S. Borin[1], T. Brusa[1], A. Favini[1], C. Corselli[2], G. D'Auria[3], M. Yakimov[3], L. Giuliano[3], T.J. McGenity[4], A. Sass[4], C. Tamburini[5] and D. Daffonchio[1]

[1]University of Milan, DISTAM, Via Celoria 2, 20133 Milano, Italy, e-mail:sara.borin@unimi.it
[2]University of Milan-Bicocca, DGSG, P.zza della Scienza 4, 20126 Milano, Italy
[3]CNR, Istituto Sperimentale Talassografico, Spianata S. Raineri 86, 98100 Messina, Italy
[4]University of Essex, Dept. Biological Sciences, Central Campus, Wivenhoe Park, Colchester, U.K.
[5]CNRS-INSU UMR 6117, Microbiologie Marine, COM, Case 907, Campus de Luminy, 13288 Marseille Cedex 09, France

MICROBIAL COMMUNITIES IN THE WATER COLUMN OF THE URANIA BASIN (EASTERN MEDITERRANEAN SEA)

Keywords: Mediterranean sea, deep hypersaline anoxic basin, Urania basin, water column, microbial community

The Urania basin is a deep hypersaline anoxic lake located in the eastern Mediterranean Sea; the Urania brine is an extreme environment, characterised by absence of oxygen, high salinity, high sulphide content and high pressure. The brine has a very high density and presents a steep chemocline at the seawater-brine interface which acts as a particle trap, and could be inhabited by a rich microbial community with high activity, as compared with the overlying deep seawater. We studied changes in microbial abundance, diversity, and activity with depth in the Urania basin, from seawater (1500 m deep) to the brine-sediment interface (3500 m deep), sampled during the R/V Urania cruise in August 2001. The brines interface had more microorganisms than the overlying deep seawater, as shown by total cell counts performed with 4,6-diamidino-2-phenylindole and by quantification of total DNA: total microorganisms in the interface were one order of magnitude higher than in the brines (1,5 10^5 cells/ml), which were slightly higher than in the overlying seawater. Moreover, aminopeptidase and phosphatase activities, and bacterial production rates confirmed that the seawater-brine interface represents a water layer with high microbial activities relatively to the "oxic" seawater above. These results have been confirmed by Real-Time PCR quantification of total prokaryotic rDNA, using universal primer and TaqMan probe systems. *Archaea*/*Eubacteria* relative proportions have been established with Fluorescent *In* S*itu* Hybridisation (FISH), using probes specific for the two prokaryotic domains. Results showed that *Archaea* increase from the seawater-brine interface to the brines, while the number of *Eubacteria* decrease with the depth. The diversity of microbial communities inhabiting DHABs was analysed with different DNA-fingerprinting methods based on the amplification of 16S rDNA (DGGE, ARDRA, T-RFLP) and on the 16S-23S rDNA spacers (ARISA and ITS-HHP) using primers specific for *Eubacteria* or *Archaea*. Comparison of the fingerprints showed that the seawater-brine interface and the brine are inhabited by specific microbial populations which are very different from those in the upper seawater. This work has been done in the ambit of the BIODEEP project which is a FP5 EC Project (Contract EVK3-2000-22057), http://www.geo.unimib.it/BioDeep/Project.html