7. Jährlicher DAbG Workshop



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Microbial life in the Barrancas Blancas plain –a harsh mountain desert environment –in a Mars analog region of the high Atacama Andes (Chile)

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The Barrancas Blancas Plain (~5000 m a.s.l., 68°39' W, 27°02' S) in the high Atacama Andes of Chile is a unique place that combines the harsh characteristics of the mountain desert environment with the presence of ice-rich permafrost. This place is situated in a Mars analog region and is therefore considered to be a natural laboratory for the study of extremophilic microbes, aiming to understand life on and the potential for life beyond Earth. Due to seasonal changes, temporal lakes are created in this area which give us the opportunity to explore the effect of water on microbial life in a desertic environment. For this reason, we performed a sampling campaign to understand how microbial life can survive and thrive under these extreme conditions and what the role of the temporal lake is in shaping the microbial community. We sampled three transects along a moisture gradient, starting from soil pit 1 (P1) on the shoreline of the lake until P5, ~70 m away with apparent nonwater interaction. We used a novel protocol to separate the living community (represented by intracellular DNA) from the dead or past communities (represented by extracellular DNA). Since this study focused on the potentially active microbial community, only the iDNA pool was considered. The results showed a clear separation between the water-affected samples from the reference site and a highly specialized microbial community, mainly composed of Proteobacteria, Gemmatimonadota, Actinobacteria, and Acidobacteria. We found that the 16S rRNA gene copy number and the ATP content have the highest values in the surface samples, particularly the P4 surface sample, at a third of the moisture gradient, which had the peak of activity. The correlation analysis indicated that these two parameters are positively correlated and negatively correlated with moisture. Additionally, co-occurrence network analysis revealed that the community is clustered into two major depth-dependent groups. The surface-related module 3 (M3) matched the ATP signal. Therefore, we expect that those ASVs might be involved in the metabolic functionality of the microbial community in this place. The study indicates that the temporal lake is a hotspot for life in this high-altitude desert, providing insights into how water shapes its specialized microbial community and controls the potential microbial activity.

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