapping paths was developed. This conception will be implemented after it does discuss with colleagues from EU-ASF-RL. In frames of academician program the study of soft ticks' distribution started since its play as major factor of ASF natural foci formation. For this purpose we began the development of the techniques to porcine acarological seromonitoring. During June–August 2010 we checked 28 serum samples from swine herds (n=2) which had sporadically hemorrhagic diathesis in anamnesis and originated from Ukrainian survived zone (near border of Russian Rostov' Region). ELISA, IB and PCR tests demonstrate the negative results for ASF presence.

Conclusion: NSC "IECVM" implemented the ASF diagnosis SOP of European Union (CISA-INIA, SPAIN) and consequently became ready to conduct monitoring ASF for fulfill of EU and UKRAINE biosafety. Treat of ASF invades in Ukraine is still raised.

21.098 **Appropriate time-interval dosage of alcohol hand gel on reducing influenza-like illnesses among preschool children: A randomized, controlled trial**

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Background: School outbreaks of influenza-like illness have been difficult to control as most preventive bundles are difficult to follow.

Objective: 1) To study the efficacy of alcohol gel as a single, simple and in-expensive preventive strategy for Influenza-like illness among preschool children. 2) To evaluate the most appropriate time-interval hand hygiene with alcohol gel.

Methods and Materials: A cluster randomization (by classrooms) was performed at a kindergarten school in Bangkok, Thailand. A total of 1,437 students were categorized into 3 arms: use alcohol gel only before lunch (q lunch), every 120 minutes (q 120) and, every 60 minutes (q 60).

The absenteeism rates of Influenza-like illness among the groups were compared during endemic season (December 2009-February 2010). Each group was stratified for age, sex, household smoker, utilization of school bus service, history of breast feeding as well as history of vaccination.

Results: The absenteeism rates of Influenza-like illness (person sick days/ person present days) were 0.026, 0.021, and 0.015 in the group that use alcohol gel q lunch, q 120 and, q 60 respectively. Significant effects on reduction of absenteeism rates detected in comparing q 60 to q 120 (p=0.008) and comparing q 60 to q lunch (p=0.002); but not between q 120 and q lunch (p=.74).

Conclusion: Using alcohol gel in a regular 60-minute schedule could reduce the absenteeism rate of Influenza-like illness among preschool children. Day care centers and kindergarten schools should consider adopting this practice to reduce the common illnesses among children during epidemic.

21.099 **A rubella outbreak appears in unvaccinated border hilly districts of Chamba-Kangra, Himachal Pradesh, India, 2007**

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Background: A community member reported on 29th October, 2006 for increased number of cases of febrile rash with swollen neck glands in some villages of Chamba district. We investigated suspected measles cases to confirm diagnosis and propose control & prevention measures.

Methods and Materials: We defined a case of measles as occurrence of febrile rash in any resident of the eight villages between 20th October to 16th January, 2007. Having line listed case patients, we collected information on age, sex, residence, date of onset, symptoms, traveling, treatment history, vaccination status and pregnancy status. We described the outbreak by time, place and person characteristics. We confirmed diagnosis clinically, epidemiologically and serologically; first to measles, scrub typhus and later to German measles viruses.

Results: We identified 116 case patients in eight villages (112/116 clinically and 04/116 laboratory confirmed case patients). The overall attack rate (AR) was 11%; highest in the age group of 11-20 years (Range 13% to 44%, Median age 12 years). Sex specific AR for males was 12%. Complication rate was 05% but no death reported. No pregnant woman was affected. The number of cases peaked on 28th November and the last case was reported on 16th January, 2007. None of them were immunized against rubella. Of 116 case-patients, 113 were immunized against measles including (5/116) 4% with MMR immunization privately. Four tested positive for IgM antibodies to rubella out of eight samples. Only 33% (38/116) case patients took allopathic medicines.

Conclusion: German measles outbreak was confirmed. Frequent traveling of Bengali colony food vendor patients flared the outbreak. We advised the local health authorities to provide MMR vaccination to the unexposed in eight affected and neighboring villages.

21.100 **Utility of phosphorodiamidate morpholino oligomer (PMOplus™) technology in rapid response to RNA virus pandemics and epidemics**

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Background: RNA viruses are responsible for a number of emerging infections of pandemic or epidemic proportion, including influenza virus and dengue virus. Successful control is dependent on rapid identification of potential therapeutic agents. The anti-viral effect of phosphorodiamidate morpholino oligomer (PMO)-based technology can be enhanced by the addition of limited positionally specific positively charged piperazinyl moieties to form PMOplus therapeutics that increase selective interaction between the drug and its target.



Methods and Materials: Two rapid response exercises using PMOplus-based technology were initiated, one to identify a potential therapeutic against the 2009 pandemic H1N1 influenza virus strain and a second against dengue virus. In both exercises, conserved genome sequences were identified and candidate drugs were identified, synthesized and tested in efficacy models as quickly as possible.

Results: Rapid responses to the 2009 H1N1 pandemic influenza strain and to dengue virus were achieved in 7 and 11 days, respectively. For the H1N1 pandemic strain, conserved genome sequences were identified using the NCBI influenza database. The H3N2 mouse model was used to identify a lead PMOplus candidate (AVI-7100) targeting a viral segment translation start site. Efficacy against the non-adapted H1N1 strain was confirmed in a ferret infection model. For dengue, conserved genome sequences had been identified based on previous experiments using PMOs. The AG-129 mouse model was used to identify a lead PMOplus candidate (AVI-6006), and efficacy was confirmed in a non-adapted ferret model.

Conclusion: PMOplus technology is well-suited to provide rapid responses to newly emerging RNA virus pathogens.

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21.101 Effective planning for outbreaks by emerging infections: Pathogen traffic and activities of daily life

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Background: Government, industry, communities and households have an obligation to provide education and procedures to protect employees and maintain services during outbreaks of emerging infectious disease. The concepts of pathogen traffic—lifecycle and transmission strategies—is fundamental for the design of training programs for occupations with routine risks for exposure to infectious pathogens. The intersection of pathogen life cycles and the commonplace activities of animals and humans are the focal points of transmission of pathogens. Many examples illustrate the utility of identifying the risks of particular tasks and job assignments, what we have labeled the Job Risk Analysis.

Methods and Materials: During the 2009–2010 H1N1 influenza pandemic, industry and government programs to reduce staff illness emphasized general precautions. New York City with its large variety of municipal services developed a training model that categorized the risks of the daily tasks of staff according to possible exposure to influenza viruses. Specific modules for teachers, police, fire, food service staff, for example, were developed to be applied throughout the city's departments by managers trained to present the material.

Results: The enthusiastic reception and success of the Job Risk Analysis approach encouraged development of training programs for other infectious diseases. For example, mosquito transmitted and water borne infections among sanitation workers and blood borne infections among police, fire, and emergency response workers.

Conclusion: This Job Risk Analysis approach could be applied to other industries and government agencies.

21.102 Diffuse outbreak of hepatitis A suspected by national case based surveillance in Japan, 2010

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Background: Hepatitis A virus (HAV) is primary spread by faeco-oral route. Improved sanitation can reduce the chance of HAV exposition in childhood; however, as severity of the disease increases with age, people who have grown up without acquiring immunity may have substantial morbidity. In Japan, only less than 200 cases per year were reported to the national case-based surveillance for the last three years. The seroepidemiological study in 2003 indicates that about 98% of people less than 50 years old are susceptible to HAV. Therefore, when the number of HAV infection cases increased in 2010, several approaches to identify etiologic agents have done.

Methods and Materials: Infectious Disease Control Centre (IDSC), which analyses surveillance data and diffuses to the public, studied the reported cases confirmed by PCR or testing positive for HA-specific IgM antibody including no symptomatic cases. IDSC also worked with reference laboratories and related local health authorities for PCR testing and collecting epidemiological information.

Results: In week 10 of 2010, more than twice the number of HA cases were reported relative to the baseline. Through Ministry of Health, Labour and Welfare, IDSC had asked all local governments for PCR sample collection and epidemiological investigation until week 27 of 2010. There were 268 cases reported from various areas between week 1 and 28 of 2010. The reported number peaked at week 13 and 19, and then was reduced to less than the baseline in week 26 and 27. Median age was 47 (range: 5-88). Seven (3%, in their 40s-60s) developed fulminant hepatitis including one death. Histories of eating seafood such as oysters were most commonly reported and yet the long incubation period of HA prevented defining causative food and tracing them back. PCR testing was analysing in 59 cases as of week 34 (among 296 reported cases). Their results were being analysed and shared among municipalities through the newly started web system.

Conclusion: Although no etiologic agent was identified, the findings of not a few fulminant hepatitis cases appeal for rapid outbreak response. Analysing PCR data is expected to find commonalities and assist epidemiological investigation in the future.

21.103 Epidemiological features of Crimean - Congo hemorrhagic fever and description of control measures, South Kazakhstan oblast, Kazakhstan, 2009–2010

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Background: Crimean-Congo Hemorrhagic Fever (CCHF) is an emerging disease in Europe of varying risk of mortality, recently 3.2% in Russia. The virus is transmitted to humans through tick bites, exposure to viremic livestock, or contact with blood. South Kazakhstan oblast (SKO), an endemic area, has reported <11 human cases annually since 2000 but in 2009 and 2010 the numbers of cases increased dramatically. We describe the epidemiology of CCHF cases in SKO and the introduction of control measures.

Methods and Materials: During 2009–2010, epidemiologic, clinical and environmental data of cases were collected weekly from all SKO districts using a special report form. Data on hospital prevention and tick control measures were obtained through interview with Sanitary Service workers and veterinarians.

Results: In 2009–2010, 39 cases were reported with 30 confirmed by serology; 11 (28.2%) resulted in death. Thirty-one (79.5%) cases were >17 years old. Twenty-two (56.4%) cases had tick bites suffered near households or worked with livestock affected by ticks, six (15.4%) cases were acquired nosocomially, one (2.6%) case occurred in a neonate born to a mother with CCHF and 10 (25.6%) cases were acquired via unknown means. In 2009-2010, >15,300 people with tick bites were registered in the SKO tick bite program meant to identify persons at risk for CCHF. For control of ticks, zones of treatment were created around households and livestock were treated, once in 2009 and thrice in 2010. In 2010, hospital personnel were additionally trained on recognition of CCHF and use of personal protective equipment (PPE) but existing PPE included cotton masks which do not adequately protect against CCHF. Livestock workers did not use personal tick protection measures.

Conclusion: The reason for the upsurge in cases in 2009-2010 is uncertain, with the main modes of transmission being tick bites and nosocomial. Control measures were based on this epidemiology but need to be evaluated. In particular, the effectiveness of tick bite reporting and tick control measures need to be assessed and the high proportion of cases acquired nosocomially indicates PPE measures must be strengthened. Reasons for the high case-fatality rate must be determined.

**21.104 Investigation of a multi-prefectural outbreak of Enterohemorrhagic Escherichia coli O157 infection—Japan, 2009**

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Background: In the last decade in Japan, approximately 4,000 patients with Enterohemorrhagic *Escherichia coli* (EHEC) infection have been reported annually, and the number has not decreased. Previous food poisoning outbreak investigations have not focused on the intermediate meat processing factories (IMPFs) as potential sites of contamination or intervention. In November and December 2009, a multi-prefectural outbreak of EHEC O157 associated with Korean-style barbecue chain restaurants was reported. We investigated this outbreak and identified structural cross-contamination risks at an IMPF.

Methods and Materials: We investigated 21 laboratory-confirmed patients with detailed dining history within 14 days before symptom onset, conducted an innovative matched case-control study enrolling controls among customers of the same chain restaurants during the outbreak period using the Internet and investigated a traced-back IMPF in collaboration with the 14 local health departments. Various food samples were collected and cultured for EHEC. We also quantified the proportion of contamination for 50 specimens of the implicated meat after the IMPF for five days. However the unprocessed lot of the meat was not left to test.

Results: Based on descriptive epidemiology and a case-control study, beef diaphragm (hanging tender) imported from Canada was identified as the source (odds ratio=14.6; 95% confidence interval 2.3–91.7). Once it was removed from the menu, the outbreak ended. Two hundred kilograms of diaphragm, equivalent to 2,000 servings at restaurant, per day had been simultaneously processed at the IMPF. On average, over the five days investigated, the proportion of contamination was 34% (95% confidence interval 22.4–47.9%) equivalent to 3,400 servings.

Conclusion: The cross-contamination at the IMPF magnified the outbreak. However, unclear food safety regulations for IMPFs made public health intervention difficult. Based on our findings implicating the IMPF in EHEC transmission, the National Committee for Food Safety highlighted the importance of assessing and managing risk at IMPFs in its recommendations to the Ministry of Health, Labour and Welfare (MHLW). In addition, MHLW shared the result of this investigation as precaution with the Canadian government several months later.

21.105 Causes of death as reflected by hospital records in Pakistan

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Background: The information on the magnitude and pattern of mortality is essential for planning and evaluating health policies and programs. However, like many other developing nations of the world, Pakistan lacks an established system for generating mortality data and if it is recorded mostly ignore cause of death. Whereas, using standard and reliable case definitions for labeling a cause of death is important to assess the mortality patterns. It helps decision makers to take evidence based decision making. Keeping in view its importance and the problems of the ground situation, the National Health Management Information System (HMIS) Cell designed a study in collaboration with the WHO. The main objective of this study was to assess the mortality patterns reflected through the hospital records in Pakistan by using the WHO's ICD-10 criteria.

Methods and Materials: Twenty three major hospitals were selected in all the four provinces and Azad Jammu and Kashmir (AJK) and then data was collected through examining the hospitals records. The data collection forms and guidelines were already circulated to all the hospitals in order to consolidate their mortality information according to ICD-10 classification. While extracting the mortality data, age, sex and cause of death were taken into account.

Results: The analysis of the major causes of death shows that total deaths belonged to four major groups which include Cardiovascular diseases, Other infections/parasitic infections, Unintentional injuries and Respiratory infections. Among Unintentional injuries 56% are Road Traffic Accidents which is often neglected aspect in the developing countries. In children Meningitis, Measles and Tetanus was found to be the leading causes of deaths. Among infants Pneumonia is the highest contributor of the total infant deaths followed by Neonatal Sepsis and Septicemia, low birth weighed/ Prematurity and Respiratory distress of Newborn. These analyses give very clear picture about which group and disease need to be targeted.

Conclusion: Like other developing countries, Pakistan lacks an efficient health information system at the hospital level with a potential to provide the basic evidence information on disease and mortality patterns. There is also need for establishing the vital registration systems and integrating these with the hospital based registration system.

21.106 Cluster of cutaneous mycobacteriosis in a school in Rome, school year 2009–2010

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Background: On February 10th 2010, a dermatology hospital in Rome notified seven cases of non-tuberculosis mycobacteria (NTM) in children attending the same school with a swimming pool. An epidemiological investigation was initiated to describe the cluster and prevent further cases.

Methods and Materials: A case was a person attending the school in 2009-2010, with skin lesions based on clinical examination (suspect), histopathology results of skin biopsies (probable), and positive culture (confirmed). To identify new cases, we screened students aged three to ten years for skin lesions between March-May 2010, and collected information on swimming pool use. Cases' parents were interviewed. Environmental samples were collected from the school and swimming pool.

Results: Until June 2010, 18 cases were identified (two confirmed, six probable, ten suspect) among 514 primary school children (3.5%). All cases (six boys, 12 girls) attended the swimming pool between October 2009 and March 2010. Onset of symptoms of all the cases was between November and February. None had an underlying health condition. Among nine available samples for culture examination, two tested positive for *Mycobacterium chelonae* complex (Group III, *M. abscessus*). Attack rate for swimming pool use was 13.1% (17/130), with a relative risk of 54.7 (9.4 - inf). No cases were reported among students not frequenting the swimming pool. Consistent with previous reports, we could not identify any evidence of person-to-person transmission.

Environmental samples were positive for NTM but could not identify *M. abscessus*. The swimming pool was treated in April 2010 following WHO-guidelines for recreational waters. No cases were reported thereafter.

Conclusion: We report on the second largest cluster of cutaneous *M. abscessus* suspected to be related to a swimming pool. No specific guidelines exist on prevention of NTM, which are not included among water quality indicators in Italy. Furthermore difficulties in diagnosis, characterization, and environmental investigation hinder the establishment of a strong correlation between exposure to the swimming pool and disease among children.

**21.107 Evaluation of preparedness status of provincial laboratories in Kenya to respond to public health emergencies, 2010**

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Background: Public health laboratories play a key role in the diagnosis, management, monitoring and prevention of outbreak prone diseases. In Kenya, questions have been raised on readiness and ability of our provincial laboratories to detect, predict and respond to public health emergencies of communicable diseases such as cholera outbreaks. We assessed provincial laboratories to identify gaps in disease outbreaks response and emergencies preparedness.

Methods and Materials: WHO laboratory assessment checklist was administered to the staff of the eight provincial laboratories and Centers for Disease Control and Prevention enteric laboratory. Specific indicators were equipments, reagents, data analysis, reporting and outbreak participation. Frequencies and proportion were calculated.

Results: Nakuru provincial laboratory had the highest score of 82% while Kakamega provincial laboratory had the least score of 52%. The scores for specific indicators varied across the provincial laboratories. Average equipments score for provincial laboratories was 48% (range 27–61) compared to CDC laboratory score of 60 % ($p < 0.001$), and average reagents score for provincial laboratories of 70% (range 39–95) compared to CDC laboratory score of 62 % ($p < 0.05$). Analysis and tests performed by provincial laboratories scored on average 70% (range 48–135) compared to 21 % ($p < 0.05$) of CDC laboratory. Reporting, analysis and communication score was 55% (range 35–86) compared to CDC laboratory score of 100% ($p < 0.05$), and in outbreak participation the provincial laboratories average score was 40% (range 7–75) compared to the CDC laboratory score of 71 % ($p < 0.05$).

Conclusion: There were significant differences between provincial laboratories and CDC laboratory in all the indicators assessed. There is need to improve laboratory infrastructure, maintenance of equipments, supply of reagents, reporting of diseases in order to effectively monitor and respond to public health emergencies.

21.108 Highland malaria outbreak in Homeyo District, Papua Province, Indonesia: an entomological investigationA. Oktavian¹, H. Kawulur¹, M. Widiyanti¹, M. Raharjo¹, D. Triboewono²¹National Institute of Health Research and Development for Biomedicine, Papua Province, Jayapura, Indonesia, ²Research and Development Centre for Vector and Disease Reservoirs, Salatiga., salatiga, Indonesia

Background: The first highland malaria outbreak and associated deaths was reported in May 2010 from several villages in Homeyo District, Papua Province. Homeyo is located more than 1900 M above sea level with 15–25°C air temperature, an uncommon condition for mosquitoes to breed. The epidemiological and parasitological survey in June 2010 conducted by the Papua Health Department found Plasmodium Falciparum Rate (PFR) in Bamba, Sanepa, Pogapa and Degesiga villages were 44.23%, 6.73%, 20.27% and 7.40%, respectively. Based on verbal autopsy, the team found 36 death cases due to malaria suspect.

Methods and Materials: The entomological survey was intended to identify the species and breeding habitat of suspected mosquito vectors, and the distribution of the highland malaria cases related to the village location and human behavior.

The survey was carried out from 30 August to 3 September 2010. We collected larva and adult stage mosquitoes from the breeding habitat, malaria case mapping with Global Positioning System based on the location of case's houses, environmental observation, short interview and blood test using Rapid Diagnostic Test.

Results: Although neither larva nor adult stage of Anopheles Sp was caught due to the heavy rain and limited time of survey, we found that the opening of new land program were likely to play an important role in creating a new mosquito breeding site, including many new ponds with no fish and ground pools with ideal temperature, salinity and pH. Further, the indigenous Papuan live in traditional wooden houses (called Honai),

without window and light and only fireplace at night. The case's houses were located close to the breeding habitat and within a flight range of Anopheles.

Conclusion: A more systematic and sustainable health education program is needed to raise public health awareness. The use of Long Lasting Insecticide Nets is the best choice for this area.

21.109 Epidemiology, clinical and paraclinical features of definite cases of influenza A (H1N1) in Kashan-Iran 2009A. Hasan¹, M. Momen Heravi¹, Z. Soleimani², A. Sharif¹¹Kashan University of Medical Sciences, Kashan, Isfahan, Iran, ²Kashan University of Medical Sciences, Kashan, Isfahan, Iran

Background: Influenza A(H1N1) is considered as a major concern for health care system and imposes a considerable burden on the community. This study was conducted to evaluate the pattern of the disease in influenza A(H1N1) patients in Kashan.

Methods and Materials: This descriptive study was carried out on 87 definite cases of influenza A(H1N1) diagnosed from July to January 2009 in Kashan. RT-PCR was performed in all patients with severe flu like symptoms for confirm diagnosis. The demographic and clinical and paraclinical information through reviewing medical records were collected and analyzed by SPSS.

Results: 44(50.6%) of patients were male and the rest (49.4%) were female. The majority of patients were in age group 16–25 years with mean age 30.1±18.5. The most common clinical symptoms were fever(92%),cough(78.2%),dyspnea(54%).Fever was the most common physical findings.The most important paraclinical findings were: leukocytosis(41.3%),increased ESR(46.6%),positive CRP(48.7%),Abnormal liver function test(19.1%) and increased CPK(29.5%) and LDH(73.7%).The most common underlying disease was chronic renal failure. The mortality was seen in 8 patients(9.2%).

Conclusion: Regarding to mortality of influenza A(H1N1), early and good management of each severe case of influenza is recommended. Because of majority of death has occurred in patients with underlying disease, annual prophylaxis by influenza vaccination and early treatment to prevent of morbidity and mortality is recommended.

21.110 Inactivation of several BSL3 viral pathogens by disinfectants and nucleic acid lysis buffersF. X. Abad¹, D. Solanes¹, M. Domingo²¹Centre de Recerca en Sanitat Animal, CReSA. UAB-IRTA, Bellaterra, Barcelona, Spain, ²CReSA. UAB-IRTA, Bellaterra, Barcelona, Spain

Background: The research in BSL3 and BSL4 viral pathogens, some of them emergent, has been strongly increased in the last years all over the world. The increase in their handling and experimentation can lead to an increase of incidents, accidents, spillages, spillovers, which have to be faced up to by disinfection. Routine disinfection also needs real data on effectiveness of currently used disinfectants. Also, safe transfer of inactivated material is only possible if we trust on our nucleic acid extraction procedures.

Methods and Materials: Suspension test of disinfectants (70% ethanol, Virkon 1% and 0.1%, Limospetic 1%, 4% acetic acid, 500 ppm and 50 ppm free chlorine from house hold bleach) at currently applied contact times on West Nile virus (WNV), H7N7 and H7N1 highly pathogenic avian influenza virus (AIV), virus Chikungunya (CHIKV) and swine vesicular disease virus (SVDV) were performed. Some lysis buffers from marketed nucleic acid extractions kits were also assayed, following manufacturer's instructions, in their ability to inactivate the aforementioned viruses. Each disinfectant, and lysis buffer, was assayed in triplicate and titrated twice.

Results: All disinfectants succeeded in the inactivation of the assayed viruses when suspension tests were performed. The reduction in viral infectious titres was reported between 2 and 5 log₁₀ TCID₅₀ taking into account the specific toxicity of each disinfectant formulation. No residual infectivity was observed at the end of contact times for all the enveloped viruses, meanwhile residual infectivity of SVDV was recorded in some disinfectants and conditions.



Most of the marketed lysis buffers were also effective in the reduction of viral infectious titres. However some of them failed in the complete inactivation of SVDV.

Conclusion: Results indicate that currently used disinfectants in our facility can overcome the potential risk of an incidental overspill of BSL3 pathogens. Lysis buffer were mostly but not totally effective, so a general rule can not be set up and a case by case rule with in house assays should be performed.

21.111 Control measures and response on West Nile Virus during the outbreak in Northern and Central Greece

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Background: In early August an outbreak of West Nile Virus (WNV) was detected in the region of Central Macedonia in Northern Greece. The first cases were hospitalized with symptoms of meningo-encephalitis at the Hospital for Infectious Diseases in Thessaloniki. Laboratory confirmation of the cases has been performed at the Reference Laboratory for Arboviruses. As of 17/09/2010, 230 cases including 23 deaths of WNV had been reported along with five cases in horses.

Methods and Materials: To control the outbreak, a Crisis Management Team has been appointed and Public Health Measures were applied in five axes:

- Surveillance of human and animal vectors, increasing awareness of health care professionals and general population on West Nile Disease
- Control of mosquito population in areas where cases occurred and in areas where large population of mosquitoes was monitored
- Sensitization of the affected population
- Implementation of blood safety measures

Results: Healthcare workers in 19 hospitals and 49 health care centers were trained and health education was provided to general population of 74 affected locations. Moreover, 149 sprayings with ultra low volume were applied in order to control mosquito population.

Integrated mosquito control includes source reduction such as appropriate sanitation and water management, which are the most drastic and cost-effective methods to eliminate larval habitat breeding and to provide long-term mosquito control.

Conclusion: The expected result is the reduction of WNV cases. This can be achieved through the elimination of mosquito population and the sanitization of breeding sites. Moreover, in order to evaluate the efficacy of the implemented measures and to plan further intervention, reliable epidemiological data regarding vector population are needed.

With the above mentioned measures and interventions the maximum positive effects on Public Health can be achieved.

21.112 Characterization of *Cronobacter sakazakii* strains from two recent neonatal meningitis cases and comparison of historical archival strains using PATRN, a novel global web-based pathogen tracking system

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Background: Food and Drug Administration of US of America (FDA) is developing a pilot scale project named "Pathogen Annotated Tracking

Resource Network (PATRN) system (www.patrn.net)" to assist its efforts in outbreak surveillance and management. We are presenting an unexpected application of this database system in the analysis of an recent outbreak. In the summer of 2010, two cases of *Cronobacter* spp. associated neonatal meningitis occurred in the United States.

Methods and Materials: Three isolates were obtained from blood and cerebral spinal fluid cultures and a fourth isolate, derived from an infant's pacifier, was obtained from one of these cases. All four isolates were identified as *Cronobacter sakazakii* by phenotypic and *rpoB* PCR analyses and they were positive by PCR for the genus-specific target, *zpx* (zinc-metalloprotease). They all possessed the O2 LPS molecular serotype determinant. PFGE analysis showed that there were three band differences among the strains (97% relatedness) which by optical mapping were shown to be due to the presence of three indel regions (59, 37, and 14 kb). Plasmid analysis using *repA* PCR revealed that all isolates harbored a pESA3-like (RepFIB) and a pCTU3-like (incH12/incLM) plasmid, but not a pESA2-like (incFII) plasmid. PCR analysis of seven RepFIB plasmid-borne loci showed that the plasmids carried *aitCBAD* and *iucABCD/iutA* (iron acquisition systems), *cpa* (*Cronobacter* plasminogen activator), and a type VI secretion system locus, but not *thaB* (filamentous hemagglutinin gene).

Results: This data was compared against the strain information in the PATRN system. Simple cluster analysis showed that the four outbreak strains matched two known records. Hierarchical cluster analysis of these plasmid loci showed that these strains grouped within Clade 1A which previous studies had shown to contain the sequenced strain, BAA-894. One of which, Jor172 was isolated from an unknown spice sample in Jordan in 2008; and the other, E772 was isolated from a milk powder sample in France in 2006.

Conclusion: In summary, the combination of molecular methods with bioinformatics tools in PATRN was highly effective in connecting related strains from two recent cases to known archival strains. PATRN is a useful resource tool for the food safety scientific community.

21.113 *C. difficile* in a hospital in Vienna before and after implementation of CDI control measures, Austria, 2009–2010

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Background: The occurrence of *C. difficile* ribotype 027 has been associated with hospital outbreaks of *C. difficile* infection (CDI). In Austria, only sporadic cases were documented until March 2009, when an increase of CDI cases was observed in a 1146-bed hospital in Vienna (Hospital X). The dominant ribotype was 027. The study objectives were to describe the 027 CDI outbreak and to assess the effect of implementing evidence-based CDI control measures in August 2009.

Methods and Materials: Surveillance case definition for hospital-associated CDI was used according to the European Study Group for *Clostridium difficile* (ESGCD). CDI cases associated with Hospital X that occurred between March 2009 and November 2010 were included. The National Reference Center for *C. difficile* performed PCR ribotyping of submitted *C. difficile* isolates, as described elsewhere. An outbreak case was defined as a patient with hospital X-associated 027 CDI, who became ill between March and July 2009. We compared the number of hospital X-associated CDI cases before and after intervention (March-July vs. August-December). We analysed the annual trend of Hospital X-associated CDI cases in 2010.

Results: From March to July 2009, 152 hospital-associated CDI cases were identified in Hospital X. Out of these, 32 cases fulfilled the definition of a 027 CDI outbreak case. After introduction of the control measures, a 48.7% reduction of hospital-associated CDI cases was observed (March-July: 152 cases; August-December: 78 cases). In 2009, ribotype 053 accounted for 34.2% of the 152 isolates typed, and ribotype 027 for 24.3% in Hospital X. In 2010, a total of 336 patients with CDI were identified in Hospital X: among 72 isolates ribotyped, 027 (20.8%) was the dominant strain followed by ribotype 239 (12.5%) and 053 (9.7%).



Conclusion: Achieving a 50% case reduction following the introduction of CDI control measures indicates moderate effectiveness of the CDI control measures, which might be due to insufficient compliance with the recommendations. Ribotype 027 is still the dominant *C. difficile* strain in this hospital that experienced the first documented outbreak of 027 CDI in Austria.

21.114 Sero prevalence of Dengue 2 virus infections in patients presenting with febrile illness in selected health facilities in Trans Nzoia Region, Kenya

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Background: The Dengue virus is a Group IV +sense ssRNA ~10.5kb, member of the virus family *Flaviviridae*, *genus flavivirus* and species Dengue virus. It is an enveloped, spherical virus, measuring 40-60nm in diameter. There are four serotypes of Dengue Virus (DENV).

Methods and Materials: Sample was serum from blood collected from hte patients who gave consent.

- Plaque reduction neutralization assays
- Indirect IgG and IgM capture ELISA

Results: Although the study was focused on Trans Nzoia, patients who visited the selected health facilities came from 5 Provinces, with majority from Rift Valley Province. Females were more than males with the ages of 5years and above being involved in the study. Clinical Presentation There were seven symptoms presented by the patients, with some of the symptoms more common than others . Fever was the most common symptom in all the patients. A total of 1121 patients were screened for Dengue 2 virus infection from Trans Nzoia by ELISA, out of which 50 were found to be positive. The health facilities did not get the same number of positive patients. Kitale district hospital had the highest positive cases followed by Andersen medical centre. Endebs had only two cases Confirmation of Positive Samples by PRNT was done on all the 50 positive samples by ELISA procedure to check for the presence of neutralizing antibodies in the patient's serum, but only 5 samples completely neutralized.

sero prevalence found to be 0.9% with most of the positive patients from Kitale district hospital.

Conclusion: Considering that Trans Nzoia District is far from the coastal regions where Dengue 2 virus epidemic was first reported in Kenya, the sero prevalence shows that it might be a re-emerging infection which could now be spread throughout the Nation. The rate at which it is spreading should not be taken lightly because the sero prevalence might be high at the coast and the regions around it. Although DHF has never been reported in Kenya, it might eventually occur if dengue infections are not controlled because the vectors might be on the increase.

21.115 New flavivirus in Europe: Bagaza virus outbreak in partridges and pheasants in Southern Spain, 2010

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Background: In the past two decades, several arboviral diseases, and particularly, diseases caused by flaviviruses, have undergone remarkable invasions to territories beyond their traditional geographic range. West Nile virus in America, Usutu virus in Europe and Japanese encephalitis in Australia are notable examples of these flavivirus "leaps". Here we describe an outbreak of disease in wild birds (partridges) that occurred in the province of Cádiz, Southern Spain, in September 2010, caused by a flavivirus, Bagaza virus, which has not been reported before in the European continent. Bagaza virus (BagV) was first isolated in Bagaza,

Central African Republic, in 1966, from a pool of *Culex sp.* mosquitoes. Subsequently, it has been isolated also from mosquitoes in different Western African countries and in India, where serological evidence suggests that this virus could be able to infect humans, though its pathogenicity in this species remains uncertain.

Methods and Materials: Virus detection and identification in samples from affected birds was achieved by heminested pan-flaviviral RT-PCR followed by nucleotide sequence of the amplicon. Virus isolation was performed by inoculation of embryonated chicken eggs and confirmed by heminested RT-PCR and sequencing. Complete nucleotide sequence of BagV was achieved from organs of one of the affected partridges, through RT-PCR amplification and subsequent nucleotide sequencing of the amplicons using a set of 27 primer pairs specifically designed for this work based on the BagV sequences already available in GenBank. A phylogenetic tree was built with the complete sequence of the BagV from this outbreak and other 32 complete nucleotide sequences comprising a wide range of flaviviruses, including two BagV representatives.

Results: Diseased wild birds (red legged partridges and common pheasants) were negative for West Nile virus, but resulted positive for flaviviral genome. Bagaza virus was identified after partial nucleotide sequence analysis, which was confirmed after complete nucleotide sequence analysis. The virus was isolated in embryonated chicken eggs. Phylogenetic analysis showed a close relationship to Bagaza viruses from Central African Republic and India (94.1% and 92.8% identity, respectively).

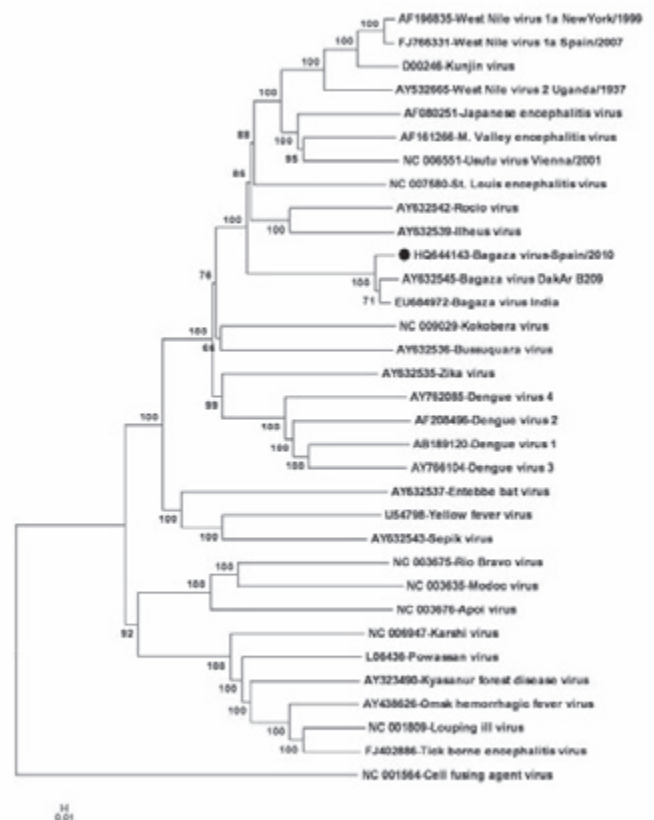


Figure 1. Phylogenetic tree showing relatedness between BagV full-length nucleotide sequence from this work (closed dot) and 32 complete sequences from other flaviviruses.

Conclusion: Bagaza virus, an as yet unknown flavivirus species in Europe, has been detected, and isolated, for the first time in Spain, affecting lethally a flock of partridges and pheasants.

**21.116 Invasive *Klebsiella pneumoniae* liver abscess syndrome broadens its horizons**D. O'Shea¹, R. Moore², G. Sheehan³, T. Geoghegan²¹Mater Misericordiae Hospital, Dublin, Ireland, ²Mater Misericordiae University Hospital, Dublin, Ireland, ³Mater Misericordiae University Hospital, Dublin, Ireland

Background: Primary liver abscess due to *Klebsiella pneumoniae* is an emerging infection, first described in Taiwan in 1986 by Liu et al. They reported seven cases associated with endophthalmitis occurring between 1981–1985. The specific entity of primary invasive liver abscess due to *K pneumoniae* has now been widely reported within Asia and also in other regions throughout the world. A strong association with diabetes mellitus and impaired glucose tolerance exists. Capsular serotypes K1 and K2 are considered the most virulent strains and are associated with metastatic sites of infection, a cause of significant morbidity. Other virulence factors have also been identified such as *rmpA* and *magA*. Quoted mortality rates are considerably lower than historical mortality rates attributed to pyogenic liver abscess. To date there have been few case reports in the literature of this syndrome in Europe and none within the United Kingdom(UK) and Ireland.

Methods and Materials: We present a case series of primary invasive liver abscess due to *k pneumoniae* from Ireland, involving a native Irishman and two immigrants from the Philippines and China respectively. All had *k pneumoniae* in blood cultures on admission in association with a liver abscess.

All *Klebsiella* isolates were sent to the Health Protection Agency in the UK for serotyping. Analysis was conducted using a Qiagen multiplex PCR kit to identify, a) serotype specific targets for capsular types K1, K2, K5, K54, K 57, K20; and b) the presence of the virulence factor *rmpA*.

Results: All patients were diabetic; two of the patients diagnosed on presentation; the other having been recently diagnosed. One patient had evidence of metastatic infection at presentation. All patients achieved cure following percutaneous drainage and prolonged anti-microbial therapy.

Two of our samples were found to be K2 capsular type and *rmpA* positive. The other was K1 serotype, *rmpA* negative.

Conclusion: *Klebsiella pneumoniae* primary invasive liver abscess syndrome continues to emerge worldwide outside of Asia. Our experience adds to the body of literature on this emerging condition and further identifies its presence in Europe. All clinicians should be aware of this condition and its potential sequelae. Prompt recognition and management are vital to achieve optimal outcomes and facilitate cure.

21.117 Dengue in East AfricaF. Vairo¹, E. Nicastrì², N. Bevilacqua², S. Meschi³, B. Nguhuni⁴, M. Sane Schepisi², A. Di Caro⁵, G. Ippolito⁶¹National institute for Infectious Diseases "L.Spallanzani", Rome, Italy,²National Institute for Infectious Diseases "L.Spallanzani", Rome, Italy,³National Institute for Infectious Diseases "L.Spallanzani", Rome, Italy,⁴Dodoma Regional Hospital, Dodoma, Tanzania, United Republic of,⁵National Institute for Infectious Diseases INMI "L. Spallanzani",Rome, Italy, ⁶National Institute for Infectious Diseases "L.Spallanzani", Rome, Italy

Background: Recently, reports of dengue (DENV) cases in East Africa lead the attention to the circulation of the virus in this Area. DENV is not officially reported to WHO by countries in the area and the poor awareness of clinician and the lack of proper tests for the diagnosis could underestimate the spreading of this infection. Aim of this review of reported cases and epidemics is to explore the documented DENV cases in East Africa

Methods and Materials: EastAfrica was defined referring to UN world macro regions and components. Publications from year 1948 up to the 31st of August 2010 from National Library of Medicine database were searched using for each country the combination of "Dengue" and the Country Name as MeSH terms. The same combination was used on the Search Archive webpage of Promed Mail.

Results: We review 22 abstracts and 16 Promed Mail Reports. 10 abstracts and 5 Promed Reports were excluded because of reporting not confirmed cases or because a more recent and detailed report was included. One article reported cases from different countries: the cumulative number of outbreaks is 24

The majority of outbreaks (66.6%) occurred in residents in the area. The cumulative number of confirmed cases was 534. Only two severe cases were reported, both in non residents. The involved serotype was reported in 16 outbreaks. All serotype except DENV 4 were involved with DENV 1, 2 and 3 accounting for the 18.7%, 43.7% and 43.7% of the outbreaks, respectively. 16 outbreaks occurred in the last 10 years, 10 (58.8%) of them in 2010.

Conclusion: The most common serotypes are 2 and 3 in accordance with an introduction of the virus from Asia. We observed an increase of the reports in the last years probably due to the spreading of the new reporting e-tools. Nevertheless, new countries experienced outbreaks in last 5 years, such as Tanzania, Madagascar, Mauritius. The incidence of severe cases is substantially low. This could be explained by the occurrence of a low cytopathogenicity DENV strains and/or a protective host genetic interaction. New studies on the prevalence of DENV in this area are needed.

21.118 Sporadic circulation of Dengue in febrile outpatients in Tanzania mainland and in Pemba Island, ZanzibarF. Vairo¹, E. Nicastrì², S. Meschi³, M. Sane Schepisi², M. Paglia², N. Bevilacqua², S. Mangi⁴, M. Jape⁵, V. Racialbuto⁶, M. Capobianchi², A. Di Caro⁷, G. Ippolito⁸¹National institute for Infectious Diseases "L.Spallanzani", Rome, Italy,²National Institute for Infectious Diseases "L.Spallanzani", Rome, Italy,³National Institute for Infectious Diseases "L.Spallanzani", Rome, Italy,⁴Tosamaganga Missionary Hospital, Iringa, Tanzania, United Republic of,⁵"Ivo De Carneri" Public Health Laboratory, Pemba, Tanzania,United Republic of, ⁶Italian Development Cooperation, Italian Ministry ofForeign Affairs, Rome, Italy, ⁷National Institute for Infectious DiseasesINMI "L. Spallanzani", Rome, Italy, ⁸National Institute for Infectious

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Background: In eastern Africa, so far the available evidence indicates that Dengue-1, -2 and -3 appear to be common causes of acute fever. Recently, 4 reports on Dengue infection in travellers and residents have raised concerns on the dengue fever occurrence in Tanzania and Zanzibar. Nevertheless, incidence and prevalence data on dengue infection in Tanzania are lacking.

Methods and Materials: The study was conducted at two peripheral hospitals in 2007 in Pemba Island, Zanzibar and in the Iringa region, Tanzania. Inclusion criteria were age ≥ 1 year and a $\geq 38^{\circ}\text{C}$ temperature for < 10 days. Dengue IgG and IgM Ab were determined by Indirect Immunofluorescence Assay using home-made slides carried out with a mix of uninfected and Dengue-2 (New Guinea C strain) infected Vero E6 cells. Total RNA was extracted and screened for Dengue RNA by using a heminested RT-PCR that amplifies a 250-bp portion of NS5 region of human pathogenic flavivirus.

Results: A total of 202 febrile patients from Iringa (111, 55%) and from Pemba (91, 45%) were studied. 99 of them (49.1%) were adults; 103 (50.9%) were under 15 years of age and were equally represented in both sites. Dengue IgG Ab were found in 9 out of 202 patients (4.5%). The IgG prevalence was significantly higher in Pemba than in Iringa (7.7% vs 1.8%, $p=0.046$, respectively), and in adults than in < 15 (8.1% vs 1.0, $p=0.03$). In under 15, anti-Dengue IgG Ab were detected in only one case, a 11 year old male subject in Pemba. All 165 PCR-tested patients (81.7%) were negative for dengue RNA

Conclusion: In this cross-sectional analysis, a sporadic transmission of dengue infection with a 4.5% seroprevalence rate was detected. A significant higher virus circulation was reported among adult patients from Pemba Island. No acute cases and no previous infections among patients under 11 years old were detected. These findings provide baseline data on the circulation of the virus in the country in recent years, highlighting the absence of recent dengue virus circulation in Tanzania and the detection of the virus in Zanzibar archipelago up until the early '90.

**21.119 Does source matter?: Comparing the timeliness of outbreak reports from governmental and non-governmental sources**

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Background: Non-governmental (or informal) information sources have been credited with raising earlier warnings of disease threats compared with traditional governmental reporting systems, and thus facilitating the rapid recognition and response to potential pandemics and emerging disease outbreaks. Despite an increased global reliance on informal reporting systems (including ProMED-mail, Global Public Health Intelligence Network (GPHIN), HealthMap and others), little empirical evidence exists to support this assertion. We tested (1) whether the original source of outbreak information (governmental or non-governmental) was an explanatory factor in the timely reporting of outbreaks, and whether (2) the initial source of outbreak information varied by source pre/post the 2003 SARS outbreak or by region.

Methods and Materials: Using a database of 398 unique human infectious disease outbreaks selected from the World Health Organization's (WHO) "Disease Outbreak News" from 1996–2009, we identified the source(s) and date of the original outbreak report (either local or international, verbal or written) from ProMED-mail's archives. Negative binomial regression models were used to test for differences and improvements in the timeliness of reporting, relative to the estimated start date of an outbreak, by source. Spearman rank correlation coefficients were used to test for trends in median days to outbreak communication by year for both governmental and non-governmental sources.

Results: We found no statistically significant differences in reporting timeliness between governmental and non-governmental sources from 1996–2009 (IRR=0.93, 95% C.I. [0.74, 1.17]), suggesting that the source of information is not an explanatory factor for timely reporting of outbreaks. Surprisingly, we also found no significant difference in reporting timeliness by governmental/non-governmental source pre/post SARS, or by geographical region. Further, no significant annual trends in reporting timeliness were found for either category of source.

Conclusion: To our knowledge this study is the first to compare timeliness of outbreak reports by governmental and non-governmental sources. No statistically significant differences in timeliness of outbreak reports by source were found over time or by region, though the study was limited to a sample of WHO-confirmed outbreaks. Further research is needed to confirm these results.

21.120 Is *Vibrio fluvialis* emerging as a predominant pathogen causing epidemics of diarrhea in coastal regions of Eastern India?

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Background: Sundarban, a delta region in the eastern parts of India, is an important international tourist destination. Several villages of the delta islands were affected by a diarrhea epidemic following cyclone 'Aila' on 26th May 2009. The village of Pakhrala experienced the worst epidemic.

Methods and Materials: In the affected villages, all patients with moderate to severe dehydration were treated and/or admitted at nearby health facilities. Stool samples/rectal swabs were collected from eligible and willing patients after obtaining verbal consent. Admission registers of hospitals were consulted to ensure broader geographic distribution of cases. However, due to lack of facilities, only 10 stool samples from Pakhrala and 27 from the other affected villages reached the laboratory (situated 70 kms into the mainland) on time for bacteriological confirmation.

Results: In Pakhrala about 91% (3,529/3,871) of the residents were affected by watery diarrhoea within a span of six weeks (5 June–20 July 2009). Of those affected, 26% (918/3,529) had moderate to severe dehydration. In other villages 70% (28,550/40,786) of the population was affected

by diarrhea and 14% (3997/28,550) had moderate to severe dehydration. So, the attack rate and the severity of the cases were significantly higher ($p < 0.05$) in Pakhrala compared to other affected villages.

In Pakhrala, 62% of the patients reported blood in their stool. But this feature was absent in patients from other villages.

On laboratory examination, *Vibrio fluvialis* was found to be the predominant organism in Pakhrala (5 of 6 microbiologically confirmed pathogens were *V. fluvialis*). But, *V. cholerae* O1 Ogawa was the predominant pathogen in other affected villages (7 of 9 microbiologically confirmed organisms were *V. cholerae* O1 Ogawa).

Conclusion: Based on attack rate, severity and clinical symptoms, the epidemic at Pakhrala appears to be different from that of other villages. The pathogen that caused epidemic in Pakhrala appears to be more virulent. Laboratory results further support the view that epidemic in Pakhrala was primarily caused by *V. fluvialis* and that in other villages by *V. cholerae*. The epidemic potential and higher pathogenicity of *V. fluvialis* compared to *V. cholerae* is of great concern and requires further in-depth studies.

21.121 Outbreak of West Nile Virus in Cádiz (Andalusia, Spain)

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Background: Infection with West Nile Virus (WNV) is presented in 80% of cases as asymptomatic, 20% as a flu-like illness, and <1% with severe neurological impairment. It is transmitted by *Culex pipiens* mosquitoes, and the reservoir is birds. Horses and humans are final hosts. In recent years, there have been outbreaks in humans with high proportion of severe cases in temperate regions of Europe and North America, becoming a public health threat. In Spain only had detected a human case from Portugal in 2004. In September 2010 were reported in Cadiz (Andalusia, Spain), several cases of WNV infections in horses. Until today there have been 41 affected horses and 10 dead in three provinces of Andalusia. In this situation, the Epidemiological Surveillance Service of Andalusia activated a surveillance protocol of human infection in the affected areas.

Methods and Materials: This protocol containing clinical criteria (patients with meningitis or encephalitis), laboratory criteria (WNV in blood or CSF, or detection of WNV nucleic acid in blood or CSF, or specific antibody response against WNV IgM in CSF, or elevated serum WNV IgM with IgG detection and confirmation of virus neutralization), and finally epidemiological criteria (live or have traveled to an endemic area for animals).

Results: 2 cases were detected in men aged 60 to 77 years in the Hospital Universitario Puerto Real (Cádiz), in September and October. Both lived in rural areas in the province of Cadiz. The two attended with symptoms of encephalitis, and one of them very serious and required admission to the ICU.

Conclusion: The WNV outbreak in the province of Cadiz, highlights the need for vigilance against emerging diseases. These new diseases are forced to work in coordination to various services (health, agriculture, environment) and different countries, because these diseases are strongly influenced by the environment.

21.122 The Confirmation of *psaA* by PCR in the different serotypes of *Streptococcus pneumoniae* isolated from nasopharynx of healthy children

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Background: The gene encoding the pneumococcal surface adhesin A (PsaA) encodes a 37-kDa putative pneumococcal surface adhesin. Although its complete nucleotide sequence has been determined, its contribution to the pathogenicity of *Streptococcus pneumoniae* has not previously been assessed.



Methods and Materials: In this study, nasopharyngeal swabs were taken from healthy children recruited from randomly selected daycare centers and primary schools in Tehran. To detect the gene we used a PCR-amplified internal fragment of the *psaA* gene.

Results: Our objective was to detect the *psaA* gene in different serotypes of *S. pneumoniae* found in the upper respiratory tract of healthy children.

Samples were collected from 485 children. *Streptococcus pneumoniae* were isolated from 228, (47%), specimens; fifteen different serotypes were identified. PCR detected the *psaA* gene in 164 cases (70%).

Our results confirm that *psaA* is present and detectable in heterologous serotypes of *Streptococcus pneumoniae*

Conclusion: These results indicate that *PsaA* can be used for the identification and diagnosis of pneumococcal diseases and utilized as a virulence determinant for vaccine development instead of using polyvalent vaccination for the prevention of Pneumococcal disease.

21.123 The study of Phospholipase C genes in Beijing strains of mycobacterium tuberculosis

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Background: The Beijing strain of *mycobacterium tuberculosis* has high transmission potential and there was a significant correlation between Beijing strain and multidrug resistance. Phospholipase of *mycobacterium tuberculosis* has important role in pathogenesis by breaking up phospholipids and then the production of diacylglycerol.

Methods and Materials: DNA extraction was performed using CTAB from positive culture specimens in tuberculosis patients. Then followed by differentiation of the Beijing strains from Nonbeijing strains with spoligotyping and PCR for amplifying of Phospholipase C region.

Results: The current study showed that, of 200 specimens 19 (9.5%) were Beijing strain and 181 (90.5%) were non Beijing strains using spoligotyping. Using PCR method for *plcA*, *plcB*, *plcC* genes in Beijing strains, 16 specimens (84.2%) were positive for *plcA*, 17 (89.4%) were positive for *plcB* and 17 (89.4%) were positive for *plcC* genes. These segments were compared with standard strain (H37RV) and have the same size with it.

Conclusion: The majority of Beijing strains have phospholipase C genes that can pertain to their pathogenesis but we need complementary studies to confirm the role of phospholipase C in pathogenicity of *mycobacterium tuberculosis*.

21.124 Emergence and spread of Vibrio cholerae O1 El Tor with classical ctxB genotype 1 and tetracycline resistant strains in Assam, northeast India

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Background: Cholera is reemerging with increasing morbidity & mortality in developing countries with inadequate sanitation made worse by natural calamities like floods and earthquakes. Recent cholera outbreaks with high case fatality rates (CFR) in Assam, a state in northeast India, were investigated in 2007, 2008, and 2010 to know the pattern of *V. cholerae* strains circulating in the region.

Methods and Materials: Our study analyzed 40 *V. cholerae* isolates collected from outbreaks of cholera in tea tribe communities from different districts of Assam and identified by conventional biochemical test. The isolates were subjected to serotype & biotype identification and antibiogram using standard operating protocols. The strains were further subjected to a mismatch amplification mutation assay (MAMA) based PCR for detection of *ctxB* allele and confirmed by DNA sequencing of the *ctxB* gene of cholera toxin (CT).

Results: All the 40 isolates were found to be *V. cholerae* serogroup O1 biotype El Tor with 19 and 21 isolates being Ogawa and Inaba serotype respectively. By disc-diffusion method, 100% strains were susceptible to Ciprofloxacin and Amikacin while 100% were resistant to Trimethoprim

and 40 % were resistant to tetracycline. All the tetracycline resistant strains had MIC of 8 mg/L. All isolates subjected to MAMA based PCR were found to harbour classical *ctxB* gene allele. DNA sequencing of *ctxB* gene of CT confirmed the amino acid residue substitution at position 68, 46 and 39 by threonine, phenylalanine & histidine respectively, denoting the genotype 1 of *ctxB*.

Conclusion: The *V. cholerae* O1 strains circulating in Assam India; causing high CFR are due to altered El Tor biotype carrying classical *ctxB* genes. The high CFR in recent cholera outbreaks may be due to the production of classical like CT by the El Tor biotypes. The emergence of tetracycline & trimethoprim resistant strains necessitates the review of the guidelines for antibiotics use for severe cholera.

21.125 How to introduce the subject of conservation medicine into veterinary studies? First experiences at JLU Giessen, Germany

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Background: Conservation medicine represents a growing field in the biological sciences. Especially emerging and reemerging infectious diseases, as well as growing knowledge of environmental effects on population health have risen the necessity to bring together people from different health, biology and environment related fields to adequately address these topics. Students of veterinary medicine get into contact with various conservation medicine related topics, hence being well prepared to connect issues of public health, animal health and ecological concern. Yet, conservation medicine as a subject is scarcely taught in Germany and not part of the study curriculum.

Methods and Materials: Elective course on conservation medicine for semester 6 and 8, consisting of lectures on emerging viruses, introduction to conservation medicine in zoos at Opel-Zoo Kronberg and student presentations on selected animal species.

Results: The meaning of conservation medicine was not definable by most students at the beginning of the course. Most students regarded the term conservation medicine as equal to zoo and wildlife medicine. The opportunity to independently search for aspects of ethology, reproduction and disease impact of several zoo animal species and to make suggestions for improvement of holding facilities was well received by the students. Focusing lectures on emerging viruses restricted the content of the elective course, missing out on bacteria, fungi, parasites and environmental stressors related to conservation medicine.

Conclusion: Knowledge about conservation medicine is scarce in students of veterinary medicine and hence lectures about conservation medicine are required to close this gap. Methods how to best introduce conservation medicine into the curriculum and to the students should be discussed. As the fields covered by conservation medicine are so diverse, input and willingness to give guest talks of people working with all different aspects of conservation medicine are needed and appreciated.

21.126 Evaluation of the effectiveness of animal diseases reporting system in Oyo State, Nigeria (1995–2005): The relevance of ProMED-mail

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Background: Under-reporting of animal disease outbreak is a common feature in most developing countries with poor Animal Disease Reporting System, the official disease reporting system of the International Office for Epizootics (OIE/WAHO). The same situation has been reported in Nigeria

Methods and Materials: The operational efficiency of the Animal Disease Reporting System of Oyo State, Nigeria between 1995 and 2005, was evaluated by examining the accuracy, completeness and speed of reporting of six major animal diseases on the list 'A' of the old Classification of Diseases Notifiable to the OIE. These diseases were African swine fever (ASF), Foot and Mouth Disease (FMD), Contagious Bovine Pleuropneumonia (CBPP), Avian Influenza (AI), Rinderpest and Peste des petite ruminants (PPR).



Results: For the 10 year period, one case each of CBPP and FMD were reported in 1995, there were no reported outbreak between 1996–2000, 2002 and 2003, eleven cases of ASF outbreak were reported in 2001, one case of FMD in 2004 and two cases of FMD in 2005. Trace-back investigation revealed that the two FMD cases reported in 2005 was a case of dual notification of the same outbreak. Only 18.2% of all reported cases were confirmed. The major impediments identified included poor awareness by farmers of the need for prompt disease, notifications, a too long chain of reporting, inadequate qualified veterinary personnel, lack of communication facilities and poor diagnostic facilities. Recommendations were made for improve the system's optimal effectiveness

Conclusion: Animal Disease Reporting System in Oyo State, Nigeria was found to be inaccurate, grossly under-reported, late and generally inactive between 1995 and 2005. This is typical of the other 35 states in Nigeria. There is a very relevant need to promote alternative to the official disease reporting for effective disease outbreak diagnosis, monitoring, surveillance and control such as the ProMED-mail (the Program for Emerging Diseases, a program of the International Society for Infectious Diseases). The start off of ProMED-East Africa (now ProMED- Anglophone Africa) to increase access to information on the part of health care professionals from both the human and animal health sectors throughout English-speaking Africa is a welcomed response.

21.127 Active immunization using exotoxin A confers protection against *Pseudomonas aeruginosa* infection in a mouse burn model

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Background: *Pseudomonas aeruginosa* is an important cause of nosocomial infection and may lead to septicemia and death. We evaluated the immunogenicity of semi-purified exotoxin A from the bacterium in a mouse burn model

Methods and Materials: The toxoid was prepared from exotoxin A taken from toxigenic strains of *P. aeruginosa* (PA 103). 50 mice were immunized with the toxoid, burned with hot metal and infected with 1×10⁸ CFU of toxigenic strains of *P. aeruginosa* (experimental group); 25 non-immunized mice were also burned and infected (control group). The mortality rate and presence of any exotoxin and *P. aeruginosa* in the sera, liver and spleen were determined

Results: In the experimental group, 2 mice died before the burns were administered and were excluded from the study. The remainder (48 mice) were challenged with a lethal dose of *P. aeruginosa* and followed for 70 days. 3 of these mice died. Neither *P. aeruginosa* nor exotoxin A was not detected in the liver, spleen or sera of the surviving mice. The protective efficacy of toxoid vaccination was therefore 93.8%. In the control group, all mice died from bacteremia and septicemia, most (80%) within 6 days, and *P. aeruginosa* and exotoxin A were isolated from sera, spleen and liver

Conclusion: Active immunization of mice using a semi-purified exotoxin A derived from *P. aeruginosa* was 93.8% effective at protecting mice from subsequent *P. aeruginosa* infections in a mouse burn model

21.128 Pertussis outbreaks and associated factors, Taiwan, January 2006–June 2010

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Background: Taiwan implemented the national diphtheria-tetanus-pertussis vaccine program in 1955. Vaccine coverage was >95%. In recent years, however, pertussis cases and outbreaks increased. To improve the pertussis control strategy, we analyzed reported outbreaks to identify possible associated factors.

Methods and Materials: Information on case demographics, vaccination status, possible source of infection were collected from pertussis outbreaks reported during January 2006 to June 2010. A cluster was defined as ≥2 epidemiologically linked cases. A case was clinically compatible illness in a person who also was laboratory confirmed or epidemiologically linked to a laboratory-confirmed case.

Results: During January 2006 to June 2010, there were 151 cases in 40 outbreaks. Of the 151 cases, 79 (52%) were female; 70 (45%) were aged 7–18 years and 40 (28%) ≥19 years. Laboratory confirmation was obtained in 107 (71%) of the cases. Seventy-three (48%) were students. Clinical presentations include: cough (77%), paroxysmal cough (46%), rhinorrhea or mild fever (35%), cough for over 21 days (27%), and cyanosis (10%). Of the 89 cases with known vaccination status, 58% had at least 4 doses of pertussis-containing vaccine. Among the 40 outbreaks, 31 (78%) occurred within families and 6 (14%) in schools. There were 24 (60%) index cases aged ≤18 months. Delayed diagnosis (>21 days after symptom onset) was noted in 15 (38%) index cases. Outbreak investigations revealed that sources of infections were child-caregivers 16 (47%), siblings 9 (23%), and classmates 6 (18%).

Conclusion: Caregiver of underimmunized infants, who were at increased risk of complications, was the most commonly identified infection source. Increasing physician awareness to shorten the time needed for pertussis diagnosis and encourage child-caregivers to receive pertussis vaccine booster may decrease outbreaks.

21.129 Vaccination coverage against influenza, pandemic and seasonal in the Canary Islands, 2009–2010 Season

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Background: The confluence in the 2009-2010 season, two influenza vaccination campaigns, seasonal and pandemic was a factor that complicate the improving coverage in the population over 60 years. Seasonal vaccination is indicated for the entire population over 65 years, while the pandemic, following the technical recommendations to the population over 60 with risk factors. We present the results obtained in the Canary Islands in both campaign.

Methods and Materials: We studied vaccine coverage for seasonal and pandemic health area. As the numerator we use the number of both vaccines administered respectively and the denominator, the population over 65 years for the seasonal and the population over 60 with risk factors for the pandemic.

Results: While coverages obtained with the seasonal vaccine were the highest ever achieved in this group in the Canary Islands (77.5%), those obtained against the pandemic vaccine in the population group studied were very low (13.5%). In general, in the two groups, the results obtained in the outer islands were higher than those of the main islands.

Conclusion: The difference in the results compared with the two vaccines, it may indicate the different perception of risk that the study population was against both flu and to the characteristics of the two vaccines. We must emphasize the high coverage obtained with seasonal influenza vaccine.

21.130 Genetic profile of new porcine parvovirus isolates and high rate of viral evolution in the capsid protein gene

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Background: Porcine parvovirus (PPV) is a widespread single-stranded DNA virus that causes reproductive failure in swine. The virus is considered to be conservative, with substitution rates near to their host. In the last years, it was shown that some parvoviruses exhibit a similar substitution rate to that determined for RNA viruses. In order to monitor and evaluate PPV mutations, recent PPV field isolates from Austria, Brazil, Germany and Switzerland were sequenced and analyzed.



Methods and Materials: These samples, together with sequences retrieved from GenBank, were included in three datasets [viral protein complete gene (n = 34), viral protein partial gene (n = 64) and non-structural protein complete gene (n = 32)]. For each dataset, the nucleotide substitution rate was determined and a molecular clock estimated.

Results: The analysis of the PPV field isolates revealed that a recently described amino acid substitution S-436-T in the VP2 protein appears to be common in the Austrian, Brazilian and German virus population. Furthermore, new amino acids substitutions were defined, mainly located in the viral capsid loops. A higher divergence in the capsid protein was also found in the phylogenetic analysis, with three well defined clusters (posterior probability = 1.0). By inferring the evolutionary dynamics of the PPV sequences, a nucleotide substitution rate of approximately 10-5 nucleotide substitutions per site per year for the non-structural protein gene and 10-4 for the capsid protein gene (for both viral protein datasets) were found. The latter rate is similar to that commonly found in RNA viruses. An association of the phylogenetic tree with the molecular clock revealed that the mutations on which the divergence for the capsid protein (for both viral protein datasets) is based, occurred in the last 30 years. In contrast, the analysis for the non-structural protein dated at 10 to 125 years ago

Conclusion: Based on these findings, we conclude that PPV variants are continuously evolving, and the vaccines (mainly based on strains isolated some thirty years ago) may well be redesigned.

21.131 **Changes in the circulating rotaviruses genotypes detected during the Surveillance and its implications for the rotavirus vaccination in Colombia, South America**

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Background: Rotavirus is the main cause of diarrhea in infants less than five years old worldwide. Rotavirus causes about 246.401 infections cases, 108.417 patients visits, 37.258 hospitalizations and 560 deaths per year, among children below five years old in Colombia. The establishment of a National Sentinel surveillance program of acute gastroenteritis at the end of 2008, has allowed us to see several changes in the distribution of rotaviruses genotypes as well as the finding of new strains which have not been seen before introduction of a monovalent vaccine in the regular vaccination program against rotavirus in our country, occurred in January 2009.

Methods and Materials: We have genotyped 70 rotavirus positive samples by the seminested-PCR method. All samples were collected from the central, north and west region of the country during 2009 and 2010.

Results: The analysis showed a high frequency of G1P[6], mixture of G1G2P[4]P[6] and a variety of genotypes with an increased frequency of G9; this genotype was seen before in our country in a very low frequency. Also we found a high frequency of P6 genotype and a wide variety of mixed genotypes containing G9 and P6.

Conclusion: These findings suggest that currently monovalent vaccine which has a cross immunity against strains in the same [Wa] genogroup, will be challenged by P[6] and G9 genotypes which we have found in a relatively high frequency in our country.

21.132 **Characterization of candidate vaccines by a new bioanalytical approach—gas-phase electrophoretic mobility macromolecular analysis with an electrostatic nanoparticle sampler**

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Background: The development of new biopharmaceuticals as vaccines often goes hand in hand with the search for new bioanalytical technologies. So the focus of this work is to establish a new analytical platform (array of methods) for size, shape and activity characterization of virus particles in candidate vaccines.

Methods and Materials: The candidate vaccines investigated are inactivated, whole virus samples of enveloped viruses like Tick-Borne Encephalitis Virus, West Nile Virus and Ross River Virus. A nano-electrospray (NanoES) gas-phase electrophoretic mobility macromolecular analyzer (GEMMA) was used for the size determination of the vaccine particles. This method reveals information on electrophoretic mobility diameters (EMD) of positively or negatively singly-charged particles, in particular the whole virus particle, which can be further correlated to respective molecular weights in a very broad mass range (kDa - MDa). The sample preparation of candidate vaccines was performed with size-exclusion chromatography (SEC) prior to GEMMA with subsequent sample collection by an ENPS (electrostatic nano particle sampler). NanoES GEMMA of separated nanoparticles were collected on nitrocellulose membrane for immunological activity testing, on mica sheet for AFM (atomic force microscopy) and on carbon-covered grid for TEM (transmission electron microscopy) measurements.

Results: These data were correlated to the GEMMA-derived particle diameters of the intact whole virions. NanoES GEMMA results were compared with tapping-mode AFM and TEM measurements of untreated and SEC-purified candidate vaccine samples. AFM and TEM images provided additional information on size, shape, virus integrity and aggregation behavior. NanoES GEMMA turned out to be a suitable sizing method, a quick control for the presence of intact whole viruses and suitable as a size-selection step prior to AFM or TEM sample preparation as just the particles with the selected EMD are collected. Finally data of biological active samples after collection will be presented.

Conclusion: All results of the newly established methods and strategy correspond well to published data. The size measurements of the candidate vaccines with the NanoES GEMMA system were shown to be a very quick as well as reliable and in combination with the ENPS ideal for further sample characterization (AFM, TEM and bioactivity).

21.133 **A measles and rubella laboratory based surveillance report in Tanzania, 2008**

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Background: The Measles Surveillance System in Tanzania started in 1995. The objectives of this system are to establish disease early detection, prevention, control of its outbreak, monitor disease pattern and integrate enhanced surveillance for polio and measles cases

Also to estimate how many persons become sick or die from measles (establish a periodic disease burden). To detect any measles outbreak as early as possible and promptly institute appropriate control measure/intervention. To identify population at risks for measles outbreaks and their risk factors. To monitor progress of measles control measures and impact of vaccination campaigns.

Methods and Materials: *Specimens:* Blood was gathered from reported cases of measles and rubella through the reporting system by District focal persons. *Serological Testing:* IgM and IgG antibodies for measles /rubella: Enzygnost Anti-Masem- virus /IgM, Enzygnost Anti-Masem- virus/IgG, Enzygnost Anti-Rubella- virus/IgM, and Enzygnost Anti-Rubella- Virus/IgG (Dade Behring, Marburg, Germany) were used.

Results: A total of 244 samples from Measles/Rubella suspected cases were received at National Measles Laboratory in 2008 for serological confirmation.

One hundred sixty one 161/244, (60%) measles cases were confirmed from the reporting system. Twenty seven rubella cases 27/244, (11.1%) of total reported cases were also confirmed.



Among the reported measles cases, 190 cases (190/244, 77.9%) were below the age of 10 years and 2 cases were more than 40 year old. Gender distribution of suspect cases 142 (58.2%) were female. The majority of confirmed measles cases 126/161 (78.3%) were below than ten years old, (Table 1) and only 6/27 (22.2%) of confirmed Rubella cases were older than ten years old. The vaccination status of measles confirmed cases, only 5/161 (3.1%) has last vaccination dates recorded and Rubella confirmed cases 16/27 (59.2%) were recorded to be vaccinated against measles.

Conclusion: As revealed in this analysis results, there are several older age cases which suggest that the population has more susceptible hosts for measles, so there is a need for regular vaccination campaigns to provide higher degree of coverage as well as to strengthen the herd immunity in the population.

21.134 Vaccine-derived poliovirus infection in an Colombian infant with congenital agammaglobulinemia

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Background: Recent world-wide immunization against polioviruses causing poliomyelitis are resulting in almost their eradication, however vaccine-associated paralytic poliomyelitis (VAPP) remains a significant problem in countries where oral polio vaccine (OPV) is still used. We report VAPP in a child that later diagnosed with congenital agammaglobulinemia.

Methods and Materials: Medical records were reviewed and vaccine-derived poliovirus (VDPV) diagnosis was established according to WHO criteria. Immunological tests included serum Ig and lymphocyte populations in peripheral blood (PB) by flow cytometry. The virus was isolated from feces and analyzed for sequence variants at the Center for Diseases Control (Atlanta, GA).

Results: A 15 month-old patient was hospitalized with acute flaccid paralysis and global hemiparesis. Previous medical records showed only 1 episode of otitis media and recurrent fevers. He had received his third scheduled dose of OPV 11 months before admission. An EMG showed axonal and demyelinating polyneuropathy affecting the 4 limbs and a brain MRI showed bilateral damage of both cerebral peduncles. CSF analysis showed no cells, 60 mg/ml proteins, 73 mg/ml glucose and cultures were negative. Serum IgA was 6 mg/dl (Ref: 10-254), IgG was 18 mg/dl (Ref: 440-2064) and IgM was 0 mg/dl (Ref: 36-239). CD19+ B cells in PB were 0,09% (Ref: 15-39%) corresponding to 8 cells/uL (Ref: 600-2700). Sequencing of viral isolates showed 1.55% genetic changes in the major capsid protein (VP1) of the Sabin virus. The child died 60 days after admission from respiratory failure.

Conclusion: VDPV appears to be very rare, however it can become significant especially in immunocompromised children. Since a community may become susceptible to the emergence of all types of VDPV in these situations, new vaccination strategies should be implemented in countries that still use OPV to avoid future VDPV cases.

21.135 Lyophilization of *Brucella abortus* S19 vaccine using two different preservatives in the Sudan

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Background: Brucellosis is a disease of major financial significance. As a result, a policy for its control is necessary in endemic areas. Brucellosis control efforts are directed to detection and prevention because no practical treatment is accessible (Merck vet. manual, 2008).The most

widely used vaccine for the prevention of brucellosis in cattle is the *Brucella abortus* S19 vaccine (OIE, 2009).Strain 19 vaccine used as a live vaccine and is normally given to female calves aged between 3 and 6 months as a single subcutaneous dose of 5–8 × 10¹⁰ viable organisms. A reduced dose of from 3 × 10⁸ to 3 × 10⁹ organisms can be administered subcutaneously to adult cattle (OIE,2009). In the present production system where the vaccine cannot be valid for a long time, lyophilization is the suitable solution. The Sudan is planning to carry mass vaccination of the different animal species against brucellosis,so it is expensive to import a vaccine for over than 140 million head of livestock.

Methods and Materials: *Brucella abortus* S19 vaccine was produced with *B.abortus* S.1119-3 supplied by the USDA using the procedures of the OIE (2008).Propagation of *Brucella* cells were carried out on potato agar medium in Roux flasks. Two preservatives were used, sterilized 4% skimmed milk and a stabilizer. Viable counts of the vaccines were determined according to Miles and Misera (see Alton *et al.*, 1975). The vaccines were dispensed in sterilized vials and lyophilized under aseptic conditions. The lyophilized vaccines were preserved at three different temperatures; at the room temperature, 4C and -20 C. The viable counts of the two vaccines were checked monthly for six months.

Results: The two suspensions were pure Gram negative coccobacilli and were not agglutinated with the acriflavine. Viable counts of the two vaccines were 8X10¹¹ and 7X10¹¹ CFU/ml for skimmed milk and stabilizer vaccines before lyophilization, respectively and were 8X10¹⁰ and 7X10¹⁰ CFU/ml after lyophilization. The two vaccines viable counts results during six months were expressed in log viable counts /CFU/ml.

Conclusion: The vaccine that lyophilized using skimmed milk was more stable than the stabilizer when stored in the refrigerator at 4C.

21.136 Measles outbreak in South of Iran

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Background: Measles is an important vaccine-preventable childhood disease which causes considerable mortality and morbidity in developing countries. Although measles vaccination is highly effective in children in the developing world when performed in carefully monitored settings, vaccination programs have not been uniformly successful.

Methods and Materials: A measles outbreak was recorded during a 6 month period in towns and districts of Hormozgan province of Iran from February 2010 till July 2010. In this study, reported cases of measles were recorded and a questionnaire containing information on the place the case was reported from, the history of vaccination, the history of contact with measles, the history of measles vaccination in mother, and the status of vaccination (incomplete, complete, and not vaccinated) was filled out.

Results: During a 6 month period 54 cases of measles were reported. Of these cases, 7.4% (4) cases were subsequent to vaccination. 35% were male, 13% were Afghan, 6% were Pakistani, 50% (27) were reported from Bandar Abbas, 32% (17) were reported from JAsk, and the rest from other towns and districts. 46% were reported from urban areas. Age of 22% of cases was less than 1 year, 33% between 1–5 years, 17% were between 5–12 years and 20% older than 12 years. In Bandar Abbas, 41% were not vaccinated, 26% had incomplete vaccination, 22% were aged less than 1 year and the rest had complete vaccination. In Jask 69% had complete vaccination, 17.6% incomplete vaccination, 17.6% aged less than 1 year, and the rest had incomplete vaccination.

Conclusion: According to the results, the main problem in the vaccination program in Bnadar Abbas is incomplete vaccination or absence of vaccination, but in Jask most of the cases reported had a complete vaccination and this indicates a fault in cold chain and that the cold chain is incomplete.

**21.137 Emerging human rotavirus strains, 2006–2010, Hungary**

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Background: Vaccination is the main strategy to control severe dehydrating gastroenteritis caused by rotaviruses in infants and young children. After recent introduction of new generation rotavirus vaccines in several countries worldwide, post-vaccination strain surveillance has begun to assess the impact of vaccines on prevalence of circulating rotavirus strains.

Methods and Materials: A post-vaccination surveillance study was conducted in different parts of Hungary, from 2006/2007–2009/2010. Rotavirus positive stool samples were collected from patients mostly under 5 years of age with acute gastroenteritis. Extracted genomic RNA was subjected to genotyping using multiplex RT-PCR assay. Type specific primers targeted the medically most important 8 G and 6 P specificities. When needed, sequencing of the VP7 and/or VP4 genes of non-typeable strains and selected unusual strains was performed.

Results: Of the 1712 rotavirus-positive samples, both G and P type specificities could be assigned for 1607 strains. During the 4-year surveillance we observed the dominating prevalence of genotype G1P[8] (42.23%) strains, followed by G4P[8] (26.52%), G2P[4] (12.21%) and G9P[8] (6.13%) genotypes. Reassortment events of common genotypes (eg, G1P[4], G2P[8], G9P[4]), as well as potential zoonotic and human-animal reassortant strains (eg, G1P[6], G2P[6], G3P[9], G4P[6], G6P[9], G9P[6], G9P[4], G8P[8], G10P[6], G12P[6], G12P[8]) were seen during the study period.

Conclusion: Our results demonstrate large antigenic diversity among co-circulating rotavirus strains in Hungary during this 4-year surveillance. The majority of identified rotavirus genotypes are covered by vaccines, which at present, are available on private market. A better understanding of potential long term effect of vaccine use on epidemiology and evolutionary dynamics of co-circulating wild type strains requires continuous strain surveillance.

21.138 Batch release of veterinary vaccines in Finland

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Background: Finnish Food Safety Authority Evira is an Official Medicines Control Laboratory (OMCL) for veterinary immunologicals and thus responsible for batch release and testing of veterinary vaccines in Finland. The market of veterinary medicinal products in Finland is small. For many indications there is only one vaccine available, thus the market is vulnerable for production interruptions. Vaccines are needed quickly if a new disease emerges (swine influenza) or there is a threat of new disease (bluetongue). Then special license granted by the Finnish Medicines Agency Fimea is only way to get products on the market.

Methods and Materials: National review of manufacturer's batch documentation has been in place since 1980's. Official batch release in accordance to the articles 81 and 82 of the veterinary medicines directive has been in place since 2008 i.e. Evira recognises the certificates granted by other OMCLs and certifies vaccine batches if no certificate is available. For live rabies bait vaccines Finland applies the article 82 of the veterinary medicines directive, thus these vaccine batches are tested by the OMCL before the certification.

Results: Annually, 250–310 batches of veterinary vaccines are being released by Evira. National release of batches (30 % and 24 % in 2008 and 2009, respectively) has often been necessary in order to have vaccines on the market. For the OMCL the situation is challenging because high quality of products should be guaranteed but on the other hand lack of product can cause major disease outbreaks.

Conclusion: Currently, majority of vaccine batches have certification by the OMCL. In order to guarantee that there are products available for veterinarians, the national release is used 1) if there is no product available, 2) if the product is on special license, 3) if there are minor deviations from the specifications in the batch which is urgently needed, and 4) until July 2010 for batches, for which the manufacturer confirmed that Finland was the only country applying official batch release for the batch in question.

21.139 Outbreaks of Hepatitis A among children in orphanages

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Background: Hepatitis A is an acute infectious disease of the liver that can cause mild to severe illness. Hepatitis A immunization in Macedonia is not obligatory, despite the intermediate level of transmission. The most affected target is children from 5 to 18 years of age. The aim of this study is to present Hepatitis A outbreaks among children in orphanages as well as our hygiene and sanitary procedures to prevent epidemic outbreaks.

Methods and Materials: Active epidemiological research, elaborated initial and final information by the Department for Epidemiology at the Centre for Public Health-Skopje, as well as laboratory examination samples.

Results: From 21.08.2009 until 26.10.2009, in an orphanage with 80 children, we registered 22 (27, 5%) cases of Hepatitis A. The disease was detected among children between 5 to 18 years of age (2 cases of 6 year old children, 8 cases of 7-9 years old children, 8 cases of 10-14 years old, and 4 cases of 15-18 years old teenagers). After the first two cases, in order to prevent the outbreaks of Hepatitis A, 130 blood samples were examined for AST-GOT (U/L) ALT-GPT (U/L) twice, during which 9 children (without symptoms) were detected. After a couple of days, 6 of them developed the symptoms, whereas 3 children were asymptomatic.

The hospitalization rate was 86, 6% (19 cases).

Conclusion: Outbreaks of Hepatitis A continue to occur, despite all epidemiological measures, personal hygiene (hand washing), disinfection of the living room, attention to proper food preparation, as well as workshops regarding personal hygiene.



The outbreaks could not to be brought under control because of the close contact of the children and the three asymptomatic cases.

After the first three cases, we suggested a Hepatitis A immunization for all children, but the experts were undecided whether children should be vaccinated during outbreaks of Hepatitis A.

21.140 Tularemia in Oppland and Hedmark counties, Norway, 2003–August 25, 2010

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Background: Tularemia, caused by *Francisella tularensis* is notifiable to the Norwegian Notification System for Infectious Diseases (MSIS). In Sweden many hundred cases are notified annually, whereas in Norway around 10-70 cases are notified per year. The main Norwegian mode of transmission is close contact with rodents and their excreta and secreta. In Sweden, however, there seems to be quite a number of cases due to tick bites – URL: [http:// www.smittskyddsinstutet.se](http://www.smittskyddsinstutet.se).

Methods and Materials: The Laboratory for Medical Microbiology, Sykehuset Innlandet Trust forwards specimens suspect of tularemia to St. Olavs Hospital, in Trondheim, using the polymerase chain reaction for bacterial cultures and microagglutination enzyme immuno assay for detection of specific antibodies. Cases are notified to the Norwegian Notification System for Infectious Diseases (URL: <http://www.msis.no>), with name and personal identification data.

Results: Tularemia in Oppland and Hedmark counties by year 2003–August 25, 2010 (year of notification and number of cases)

	2003	2004	2005	2006	2007	2008	2009	2010
HEDMARK	6	0	1	0	2	1	2	0
OPPLAND	3	2	3	2	1	1	0	1

The total number of cases was 25. Oppland had 13 notifications, whereas Hedmark had 12—throughout the time span described.

Conclusion: The number of cases is rather low. Therefore it is difficult to assess the seasonal distribution, however, many cases are detected and notified during the first and fourth quarters. The variation in incidence, as for haemorrhagic fever with renal syndrome (HFRS), seems to be due to fluctuation in the sizes of various rodent populations. The Norwegian vectors when it comes to tularemia comprises hares, rats, mice and ticks, whereas the vectors for HFRS belong to the genera *Myodes* and *Apodemus* exclusively.

The trends in Oppland and Hedmark counties, reflect that of the national situation. The increased incidence in year 2003 co-incides with an increase in the rodent population that year. Why Norway has such low incidences of tularemia as opposed to Sweden is unclear, given that the rodent and arthropod vectors are the same and that the vectors do cross national boundaries.

21.141 Haemorrhagic fever with renal syndrome (HFRS) in Oppland and Hedmark Counties, Norway, 1981–2009

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Background: Our laboratory serves Oppland and Hedmark counties, Norway. We have the highest incidences of HFRS in Norway. The main vectors are *Myodes glareolus* and *Apodemus sylvaticus*. The population has varied from 1981 to 2009, peaking 1998. The Norwegian, indigenous strain of Hantavirus, is the Puumala virus. Cases are notified to the Norwegian Public Health Institute—which is in charge of The Notification System for Infectious Diseases. From 1980 to around 1985 the Norwegian mean temperatures were below “baseline”—ranging from “pre-1980s baseline values”—to minus 0.5 degrees below baseline. From 1985 there was an increase—up to plus 0.5 degrees (in 1990). In the period 1990–1995, a decrease was observed—i.e. from approx. plus 0.5 degrees in 1990 to approx. plus 0.4 degrees in 1995. From 1995 to 2000 a new increase occurred, i.e. from approx. plus 0.4 degrees in 1995 to approx. 0.9 degrees in the year 2000. Another small increment occurred 2000–2008, peaking at approx. 1 degree above baseline, around 2008.

Methods and Materials: The Department of Medical Microbiology, Sykehuset Innlandet Trust diagnoses IgG and IgM antibodies against the Puumala virus.

Results: From 1981–2008 Oppland and Hedmark had 658 laboratory-confirmed cases of HFRS. The cumulative incidence 1981–1988 was 56, whereas, 1989–2009, it was 602.

Conclusion: The incidence, in 1998, (106 notifications) co-incided with a peak in some rodent populations. The lowest incidence, before 1988, was in 1984, with zero cases. The lowest incidence, after 1988, occurred in 2006, with seven cases. In 2008 there were 17 cases, compared to 1988, with 26 cases. An examination of the yearly incidences gives a somewhat different picture than looking at cumulative totals, in two different climatic periods, 1981–1988 compared to 1989 to 2009. It may seem that variations, in the size of our rodent population, has demonstrated a higher degree of co-incidence with cases notified than meteorological parameters per se. Whether or not the rather large vector population, in 1998, may be due to variations in ambient temperatures, as well as, other factors—including ecological ones—will not be discussed in detail.

21.142 High incidence of rickettsiosis correlated with the prevalence of *Rickettsia japonica* among *Haemaphysalis longicornis* tick associated with Japanese deer density in Shimane Prefecture, Japan

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Background: In Shimane Prefecture, 110 cases of Japanese spotted fever(JSF) were confirmed between 1987 and 2009, of which 102 cases were found in Misen mountains situated in the westernmost end of Shimane Peninsula. In that regions, Japanese deer showed high population density and were important hosts of ixodid ticks. To determine why an endemic focus of JSF was found in the Misen mountains, we performed genetic studies to identify the most competent ixodid ticks of the pathogenic *Rickettsia*, and considered their relationship to deer density in Shimane Peninsula.

Methods and Materials: Between 1999 and 2009, we captured 2099 adult ticks including 2 genera and 8 species by the flagging method on the Shimane Peninsula and other parts of Shimane Prefecture. We extracted DNA from 2099 ticks individually, and investigated the presence of *Rickettsia* 17-kDa gene and *gltA* gene, which were amplified by PCR using previously published primer pairs, R1 and R2, and RpCS877p and RpCS1258n, respectively. Following PCR amplification, DNA sequencing was performed using an ABI Prism 3130 Genetic Analyzer. The nucleotide sequences were compared with the corresponding sequences deposited in DNA Data Bank of Japan using BLAST(<http://blast.ddbj.nig.ac.jp/top-j.html>)

Results: Of 2099 ticks, 1149 were collected in the Misen mountains(Area A), and 584,294, and 117 ticks were collected in the area east of Misen mountains(Area B), in the eastern half of Shimane Peninsula(Area C) and in the Chugoku mountains in the southern part of Shimane Prefecture(Area D), respectively. These collection sizes were positively correlated with the incidence of JSF cases and deer density in the 4 areas,with Area A, as the most endemic area. The *Rickettsia japonica* DNA was detected from 15 *Haemaphysalis longicornis*(4.19%) in Area A, and one *H.longicornis*(0.55%) in Area B.

Conclusion: These analyses suggested that *R.japonica* is highly prevalent among the population of *H.longicornis* ticks inhabiting the Misen mountains on the Shimane Peninsula. *H.longicornis*, with an affinity for Japanese deer, were dominant in the Misen mountains. In Shimane Prefecture, JSF cases are endemic around the Misen mountains, which might be explained by the dominance of tick fauna depend on a high deer population density.

**21.143 Temporal trends of Malaria Cases and Deaths—Nigeria, 2003–2009**

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Background: Nigeria accounts for a quarter of malaria morbidity in sub-Saharan Africa, 60% of outpatient visits to health facilities, 30% of childhood deaths and 11% of maternal deaths. In 1998, the national malaria surveillance system was set up by the Federal government to support prevention, treatment and control efforts. We analysed the National malaria surveillance data from 2003–2009 to identify changes in temporal trend.

Methods and Materials: We reviewed 2003–2009 surveillance data on all malaria cases and deaths using Microsoft Excel. We conducted a descriptive analysis of the data on uncomplicated (UM) and severe malaria with anaemia (SMA) in children under 5 years (U5) in relation to overall malaria morbidity and mortality; using 2003 as baseline year

Results: Totally, the annual incidence (AI) and mortality rate (MR) increased steadily and was 1.6 times the baseline in 2009 (AI= 43 cases/1,000 population; MR= 8 deaths/100,000 population). Case fatality rate (CFR) remained stable at 0.2% annually. AI of UM in U5 increased exponentially and accounted in 2009 for 30% (1,952,419/6,567,575) of total cases. MR of UM decreased yearly by up to 50% until 2006 but reached the highest level ever in 2009. CFR decreased by 80% in 2009 compared to baseline. The AI of SMA increased over the reporting period to 7 cases/1,000 population while MR has been stable up to 2007. In 2008 and 2009, MR increased to 12 and 5 deaths/100,000 population, respectively. CFR decreased by 70% in 2009. Cases of malaria in pregnancy (MIG) increased exponentially and accounted for 6.9% of total cases (456,275/6,567,575) in 2009. However, CFR decreased yearly by up to 75% until 2006 but it reached the highest level ever in 2007. In 2009, CFR decreased by 81% compared to baseline.

Conclusion: Malaria remains a public health problem in Nigeria. The AI and MR are increasing in the U5. A significant reduction in death due to MIG was observed despite increasing cases. There is a need for early identification of cases, appropriate treatment and prioritising access to preventive measures for U5. The use of Sulfadoxine-pyrimethamine for the intermittent preventive treatment of malaria in pregnant women should be sustained.

21.144 Ten years experience of Crimean-Congo Haemorrhagic Fever as a vector borne disease in Iran

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Background: Crimean-Congo Haemorrhagic Fever (CCHF) is a tick borne viral haemorrhagic zoonosis with 50% mortality rate, caused by CCHF virus (CCHFV) belonging to the genus Nairovirus, family Bunyaviridae. In the transmission cycle of the disease, ticks play both vector and reservoir roles for CCHFV. Routes of transmission of CCHF are tick bites, handling of infected livestock organs, blood or tissues and nosocomial infection

Methods and Materials: Since 2000, the laboratory of Arboviruses and Viral Haemorrhagic Fevers of the Pasteur Institute of Iran, as the National Reference Laboratory, has performed advanced laboratory diagnosis

consisting of specific Elisa for IgM and IgG detection for CCHF in the sera of CCHF probable patients and also RT-PCR and Real time RT-PCR for detection of CCHFV genome in patients sera. These researchs have conducted us to the following facts and observations in our one decade experience on CCHF in Iran:

Results: Most cases are between 21–40 years (in their active years) and 77% are male. The most infected professions are those in contact with infected blood or organs of livestock such as slaughterer, butcher, farmer and housewives in rural area. Most cases have occurred in the south-east of Iran in the vicinity of Afghanistan and Pakistan which are endemic countries, particularly in the Sistan Baluchestan province of Iran.

Conclusion: CCHF is the most important haemorrhagic fever in Iran.

Although ticks play a very important role as both the vector and the reservoir of the virus and tick bite is one of the routes of transmission of the disease, we have observed in our country that most cases have occurred by handling infected blood or organs of livestock.

Sistan Baluchestan province, which has a very long border with Pakistan and Afghanistan, is not only the most infected province but also we saw that in all these 10 years was the first contaminated province of Iran and also by performing phylogenetical studies we have found that the Iranian CCHF strain is very similar to the Matin strain of CCHF in Pakistan.

21.145 Using Ross River virus outbreak models to deliver practical management tools for mosquito control efforts in the Northern Territory, Australia

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Background: In Australia there are on average 4800 Ross River virus (RRV) disease notifications annually. Although non-fatal, RRV infection is of economic concern as the subsequent fatigue may be debilitating for up to six months. Models can predict RRV outbreaks, although these 'early-warning systems' rarely deliver more than timeliness of a public warning to avoid mosquito contact, rarely can they be used to assist in the control mosquitoes.

We sought to create a rainfall threshold which can pre-emptively notify of RRV disease outbreak conditions, such that vector control measures can be initiated before mosquito numbers peak.

Methods and Materials: Laboratory confirmed cases of RRV infection in the Northern Territory (NT) over 16 years, together with climate and tidal data were used to create logistic regression models of RRV disease outbreaks for each of the major townships of the NT. Following this; a cumulative monthly rainfall threshold was generated using the post-estimation cross-over between sensitivity and specificity.

Results: All models were highly significant. The accuracy of each was represented using the receiver operator characteristic. Rainfall thresholds were produced for each of the major townships, Darwin urban had the highest and Alice Springs the lowest.

Conclusion: We have produced accurate models for RRV infections for the main townships in the NT using climate-only parameters. Furthermore, the rainfall threshold, created when used in conjunction with the tide-cut-off should eliminate the need to resort to predictive models which require constant maintenance. These rainfall thresholds will enable medical entomology to provide tighter control of vector mosquitoes, thus decreasing RRV disease outbreaks.

21.146 Effectiveness of alpha-cypermethrin (Cyperthor) and lambda-cyhalothrin (Demand) in the reduction or prevention of Aedes mosquito breeding in tyres under tropical conditions

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Background: *Aedes aegypti* is not endemic in the Northern Territory, however imports have led to its establishment in 2004 in Tennant Creek and on Groote Eylandt in 2006. Bifenthrin provides limited residual control (approx. 2 wk) in tyres under tropical conditions.

We compare the effectiveness of alpha-cypermethrin (Cyperthor) versus lambda-cyhalothrin (Demand) at preventing colonisation and killing adult *Aedes* mosquitoes in tyres under tropical conditions over a 24 week study period.



Methods and Materials: Larval colonisation: *Aedes* colonisation defined as the presence of 3rd stage instars or higher of *Ae. notoscriptus* in any tyre over the study period. Cross-sectional logistic regression models were used to compare the treatments and application techniques.

Adult mortality: Numbers of tyres positive with dead *Aedes* adult mosquitoes, within treatment and control tyres during the study period were collated. A GLM- binomial distribution with logit link was used to fit the data, this was repeated using only the first 10 weeks of the study. Statistical analysis was performed using Intercooled Stata 10.0 (Stata Corp., College Station, TX, USA).

Results: Larval colonisation: There was a highly significant difference between the treatment groups and the controls ($p < 0.0001$), as indicated by the absolute numbers over the 24 weeks of the study, with 67 incidents of *Aedes* colonisation occurred in all five control tyres. One treated tyre alpha-cypermethrin - dry application was colonised in week 22. Both insecticides using both application modes prevented *Aedes* colonisation for a minimum of 22 weeks.

Adult mortality: Adult mosquitoes had an increased risk of death (OR 2.5, $p = 0.090$) in tyres receiving alpha-cypermethrin application, regardless of application type (wet or dry), than those applied with lambda-cyhalothrin. The risk of death to mosquitoes rose to OR 11.2, $p = 0.023$, when analysis was restricted to the first 10 weeks of the experiment.

Conclusion: These results suggest prevention of colonization of dengue vectors *Ae. aegypti* and *Ae. Albopictus* over a substantial period is possible when sprayed with lambda-cyhalothrin or alpha-cypermethrin, regardless of water presence. This has applications for prevention of dengue vectors in dengue outbreak situations as well as a pre-emptively eliminating or eradicating dengue vectors in non-outbreak situations.

21.147 Current status of Q fever in Ukraine and needs for expanded surveillance of *Coxiella burnetii*

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Background: Since the 1950s, the incidence and distribution of Q fever has been monitored in Ukraine. Local outbreaks of the disease have been identified. Only sporadic cases of Q fever have been identified among the human population. The majority of these were in areas of southern Ukraine where intensive sheep breeding is located, with aerosolization serving as the primary means of transmission. The study was aimed to assess the present situation of Q fever in western Ukraine.

Methods and Materials: This study (project P364/UP-1) was conducted as a component of a larger serosurvey of zoonotic diseases in Ukraine. Serologic assays (ELISA, IFA, and CFT) were used to assess antibody levels against *Coxiella burnetii* in serum samples from healthy volunteers ($n = 1000$) collected in a survey at a single region in western Ukraine.

Results: Of the 1000 serum samples, 36 samples reacted positively in the screening ELISA. Of those screen positive samples, only one individual gave positive IFA tests. While this study indicated a seroprevalence in this area, we are going to study the contribution of *Coxiella burnetii* to acute febrile illness in future. It is possible that some individuals, such as Ukrainian residents who work in agriculture in Europe, may become infected while working and/or living in Q fever enzootic areas outside of Ukraine. However, it is known that *C. burnetii* still circulates in natural foci within Ukraine despite a decrease in morbidity among the population. The pathogen was transmitted by vectors from enzootic areas in some parts of Ukraine to other regions thereby creating new foci. Thus, further understanding of natural maintenance of *C. burnetii* in ticks, reservoir hosts, and the contribution to human disease in Ukraine is critical to the future study and implementing appropriate epizooto-epidemiological prevention and control measures.

Conclusion: The importance of Q fever has been increasingly recognized in Ukraine. The current status of Q fever in Ukraine requires further epidemiological investigation. This preliminary study provides the basis for future efforts aimed at improving the ability to detect Q fever among acute patients and to enhance our understanding of the natural foci of infection.

21.148 Visceral Leishmaniasis (V-L) in pregnancy: Case report

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Background: Visceral leishmaniasis (VL) is usually transmitted by phlebotomies sandflies. Visceral Leishmaniasis (V-L), called also kala-azar is an endemic disease in Albania. During the last two decades it is noticed an increase in the number of cases with V-L at grown-ups, consequently appearing at pregnant women. We think that this situation has raised the possibility or the risk for the vertical transmitting of the parasite

Methods and Materials: We are describing a symptomatic case of VL in a Albanian pregnant women, who was not treated during the pregnancy for V-L, but after the nascence. It was accompanied with a vertical transmitting of the parasite to the child. No evidence exist for congenital leishmaniasis in Albania. Mother and baby were followed up for about 12 months after nascence.

Results: In our report, we demonstrate the history, the course and the treatment of the mother and the baby infected with V-L. The treatment has been done with pentavalent antimonial agents(Glucantini). Result of the treatment for both mother and baby was with good outcome.

Conclusion: Albania is endemic country for visceral leishmaniasis (V-L). This is the first case of vertical transmission of (V-L) published in Albania.

21.149 WNV monitoring activities implemented in Veneto region from 2008 to 2010

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Background: In 2008, the West Nile Virus (WNV) was detected in Northern Italy. This study describes the results of the surveillance activities implemented in the Veneto region in 2008–2010, in order to monitor the spread of infection and to identify the high-risk areas for virus circulation.

Methods and Materials: In 2008, horses from a total of 421 premises were sampled, testing only the horses that had not moved from Veneto or that showed WND symptoms. In the 2009–2010 biennium the surveillance activities were carried out mainly in the municipalities within 20 km from the most outlying farms that resulted positive. In the WNV circulation area only the horses that tested negative in the previous years or showed WND symptoms were tested.

Active and passive surveillance on wild birds and entomological surveillance were also performed.

A number of preliminary risk maps combining the surveillance data on the horse premises and the environmental variables (mainly vegetation, temperature and precipitation) were created to identify the most important ecological variables related to the presence of the disease.

Results: A total of 391/2287 (17%) horses in 199 (28.4%) farms tested positive for WNV in 2008–2010. In 2009 active surveillance 10 wild non-migratory birds tested positive at serological essay for WN while in passive surveillance a blackbird (*Turdus merula*) resulted positive to Usutu virus (USUV) and in 2010 one collared dove (*Streptopelia decaocto*) resulted positive for WNV.

Between 2008 and 2009 the results on the totality of the mosquito pools tested was negative for WNV, while 5 pools were USUV positive. In 2010, 9 and 23 pools of *Culex pipiens* out of 2652 pool resulted positive for WNV and USUV respectively.

Conclusion: Surveillance results of the WNV in 2008–2010 and recent evidence of USUV circulation stress the need to develop tools to: (a) properly monitor the presence of mosquito borne diseases; (b) promptly detect the circulation and further spread of WNV and USUV and; (c) correctly identify the wild reservoirs.



To provide an effective surveillance plan tools need to approach data analysis in a new way and surveillance data must be integrated with ecological and climate variables.

21.150 Comparative analysis of the genomic sequences of dengue type 2 viruses associated with different genotypes/sampling times/epidemics/disease severity in Thailand from 1964 to 2001

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Background: Dengue has re-emerged as one of the most prevalent mosquito-borne viral diseases in the world. Dengue is caused by the dengue viruses (DENVs), which are single-stranded, positive-sense RNA viruses in the *genus Flavivirus, family Flaviviridae*. All four antigenetically distinct DENV serotypes (DENV 1-4) have been associated with human disease ranging from dengue fever to dengue hemorrhagic fever. The prevalence of all four DENVs serotypes has increased dramatically in recent years in many tropical and sub-tropical countries accompanied by an increase in genetic diversity within each serotype. This expansion in genetic diversity is expected to give rise to viruses with altered antigenicity, virulence, and transmission potential.

Methods and Materials: A comparative analysis of complete viral genomic sequences was performed for 19 Thai DENV-2 clinical isolates associated with different genotypes, sampling times, epidemics, and disease severity sampled during the period of 1964-2001, using computer software programs of Clustal W (1.81) and MFOLD.

Results: The analysis revealed: (1) remarkable inter-genotype genetic variations across viral genomes, which may be responsible for genotype dominance within a community; (2) an increase in the total number of amino acid/nucleotide substitutions over time corresponding with increasing dengue incidence in Thailand; (3) an association between the increased DENV-2 epidemic activity and specific amino acid/nucleotide substitutions in the capsid/pre-membrane/envelope/non-structural 1 (NS1)/NS2A/NS4A proteins and 3'untranslated region; (4) some amino acid and nucleotide substitutions were fixed in the virus genome, suggesting a process of micro evolution acting on the DENV-2 genome over time; and (5) the absence of well defined genetic markers that correlated with disease severity.

Conclusion: This study has identified many potential genetic sites possibly responsible for the predominance of DENV-2 genotypes and the serotype itself in Thailand over the 37-years during the sample collections. The invariable observation of specific amino acid and nucleotide changes that are associated with epidemics of intermediate intensity suggests a link between these changes and DENV transmission thorough human hosts. The visual timeline of DENV genome evolution in a specific community provided by this study will hopefully lead to more comprehensive studies of the effects of mutations at particular genomic sites on virus phenotype and, ultimately, novel strategies for disease control.

21.151 Visceral leishmaniasis in Kairouan, Tunisia: Clinical and Epidemiological characteristics and factors of bad prognosis

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Background: Visceral leishmaniasis (VL) is an emergent disease in Tunisia since the early 90's. It presents an increase of its incidence and an extension of its geographical distribution. The aim of this study is to update the current epidemiological and clinical features of VL and to analyze the factors of bad prognosis.

Methods and Materials: Data of 133 VL cases diagnosed from 2004 to 2008 in the pediatric department of Kairouan hospital were collected from the medical records. All patients were treated with Meglumine antimoniate as recommended by WHO. Epidemiological, clinical and biological parameters were analyzed using SPSS program.

Results: Children less than 5 years old were the most affected (94.6%, mean age of 2 years and 1 month). The geographical distribution of cases confirmed the recent spread of the disease to the Central and even Southern districts of the governorate. No difference was found according to sex (Sex Ratio M/F=0.98). Diagnostic delays (mean of 36 days) have considerably shortened compared to previous reports.

The most observed clinical symptoms were fever (all cases) and spleen enlargement (97.7%). Biological disturbances concerned mainly anemia (hemoglobin level <9g/100 ml in 86.6%), thrombocytopenia under 100000 platelets/ml in 67.7%, leucopenia (46.6%) and an increase of γ globulin level (42.4%).

PCR, Bone marrow aspirates exam and Serology (IFAT), showed respective sensitivities in the confirmation of the disease of 100%, 86% and 97.5%. Iso-enzyme typing of isolated strains according to Rioux *et al* method identified *Leishmania infantum* species in all cases.

The lethality rate was of 5.3% (7 deaths). Factors associated with bad prognosis were hemorrhage ($p<0.01$), stibio-intoxication ($p=0.017$), leucopenia ($p=0.038$) and severe anemia ($p=0.047$).

Conclusion: Compared to previous reports, it seems that VL cases are better managed in Tunisia. However, efforts should be maintained to reduce more diagnostic delays and to improve the disease prognosis.

21.152 A metapopulation model to simulate West Nile virus circulation in southern Europe and the Mediterranean basin

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Background: In Europe, recent studies suggest that a recurrent circulation of West Nile Virus (WNV) could exist in some areas. Whether this circulation is permanent due to overwintering mechanisms or not remains unknown. The current conception of WNV epidemiology combines an enzootic WNV circulation in tropical Africa with seasonal introductions of the virus in Europe by migratory birds. The objectives of this work were to (i) model this conception of WNV global circulation; (ii) evaluate whether the model could reproduce data and patterns observed in Europe and Africa

Methods and Materials: The model is a deterministic discrete time meta-population model with a daily time step. The epidemiological system is represented by a set of host populations that share during their annual life cycle a set of locations where vector live. Incidental hosts (sentinel chickens and horses) also are living in each location and are exposed to infectious bites. Three locations were considered: a wet African area, a dry African area, and a European Mediterranean area. Three resident bird populations live in these areas, as do three vector populations. Two migratory bird populations link the three areas: long distance migrants (wet African area-European area) and short distance migrants (wet African area-dry African area). Population dynamics of both vectors and hosts as well as Infection dynamic parameters were fixed according to literature data. Age-specific bite relative risk and site-specific vector-host ratios were estimated using published seroprevalence data coming from these 3 zones. Two age classes were considered for the variations of the bite relative risk: nestlings, chosen as the reference class, and flying individuals (juveniles and adults). A systematic univariate sensitivity analysis was conducted to study the effects of parameter variations on the estimated values of the juvenile and adult bite relative risk, and of site-specific vector-host ratios.

Results: The model was validated using independent published studies. According to this model, overwintering mechanisms are not needed to reproduce the observed pattern. However, the existence of such mechanisms cannot be ruled out.

Conclusion: This model will be used to test the efficiency of several surveillance system (sentinel horses and chickens, mosquito trapping) as well as climatic scenarios.

**21.153** **Bluetongue disease in wild ruminants in the Czech Republic**

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Background: Bluetongue (BT) is a non-contagious viral disease of ruminants transmitted by *Culicoides* midges (Diptera: *Ceratopogonidae*). The disease is caused by an orbivirus of the family *Reoviridae*, with 24 serotypes of the bluetongue virus (BTV-1 to BTV-24) being recognized at present. The clinical signs of BT include fever, hyperaemia and ulceration of the oral mucosa, oedema and coronitis, but infection is often clinically inapparent. In 2006, a BTV-8 virus was unexpectedly isolated in the Benelux countries, Germany and France and, in November 2007, it was detected in the Czech Republic; since then 14 outbreaks have been reported there. In 2008 compulsory emergency vaccination of domestic ruminants with inactivated BTV-8 vaccine was started in our as well as other European countries. However, wild ruminants, possible BTV reservoirs, are not vaccinated and their role in the transmission and spread of BT is poorly understood. The objective of this study was to detect BT in wild ruminants living in the territory of the Czech Republic by blood sample examination.

Methods and Materials: From 2008 to 2010, a total of 436 samples of blood sera or full blood (with EDTA) were obtained from eight different wild ruminant species. Of these, 405 plasma or serum samples were tested for the presence of specific antibodies against BTV by ELISA. In addition, 39 full blood samples were examined by the RT-nested PCR assay detecting the RNA sequence specific for BTV-8.

Results: The serological examination revealed only one positive result in the plasma sample taken from a roe deer in 2009. All 39 PCR-examined samples tested negative for the presence of BTV-8-specific RNA.

Conclusion: Our results indicate that at present the role played by wild ruminants in the epidemiology of BT in the Czech Republic is minimal. However, a similar situation was recorded in some European countries in early surveys for BT in wild ruminants later showing a high BT seroprevalence, and this fact warrants further investigation into the issue. The study was supported by the Research Project no. 6215712403 from the Ministry of Education, Youth and Sports of the Czech Republic.

21.154 **Four years of mosquito-based arbovirus surveys in Emilia-Romagna Region (Northern Italy)**

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Background: In recent years human diseases due to mosquito-borne viruses were increasingly reported in Emilia-Romagna region (Italy) - chikungunya virus in 2007, West Nile virus (WNV) in 2008 and Usutu virus (USUV) in 2009 - suggesting the need for an investigation to determine the presence and geographic distribution of arboviruses. For this purpose, a mosquito based survey was started in late summer 2007; this plan was implemented to cover the whole season in 2008, the survey continued in 2009 and finally in 2010 network of evenly distributed, regularly working sampling stations were activated over the whole Region.

Methods and Materials: Mosquitoes trapped by modified CDC traps baited by CO₂ were pooled according to date, location and species, with a maximum number of 200 specimens per pool. The pools were grinded and centrifuged and an aliquot of supernatant was collected, RNA was extracted and retro-transcribed then analyzed by different genus-PCRs targeting flaviviruses, alphaviruses and orthobunyaviruses and specific-PCRs targeting WNV and USUV. The obtained amplicons were sequenced.

Results: A total of 678,236 mosquitoes, grouped in 5,796 pools, were analyzed from 2007 to 2010. The most tested species resulted *Culex pipiens* (86.4 % of total mosquitoes), followed by *Aedes caspius* (9.2 %), *Ae. vexans* (3.4 %) and *Ae. albopictus* (0.6 %).

The survey allowed the detections of WNV in 32 pools (2 in 2008, 27 in 2009 and 3 in 2010), USUV in 147 pools (56 in 2009, 91 in 2010) and Tahyna virus in 3 pools (one per year from 2008). Furthermore sequence

data showed the presence in tested mosquitoes of RNA of mosquito-only flaviviruses.

Conclusion: The inquiry conducted on sampled mosquitoes pointed out important epidemiological data on temporal and geographic diffusion of the detected viruses in Emilia-Romagna and their spreads in mosquitoes. These results confirmed that, if mosquito trapping effort is intensive, detection of viruses in mosquitoes might precede detection of virus activity by other surveillance tools.

The results obtained by the described survey are encouraging and show how this mosquito-based surveillance could constitute the foundation for a public health alert system targeting mosquito borne arboviruses.

21.155 **Acaricide use and the control of *Theileria parva* infection at the wildlife-livestock disease interface in Kenya**

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Background: In many parts of Kenya, wildlife share grazing land with livestock, leading to the potential for disease transmission across species. *Theileria parva* is a tick-borne protozoan which infects cattle and buffalo in eastern and southern Africa, causing a variety of clinical syndromes including East Coast fever and Corridor disease. The epizology of the disease is complex because of the interaction between wild buffalo and domestic cattle, which are treated with acaricides to kill ticks. Previous studies have focused exclusively on cattle and have only speculated about the influence of buffalo on the dynamics of the disease or about the influence of extensive acaricide use on transmission. We investigate the impact that acaricide use has on the ecology and epizology of *Theileria parva* especially in terms of disruptions of a state of enzootic stability.

Methods and Materials: We gathered data on tick populations and disease prevalence in cattle at two ranches in Laikipia, Kenya which apply acaricides at different frequencies (weekly or fortnightly). Based on this data and on the literature, we developed a continuous time compartmental model of disease transmission by ticks to both cattle and buffalo.

Results: More frequent acaricide use depresses environmental tick population levels, but this is unlikely to be sufficient to disrupt enzootic stability in buffalo populations. However, acaricide use maintains cattle population in an unstable state of low disease incidence.

Conclusion: The results of this study indicate that frequent acaricide use has an impact on the dynamics of *Theileria* transmission in cattle and buffalo and is not a sustainable strategy for tick-borne disease control. The interactions between *Theileria parva*, ticks, cattle and buffalo are complex and merit further study, especially *Theileria* infection in buffaloes about which very little is known. We propose the use of an integrated and adaptive management strategy for ticks on cattle that combines immunization with acaricide use only as needed and offer suggestions for its implementation.

21.156 **Dengue surveillance in Kerala, South-India, from 2007-2010: A laboratory-based analysis**

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Background: Dengue has been prevalent in the Indian-subcontinent for more than 100 years. All the 4 serotypes of the dengue virus circulate in the Indian sub-continent. However, there have been very less study on the genotyping aspects of the dengue virus in the southern parts of India, which is surrounded by highly dengue infected south-east Asian countries. Our laboratory has been involved in carrying out the genotyping of the dengue viral isolates from Kerala, South India, for the past 3 years.

Methods and Materials: Clinical blood samples suspected of dengue fever were collected from various health centers and hospitals. Dengue viral detection was done using RT-PCR and further serotyping by a semi-nested PCR. Full-genome sequencing and phylogenetic analysis was carried out with selected samples from different time periods and of different serotypes. The evolutionary status of the dengue virus as well as the currently circulating serotype was then determined.



Results: The predominant serotype in 2007 was of Dengue Type 1. However, 2008 saw the emergence of other serotypes mainly type 2 and 3 along with type 1. The year also witnessed an outbreak with concurrent infection with serotype 2 and 3 as the major serotypes. Phylogenetic analysis showed serotype 3 to be of a separate lineage different from those already reported from India. On the other hand, 2009 saw another dengue outbreak caused mainly by serotype 1. Phylogenetic analysis of these samples showed the type 1 to be of a separate lineage. Full genome analysis of selected samples of serotype 1 from 2007-2009 showed recombination events in the samples of 2008 and 2009. Phylogenetic analysis of the samples from 2010 showed the newly emerged type 1 lineage to be circulating in these regions till date.

Conclusion: Local-evolution of the dengue virus leading to the formation of a separate lineage may be one of the factors responsible for the outbreak. Co-circulation of all 3 serotypes can cause concurrent infections again in future which may have greater consequences. This study further emphasis on the fact of early detection mechanisms in dengue surveillance and outbreak control.

21.157 A clinical, immunological and neuroimaging study in Lyme Neuroborreliosis

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Background: Lyme Neuroborreliosis (LNB) results when systemic infection with the spirochete *Borrelia burgdorferi* (Bb) leads neurologic involvement. The objectives of the study consisted in the evaluation of the central nervous system (CNS), peripheral nervous system (PNS) alterations and the associated lesions in the Bb spirochete infection through the clinical, immunologic and neuroimaging data.

Methods and Materials: We performed a retrospective study on a number of 50 patients admitted in Targu Mures, Infectious Disease Clinic from 30 September 2006–30 October 2010. In order to avoid a diagnosis excess, the enrolment of the patients in this study was done according to the CDC criteria, patients being assessed using: clinical and paraclinical parameters (cerebrospinal fluid—CSF, microscopic examinations, simultaneous serum and CSF serology and different immunologic techniques—ELISA, Western Blot). The patients who showed meningeal, cerebral determinations, were examined using cerebral CT – scan and MRI, EEG recordings.

Results: In this study 97% of the patients were included in the acute phase of the disease (early LNB) and 3% of them in the late phase of the disease. CNS and PNS impairment in this study was certain revealing meningeal determinations in 86% of the patients, cerebral 72%, facial nerve lesions 38%, radiculonevritis 24%, spinal lesions in 12% of the patients. Serologic findings using a concomitant ELISA and Western Blot techniques from serum and CSF in order to prove the intratecal anti Bb antibodies synthesis and to confirm the diagnosis of LNB have shown total antibodies positive serum titres in 100% of the cases, Ig M (72%), Ig G (14%) of the cases; CSF total antibodies positive titres in 96%, Ig M (64%), Ig G (20%) of the cases.

Conclusion: The diagnostic tests for LNB must be mandatory for the patients suffering from CNS or/and PNS alterations without a definite aetiology.

21.158 Experimental Tacaribe virus infection of Jamaican fruit bats

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Background: Bats represent nearly one fourth of 5400 known species of mammals and it is now evident that bats are reservoirs or potential reservoirs of many human and veterinary pathogens. Tacaribe virus (TCRV, family *Arenaviridae*) is closely related to the viruses that cause the South American hemorrhagic fevers in humans, although TCRV is

not known to cause severe human disease. Arenaviruses with known hosts are rodent-borne with the exception of TCRV, which has only been repeatedly isolated from Jamaican fruit bats (*Artibeus jamaicensis*) and great fruit-eating bats (*Artibeus lituratus*) in Trinidad and Tobago. However, it is unknown if these species are natural reservoirs of TCRV or if the bat infections were incidental. While experimental infections with TCRV have been conducted in mice, very little is known about infection in bats.

Methods and Materials: We performed experimental infections with TCRV on Jamaican fruit bats to examine pathology, virus tropism, shedding and transmission. We assessed infections by detection of viral RNA by PCR and virus isolation. Tissues were collected for histopathological evaluation.

Results: Low dose inoculations led to persistent infection in many bats, while high dose inoculations resulted in death of most bats. Prominent symptoms included nonresponsiveness to stimuli and tremors, with deaths occurring as early as 11 days post-infection. Histopathology indicated multi-organ involvement, including pathology of the liver, lungs, and hearts, and in the brains of all bats that exhibited tremors. No transmission was observed, although virus was detected in and recovered from most tissues examined. These symptoms are similar to those observed in Argentine hemorrhagic fever.

Conclusion: Jamaican fruit bats are susceptible to TCRV and disease is dose-dependent. This model is suitable for studying virus infection of captive fruit bats. The pathology and symptoms exhibited by some infected bats suggest this may be a suitable animal model for this disease.

21.159 Abundance of *Culicoides sonorensis* (Diptera: Ceratopogonidae) in Southern Alberta (Canada) and Montana (USA)

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Background: Bluetongue (BT) and Epizootic Hemorrhagic Disease (EHD) are *Culicoides*-transmitted diseases of ungulates caused by closely related viruses of the genus *Orbivirus*. The main vector for BT and EHD in North America is considered to be *Culicoides sonorensis*. BT and EHD occur regularly throughout the United States. In Canada, outbreaks of EHD were reported in the Southwest (Alberta and British Columbia) in 1962, 1987/1988 and 1999 and outbreaks of BT were reported in South western Canada (Okanagan Valley, British Columbia) in 1975/1976, 1987/1988, 1998 and 2004. BT is a notifiable disease in Canada. Knowledge of the distribution and abundance of *Culicoides sonorensis* is important to inform risk assessment and surveillance efforts by ensuring identification of factors favouring the presence of BT vectors. In this poster we present entomological data collected in Montana and Alberta (2002–2003). Current and future sampling plans will also be discussed.

Methods and Materials: Biting midge were trapped in eight feedlot locations (years 2002–2003) of Southern Alberta and in thirty-one (2002) and nineteen (2003) locations throughout Montana. *Culicoides* sp. were collected using black light traps. In south-western Alberta sampling began in May–June and continued until October for both years. In Montana the trapping started in mid July and extended through September in 2002. For year 2003, black light traps were run from May to September at most locations. Samples were sorted to species and the parity of the *C. sonorensis* determined.

Results: *C. sonorensis* was captured in all the sites of Southern Alberta. Twenty-five (80%) of the 2002 Montana sites were positive for *C. sonorensis*. In 2003, *Culicoides sonorensis* was found in fourteen (73%) of the Montana sites.

Conclusion: Several factors determined the presence and abundance of *C. sonorensis* throughout Alberta and Montana in 2002-2003. To gain a better understanding of these factors, targeted entomological studies along with examination of climate and vegetation data are underway in Southern Alberta. This data will be used to inform risk assessment and vector distribution models.

**21.160** **Diagnosis of tick-borne encephalitis (TBE) based on the detection of NS5 gene sequences by the qRT-PCR in canine samples**

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Background: TBE (Flaviviridae) is the most important and widespread viral disease transmitted by ticks in Europe. This infection can cause serious health involvement with permanent sequelae in humans. Since 1990 the number of human cases has risen and new endemic areas have appeared. Except humans also dogs are susceptible to clinical course with nervous manifestation. Dog is the closest pet-animal to people (which is also connected with travelling to hazardous areas) - that is why the risk of TBE in dogs grows and more cases have been diagnosed. In this study, the diagnosis of TBE virus in dogs was based on use of the qRT-PCR for the detection of flavivirus NS5 gene sequences in the samples of canine whole blood (with EDTA), serum and cerebrospinal fluid. Also deep-frozen samples can be used for retrospective diagnosis (because the phase of neuronal symptoms appears after viraemia and blood samples are usually negative). In addition to TBE, West Nile fever virus (as the second Flavivirus) can occur in our geographic area - the circulating in nature is foreshadowed by wild animal serologic monitoring. But main hosts suffering from encephalitis are humans and horses.

Methods and Materials: The samples were obtained from dogs with the signs of encephalitis of unclear aetiology (donated by MVDr. Pavel Schánílec, University of Veterinary and Pharmaceutical Sciences Brno, Dogs and Cats Clinic). A total of 13 samples were analysed.

The qRT-PCR was chosen for its high specificity and sensitivity. The target sequence NS5 is very conservative and therefore appropriate for the detection of flaviviruses. Primers were designed according to Scaramozzino et al. (2001) and Kubiček. For RNA isolation, the NucleoSpin RNA II protocol 5.1 and a ZR-whole-blood Total RNA kit were used. For amplification, a qPCR 2x SYBR Master Mix (Top-Bio, s.r.o.) was used.

Results: One positive sample was detected. The use of positive controls confirmed that this method would be effective for the detection of TBE virus in canine fluid and tissue samples.

Conclusion: Since there is a growing threat of TBE infection spread in Central Europe, it is necessary to have a reliable method for its diagnosis.

21.161 **Seasonal abundance and prevalence of *Culicoides* biting midges in Sicily, Italy**

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Background: Bluetongue is an infectious, non-contagious arboviral disease thought to infect all known ruminant species. Bluetongue virus is transmitted by biting midges, *Culicoides imicola*, is the major vector in the old world. In Italy other species have been incriminated as vectors: *C.pulicaris* in Sicily and *C.obsoletus* in Central Italy. In this paper the seasonal abundance and the prevalence of positive captures for *C.imicola*, *C.pulicaris* and *C.obsoletus* is valued.

Methods and Materials: The study was carried out at a sheep and goat mix breeding in Palermo province, Italy, from 2005 to 2009, 211 light-trap collections were made, using Onderstepoort-type blacklight trap. *C.imicola*, *C.obsoletus* and *C.pulicaris* were counted, and was calculated the abundance (total number of insect from the same species divided by the total number of catches) and the prevalence (positive catches for a species divided by the total number of catches %).

Results: The results shows that *C.imicola* was present only from July to November, instead both *C.obsoletus* and *C.pulicaris* were present all over the year. *C.obsoletus* had the high prevalence of positive catches with peak in May (100%) and in October (95%), *C.pulicaris* shown low prevalence value with two peaks, in May (83%) and December (77%). As regarding the abundance, *C.imicola* shown very low value, the peak was in October with a value of 0.4 midge. *C.pulicaris* had low value with the peak on April (21.0 insects) and in November (9.5 insects). *C.obsoletus* shown high value with one peak in April (956.7 insects).

Conclusion: Several studies reported a minor vector role for species of *Culicoides obsoletus* complex, presumably high abundances and high survival rates can compensate for low levels of vector competence. On the other hand, *C.pulicaris* shows a relatively higher vector competence, that probably compensate its lower abundance, allowing to act as a vector. This data suggest that different species of *Culicoides*, even though with different vector competence, can play a role to maintain the circulation of BTV in an endemic area. Authors thanks Franco Ferraro and Rosa Filippi for their precious support.

21.162 **Molecular characterization of *B. bovis* Merozoite surface antigen 2c (Msa2c) from Italian strains**

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Background: The merozoite surface antigen-2 (msa) gene family of *Babesia bovis* encodes membrane glycoproteins involved in erythrocyte invasion. The genomic locus of the Mexican Mo7 strain contains four tandemly arranged copies of msa-2 genes, that were shown to be transcribed and expressed. In vivo immunization studies showed the presence of highly immunogenic, conserved B-cell epitopes that elicit neutralization-sensitive antibodies in cattle. The present study was aimed to investigate the degree of conservation of one member of this family, MSA-2c, comparing sequences of Italian and geographically distant strains of *B.bovis*.

Methods and Materials: Genomic DNA from *B.bovis* naturally infected calves positive at the diagnostics PCR (Figuerola et al, 1993) from Sicily and from Campania regions were amplified for msa- 2c gene by PCR (Dominguez et al, 2010). Purified PCR products were cloned in Invitrogen pCR2.1 TOPO TA cloning vector and plasmids were sequenced. The results were obtained using the following software: ClustalW2.0.10, Bioedit, MEGA, DAMBE, SignalP and big-PI Predictor, Predicting Antigenic Peptides.

Results: The whole coding region of the Msa-2c gene was amplified and sequenced from two different Italian strains of *B.bovis*. The comparison of the sequence of *B.bovis* Msa-2c gene of the Italian strains to those coming from Mexico (Chiapas), Argentina (R1A), and USA (T2Bo) showed a high degree of similarity. The overall average of identity at the nucleotide level resulted 96% and at aminoacidic level was 93,8%. The Italian strains conserved a signal peptide at the N-terminal region and a GPI-anchor site at the C-terminus. Furthermore, the predicted immunogenic regions of Msa-2c from Italian strains seemed to maintain a good degree of conservation. The phylogenetical analysis revealed that the groups identified do not cluster accordingly to their geographic regions of origin.

Conclusion: This work reports a molecular characterization performed for the first time from Italian strains of *B. bovis*. The *in silico* analysis revealed a high degree of conservation with foreign isolates and confirmed the key role of Msa-2c as vaccine candidate. (Financed Italian Health Ministry by IZSSI02/07). Authors would like to thank Franco Ferraro and Rosa Filippi for their precious support.

21.163 **Characterization of *Rickettsia* infections in Sicily, Italy**

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Background: Spotted fever group (SFG) are due to obligate intracellular bacteria of the genus *Rickettsia* within the family Rickettsiaceae in the order Rickettsiales. These zoonoses are among the oldest known vector-borne diseases. For *Rickettsia* species classification, gene sequences of 16S rRNA, *gltA*, *ompA*, *ompB*, and D are used. In this study a phylogenetic



analysis of *Rickettsia* strains isolated in Sicily from humans, animals and ticks was performed using 17KDalton gene as target for molecular characterization.

Methods and Materials: From 2002 to 2008, 2299 samples have been analyzed for *Rickettsia* spp. 16SrRNA gene. From seventy-one positive samples, 17KDalton gene was amplified for a region of 256bp and for a 430bp fragment. Sequences obtained were analysed using the software ClustalW2.0.10, Bioedit, MEGA and DAMBE.

Results: A phylogenetic tree was constructed using the 17KDalton gene 256bp fragment. The tree had three major groups, one including *R.belli*, one including *R.typhi*, *R.prowazekii* and *R.felis*, while the last including the group of *R.conorii* subsp. *conorii* Malish7, *R.rickettsii* and *R.sibirica*. Out of tested samples, forty-six strains clusterized with the group of *R.conorii* subsp. *conorii* Malish 7, that included also *R.conorii* subsp. *israelensis* present in Sicily. A Sicilian strain of *R.massiliae*, identified by other genes, and six other strains clusterized with *R.massiliae* and *R.rhipicephali*. Other Sicilian strains clusterized with a candidatus *R.gravesii*, four Sicilian strains clusterized with a candidatus *R.hoogstraalii*. Sequence analysis of 17KDalton gene 430bp fragment allowed to differentiate *R.conorii* subsp. *conorii* Malish 7, *R.conorii* subsp. *israelensis* and *R.massiliae*, for the presence of point mutations.

Conclusion: The analysis performed allowed to distinguish *Rickettsia* species spread in Sicily. At least 25 strains were different from *R.conorii*, among these new species of *Rickettsia* spread in Sicily could be present. Five out of them were strains of human origin and clusterized with *R.massiliae* and *R.hoogstraalii*. This study has provided also important information about 17KDalton gene, suggesting it can be used for phylogenetic analysis. Authors would like to thank Franco Ferraro and Rosa Filippi for their precious support. (Financed by Italian Ministry of Health IZSSi 07/08)

21.164 Serologic and genetic evidence of Dobrava-Belgrade and Saaremaa hantaviruses among Apodemus mice in Hungary and Northern Croatia

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Background: Dobrava (DOBV) and Saaremaa (SAAV) hantaviruses belong to the genus *Hantavirus*, family *Bunyaviridae* and carried by yellow necked (*Apodemus flavicollis*) and striped field (*Apodemus agrarius*) mice. The goal of this study was to determine the prevalence of DOBV and SAAV in *Apodemus* rodents in Hungary and in Northern Croatia.

Methods and Materials: Rodents were trapped in seven different locations during the summer and autumn seasons of 2005-2007. Rodents were dissected and lung tissues were used for hantavirus detection by SYBR Green-based real-time PCR. A representative DOBV strain (DOB/Pécs/242Af/06) was selected for protein expression. Truncated nucleocapsid protein (rNP50) was expressed in *BL21 Rosetta (DE3) pLysS Escherichia coli* cells using pET28a expression vector. Presence of antibodies against DOBV and SAAV in the collected rodents was determined by ELISA reaction.

Results: During the study period a total of 125 *Apodemus* sp. (67 *A. agrarius*, 58 *A. flavicollis*) was tested for the presence of hantaviruses. DOBV and SAAV were detected from 21 *Apodemus* rodents by RT-PCR and/or ELISA. Five rodents were RT-PCR and ELISA positive and also 5 animals were positive by RT-PCR only. 11 small mammals were ELISA positive only, while 104 rodents were negative with both methods. The prevalence based on the results of these two detection techniques was 17% (21/125).

Conclusion: In this study we concluded that prevalence of DOBV and SAAV is much higher as it was expected before, and the parallel use of molecular and serological techniques is the more reliable way to detect hantavirus infections.

21.165 *Dirofilaria repens*—occurrence and emergence in Austria

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Background: The number of reports on cases of dirofilariosis caused by *Dirofilaria repens* in pets and humans in Europe is increasing in the last decade. It is not yet known if this is a matter of emergence of this parasite or if this is based on an increased effort to detect it due to increase in available information in the scientific community. In Austria 2009 the first supposed autochthonous case was reported in the most eastern part of the country. Especially the countries bordering to Austria in the north and east show high prevalences of *D. repens* in dogs up to 30%. This led to a preliminary investigation in northeast and eastern Austria.

Methods and Materials: In 2009 dogs originating from the eastern and northeastern parts of Austria were sampled. On the whole 142 blood samples were investigated by Knott-test and PCR with specific primers for *D. repens* and *D. immitis*. To overcome logistic problems in further studies a modified filter technique was evaluated to simplify the sampling.

In 2010 vets of these areas were supplied with filter cards and to date cards with samples of 85 dogs have been returned.

Results: Investigation 2009: 12 of the 142 dogs could be identified positive for *D. repens*. At least 5 of the positive dogs were supposed to have acquired their infection in Austria due to the fact that they never had been abroad according to the owners' statements. None of the samples were positive for *D. immitis*.

Investigation 2010: 1 imported *D. repens* - positive dog among 85 could be identified.

Conclusion: In Austria we have positive cases of *D. repens*. Some of them might be imported, others are most likely autochthonous. This has to be proven in further investigations. Due to the fact that dogs with circulating microfilaria are available for capable vectors an establishment of new endemic foci is possible. Due to the zoonotic nature of this infection positive dogs should be treated with adulticidal drugs with good efficacy as demonstrated in recent investigations to avoid spreading of this disease.

21.166 Association between Anaplasma phagocytophilum in ticks and anaplasmosis in dogs in Latvia

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Background: Tick-borne encephalitis and Lyme disease are common tick-borne diseases in humans in Latvia. Since 2001 65 cases of human anaplasmosis have been registered. Six cases of canine anaplasmosis have been diagnosed in Latvia. We hypothesize that there could be an association between the prevalence of *Anaplasma phagocytophilum* in two *Ixodes* tick species and anaplasmosis cases diagnosed in dogs in certain regions of Latvia.

Methods and Materials: Ticks collected by flagging were analysed in pooled samples that contained 5 imago or 10 nymphs: *Ixodes ricinus* (248 imago, 40 nymph pools) and *Ixodes persulcatus* (87 imago, 8 nymph pools). The prevalence of *A. phagocytophilum* in ticks was evaluated by nested 16S rRNS PCR.

Peripheral venous blood samples were collected from 301 clinically healthy dogs (healthy dogs) and from 27 dogs with clinical suspicion of a tick-borne disease (sick dogs). Seropositivity for *A. phagocytophilum* was detected by SNAP 4Dx tests (IDEXX). Percentage of the canine seropositivity for *A. phagocytophilum* was correlated with the prevalent tick species in the region (z test).

Results: *A. phagocytophilum* was detected in 6% (17/248) of *I. ricinus* imago pools. All nymph pools and *I. persulcatus* imago samples were negative. Seropositivity in healthy and sick dogs was 10% (32/301) and 22% (6/27) respectively. Based on the geographical prevalence of the tick species, higher seropositivity of 15% (36/233) was noted in Central and



Western Latvia – the region that is inhabited by *I. ricinus* ticks. Dogs from Eastern part that is inhabited mostly by *I. persulcatus* were significantly less seropositive 4% (4/95, $z=2.604$, $\alpha=0.5$).

Conclusion: *A. phagocytophilum* were found only in *I. ricinus* imago ticks. More seropositive dogs were noted in areas where *I. ricinus* are prevalent over *I. persulcatus*.

21.167 Malaria in rural Zimbabwe: Are WHO's goals for disease control being achieved?

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Background: Globally, more than three billion people are at risk for malaria infection. Every year, 247 million cases are reported worldwide causing 1 million deaths. Although Africa represents 91% of deaths burden, epidemiological data from rural areas of high transmission are imprecise. In Zimbabwe, with nearly 13 million inhabitants, WHO reported 1.5 million cases of malaria in 2005, with 56% of the population living at high risk. Since the Roll Back Malaria Partnership was launched in 1998 to accelerate malaria control, WHO's goal was to reduce the burden of malaria by 50% by 2010 from 2000 estimates. We report data collected from a rural Zimbabwean town.

Methods and Materials: Chireya is a rural village, located in the Gokwe district of Zimbabwe. This area is meso-endemic for malaria transmission. Chireya's last census showed a population of 26973 individuals. A non-interventive, observational epidemiological survey was conducted between February and April 2009. 3081 febrile patients attending a rural clinic were tested for falciparum malaria using Paracheck Pf®. Demographic, clinical, treatment characteristics and outcome data was checked for consistency and analyzed using descriptive statistics.

Results: 55.5% of patients tested positive, this represents 6.4% of Chireya's population. 29% were children under five, 11% were 5–15, and 60% were older than 15. The number of patients with clinical criteria for severe malaria was 302 (17.65%). From these 61% were aged under five, 18% were 5–15 years old and 21% were older than 15. Ten deaths occurred, all of them in children under five.

Conclusion: The two-month's malaria incidence observed was more than half of what was globally reported for Zimbabwe in 2005 (6.4 vs. 11.5%). This suggests that, at least on the micro-scale, the targets for malaria control, set by WHO in 2005, were not being achieved. Moreover, concerning the endemicity of the area surveyed, the majority of cases were supposed to be found in children due to the species and the stage-specific acquired immunity present in adults. Unexpectedly, 60% of cases were of symptomatic adults. The role of erroneous disease mapping and/or the effect of co-morbidities, such as malnutrition and HIV infection on the ability to develop immunity, need further clarification.

21.168 Humoral immune response to rickettsial pathogens in dogs regularly infested by ticks in Eastern Austria

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Background: Dogs may serve as a biological indicator for the presence and prevalence of *Rickettsia* spp. known to be pathogenic for humans and animals.

Methods and Materials: 31 dogs from Eastern Austria were examined daily for tick infestation for 6 months. Canine blood samples ($n=31$ after 6 months, $n=4$ after 12 months) were tested for antibodies to *Rickettsia slovaca*, *R. helvetica*, *R. conorii* by specific IFAT's (MegaCor, Austria). Sera were also tested for antibodies to *Anaplasma phagocytophilum* and *Babesia canis* to evaluate possible cross-reactivity. 12 ticks were tested for rickettsial DNA by rrl-rrf ITS PCR.

Results: 460 ticks were collected: 326 *Ixodes* spp., 92 *Dermacentor reticulatus*, and 37 *Haemaphysalis concinna*. Seroprevalence for *R. slovaca*, *R. helvetica*, and *R. conorii* was 20 %, 26 %, and 29 %, respectively. 3/5 positive titres returned to negative when retested after 6 months. Antibodies to *A. phagocytophilum* were found in 57 % and to

Babesia canis in 17 %. All samples that tested positive for either *R. slovaca* or *R. helvetica* were also positive for *R. conorii* and *A. phagocytophilum*. Antibodies to *B. canis* did not correlate with the results of the rickettsial tests. The PCR on 7 ticks originating from 5/31 dogs delivered positive results for *Rickettsia* spp. According to their sequences three groups could be formed: 1) *R. helvetica* isolated from two *I. ricinus*; 2) from two *D. reticulatus*, showing high similarity to *R. massilae*, but the alignment revealed a gap of about 60 bp between the sample and the GenBank entry for *R. massilae*; 3) samples from *I. ricinus* showed a high similarity with an undetermined genus entry in the data base.

Conclusion: Rickettsial pathogens could be detected in ticks collected from dogs. Seroprevalence in dogs ranged from 20-29 % making regular infection very likely. Titres do not seem to be stable over 6 months without reinfection. Results make cross-reactivity of antibodies to the pathogens very likely, as *R. conorii* is unlikely to occur in Eastern Austria as the vector (*Rhipicephalus sanguineus*) is not endemic. *A. phagocytophilum* may also be responsible for cross-reactive antibodies, whereas *Babesia canis* is not.

21.169 Serological evidence of Toscana virus in Portugal

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Background: Toscana virus (TOSV) is an emerging sandfly-transmitted *Phlebovirus* of growing interest as a human neurovirulent pathogen in the Mediterranean basin. In Portugal however there is a lack of knowledge about the prevalence of TOSV infection in the population. The aim of this work was to perform a seroprevalence study in a group of patients with clinical manifestations compatible with TOSV infection.

Methods and Materials: A total of 538 patients admitted to different hospitals, from all over the country, with neurological disease, or requested for arboviruses laboratorial diagnosis, were studied from 2004 to 2008. All samples were analysed by in house indirect immunofluorescence assay (IFI). Positive and borderline results by IFI for TOSV were confirmed by ELISA commercial kits. Positive samples by IFI and ELISA were also tested by plaque reduction neutralization tests (PNRT) with the TOSV ISS. PhI.3 Italian strain.

Results: Overall twelve patients (2.23%) presented IgG antibodies. Five (3.0%) of the patients with neurological disease presented both IgG and IgM antibodies against TOSV by IFI assay and ELISA. Two patients' samples were confirmed with PNRT with the TOSV ISS. PhI.3 Italian strain.

Conclusion: This work showed that Toscana virus is present and causing illness from north to south of Portugal. Our results indicate a need for clinical awareness about the virus circulation in Portugal and the need for consideration of TOSV diagnostic request in compatible human disease suspicion, namely in neurotropic viral diseases. The probable circulation of different phleboviruses genotypes emphasizes the need for further studies.

21.170 Abundance and distribution of potential West Nile Virus mosquito vectors in North Western Canada

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Background: West Nile Virus (WNV) has rapidly spread across North America in the last decade. Mosquitoes of the genus *Culex* are considered to be the main vector in Canada, however, during years of high virus pressure, infected *Culiseta* spp – a genus mainly feeding on large mammals – were detected during surveillance efforts. The aim of the presented study is to evaluate presence and abundance of *Culex* and *Culiseta* mosquitoes in North West Canada in order to evaluate the possible risk of a northward spread of the virus.



Methods and Materials: Mosquito trapping was conducted over the field season (May to September) of 2010 in five locations in northern Alberta and three locations in the southern Northwest Territories. Sampling was performed every second week by means of CO₂ baited CDC traps. Samples were sorted to species and faunistic richness and evenness were determined. Screening for the presence of West Nile and other *Flaviviruses* was performed using Real-Time RT-PCR.

Results: *Culiseta* spp were collected at all sampling locations. Peak abundances were noted in early - mid June. The main species present were *Culiseta alaskensis* and *Culiseta impatiens*. In comparison to this, *Culex* spp were detected in fewer numbers and later in the season. Highest overall abundance and abundance relative to *Aedes* spp was found in the three North Western locations.

Conclusion: The obtained results indicate the presence of competent vectors for disease transmission in the sampled areas, notably the North Western locations sampled. This implies focusing on these regions in the coming field seasons with a view to providing more detailed data to inform future surveillance initiatives and risk assessment activities.

21.171 Evaluation of CCHF patients: Laboratory findings of the first two days

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Background: Crimean Congo Hemorrhagic Fever (CCHF) is an important disease that has been monitored in Turkey since 2002. The disease has a mild clinical course in some patients while it may have a serious course in some others. In our study it was aimed to observe how the first two days biochemical and hematologic laboratory findings affect fatality.

Methods and Materials: The study was carried out retrospectively with CCHF patients in Yozgat region between 2008–2009–2010. Patients who were included in the study had any biochemical or hematological laboratory findings within first two days after the observance of symptoms. Laboratory findings were analyzed using package programme SPSS 15.0 and Chi-Square and Mann-Whitney U tests were conducted to compare measurements of fatal and nonfatal patients.

Results: In Yozgat region there were 352 confirmed CCHF patients between 2008, 2009 and 2010 and 17 (4.82%) of these patients died. There were 244 patients that complied with the study criteria. A total of 244 patients 15 of whom were dead were included in the study. The average of age of nonfatal patients were 38.46 (SD:19.07), and average of age of fatal patients was found out to be 45.47 (SD:19.67) and the difference regarding age was not statistically significant ($p=0.234$). Fatigue (97.4%) was the most common complaint among patients and high fever (86.9%), headache (79.4%), myalgia (78.4%), nausea-vomiting (68.1%), diarrhea (27.4%) were observed in descending frequencies. When laboratory values of patients were examined, aspartate aminotransferase, alanine aminotransferase, lactate dehydrogenase, prothrombin time, activated partial thromboplastin time, international normalized ratio, white blood cell count and thrombolytic values were statistically significant for fatal cases.

Conclusion: CCHF is a disease still maintains its importance in our country, and equipment of hospitals in endemic regions of Turkey is lack of quality ICU facilities. It is critical to conjecture which patients will have a more fatal course. Since this study was performed with laboratory findings of the first two days, we believe that it holds key importance to predict earlier which patients should be transferred particularly in hospitals that have ICU.

21.172 Detection of Pathogenic Arboviral Zoonoses in Central Asia

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Background: High consequence human pathogens such as Crimean-Congo Haemorrhagic Fever (CCHF) virus, Tick-Borne Encephalitis (TBE) virus, Dobrava (DOB) hantavirus and Puumala (PUU) hantavirus are endemic throughout Eurasia, however there is a lack of confirmed reports regarding the circulation of these viral agents in the Former Soviet Republics. As part of an international collaboration established to increase epidemiological surveillance capabilities in former Soviet states, a team of British, American and Central Asian scientists undertook several clinical and field studies to assess the prevalence of high consequence arboviral zoonoses across the region.

Methods and Materials: *Arthropods:* Ticks, midges and mosquitoes were collected by local scientists across several Central Asian regions. Arthropods were crushed into PBS, then a small sample inactivated in AVL buffer (Qiagen). *Small Mammals:* Small mammals were trapped by mammalogists in both Georgia and Kyrgyzstan. Organs (typically liver, lung, spleen and salivary gland) were harvested and samples inactivated using either AVL or FTA cards (Whatman). *Human Samples:* Potential human cases of CCHF and TBE were targeted in Tajikistan and Kyrgyzstan, respectively and samples obtained by local physicians.

All materials were transported to the high containment facilities at HPA-Porton (UK) for molecular diagnosis and sequencing. Detection was carried out using in-house real-time qRT-PCR assays positive samples were confirmed with 'classic PCR' and sequencing

Results: GEORGIA: *Field Samples* (126 arthropods) – DOB 24 (19%), TBE 15 (12%), CCHF 1 (0.8%). KYRGYZSTAN: *Field Samples A* (96 mammals) – PUU: 23 (24%), TBE: 3 (3.1%), CCHF: 2 (2.1%). *Clinical Sample* (1 patient) – TBE: 1 (100%). *Field Samples B* (18 tick pools) – TBE 12 (66.7%). TAJIKISTAN: *Clinical Samples* (11 patients) – CCHF: 7 (63.6%)

Conclusion: Several high consequence pathogenic viruses have been detected in arthropod, mammal and human samples across Central Asia. Real-time qPCR and serological assays are being transferred to several laboratories across the region in order to allow continual epidemiological surveillance, clinical diagnosis and to assess the burden of disease across the region

21.173 Identification of an inhibitor of Flavivirus protease with antiviral activity

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Background: The objective of our study is to identify inhibitors of the Flavivirus protease.

Flavivirus, members of Flaviviridae family, are arboviruses. They are responsible of fevers, haemorrhagic fevers, encephalitis and variable severity poly-visceral attack in human. Their annual cumulated impact is between 50 and 100 million cases. No therapeutics exists.

Methods and Materials: During past works, we expressed, purified and characterized the serine protease of 7 different Flaviviruses that are assumed to be representative of all flavivirus genus members. We set up and optimized *in vitro* assays for those proteases that enabled us to test inhibitory molecules. Protease activity was measured using fluorogenic synthetic substrate on a spectrophotometer. Cytotoxicity on Vero cells and effect on cell growing were tested. Effect on virus proliferation was determined by qRT-PCR.



Results: *In vitro*, we observed inhibitory activity of one compound (S1) on all assayed proteases. A decrease of 70% to 80% of protease activity for enzyme:inhibitor ratios of 1:100 and 1:80 respectively. This inhibitor mimics a consensus peptidic sequence of flavivirus proteases substrate and is non-splittable. We found that it is a competitive inhibitor for Saint-Louis Encephalitis virus protease and surprisingly, a non-competitive inhibitor for other proteases tested. The fixation site for non-competitive inhibition is being determined. This compound is specific for the protease of the flaviviruses since it does not have any effect on other serine protease as trypsin.

In vivo, S1 has antiviral activity: ED50 (concentration of inhibitor that reduces quantity of virus of 50%) was 100µM. No effect was observed on a control virus (Chikungunya, an Alphavirus). CC50 (concentration of inhibitor that reduces cells viability of 50%) was 410µM. IC50 (concentration of inhibitor that reduces cells growth of 50%) was estimated as 380µM. S1 is considered as non cytotoxic.

Conclusion: Our results indicate that S1 is an inhibitor of several flavivirus proteases. This inhibitor appears to have better CC50 and IC50 for flaviviruses than any other published compound. Low ED50 shows that this inhibitor interferes strongly with viral replication. To our knowledge, it's the first time that an inhibitor targeting all members of a viral genus is developed.

21.174 Viral features associated to Chikungunya virus emergence in metropolitan France

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Background: Chikungunya virus (CHIKV), an alphavirus transmitted to humans by the bites of *Aedes species* mosquito vectors, is responsible for numerous outbreaks in Africa, Indian Ocean, India and South East Asia.

Methods and Materials: To face a possible emergence of CHIKV infection in France, a surveillance system has been implemented since 2006 in six departments from southeastern France where *Aedes albopictus* is present.

Results: In August 2010, an imported case from Rajasthan (India) of CHIKV infection was detected in Fréjus (Var, France). Three weeks later, two cases of autochthonous transmissions of CHIKV were identified by the surveillance network. Both patients had no history of travel in endemic areas for CHIKV but they had spent two days in close vicinity of the imported case. Early intensive mosquito control measures were undertaken around all confirmed cases and no additional autochthonous infection was reported in Fréjus.

Envelope E2 and E1 genes sequences were determined for CHIKV isolates (France/2010 CHIKV) from autochthonous and imported human cases. These two strains showed 99.97% identity at the nucleotide level and 100% at the amino acid level. Phylogenetic analysis evidenced that these France/2010 CHIKV clustered with Indian strains within the East Central South Africa (ECSA) lineage. Noteworthy, the two France/2010 CHIKV strains carry an Ala residue at the position E1-226, whereas a Val residue at this position has been identified as a crucial determinant for *Aedes albopictus* adaptation.

Conclusion: The successful local transmission of CHIKV strains with Ala at the position E1-226 provides a new insight into the vectorial capacity of *Aedes albopictus* in Western Europe. The different introductions of CHIKV in La Réunion island and the two recent emergence events of CHIKV virus in Europe (Italy, 2007; France, 2010), due in both cases to a unique viremic patient, indicate that an efficient transmission of CHIKV may occur with a wide spectrum of viral genetic background and whatever is the vector specie(s) present in the country of origin of the imported isolate. Thus an appropriate surveillance schedule should be recommended in all European countries facing the expansion of *Aedes albopictus*.

21.175 The role of South American camelids in bluetongue virus serotype 8 epidemiology

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Background: Bluetongue (BT) is one of the most important diseases of domestic livestock worldwide and is caused by *Bluetongue virus* (BTV), an *Orbivirus* transmitted by *Culicoides* biting midges. In South American camelids (SAC), serological evidence indicated their susceptibility to BTV infection. BTV-related disease and fatalities have recently been reported in a few SAC during the BTV serotype 8 (BTV-8) and BTV-1 epizootics in Europe. This raised concerns about the role of SAC in BTV epidemiology.

Methods and Materials: Blood samples were collected from 1742 SAC in Germany from autumn 2008 to spring 2009. BTV antibodies were detected by ELISA, and seropositive samples were tested for BTV RNA with real-time quantitative RT-PCR (RT-qPCR). On three farms with seropositive SAC, *Culicoides* biting midges were caught in BG-Sentinel™ UV light traps between mid-2008 and autumn 2009. They were counted and sorted by species. Selected midge samples were tested for BTV RNA with RT-qPCR.

Three llamas and three alpacas were experimentally infected with a recent German isolate of BTV-8. Whole blood and serum samples were analysed by ELISA, serum neutralisation test, full blood count, RT-qPCR, and virus isolation. Clinical data were recorded daily. Spleens collected postmortem, three months after infection, were also tested for BTV RNA using RT-qPCR. The adsorption capacity of BTV-8 to camelid blood cells was investigated by an *in vitro* experiment.

Results: No BTV RNA was found in blood samples or *Culicoides* specimens, but 14% of SAC were seropositive. After experimental BTV-8 infection, viral RNA was only transiently detectable in low amounts in SAC blood, and was quickly cleared after seroconversion. However, spleens collected postmortem were still positive for BTV RNA. Virus isolation from SAC blood was only possible by inoculation of highly sensitive interferon alpha/beta receptor deficient IFNAR^{-/-} mice. The blood cell binding experiment demonstrated that significantly lower amounts of BTV-8 adsorbed to SAC blood cells than to blood cells of cattle.

Conclusion: Although the animal experiment demonstrated that SAC are generally susceptible to BTV-8 infection, the virological results suggest that they only play a negligible role in BTV epidemiology.

21.176 Effect of transportation on the efficacy of a formalin inactivated Rift Valley Fever vaccine.

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Background: Mozambique is one of several countries in sub-Saharan Africa where Rift Valley Fever Virus (RVFV, Phlebovirus, *Bunyaviridae* family) causes severe disease among livestock. The clinical signs vary from necrotic hepatitis with or without hemorrhagic stage to spontaneous abortions and high mortality. To combat disease among cattle, a vaccination program using formalin-inactivated RVFV vaccine (Onderstepoort Biological Products Ltd, South Africa) was introduced in the province of Zambezia. Before the vaccine is distributed to the animals it is transported within Mozambique by plane and car a distance of at



least 600km, a transport often resulting in disrupted cold-chain. The true effectiveness of the administered vaccine is therefore not known. In this study we aim to evaluate the effect of different storage condition on the efficacy of the formalin-inactivated RVFV vaccine.

Methods and Materials: The RVFV vaccine was stored under three different conditions for one week: I) +4°C, according to the manufacturers' instructions, II) similar to transportation conditions, alternating +4°C and +25°C or III) +25°C. Each vaccination group contained 10 cows, which were vaccinated two times with three weeks intermission. Twenty-five serum samples were collected from each cow during one year and the antibody responses were monitored by ELISA and IFA and the protective immunity by neutralization test.

Results: As confirmed by ELISA and IFA, 10% (3 out of 30) of the cows were sero-positive for anti-RVFV antibodies before vaccination. As expected, the anti-N antibody responses were relatively weak and did not differ between the vaccination groups. The protective immune responses, monitored by neutralization test, were also similar between the groups and no major differences could be detected in either antibody titers or duration.

Conclusion: Our results show that RVFV is present in the southern parts of Mozambique, indicating that a larger surveillance study has to be performed in order to evaluate if the livestock vaccination program should be further expanded. Since no differences in the induced immune responses could be ascribed the different vaccination groups, our results indicate that the formalin-inactivated vaccine administered in the field is still effective, despite variations in storage temperature.

21.177 Do they meet often? Genetic similarity between European populations of a potent disease vector *Culex pipiens*

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Background: Mosquitoes are vectors for a number of important insect-borne diseases that can infect both humans and domesticated animals. In Southern Europe the mosquito *Culex pipiens* is a competent vector for several types of pathogens of great medical importance, such as the West Nile Fever Virus (WNV), Rift Valley Fever Virus (RVFV), and Eastern / Western Equine Encephalitis Virus (EEEV / WEEV). Ongoing climate change combined with increasing globalization makes it possible for pathogens previously absent in Northern Europe to establish themselves in new areas. One way to estimate the rate of contact between mosquito populations that carry certain pathogens and the ones that do not, and in this way estimate the possibility of natural pathogen dispersal, is to look at the gene exchange between mosquito populations.

Methods and Materials: To measure the genetic diversity between European *Culex pipiens* populations we used 8 microsatellite markers in 10 populations of *Culex pipiens* originating from northern, central and southern Europe.

Results: Our data showed an extensive amount of gene exchange between European *Culex pipiens* populations with only a few populations being isolated.

Conclusion: We therefore conclude that pathogens presently occurring in southern areas are at favorable climatic conditions likely to disperse northward over a relatively short time period.

21.178 A model to predict areas of potential BTV outbreaks

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Background: Bluetongue (BT) is an infectious non contagious vector-borne disease of ruminants caused by Bluetongue virus (BTV), transmitted by *Culicoides* biting midges. Since 1998, several outbreaks have occurred in Europe involving different serotypes. The aim of this study was to develop a predictive model to estimate the potential spatial distribution of BTV8 serotype to detect areas of potential BT outbreaks occurrence in North-western Italy (Piedmont region).

Conclusion: From an epidemiological point of view, this model is oversimplified as it didn't evaluate the effect of animal density. However the fact that 16 outbreaks reported in Piedmont in 2009 occurred in the area underlined by the map, might be considered as a clear evidence of the validity of the predictive model.

21.179 Studies on the pathogenicity of the 2009 West Nile Italian strain (Italy/2009)

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Background: In 2008, ten years after the last outbreak, new, clinical cases of WNV were reported either in humans and in horses in Italy. The WNV strain was able to survive the winter season and cases were reported also in 2009. According to its genetic characteristic the Italian WNV strain is grouped within the lineage 1 and revealed the acquisition of a putative virulence-associated modification (NS3-T249P) when compared to the 1998 Italian strain. The same mutation has been claimed as responsible for the high virulence of the strain isolated in 1999 in New York City. To investigate the virulence of the new Italian WNV, mortality rate, pathogenicity and neuroinvasivity of the IT/09 and NY/99 were compared by using a murine model.

Methods and Materials: Four groups of five 3-4-week-old female Swiss mice were each inoculated with doses ranging from 100 to 103 TCID₅₀/ml of NY/99 or IT/09. The strains were injected intraperitoneally (i.p.) or intracerebrally (i.c.). For each inoculation route, control groups were included. Several organs were collected from death animals and the presence and titre of WNV was determined by, virus titration (VT) and qRT-PCR. For each, determined rate 95% confidence intervals was calculated using the Bayesian approach through the beta distribution.

Results: In the infected mice the brain was the organ found most frequently and heavily infected despite the strain and route used.

Lower doses (100–101 TCID₅₀/ml), of IT09 were able to kill less (P<0.05) animals (4 dead/20 infected, 95% CI 8%-41%) compared to the NY/99 (14 dead/20 infected, 95% CI 47%-85%). Similarly, after the intracerebral injection, a lower mortality rate (P<0.05) was found in the groups of mice infected with IT/09 (11 dead/20 infected, 95% CI 34%-74%) compared to the groups infected with NY/99 (20 dead/20 infected, 95% CI 86%-100%).

Conclusion: When compared to the highly virulent NY/99, although showing a similar neuro-invasiveness and capability of invading and replicating in many other different tissues and organs of mice, IT/09 demonstrated to be less pathogenic for mice either when injected at lower doses or when injected intracerebrally.

21.180 Age- and sex-specific mortality patterns in hemorrhagic fever with renal syndrome caused by Puumala virus

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Background: Hantaviruses cause hemorrhagic fever with renal syndrome (HFRS) in Eurasia and hantavirus cardiopulmonary syndrome (HCPS) in the Americas. These diseases have a case-fatality rate <40% depending on the specific hantavirus. HFRS/HCPS-causing hantaviruses are maintained in the environment by rodents, with humans serving as incidental hosts who are typically infected by inhalation of virus-



contaminated rodent excreta. In parts of Europe, including Sweden, Puumala virus (PUUV) causes nephropathia epidemica (NE), a relatively mild form of HFRS with case-fatality rates of 0.1% - 1%. For many infectious diseases, frequency of infection is generally higher, and the clinical outcome often worse, in male patients. It is known that males are over-represented in HFRS-diagnoses. However, if there are sex differences in the severity of disease had previously not been investigated.

Methods and Materials: We analyzed case-fatality rate in all NE-patients ($n = 5,282$) diagnosed in Sweden 1997-2007.

Results: The overall male:female ratio in NE cases was 1.52. The highest prevalence was observed in the age group 55-59 years for both males and females, and the mean \pm SD age at diagnosis was 49.3 ± 16.7 years for men and 50.7 ± 16.5 years for women. Of all diagnosed, 0.4 % died during acute NE (within 3 months after diagnoses), and the standardized mortality ratio (SMR) was 3.5 (95% confidence interval (CI) 2.22-5.26). Case-fatality rate increased with age; no patient below 50, but 6.5 % of patients older than 80 years of age, died. Interestingly, whereas the SMR during acute NE for females was 6.4 (95% CI 2.97-12.15) and for males 2.7 (95% CI 1.52-4.56), only women showed significantly increased case-fatality rate during the first year after diagnoses; the SMR for females was 2.0 (95% CI 1.02-3.57) and for males 0.95 (95% CI 0.58-1.49).

Conclusion: The results show that there may be age and sex differences in mortality patterns of HFRS, which should be considered in clinical studies of hantavirus infections.

21.181 Wild mammal diversity and animal keeping relationships: The link for a better comprehension of sleeping sickness re-emergence in Fontem (Cameroon) old focus

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Background: Research discoveries in the Bipindi area (Cameroon) indicated the existence of a triangular transmission scheme of *Trypanosoma brucei gambiense* (TBG) involving the vectors (*Glossina palpalis palpalis*), terminal hosts (humans) and host-reservoirs (livestock and wild mammals) in Cameroon. However, the interconnexions between livestock and wild mammals remained unknown.

Methods and Materials: Therefore, we carried out animal keeping study and wild mammal surveys in Fontem old focus of sleeping sickness located in South-West province of Cameroon in order to find out the intermingling areas between domestic and wild cycles of the disease.

Results: From the total 2793 individuals of domestic animals including fowls (2295 individuals) and mammals (498) only three species (goats, sheep and pigs) are recognized as host-reservoirs of TBG. Among these species host-reservoirs, 195 (56.67%) individuals were kept as free-range animals and 139 (43.33%) individuals confined. As for wild animals, 15 mammal species were recorded, of which 11 occurred in the undisturbed forest, 6 in farmlands and plantations (cocoa or palm oil plantations) and 6 in village-adjacent forest. Among them four species (*Cephalophus monticola*, *Cephalophus dorsalis*, *Atherurus africanus* and *Cricetomys emini*), known as reservoir hosts of TBR occurred in all habitats suitable or unsuitable for *G. palpalis palpalis*. These species are the most involved in the transmission cycle (humans / tsetse flies / wild mammals). However, in the village-adjacent forest, farmlands and plantations, suitable habitats for *G. palpalis palpalis*, these reservoir hosts are involved in the mix transmission cycle humans / tsetse fly / wild mammals / tsetse fly / domestic mammals (free-range individuals).

Conclusion: This study showed that free-range animals contributed to the spread of tsetse flies around the villages and from the village to the adjacent biotopes and forest favoring the contacts between domestic mammals, wild mammals and the flies.

21.182 Serosurvey of Crimean-Congo Hemorrhagic Fever in human populations in Kenya

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Background: Crimean-Congo hemorrhagic fever (CCHF) is a viral tick-borne zoonotic disease caused by CCHF virus, a member of the *Bunyaviridae* family, *Nairovirus* genus. CCHF is a disease with high mortality rates in humans with symptoms of more common febrile illnesses in Kenya such as malaria or rift valley fever; leading to misdiagnosis, wrong treatment and an inability to detect outbreaks of other disease agents. Evidence of CCHFV circulation in ticks in the North Eastern province indicated the need for accurate assessment of CCHF prevalence as an important step towards assessing disease burden in humans, and need for improved outbreak preparedness. The aim of this study was to determine the prevalence of CCHF in two districts in this province.

Methods and Materials: This study was a descriptive cross sectional analysis of 346 acute phase human sera from Ijara and Garissa districts. ELISA was used to detect acute infection of and prior exposure to CCHFV. Questionnaires with demographic, clinical and geographical characteristics were administered. Data analysis was performed using Epi Info software version 3.3.2. Fisher's exact test was used to determine associations while proportions was determined by frequencies.

Results: All of the samples screened for CCHF by IgM ELISA were negative whereas 26 out of 346 (7.5%) samples were IgG ELISA positive (95% confidence interval: 5.1-10.9). Of the IgG positives, males represented 53.8%, (Median age=30 years, range=16-60years).

The most affected age group for CCHF IgG positive were aged 20-29yrs (42.1%). Herdsmen were more frequently (57.7%) affected than housewives and businessmen. CCHF virus exposure was significantly associated with farming ($p = 0.0294$), travelling outside the village ($p = 0.0327$) and contact with camels ($p < 0.000$).

Conclusion: This study is the first sero-survey showing the extent of human exposure to CCHFV in Kenya. Risk factors included camel contact, farming and livestock herding. This evidence of human disease necessitates awareness creation among public health awareness on the disease existence, training on disease management and outbreak response. Further investigations on the scope of the disease in other regions with similar risk factors, reservoir hosts and vectors are critical for disease management and control.

21.183 Risk maps for mosquito-borne diseases (Diptera,Culicidae): Distribution and abundance of mosquitoes in the Canaries Archipelago (Spain)

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Background: Facts happened in archipelagoes near to that of Canaries, as the emergence of dengue fever in Santiago (Cape Verde) and the growth of the abundance of *Aedes aegypti* in Madeira (Portugal), have alerted the Spanish Health Authorities of the susceptibility of Canaries to



the emergence and re-emergence of mosquito-borne diseases. For this reason we are developing a project, whose purpose is to provide to the Canary Health Service maps with which to predict the risk of introduction or re-introduction of mosquito-borne diseases. These maps will be made on the basis of the spatial-temporal variability of abundance and population distribution of vectors, and using GIS. The first objective was to analyze abundance and distribution of mosquitoes in two of the islands, Tenerife and Gran Canaria.

Methods and Materials: The choice of sampling sites was made on the basis of published data from positive catches and to the different bioclimatic zones in the islands. Adults and larvae were captured in every sampling site, using traps of light type CDC and by mean of pipetting, respectively. The captures were realized from February 2010 until November 2010 and with a seasonal frequency.

Results: The identification showed that the captured mosquitoes belonged to seven species: *Aedes eatonii*, *Anopheles cinereus hispaniola*, *Culex arbieeni*, *Culex laticinctus*, *Culex pipiens*, *Culex theileri* and *Culiseta longiareolata*, of which *Cx. pipiens* and *Cx. theileri* turned out to be the species most abundant and distributed in both island. About these species are known its relationship with the potential transmission of viruses like the virus of the West Nile, the virus Sindbis and the virus of Rift Valley fever, and nematodes as *Dirofilaria spp.*

Conclusion: The information obtained of the distribution and abundance will be incorporated together with other data (vegetation, climate, etc.) to a GIS for the preparation of the maps, which will be useful to develop much more rational strategies of control and intervention.

The Project "Gestión integrada del vector *Aedes aegypti*" (MOSQIMAC/2/M063) has been funded by the EU (FEDER).

21.184 Surveillance of dengue in France: Different modalities for different situations and results for 2010

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Background: Dengue Fever presents extremely varied epidemiological profiles in France (Pacific Territories excluded), depending on the territory considered. The virus is hyperendemic in the French West Indies and French Guyana (French Territories in the Americas, FTA), causes usually sporadic cases and occasional outbreaks in French islands of the Indian Ocean, is threatening to emerge in the South-West of mainland France and Corsica while it poses no risk in other parts of the mainland.

Methods and Materials: France's national institute for public health surveillance (InVS) therefore established context-specific dengue surveillance frameworks, identifying specific rationales and modalities, including strategies for biological diagnosis and vector management.

Results: The risk of importation from the FTA to areas where the vector is present poses a real and immediate risk, as shown during the summer of 2010 when the first two autochthonous cases were diagnosed in the south of mainland France. This could be explained by the well-documented "importation corridor" between Mainland France and the FTA, where major epidemics were described in 2010. Autochthonous, sporadic cases were also diagnosed in the French islands of the Indian Ocean, especially in the French island of Mayotte, a part of the Comoros archipelago which also faced an important outbreak in early 2010.

Conclusion: France is the only European country with such a diverse Dengue transmission profile, shared only with a handful of countries. The authors will present the updated results for 2010 and discuss the Dengue emergence risks and surveillance strategies implemented.

21.185 First laboratory confirmed case of tick-borne fever in dairy cattle in Germany

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Background: Tick-borne fever (TBF) of ruminants is caused by the obligate intracellular bacterium *Anaplasma phagocytophilum* and is transmitted by the sheep tick, *Ixodes ricinus*, the most abundant tick in Central Europe. The disease and its causing agent were already described in the first half of the 20th century. However, scientific interest only awakened after the discovery that variants of the same agent also cause Granulocytic Anaplasmosis (GA) in humans, dogs and horses. TBF is considered endemic in Germany, because of (i) the endemic presence of *A. phagocytophilum* in ticks and (ii) the occurrence of GA in dogs and horses, but no confirmed case description can be found in a medline search.

Methods and Materials: In September and October 2010, 4 primipara XFM hybrids (Fleckvieh x Red Holstein) presented between 2 and 4 months post partum with fever, depression, anorexia, stiff walking, decreased milk production, nasal and eye discharge after being brought to the pasture. All animals received analgetic treatment, two animals with fever > 40°C were additionally treated with Trimethoprim and Sulphadimethoxine. According to a suspicion of TBF, EDTA blood was analysed with buffy coat and blood smears after Giemsa staining, *A. phagocytophilum*-specific real-time PCR after DNA-extraction, and serum was tested with commercially available IFAT slides.

Results: Smears revealed morulae of *A. phagocytophilum* in neutrophilic granulocytes in 3 out of 4 cases (Figure). Specific real-time PCR for *A. phagocytophilum* was positive in all 4 cases and the IFAT titer was up to 1:200. For the differentiation and characterization of the TBF causing agent, further PCRs targeting partial *16S rRNA*, *msp2*, *msp4* and *groEL* genes are currently being carried out.

Conclusion: In conclusion, we report here a confirmed TBF case in cattle according to the guidelines for human cases. Taken together with known prevalence data of *A. phagocytophilum* in ticks in Germany, we consider that underdiagnosing of TBF in cattle is highly likely and should therefore be considered as differential diagnosis after high fever and/or a sudden decrease in milk production in pastured animals. This adds new aspects in a public health context, as likewise human cases have not yet been found in Germany.

21.186 Ecological surveillance of West Nile virus in Catalonia 2007-2010: Continuously evolving

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Background: West Nile Virus (WNV) is a widespread zoonotic vector-borne pathogen, which circulation has been frequently reported in Europe, causing animal and human fatalities.

An ecologic surveillance system for WNV has been implemented in Catalonia (in north-east of Spain) from 2007, constituted by several components: active and passive avian surveillance, follow-up of chicken sentinels, cross-sectional surveys in feral equines, follow-up of equine sentinels, passive equine surveillance, and entomological surveillance.



Methods and Materials: The active avian surveillance consisted in serological surveys by using a competitive ELISA (cELISA), and later confirmation by virus-seroneutralization test (VNT).

The passive avian surveillance included investigations of dead birds all over Catalonia. Encephalon tissue was collected and tested by specific WNV real time RT-PCR (RRT-PCR).

The equine surveillance was based on periodical serosurveys in sentinels, cross-sectional surveys in feral horses from wetland areas, in both cases by cELISA and later VNT, and passive surveillance on those showing neurological clinical signs by testing sera, cerebrospinal fluid (CSF) or nervous tissue. The sera and CSF samples were tested by cELISA, and CSF and nervous tissue by RRT-PCR.

In the entomological surveillance, the specimens were identified and pooled, viral RNA extracted, followed by a generic RT-nPCR. Only flavivirus positive pools were tested for WNV by RRT-PCR.

Results: All birds (n=291) from passive surveillance gave negative results by RRT-PCR. In active surveillance, all sera (n=537) gave negative results with the exception, in 2010, of 5 sera from migrant species coming from African countries.

All sentinel chicken sera tested by WNV cELISA resulted negative.

All equine sera (n=572) were tested as negative by cELISA except one indigenous that was positive to cELISA and VNT (1/10), and negative to the ELISA for Ig M. All equines with clinical signs of encephalitis were negative to WNV by real time RT-PCR.

Between 2007 and 2009, 14,404 mosquitoes from 15 different species were pooled in 902 groups. Sixty one pools resulted positive to *Flavivirus* genus, although none of them resulted WNV positive.

Conclusion: From 2007 to 2009 all samples resulted negative for WNV.

However the 2010 wild bird serological surveys have pointed out that the WNV incursion is highly probable.

Although WNV circulation in mosquitoes has not been detected, the isolation of other flavivirus sequences of unknown importance in health is a concern that requires further research.

21.187 Health related quality of life and the prevalence of post traumatic stress disorder among CCHF survivors 12 months after disease

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Background: Crimean Congo haemorrhagic fever (CCHF) is a potentially fatal, endemic disease in Turkey. Many people are affected from this disease especially in summer season. Patients are held in isolated care in hospitals and many of them require blood transfusions. Also, some patients must be kept under intensive care unit (ICU) conditions. This brings the possibility of poor outcomes for the survivors. CCHF is not a recurrent disease and relapses are not expected. Once a patient recovers from CCHF no medical follow up is needed.

Methods and Materials: The present study was conducted in Yozgat province of Turkey. Patients survived CCHF after 12 months from discharge were included in the study. Turkish version of the structured clinical interview for DSM-4, Clinical Version (SCID) was first administered by our research psychiatrist. The Medical Outcomes Study (MOS) Short Form 36 (SF-36) was chosen as the functional outcome assessment in this study. It is a self administered, generic, multi-dimensional measure of health related quality of life. For the analysis of the data SPSS 15.0 software was used. Patients were divided into two groups: one with PTSD diagnosis and another one without diagnosis. For correlations Mann-Whitney U-Test and Chi Square test were used. Comparing patients with CCHF and public SF-36 test results' averages, One Sample Test was chosen. Results of analysis were accepted statistically significant if p<0.05.

Results: Our results showed that 48.1% of patients had some kind of psychiatric disorders, 18.5% of them specifically had post traumatic stress disorder (PTSD). Among patients requiring ICU setups or blood

transfusions, PTSD incidence was higher; however, none of the patients applied to health care professionals with these psychiatric problems. Quality of life assays of patients and Turkish population average were revealed that social functionality, emotional role problems and mental health were deteriorated most frequently.

Conclusion: Due to the increasing number of CCHF cases in Turkey, we believe that periodic psychiatric evaluations must be performed and precautionary preparations must be made considering this problem as an important public health measure.

SESSION 22 (Early Morning Session)

Emerging Diseases in Public Health Education

Monday, February 7, 2011

Room: Klimt Ballroom 2-3 • Upper Level

07:00-08:00

22.001 Emerging diseases in public health education: The case of field epidemiological trainings

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Background: The Epidemic Intelligence Service, initiated by the US-CDC in 1951, has set the ground to key successes in field epidemiology. The two-year program covers applied epidemiology, biostatistics, surveillance, communication, and emerging public health issues. It started to be replicated in various countries 30years ago and is now the canon for 61trainings worldwide. Thanks to this program the community of field-epidemiologists has managed to control numerous outbreaks from -sometime- unknown origins. Efforts have been devoted to expand internationally this training. But, is this 60-year-old model still adapted to currently emerging diseases? Globalization requires field-epidemiologists to be able to participate to international outbreak investigations. New disciplines(genomics, proteomics), and disciplines from social-or environmental-sciences need to be mobilized to answer the growing complexity of new emerging diseases. Are field-epidemiologists prepared to face those challenges?

Methods and Materials: We have listed Field Epidemiological Trainings(FET) registered in FET networks: TEPHINET, EMPHINET, AFENET, and SAFETYNET. Then, information was collected regarding:

- International scope,
- Technological awareness,
- Scientific excellence/recognition,
- Interdisciplinary interest.

Results: Among 52 active trainings, 7 have a regional scope and none encompass a worldwide terrain. Half of them are taught in English but only 4 are multilingual. National field-epidemiology agencies are involved in most trainings, but university/research institutions participate in less-than-half of the trainings. Only 15programs award degrees or certificates. No data could be gathered on the technological awareness of the programs. No mention of interdisciplinary acculturation has been found in any reviewed program content.

Conclusion: Our analysis suggests FETs are getting a regional perspective but not a global one yet. Core competencies correspond to current best practices, but efforts need to be made to diversify and modernize them. Links with existing academic programs could achieve that goal. Finally, new pedagogical methods like distance-learning which demonstrates benefits in tropical and low-income areas could also be worth testing, even if they do not fit the current model.

**SESSION 23 (Parallel Session)****Farm to Table: Foodborne Infections**

Monday, February 7, 2011

Room: Park Congress • Ground Level

08:30–10:30

23.001 Salmonella: Epidemics, reservoirs, and resistance**J. Threlfall**

Health Protection Agency, London, United Kingdom

Background: There are currently two major aspects of food-borne salmonellosis in *Salmonella* of particular relevance for public health in the EU. These are: the occurrence of resistance to quinolones and cephalosporins, defined as Critically Important Antimicrobials by the World Health Organisation; and the recent emergence of new drug-resistant clones of *Salmonella* Typhimurium-like organisms which have caused outbreaks of infection in several EU Member States (MS) since 2000.

Methods and Materials: Resistance to quinolone antimicrobials has increased substantially in *Salmonella* from cases of human infection in several MS since the early 2000s. Such resistance has been particularly concentrated in serovar Enteritidis and has been associated with the consumption of contaminated eggs and egg products. Resistance to quinolones in food producing animals, particularly poultry, has also increased substantially in many MS over the last 5-10 years. In contrast the prevalence of resistance to third-generation cephalosporins in *Salmonella* from both animals and from cases of human infection is currently low in all MS. An exception to this has been recently observed in the Netherlands, where isolates of *Salmonella* Java with resistance to third-generation cephalosporins has increased in recent years. The EU picture is also affected by global food imports and also human travel-associated exposure to *Salmonella*. Notwithstanding these considerations, it seems safe to conclude that the overall prevalence of resistance to third-generation cephalosporins in *Salmonella* in EU MS is at present low.

Results: Within EU countries two major clonal lines of 'monophasic S. Typhimurium' with the antigenic structure of 4,[5],12:i:- have emerged over the last two decades. One such clonal line emerged in Spain in the late 1990s and exhibits plasmid-mediated resistance to a range of antimicrobials. The second has become particularly common in several European MS since 2000 and is characterized by resistance to ampicillin (A), streptomycin (S), sulphonamides (Su) and tetracyclines (T) (= R-type ASSuT).

Conclusion: The latter class of monophasic S. Typhimurium is phage typeable using the standard panel of Typhimurium typing phages and the predominant definitive phage type is DT 193. The most common PFGE profile is that of STYMXB.0131, the predominant VNTR profile is that of 3-11-9-NA-211, and the most common sequence types (STs) are STs 34 and 19. Resistances in such strains are encoded within a chromosomal island which differs from the *Salmonella* Genomic Island 1 (SGI1), first identified in epidemic S. Typhimurium DT 104.

Such strains have now caused outbreaks and incidents of infection in at least 10 European countries, with a death reported in at least one outbreak. Because not all laboratories fully serotype all isolates of putative Typhimurium, their true incidence in the human population is unknown. The organisms seem to be associated with pigs and pig products, although their transmission to other food animals is a possibility.

There is little doubt that these S. 4,[5],12:i:- strains are becoming widely disseminated within the EU. There is an urgent need for a rationalisation of their classification to assist in determination of their true incidence, and also to assist in the formulation of legislative control measures in EU Member States.

23.002 Listeriosis on the rise**F. Allerberger**

AGES, Vienna, Austria

Background: *Listeria monocytogenes* is the causative agent of human listeriosis, a potentially fatal foodborne infection. Clinical manifestations range from febrile gastroenteritis to more severe invasive forms including sepsis, meningitis, rhombencephalitis, abortions, and perinatal infections.

Methods and Materials: In Europe, listeriosis is a reportable disease under surveillance according to EC 2119/98.

Results: In recent years, an increasing rate of listeriosis has been reported in several European countries. For instance, in Austria the incidence increased from 0.16/100000 in 1999 to 0.58 in 2009, in Germany from 0.04 to 0.48, and in Spain from 0.08 to 1.06. These increases primarily reflect a higher rate of bacteremic listeriosis in those >65 years of age and are not otherwise correlated with geography, gender, ethnicity, socioeconomic factors or infectious serotypes. In the late 1980s, an upsurge in listeriosis rates was due to the contamination of a small number of food products. However, a restricted range of strains was responsible for most of the additional cases at that time, and no evidence exists for such a pattern since 2001.

Conclusion: From a clinical perspective, the importance of isolating the pathogen as a prerequisite for an accurate epidemiological investigation and ultimately stopping transmission cannot be overemphasised. Listeriosis is essentially a foodborne disease, and this is no longer questioned. In addition to individual advice to consumers, control of listeriosis requires action from public health agencies and from the food industry. Important control strategies from public health agencies include developing and maintaining timely and effective disease surveillance programmes, as well as promptly investigating clusters of listeriosis cases. Routine characterization of human, food, and environmental isolates, and utilization of large-scale subtype-databases hopefully will facilitate European-wide outbreak detection and control in the near future.

23.003 Opportunistic food-borne infections: The burden of prevention**J. Torres**

Tropical Medicine Institute, Caracas, Venezuela

Food is an excellent vehicle by which many pathogens (including bacteria, viruses/prions and parasites) can reach an appropriate colonization site in a new host. Indeed, WHO estimates indicate that worldwide close to 1.8 million people die annually from diarrheal diseases, largely attributable to contaminated food and drinking water. This problem is not restricted to the underdeveloped world.

The exact burden of diseases caused by food-borne pathogens remains largely unknown, as data indicating trends in food-borne infectious intestinal disease is almost entirely limited to a few industrialized countries, and even fewer pathogens.

Although food production practices have changed considerably during the last decades, traditional food-borne pathogens, such as *Salmonella spp.*, *Campylobacter spp.* and *Escherichia coli*, seem able to adapt to exploit innovative opportunities and generate new public health challenges, such as antimicrobial resistance. In addition, previously unknown food-borne pathogens, many of which are agents of zoonosis, continue to emerge unremittingly, as illustrated by the newly described orally-transmitted Chagas Disease.

Overall, the microbiological safety of food remains a dynamic situation heavily influenced by multiple factors along the food chain from farm to fork.

Whereas it is evident that intestinal food-borne infectious disease, whether caused by bacteria (antibiotic resistant or not), viruses or parasites, represents a major cause of public health concern and social and economic cost globally; at least for viruses and parasites, the extent of such cost is largely unknown. Appropriate surveillance/ monitoring and research, as well as new prevention technologies and intervention are in dear need.

Recent bioterrorism attacks have shown the likelihood that someone might use contaminate food as an instrument of disruption, crime or terror.



23.004 The changing epidemiology of noroviruses

M. Koopmans

Erasmus Medical Centre and National Institute for Public Health and the Environment RIVM, Rotterdam, Netherlands

Acute gastro-enteritis with vomiting and diarrhoea due to norovirus infection is one of the most common infectious diseases. Noroviruses spread to patient contacts and the environment by fecal-oral contact and through vomiting. Once outside the host, noroviruses can stay infectious for a long time, making outbreak control a challenging task. People of all age groups may be infected multiple times, because the viruses are diverse, and immunity—if it develops—is not broadly protective.

In addition to this, the norovirus strains most often responsible for outbreaks evolve very rapidly by mutation in a manner similar to influenza A with global emergence and spread. New variants differ in their antigenic make-up but also in the way they bind to the host receptor, showing that the success of noroviruses is determined by an intricate interplay between virus evolution and susceptibility of the host. Clinically, norovirus disease is mild and self-limiting in most patients, but not in risk groups such as elderly, immunocompromised patients, and patients with other co-morbidities. Nosocomial infections are common and have resulted in prolonged illness and shedding by patients hospitalized for other illnesses, as well as substantial costs. Food-and waterborne transmission is common in noroviruses, but estimating the contribution of these modes of transmission to the total burden of disease is difficult. Of particular concern is the contamination high in the food chain, resulting from sewage exposure. In these situations, often multiple viruses are found, and simultaneous exposure of humans increases the risk of mixed infections and thereby recombination. An estimated 15% of all noroviruses in the European FBVE database are recombinant genomes, illustrating that this is not a rare event. Here, the presence of related viruses in pigs points at a potential source for novel genes to be introduced in the human population.

and 42oC for 72 h. Grey to ceramic colonies grown were picked and identified biochemically by Gram's stain and oxidase reaction. Species identification of *Campylobacter* was achieved using hippurate hydrolysis test and catalase reaction.

Results: The age of the patients ranged from 2 months to 85 years. There were 126 males and 74 females among whom 136 were adults and 64 children. *C. jejuni* was isolated from 3.5% of them. In the pediatric group, *C. jejuni* was isolated from 7/64 (10.9%) patients with higher rate of isolation (71%) from preschool children. *Campylobacter* was not isolated from any of the adult patients or from the healthy subjects. Direct culture did not yield any *Campylobacter*. Among poultry samples *C. jejuni* was the only species isolated from 11/29 (37.9%) of the intestinal samples using the filtration technique and none from cloacal swabs.

Conclusion: There is a higher prevalence of *Campylobacter* in pediatric patients suffering from acute bacterial diarrhea. Poultry is a good reservoir of *Campylobacter* and may be responsible for continued transmission to humans. Filtration technique is a better option for isolating *Campylobacter*.

24.002 SARS-Coronavirus ancestors foot-prints in South-East Asia: bat colonies and the biodiversity refuge theory

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Background: One of the great challenges in Ecology of Infectious Diseases is to understand the drivers of emergence of new pathogens and for example the relations between viruses and their hosts. In the case of the emergence of SARS, several studies have pointed out the *Coronavirus* diversity in bats as well as the existence of SARS-CoV infection in apparently healthy bats (Lau 2005, Li 2005, Tong 2009, Drexler 2010).

Methods and Materials: This integrative study combine hosts ecology, biogeography, comparative phylogeny and RNA virus features to propose one hypothesis about the making of the SARS-CoV ancestor. Polymerase sequence of *Coronavirus* has been targeted by Rt-PCR in non-invasive samples from bats collected in Thailand. Phylogenetic relations between coronaviruses have been inferred by various reconstruction methods. We have tested the effect of several parameters on the final result and tree topology.

Results: *Betacoronavirus-b* long-lasting infection in an isolated *Hipposideridae* bat colony and *Alphacoronavirus* infections of bats are reported from South-East Asia. Interestingly, viruses previously detected in Africa are related to those that currently circulate in specific areas of South-East Asia.

Conclusion: These findings are crucial points regarding the origin and the natural history of the *Rhinolophus* hosted SARS-CoV lineage. Despite their probable pathogenicity, *Betacoronavirus-b* viruses can persistently infect a medium-sized bat population. The common ancestor of *Hipposideridae* and *Rhinolophidae* families is a key taxa in the understanding of the actual repartition of *Betacoronaviruses*. Hosts phylogeny and biogeography, combined with pathogen plasticity and anthropic changes are cofactors of disease emergence.

24.003 Sentinel organisms as biomonitors for emerging zoonotic pathogens at the environmental interface of humans, wildlife, and livestock

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Background: One Health approaches to zoonotic disease surveillance require simultaneous or coordinated monitoring for pathogens in a variety of terrestrial and aquatic ecosystems at the interface of human and animal

SESSION 24 (Parallel Session)

Emerging Infectious Pathogens of Animals & Man (Oral Presentations)

Monday, February 7, 2011

Room: Klimt Ballroom 2-3 • Upper Level

08:30-10:30

24.001 Prevalence of campylobacters in patients and poultry in and around Chandigarh, India

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Background: *Campylobacter* is a bacterial enteropathogen causing mild to severe gastroenteritis. It is also associated with reactive arthritis and neuromuscular paralytic disorders like Guillain-Barre' and Miller-Fisher syndromes. Poultry is the major food vehicle of the organism. Contamination of food and water with fecal materials from poultry may result in transmission to humans. Presently, very limited Indian data is available on diarrhea caused by *Campylobacter*. We studied the prevalence of *Campylobacter* in diarrheic patients as well as in poultry from the same region.

Methods and Materials: Fecal samples were collected in thioglycolate transport medium from 200 adult and pediatric patients presenting with diarrhea, fever and abdominal pain and 21 healthy age matched subjects. Additionally 56 cloacal swabs/intestinal specimens were collected from poultry being sold from retail outlets in Chandigarh. The samples were cultured directly on to *Campylobacter* Blood Base Agar media and also after filtering through 0.45µ Millipore membrane and incubated at 37oC



activity. We have identified and tested several types of sentinel organisms integral to such ecosystems to determine their effectiveness in collecting and concentrating pathogens for laboratory analysis.

Methods and Materials: From 1997–2010, we used filter-feeding bivalve molluscs inhabiting major rivers, lakes and other aquatic sites to collect waterborne pathogens near urban and agricultural areas in North America and Europe. We used excrement-feeding flies and dung beetles occurring in agricultural ecosystems to collect pathogens from areas co-inhabited by humans, livestock and wildlife. Molluscs were collected with sediment sieves (*Corbicula*) or navigational buoys as monitoring platforms (*Dreissena*) across hundreds of kilometers of waterways. Flies and beetles were collected in baited traps, and beetles also from excavated burrows. Sentinel organisms were fixed in 75% ethanol in the field. In the laboratory, specimens were washed, homogenized, subjected to centrifugal separation of tissues and pathogens, and processed using techniques ranging from traditional biological staining to precise molecular methods including immunofluorescent antibody tags and fluorescent in-situ hybridization (FISH). Pathogens targeted for identification included the opportunistic protists, *Cryptosporidium parvum* and *Giardia lamblia*, and the human-virulent microsporidia, *Enterocytozoon bieneusi*, *Encephalitozoon intestinalis*, and *Encephalitozoon hellem*.

Results: In all sampling programs we identified target pathogens from all sentinel species. Prevalence ranged between 0–93% among mollusc samples (intensity range 1–22/sample), with substantial variability between pathogen species, locality, and date. Greater numbers of waterborne pathogens generally occurred where waterways received direct runoff from agricultural land. Prevalence of pathogens in and on terrestrial insects in agricultural settings varied with pathogen and site relative to animal reservoir species, with a range of 8–57% of flies and 100% of beetles contaminated (intensity range 3–321/beetle).

Conclusion: This demonstrates that a wide range of invertebrates are effective sentinels for collecting and concentrating zoonotic protist and microsporidian pathogens across diverse aquatic and terrestrial environments, and the pathogens can be identified with a variety of diagnostic techniques. These principles should be considered and additional sentinel organisms identified in future surveillance programs around the globe.

24.004 Zoonotic arboviruses threatening wildlife in Southern Africa

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Background: Zoonotic arboviruses in the families *-flaviviridae*, *togaviridae* and *bunyaviridae* may be the cause of severe neurological disease in humans and animals but despite many being endemic are rarely reported from Africa. Recent identification of flaviviruses (West Nile and Wesselsbronvirus); alpha viruses (togaviridae) Middelburg and Sindbisvirus as well as Shunivirus an uncharacterized bunyavirus, genus *Orthobunyaviridae* in several fatal cases of neurological disease in horses throughout South Africa, none that were well described as horse pathogens in Africa before, prompted us to investigate neurological disease outbreaks in several species of wildlife including rhinoceroses, Cape buffalo, warthogs and crocodiles during 2010.

Methods and Materials: Necropsies on fatal cases of ascending hind quarter- to quadriplegia in white rhinoceros, Cape buffalo, warthog and crocodiles were undertaken at Veterinary Pathology, University of Pretoria following outbreaks in Limpopo, North West and Northern KwaZulu Natal (KZN) provinces of South Africa. Thirty nine brain, spinal cord and spleen specimens from these species were submitted to the zoonosis Unit, Faculty of Health Sciences in 2009–2010. Specimens were screened by RTPCRs for flavivirus, alpha-, bunyaviruses and confirmed by sequencing and. Tissue was subjected to viral isolation and rabies fluorescent antigen detection assays.

Results: In 2010 positives cases of Middelburgvirus; Sindbis and Shunivirus were identified in 4 white Rhinoceros (1 Sindbis (brain from KZN); 3 Middelburg (1 brain from KZN, 1 spleen from North West

and 1 brain with Middelburg and Shunivirus (Limpopo)); 2 warthog (1 Middelburgvirus (spinal cord) 1 Shunivirus (spinal cord), Limpopo province); 1 buffalo and 1 crocodile (both Limpopo province positive for Shunivirus on spinal cord)). All cases were negative for rabies.

Phylogenetic analysis clustered Middelburg, Sindbis and shuni strains close but distinct to those identified in horses. Shunivirus showed geographical clustering distinct to the prototype strain from Nigeria.

Conclusion: This confirms that outbreaks of neurological disease and death in rhinoceros, Cape Buffalo, Warthog and crocodile in Africa may be due to Middelburg, Sindbis and Shunivirus. This surprising association of zoonotic arboviruses with severe neurological symptoms and death in a wide range of species suggests that they should be considered in neurological disease in humans and animals in Africa.

24.005 Emergence and spread of human adaptation markers in avian influenza viruses during an HPAI A(H7N7) virus outbreak

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Background: Recent human cases showed that highly pathogenic avian influenza (HPAI) A viruses can directly infect humans and might harbor markers associated with human fatal disease. This raised the concern that an HPAI virus may acquire all properties of a pandemic virus through adaptive mutations already in the animal host.

Methods and Materials: Using full-length HA, NA and PB2 sequences of human and avian viruses collected during the large A(H7N7) HPAI epizootic in The Netherlands in 2003, a Maximum Parsimony transmission network was constructed to identify farm-to-farm and farm-to-human transmission events. Virological- and epidemiological data collected during veterinary and medical outbreak control activities were combined to identify possible human adaptation markers supplemented by information on their effect, importance and origin.

Results: The transmission network demonstrated that 35% of the human viruses were identical to poultry farm sequences, while 65% had ≥ 1 nucleotide substitution compared to the suspected avian source of infection. Although 59% of these mutations resulted in amino acid substitutions, no known avian-to-human adaptation markers were identified in viruses obtained from 67/89 human A(H7N7) cases except for the PB2 E627K mutation in the virus obtained from the fatal human case. Mapping of virulence and human adaptation markers in poultry sequence data, demonstrated the emergence and spread of a multitude of mutations during the A(H7N7) outbreak in poultry. These include the independent emergence of HA mutants with increased replication kinetics, accumulation of NA mutations facilitating efficient release of virus particles from the host cell and farm-to-farm spread of virus variants harboring a mammalian host determinant in PB2.

Conclusion: The emergence and spread of both virulence and human adaptation markers in HPAI viruses isolated from poultry farms demonstrate that human tropic virus variants can arise in the absence of the human host. This emphasizes the need for global influenza virus surveillance in poultry, to rapidly identify emergence of influenza variants with pandemic potential.

24.006 Origin and genetic evolution of swine influenza A virus isolated during winter of 2008–2010 in Zhejiang province, China

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School of Public Health, Fudan University, Shanghai, China

Background: As swine are susceptible to infect with both avian and human influenza A viruses, they have been postulated to be a “mixing vessel” in which two or more influenza viruses can co-infect and undergo reassortment with potential for development of new viruses. Four lineage viruses currently circulated in swine: classical swine H1N1, Eurasian



'avian-like' swine H1N1, triple-reassortant swine and 2009 human outbreak swine H1N1 viruses.

Methods and Materials: 1750 nasal swabs were collected from healthy pigs during winter of 2008–2010 in a slaughterhouse in Zhejiang province, China. Influenza viruses were isolated in MDCK cell line and identified by RT-PCR. Eight segments of all isolates were obtained by sequencing and phylogenetic analysis was conducted by comparing with available sequences from the GenBank.

Results: During 2008–2010, two influenza A/H1N2 and seven influenza A/H1N1 viruses were isolated from nasal swabs of healthy pigs in a slaughterhouse in Zhejiang province, China. The two influenza A/H1N2 viruses were 100% identical and shown to be triple-reassortant viruses harboring genes of human (NA and PB1), swine (HA, NP, M and NS), and avian (PB2 and PA) lineage viruses, and were similar to other reassortant viruses isolated in China with genetic drift observed. Seven influenza A/H1N1 viruses were over 99.5% identical and shown to be Eurasian 'avian-like' swine H1N1 lineage, and were similar to other viruses from the same lineage with genetic drift observed.

Conclusion: There were at least two lineage swine influenza A viruses circulated in swine population nearby the slaughterhouse, and Swine influenza surveillance need to keep following for viruses were constantly varying.

24.007 Surveillance of leptospirosis in an urban slum: Using animal population surveillance data to assess human risk

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Background: Leptospirosis is a widespread but under-diagnosed zoonosis that is of increasing concern as a cause of morbidity in the urban slum context. The epidemiology of this multi-host pathogen was examined in the rodent and domestic dog populations of the Kibera urban slum in Nairobi, Kenya. The potential use of these animal data to understand the risk of human leptospirosis in this community is explored.

Methods and Materials: A cross-sectional trapping survey of the rodent population in Kibera was conducted and dog sera collected from an ongoing cohort study of the domestic dogs at this site. A total of 236 rodent kidney specimens were tested by polymerase chain reaction test specific for detecting pathogenic leptospires. In addition, 162 rodent sera and over 1400 dog sera were tested with an indirect enzyme-linked immunosorbent assay (ELISA) test utilizing mixed antigens from 15 pathogenic *Leptospira* serovars and a subset of rodent and dog sera were tested using the microscopic agglutination test (MAT) against a panel of 18 *Leptospira* serovars. To assess the potential for zoonotic transmission, a questionnaire survey was administered to investigate contacts between the human and animal populations and potential risk factors for human infections.

Results: A total of 237 rodents (195 *Mus* spp. and 42 *Rattus* spp.) were trapped within households with an overall trap success of 25%. Pathogenic leptospires were detected in the kidneys of 18% (42/228) of rodents by PCR. Antibodies against *Leptospira* were detected in the sera of <10% of 162 rodents, and the estimated seroprevalence of anti-*Leptospira* antibodies in dogs ranged from 5–36% over the course of the study. 60% of respondents in the questionnaire survey reported seeing 5 or more rodents in their house on a daily basis.

Conclusion: These data provide molecular and serological evidence of the circulation of pathogenic leptospires in the Kibera rodent population, and considerable exposure to *Leptospira* in the domestic dogs. Given evidence of frequent interactions between humans and rodents, these data indicate that the burden of leptospirosis may be heavy among the human population in Kibera.

24.008 Epidemic Intelligence (EI): Assessing event-based (EB) tools and users' perception in the GHSAG community

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Background: Founded in 2001, the Global Health Security Initiative (GHSI) is an informal international partnership for preparedness and response to chemical, biological, radiological, and nuclear (CBRN) threats. Within this framework, an early warning project based on Epidemic Intelligence (EI) and dedicated to enhancement of the detection/risk assessment of CBRN terrorism threats has been developed by Global Health Security Action Group (GHSAG), a committee of senior health officials from the seven GHSI partner nations plus Mexico.

EB systems mine unstructured data from internet media and social networks to detect events or aberrations, anomalies and social disruption that may be a sign of a potential public health threat. These tools contribute to early warning for epidemics including emerging diseases, and CBRN threats. However, the systems have to be adapted to the needs of users. The objective of this project was to describe and assess the seven EB systems used by GHSAG (ProMED, BioCaster, HealthMap, MedISys, PULS, Argus, GPHIN), taking into account EI experts' perception and search strategies.

Methods and Materials: Information on systems' characteristics and users' perception of systems' use and their expectations regarding EI was collected using questionnaires administered to GHSAG experts from November 2009 to April 2010. Systems were evaluated using common public health indicators.

Results: All seven system providers completed forms. System structures differ fundamentally in terms of intrinsic characteristics, attributes and functionalities, but also in terms of human intervention. Each system retrieves information of its own, but also from some of the other systems.

Eleven users' responses were collected from a total of six countries and two supranational agencies. Overall, users routinely access between four to seven different systems and their EI approaches vary widely. Users' perceptions resulted in high scores for the early detection indicators (timeliness and sensitivity), and all seven systems were considered useful. Weaknesses, however, were underlined, notably in terms of flexibility, representativeness and completeness.

Conclusion: Documenting the overall heterogeneity of EI data collection systems using a single assessment methodology is complex. The presented data will pinpoint strengths and weaknesses, and illustrate the added values of developing synergies and interactions between EB systems.

For the GHSAG working group*

24.009 Discovery of *Mycobacterium mungi* sp. nov.: A novel, emerging *M. tuberculosis* complex pathogen affecting banded mongoose living at the human-wildlife interface

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Background: We describe the emergence of a novel *Mycobacterium tuberculosis* complex (MtbC) pathogen, *Mycobacterium mungi* sp. nov. among banded mongoose that associate with humans while foraging and denning amongst human waste and buildings in Chobe District, Botswana.

Methods and Materials: Samples from histologically positive mongoose were examined using a variety of molecular assays including identification of regions of difference, specific single nucleotide polymorphisms, a MtbC-specific multiplex-PCR test, spacer-oligotyping (spoligotyping)



and mycobacterial interspersed repetitive unit-variable-number tandem repeats (MIRU-VNTR's) analysis. Our examination of MIRU-VNTR patterns also included *dassie bacillus*, which had not been analyzed before.

Results: *M. mungi* appears to be environmentally transmitted through the nasal planum of banded mongoose. Seven outbreaks have been documented (2000–2010), involving increasing numbers of troops. Our suite of molecular assessments provided distinct results, differing clearly from the other members of the MtbC. The unique spoligotyping pattern was identified across outbreak years (2000 to 2009) in different mongoose troops and locations and will allow identification of *M. mungi* in TB surveillance programs. While the host spectrum and transmission dynamics are unknown, MIRU-VNTR results identify substrains within and between outbreak years and troops suggesting complexity in pathogen transmission dynamics and potential evolution of the organism over the last decade.

Conclusion: This newly identified mycobacterial pathogen has many unique ecological characteristics that set it apart from other members in the MtbC complex. First, it causes high levels of mortality in banded mongooses, threatening local extinction of smaller social groups. Second, rather than having a primary respiratory transmission route with direct transmission between individuals, as is characteristic of other MtbC species; *M. mungi* appears to infect banded mongooses by means of a non-respiratory route through the nasal planum suggestive of environmental transmission. Third, clinical presentation to death in affected mongooses is generally short (2–3 months) as compared with other MtbC pathogens, which are usually more chronic in nature and can take years to cause death. The identification of a novel MtbC pathogen presents new concerns and potential threats to human and wildlife health; particularly in light of the sub-Saharan HIV/AIDS epidemic and spatial overlap among wildlife, domestic animals and humans in this region.

24.010 Zoonotic pathogens present in South African bat species

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University of Pretoria, Pretoria, South Africa

Background: Almost three quarters of emerging infectious diseases in humans are zoonotic in nature, with several of unknown etiology. A vast number have been linked to bat species. About 116 bat species occur in Southern Africa and very few studies have investigated pathogens associated with bats of this region.

Methods and Materials: Samples were collected from several bat species across South Africa during 2006–2008. Serum samples were screened with virus neutralization assays for the presence of lyssavirus antibodies and brain samples with quantitative real-time RT-PCR targeting lyssavirus nucleoprotein genes. A heminested RT-PCR targeting a conserved RNA dependant polymerase gene region was used to screen fecal samples for the presence of coronavirus RNA. Real-time PCR targeting the *gltA* and 16S rDNA gene of *Rickettsia* spp was used to screen blood samples for the presence of this pathogen. For general pathogen discovery, we used a sequence independent single primer amplification (SISPA) to screen kidney samples. All positive results were further characterized by DNA sequencing.

Results: This survey resulted in the identification of lyssaviruses, coronaviruses, *Rickettsia* and *Klebsiella pneumoniae*. Several new isolations of Lagos bat virus was made from *Epomophorus wahlbergii*, a frugivorous bat. A high seroprevalence for specific lyssaviruses viz. Duvenhage and Lagos bat virus was indicated in *Myotis spp* and *E. wahlbergii* respectively and a very low percentage of active infection (< 1%). Coronavirus sequences were obtained from several species of insectivorous bats that were related to the Alphacoronavirus group. Sequences were also detected in frugivorous bats such as *Epomophorus* which grouped with the Betacoronaviruses. Although seroprevalence for coronaviruses has been indicated before in South African bats, this is the first detection of coronavirus RNA from this country. A blood sample of a frugivorous bat tested positive for *Rickettsia* with a high similarity to *Rickettsia conorii*. *Klebsiella pneumoniae*, which is known to accumulate within the intestine of mammals, was identified from the kidney of *E. wahlbergii* using the SISPA sequence independent method.

Conclusion: This is the first report of several zoonotic pathogens from bats in South Africa. However discovering novel organisms is only the first step in understanding the mechanism through which they cause disease.

SESSION 25 (Plenary)

Plenary Lecture 5

Monday, February 7, 2011

Room: Park Congress • Ground Level

11:00–11:45

25.001 Identifying New and Emerging Viruses of Bat Origin

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Background: Bats account for 20% of all known mammal species on earth and have been identified as the reservoir hosts of a number of emerging viruses responsible for severe human and livestock disease outbreaks, including paramyxoviruses (Hendra and Nipah viruses), coronaviruses (SARS-like coronaviruses), filoviruses (Ebola and Marburg viruses) and orthoreoviruses (Melaka and Kampar viruses). When these viruses spill over and infect non-reservoir mammalian hosts, they can be highly lethal. Yet, none of these viruses seem to cause any clinical diseases either in wild bat populations or in experimentally infected bats.

Methods and Materials: New bat cell lines and improved sampling and culture techniques are employed to improve virus isolation. Mass sequencing is being used for rapid virus discovery.

Results: Preliminary results will be presented on discovery of novel viruses from bat urine samples collected in Australia.

Conclusion: Bats are increasingly being recognized as an important reservoir of new and emerging zoonotic viruses. Our group's current focus is on improvement of rapid virus isolation and characterization and better understanding of virus-bat interaction at cellular and molecular levels.



presenter = **bold** faced, abstract number: e.g. 10.019 = 10 is session number, 019 is presentation number within session

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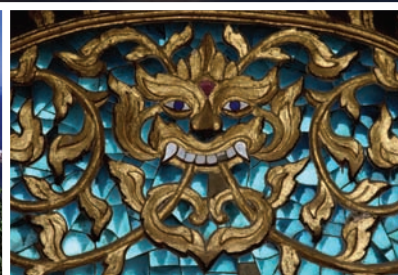
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