

## Bacterial and archaeal communities of the brine/seawater interfaces in four different brine lakes of the Mediterranean Sea.

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On the seafloor of the Mediterranean Sea several deep hypersaline anoxic basins (brine lakes) have been discovered. These brines are most likely developed by the dissolution of 5- to 8- million year old Messinian evaporites. They are well described for their geochemical parameters. However, little is known about the microflora present and their ecological role in these environments. As part of the EC project BIOTEchnology from the DEEP (BIODEEP) the microflora in the brine/seawater interface of four different brine lake (L'Atalante, Bannock, Discovery and Urania) was studied by sequencing of 16s rRNA genes. Clone libraries of bacterial and archaeal 16S rDNA were constructed and 96 clones from the brine/seawater interface were sequenced. Results show that the bacterial diversity in the interfaces was high (~ 30 operational taxonomic units, OTU, >97% sequence homology) with the highest number of OTUs in the Discovery interface. In contrast, the number of OTUs for archaea was much lower (~14) indicating a lower archaeal diversity. The brine/seawater interface showed a specific bacterial community for each brine with only one sequence being present in all four lakes. In contrast, same archaeal sequences were found in the four brines but different sequences dominated the different brine/seawater interface of the four brines. A phylogenetic survey with closest known relatives showed that sulfate reducing bacteria, sulfur oxidizing bacteria and methanogenic archaea were among the sequences found in all four brine lakes. This suggests that these bacteria play an important role in these environments, contributing to sulfur speciation as well as methane production. Furthermore, a significant amount of the bacterial and archaeal sequences are unique and show very low homology (<90% sequence similarity) with known sequences from the GenBank database indicating that a large portion of the microflora is yet unknown. This might open possibilities to try to study these novel bacterial species for biotechnological and medical applications. Overall, it can be concluded that each brine interface has a specific microbial community. It is speculated that this might be caused by the different geochemical conditions in each brine interface. In spite of this specific microbial community, microbial metabolic processes seems to be similar in the four brine interfaces.