Patterns of prokaryotic diversity in sediments of brackish to hypersaline salt lakes in Romania

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Abstract
In this work, we explored the structure of prokaryotic communities inhabiting the sediments of nine lakes with different salinities (from 84 to 344 g L\textsuperscript{-1}) located in Central and South-Eastern Romania. The 16S amplicon sequencing approach combined with geochemical measurements were employed to i) assess local molecular diversity of prokaryotic communities, ii) evaluate the geographical and environmental factors affecting the community composition among sediments of distinct geochemical conditions, and iii) infer key microbial players in the biogeochemical cycling of C, S, and Fe. High relative abundances of 16S rRNA gene reads were assigned to Actinobacteria, Alphaproteobacteria, Bacteroidia, Clostridia, Deltaproteobacteria, Gammaproteobacteria, Mollicutes, and Rhodothermia bacterial classes and to Halobacteria, Thermoplasmata, and Woesearchaeia among the Archaea. Highest richness and diversity were found in sediments containing 96 g L\textsuperscript{-1} and 300 g L\textsuperscript{-1} NaCl. Additionally, the analyzed saline sediments appeared to be inhabited by uncultured Bacteria (Gracilibacteria, Marinimicrobia, Omnitrophicaeota, Patescibacteria) and Archaea (Altarchaeota, Asgardarchaeota, Diapherotrites, Hadesarchaeota) with possible crucial roles in C and S cycling. A microbially-driven Fe cycle could be speculated from the presence of Zetaproteobacteria-affiliated reads in five sediments with different salinities. In conclusion, we provided clues about the microbial diversity and its putative functional capabilities in poorly investigated, saline aquatic habitats.

Keywords: diversity, hypersaline, microbial dark matter, sediments.

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