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BOOK OF ABSTRACTS

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Microbial diversity in the deep-sea anaerobic hypersaline environments with emphasis on the role of anaerobic haloarchaea in C and S cycles

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Abstract

Extremely halophilic archaea represented by classes *Halobacteria*, *Methanonatronarchaeia* and candidate division Nanohaloarchaea apparently originated from two distinct clades of methanogenic anaerobes. The members of class *Halobacteria* within the phylum *Euryarchaeota* are hypothesized to acquire by a massive lateral LTG event of ~1,000 eubacterial genes (30% of their genomes). As a consequence of this acquisition, most of the known *Halobacteria* species are aerobic heterotrophs inhabiting oxygenated layers of brines with very few of them possessing the ability for fermentative growth and/or anaerobic respiration. Our recent research, aimed at microbial sulfur respiration at extreme salinity in anaerobic sediments, uncovered the existence of at least two novel functional groups of strict anaerobic sulfidogenic haloarchaea. One group is using acetate as the electron donor for elemental sulfur-dependent respiration - a catabolic route overlooked previously in the whole Archaeal Kingdom. The second group uses formate and/or H₂ as the electron donor and elemental sulfur, thiosulfate or DMSO as the alternative acceptors thus, representing a first example of lithoheterotrophy in haloarchaea. The discovery of these groups of obligate anaerobic sulfur-respiring haloarchaea, widely present in anoxic hypersaline environments, including deep-sea brine lakes, showed that (i) the carbon and sulfur cycles in anoxic hypersaline ecosystems should be reconsidered and (ii) the dominant paradigm on the haloarchaeal physiology is far from completeness.

Keywords: deep-sea anoxic brine lakes, extreme halophilic euryarchaea, genome sequence, *Halobacteria*, sulphur respiration.

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