BACTERIAL COMMUNITIES IN THE SEAWATER-BRINE CHEMOCLINE IN DEEP ANOXIC HYPERSALINE BASINS IN THE EASTERN MEDITERRANEAN SEA

Borin Sara[1], Daffonchio Daniele[1] , Brusa Tullio[1], Francesco Gasparoni[2], Daniele Calore[2], Cesare Corselli3 and BIODEEP* Scientific Team

[1]University of Milan, DISTAM, Via Celoria 2, 20133 Milan, Italy

[2]Tecnomare s.p.a., San Marco 3584, 30124 Venice, Italy

[3]University of Milan-Bicocca, DGSG, P.zza della Scienza 4, 20126 Milan, Italy

Deep hypersaline anoxic basins (DHABs) in the eastern Mediterranean sea are extreme environments characterised by oxygen absence, high pressure, with the presence of brines with very high salinity and density. The seawater-brine interface presents a steep chemocline with a density gradient ranging from seawater values to brine physio-chemical parameters. Due to these characteristics, the chemocline acts as a particle trap which could be inhabited by rich microbial communities that could be adapted to the different salinity layers. In this work we investigated the microbial community structure of the different chemocline layers in the Urania and in the Bannock basins, sampled during the R/V Urania cruise in August 2001.

Using a Rosette sampler, fitted on the remote operated MODUS/SCIPACK system, several Niskin bottles were closed under CTD control, at the seawater-brine interface level. From each bottle the 10 litres content has been fractionated in 1 litre aliquots that exhibited conductivity ranging from seawater to brine salinity values. The total DNA has been extracted from the aliquots, and has been analysed with PCR-based fingerprinting techniques to describe the microbial community inhabiting each gradient layer. The microbial diversity was analysed with methods based on the amplification of 16S rDNA (ARDRA) or the 16S-23S rDNA spacers (ARISA and ITS-HHP) using primers specific for *Eubacteria* or *Archaea*. The obtained results showed relevant differences between the bacterial communities of the seawater-brine interfaces of the basins, and between the different Niskin bottles closed in each basin at different depths. We could not observe significant differences between the different fractions of each Niskin bottles exhibiting different salinity content, indicating that the physico-chemical gradient did not substantially influence the diversity of microbial community present in the chemocline.

Real-Time PCR quantification of archaeal and total prokaryotic rDNA, using universal primer and TaqMan probe systems, showed quantitative variations along the gradient. *BIODEEP is FP5 EC Project (Contract EVK3-2000-22057). http://www.geo.unimib.it/BioDeep/Project.html