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Unraveling diversity of extremophiles along salinity gradient at the sea-water interfaces of several mediterranean deep hypersaline anoxic lakes in Eastern Mediterranean Sea

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Deep Hypersaline Anoxic Lakes (DHALs) are deep subsurface brine pools located at about 3500 meter depth in the tectono-volcanic settings of the Eastern Mediterranean regions but all distantly located each other. DHALs are thought to have been by erosion and dissolution of buried Messinian evaporitic deposits in the subseafloor under various mecanism process [1, 2]. High Na/Cl ratio in brines is related to thalassic basin (ex: Médée and Atalante sites) while low Na/Cl ratio is due to bischofite dissolution in athalassic basin (ex: Kryos and Discovery sites). With extreme salinity (300 to 600 g/l salts), some of these DHALs can be impacted by subseafloor hydrothermal fluid circulation. Therefore, these ecosystems are an unique opportunity to assess extremophiles from the deep biosphere in one of the harshest ecosystem on Earth. Early investigations showed that these environments harbored an abundant and diverse microflora at the interface seawater -brine layers [4, 1]. However, over the last decades, microbial ecology studies on DHALs have been focusing on seawater-brines interfaces, varying the methodology employed and the targted biological and therefore making difficult any comparison between all DHALs [3, 4, 5, 6, 7, 8, 9]. Here, we focus on the microbial ecosystems associated to the seawater-brine interfaces from 4 DHALs, processed all altogether along the same methodology and using next-generation sequencing technology. We wish to evaluate the potential of inter-connectivity among the six differents DHALs and understand the extent of the microbial ecosystem adaptation to increased salinity at the seawater-brine interface and biogeochemical interactions of prokaryotic communities along the halocline. Diversity was first studied through 16S rRNA genes analysis by metabarcoding from DNA and reverse-transcribed RNA into cDNA with Illumina MiSeq technology. Metagenomes from a new hypersaline anoxic basin is currently investigated in order to assess potential metabolic activity, genes, functions and regulations involved in salt adaptation.

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