

Mars exploration begins on Earth: Systematic comparison of the anaerobic, intact and cultivable microbiome of extreme, anoxic, Mars-analogue environments. Perras, A.K.^{1,2}, Wink, L.¹, Duller, S.¹, Monaghan, E.³, Schwendner, P.⁴, Cockell, C.S.⁴, Rettberg, P.⁵, Beblo-Vranesevic, K.⁵, Bohmeier, M.⁵, Gaboyer, F.⁶, Westall, F.⁶, Walter, N.⁷, Cabezas P.⁷, Garcia-Descalzo, L.⁸, Gomez, F.⁸, Malki, M.⁹, Amils, R.⁹, Ehrenfreund, P.³, Vannier, P.¹⁰, Marteinson, V.¹⁰, Erlacher, A.¹¹, Mahner, A.¹¹, Bashir, M.¹² and Moissl-Eichinger, C.^{1,13},

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The concept of present and/or past extraterrestrial life is thrilling and tackled intensively throughout the last decades, yet remains notional. Some regions of extraterrestrial bodies (e.g. the Mars) are in general considered as habitable; however, are ruled by extreme physical and chemical variables, which constrain the possibility of life. Similar settings (at least to a certain extent) exist on Earth and function as analogue model sites in many studies to elucidate basic information on the limits of life. One crucial feature, which distinguishes Earth from extraterrestrial bodies, is the absence of oxygen in the atmosphere. Terrestrial Mars analogue, anoxic settings are hardly described, in particular with respect on the hosted microbial communities.

The MASE (Mars Analogues for Space Exploration) project tackled to understand specifically anaerobic life thriving in a number of various Mars analogue settings. Within the frame of this project, a diverse set of extreme and anoxic Mars analogue environments were sampled and microbiologically investigated by combining cultivation based and cultivation-independent analyses. This study included (i) a wide-scale cultivation approach targeting the anaerobic microbial fraction and (ii) an amplicon sequencing approach focusing on the viable Archaeome and Bacteriome.

We revealed a highly adapted microbiome, thriving under harsh conditions, and obtained a numerous set of cultivated space-relevant microorganisms. Even though abiotic factors vary strongly upon the sampling sites, a cosmopolitan group of microorganisms was detected to be viable in the investigated sites.

Our study provides novel and highly valuable information on microbial communities in anoxic environments, with a strong impact for the search for life in the universe.

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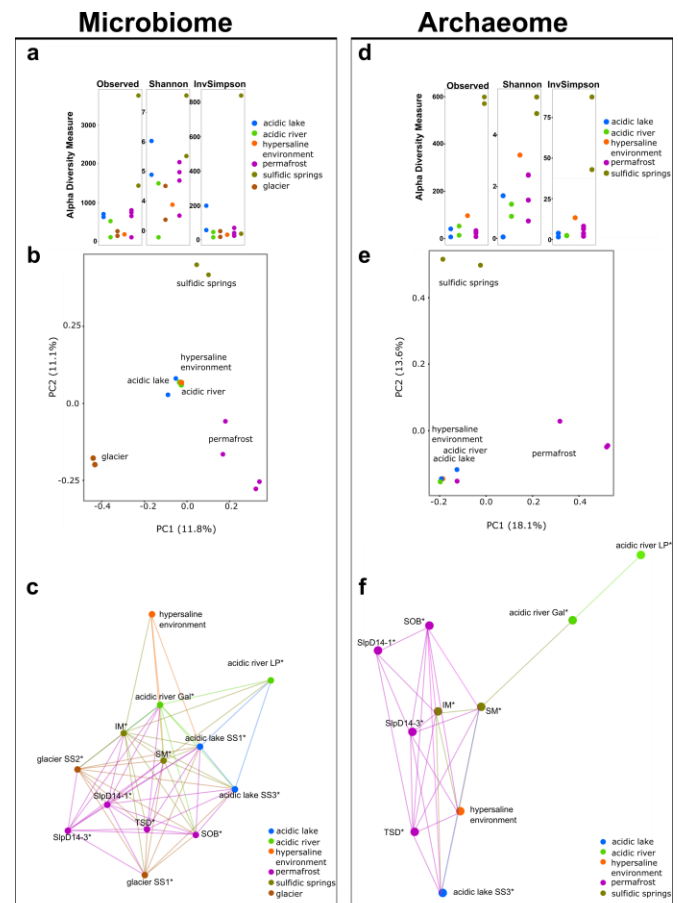


Fig.1: Microbial diversity and network analysis of microbial communities in samples from MASE sites. The left panel gives information on the general microbiome, whereas the right panel displays results from the archaeome analyses.