

10th NATIONAL CONGRESS OF THE
ITALIAN SOCIETY FOR VIROLOGY



Società
Italiana di
Virologia

ORVIETO (TR)
Palazzo del Capitano del Popolo
September 12-14, 2011



UNDER THE PATRONAGE AND SUPPORT OF



Comune di Orvieto



Programme and Abstract Book

GIV NOROVIRUSES AND OTHER ENTERIC VIRUSES IN BIVALVES

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Background: the impact of sewage discharge on the microbiological quality of shellfish is well known. Bivalves filter large volumes of water as part of their feeding activities, and thus accumulate and concentrate different types of pathogens from human fecal pollution. The aim of the study was to evaluate the presence, in these molluscs, of six different groups of enteric viruses: norovirus (genogroups I, II, and GIV), adenovirus, enterovirus, astrovirus, hepatitis A virus, and hepatitis E virus.

Methods: samples were collected from harvesting areas, restaurants, fish markets and shellfish markets (fresh and frozen) in the South of Italy. Different nested PCR-based methods followed by sequencing were carried out to detect viral presence. Cell culture assays on FRhk-4, A549 and BGM were performed to test for the infectivity of viruses.

Results: Bivalves appeared to be significantly contaminated. Four out of six classes of enteric viruses (norovirus, adenovirus, enterovirus and hepatitis A) were detected in the shellfish tested, which were often co-infected (with up to four different viral groups in a single sample). Specifically, we detected noroviruses GII.4 and GIV.1, adenoviruses types 1 and 2, Hepatitis A, and echovirus type 7. No samples were found positive for virus isolation on cell lines.

Conclusions: The present study is the first to document the presence of GIV noroviruses in shellfish. This finding, combined with the relatively high frequency of these viruses recently detected in sewage samples, highlights the potential role of GIV norovirus as an emerging enteric pathogen, along with GI and GII noroviruses. The simultaneous presence of different genotypes (and genogroups) is of particular interest, since it is believed to facilitate norovirus recombination within the human gut. Our results confirm that bivalves, eaten raw or partially cooked, can be an important risk factor for the transmission of viruses to humans.

HEPATITIS E VIRUS IN ITALY: MOLECULAR ANALYSIS OF CLINICAL AND ENVIRONMENTAL SAMPLES

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Background: Human hepatitis E virus (HEV) is considered an emerging pathogen in industrialized countries. The aim of the present study was to contribute to the body of knowledge available on the molecular epidemiology of acute hepatitis E in Italy.

Methods: HEV-specific primers targeting the ORF1 and ORF2 were used to examine serum samples collected from acute hepatitis patients, and raw sewage samples collected from wastewater treatment plants in different regions of Italy.

Results: We found a high proportion of HEV-positive sewage samples in Italy (16%, mostly G1, but also G3) evenly distributed across the entire country. As for clinical samples, seventeen patients tested HEV RNA-positive: 12 infections, due to genotype 1, were associated with travel to endemic areas (Bangladesh, India and Pakistan), while five infections, due to genotype 3, were presumably autochthonous. Risk factors identified in this group included exposure to raw seafood, pork liver sausages, and wild boar. Phylogenetic analysis showed that the environmental HEV G1 strains clustered together in a distinct clade of G1 sequences, showing relatively little similarity to clinical strains, with the exception of a single clinical sample. The reason for the different clustering of environmental and clinical isolates is difficult to explain and implies the need for further investigation.

Conclusions: Evidence that HEV could be establishing itself in our region is accumulating and may justify more active surveillance to monitor its spread.