



30° Meeting of SIMGBM - Società Italiana di Microbiologia Generale e Biotecnologie Microbiche

# *Microbiology 2013*

*September 18<sup>th</sup> - 21<sup>st</sup>*



*Ischia, Italy*

[www.simgbm.it](http://www.simgbm.it)

#### **B44. The bioremediation potential of the Priolo Harbour (SR, Italy): isolation, identification and catabolic ability of hydrocarbonoclastic bacteria**

Paola Quatrin<sup>1</sup>, Santina Santisi<sup>2,3</sup>, Valentina Catania<sup>1</sup>, Michail M. Yakimov<sup>2</sup> and Simone Cappello<sup>2</sup>

<sup>1</sup>Dip.to Scienze e Tecnologie Biologiche, Chimiche e Farmaceutiche (STEBICEF), University of Palermo, Viale delle Scienze edif. 16 90128 Palermo, Italy (paola.quatrin@unipa.it); <sup>2</sup>Istituto per l'Ambiente Marino Costiero (IAMC) – CNR U.O.S. of Messina, Italy; <sup>3</sup>Ph.D School in "Biology and Cellular Biotechnology" of University of Messina, Faculty of Sciences, Messina, Italy

The petrochemical site of Priolo-Augusta-Melilli (Sicily, Italy), is a Site of National Interest (SIN) due to high levels of contamination of the coastline and its remediation is urgently needed. Successful remediation strategies relying on the catabolic potential of marine hydrocarbonoclastic bacteria (HCB) have been described. HCB are specialised hydrocarbon (HC)-degrading marine bacteria that use HC almost exclusively as unique carbon and energy source and become dominant in oil-impacted environments. In order to identify the key hydrocarbon degraders and explore the natural bioremediation potential of the contaminated area, sediment cores and sea water were collected inside the Priolo Harbour (SR, Italy) and used to set enrichment cultures on mineral broth containing different mixtures of linear (C<sub>14</sub>, C<sub>16</sub>, C<sub>24</sub>) and aromatic (phenatrene, pyrene, biphenyl and dibenzothiophene) hydrocarbons and crude oil. The collection of HC degrading bacteria is composed of about 100 isolates that are mainly obligate hydrocarbonoclastic bacteria of the genera *Alcanivorax*, *Marinobacter*, *Thalassospira*, *Oleibacter* and other HC-degraders of the genera *Maribacter*, *Alteromonas*, *Methylophaga* and as yet uncharacterized Rhodospirillales and Oceanospirillales. Assays of HC biodegradation efficiency of some representative isolates revealed their high potential of application in bioremediation. The analysis of the key catabolic genes involved in HC degradation is in progress.

#### **B45. Culture-independent methods for assessing diversity of microbial community in biogas reactors**

Ricci Marco and Sanangelantoni Anna Maria

Department of Life Sciences - Parma University - Parco Area delle Scienze 11/A- Parma  
sanan@unipr.it

The utilization of agricultural biomass and livestock manure for production of energy is today considered a valuable alternative to fossil energy resources and, since the last decade, the production of biogas, that combines the elimination of organic waste with the formation of methane, has been increasing constantly.

The generation of biogas is driven by a complex microbial community, still poorly characterized. In this work the methanogenic archaeal community in two anaerobic digesters, fed with manure and maize silage, has been analyzed by molecular culture-independent techniques. Samples have been collected from biogas reactors during the start-up phase and during the steady-state phase. PCR amplification of 16S rDNA from total DNA extracted from the samples, followed by molecular cloning, ARDRA analysis, and sequencing of one representative of each ARDRA group, allowed the identification of several clostridia and Archaea belonging to the hydrogenotrophic and acetoclastic metabolic groups. Real Time PCR has been developed for quantification of these microorganisms during different phases of the process, and monitoring the dynamics of acetotrophic and hydrogenotrophic populations. The diversity of methanogenic Archaea has also been studied by analysis of the gene *mcrA* while the diversity of bacterial community has been analyzed by ARISA targeted to the 16S-23S rDNA spacer region.

#### **B46. Exopolysaccharides synthesized by cyanobacteria residing in Induced Biological Sol Crusts increase stability and carbon organic content of desert sandy soils**

Federico Rossi<sup>1</sup>, Giovanni Colica<sup>1</sup>, Hua Li<sup>2</sup>, Yongding Liu<sup>2</sup>, Roberto De Philippis<sup>1</sup>

<sup>1</sup>Department of Agrifood Production and Environmental Sciences, University of Florence; <sup>2</sup>State Key Laboratory of Freshwater Ecology and Biotechnology, Institute of Hydrobiology, Chinese Academy of Sciences, Wuhan, China

The introduction of Biological Soil Crusts (BSCs) in degraded soils through inoculation-based techniques (IBTs) is considered a valid pathway to counteract soil-loss and to expand cultivable areas. BSCs introduce high amount of C in the soil as extracellular polysaccharides (EPSs), mostly produced by the crustal phototrophic fraction. IBTs using *ex-situ* cultured cyanobacterial biomass were reported to induce crust formation and represent an exploitable system to increase soil fertility. Such a technology was applied in Hobq desert, China, where different sites constituted initially by bare sandy soil were inoculated with a mixed culture of EPS-producing cyanobacteria.

We investigated the effects of IBT in terms of soil C gain and phototrophic abundance. EPSs, extracted from the crusts, were analyzed for their monosaccharidic composition and molecular weight (MW) in order to investigate possible differences related with crustal development stage. Results showed that BSC induction led to a significant increase in soil total carbohydrate content and phototrophic abundance compared to control areas. EPSs showed to be constituted by moieties with different MWs and a notable complexity in terms of monosaccharidic composition, suggesting the major share of cyanobacteria in their synthesis.

The outcomes of this study underline the potential of the IBT method in restoring Soil Organic Carbon content, and represent a first step in field studies regarding EPS dynamics in BSCs.

#### **B47. Cellulase production by a wild strain of *Trichoderma* spp. isolated from wood chips from short rotation hybrid poplar plantations**

Francesca Luziatelli<sup>1</sup>, Andrea Cavalieri<sup>2</sup>, Veronica Fabbrica<sup>1</sup>, Maurizio Ruzzi<sup>1</sup>

<sup>1</sup>DIBAF, University of Tuscia, Via S. Camillo de Lellis snc Viterbo, Italy; <sup>2</sup>Dept. Plant Science, Univ. Manitoba, Winnipeg, MB, Canada

As part of an investigation on dynamics of fungal population developing on poplar wood chips of different size, whose dehydration was carried out in open-air systems under different operating conditions, we isolated several filamentous fungi capable of degrading cellulose. The cellulase production of one of these strains, identified as *Trichoderma* spp., was studied in more detail. When grown as a submerged culture with 2.5% microcrystalline cellulose (Avicel) as a substrate, this strain produced considerable amounts of filter paper degrading activity (FPase) in the extracellular supernatant. The maximum enzyme yields were obtained after 10 days of incubation at 30°C. The optimal conditions for the FPase activity were found at pH 4.8 and 60-65°C, and more than 50% of its maximal activity was retained at 35-60°C for 18-24 hrs. Crude enzymatic extract from *Trichoderma* spp. was applied in saccharification experiments using untreated lignocellulosic biomass as a substrate, and the hydrolysis yields were compared to that obtained by commercial cellulase preparations. Preliminary results indicated that glycosyl hydrolases produced from this strain could be applied in bioconversion of lignocellulosic biomass into fermentable sugars.