

# Worth their Salt: Halophiles and High Salinity Environments in Astrobiology and Space Biotechnology

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As widely recognized, the study of terrestrial analogue sites is seen as essential for: i) studying the limits of life, ii) obtaining new microbes for astrobiological exposure experiments, iii) analyzing long-term viability and preservation of microbes and biomolecules, iv) developing and testing technology for life-detection in space missions, and v) defining and refining planetary protection measures.

Within this context, we are witnessing a booming interest in high salinity environments as key analogues for conditions on Mars (and possibly beyond). Such sites encompass a diverse range of settings, which include coastal locations, inland lakes, surfaces of plants and animals, food products, deep-sea brines, or even salt-deposits in salt mines.

Members of the archaeal class *Halobacteria* are the clear champions of life in such environments and, fittingly, have been previously flagged as important model organisms for Astrobiology. *Halobacteria* are diverse, frequently polyextremophilic, and show a remarkable resilience. They have also been shown to survive or grow when exposed to several Mars-like conditions, raising important issues regarding Planetary Protection. From a more positive perspective, their relevance in biotechnology makes them essential sources for space biotechnological applications (namely for *in situ* resource utilisation- ISRU) and ensuring the sustainability of longer-term human presence in space. Another relevant aspect of members of this group is the extensive number of reports on their detection in minute brine inclusions, trapped within salt for extensive periods of time, while retaining viability.

Despite the relevance of halophiles and high salinity environments, they still remain underexplored from an astrobiological perspective. Data dispersion and increased number of species in the group makes it increasingly difficult to navigate this field. To cover this gap, we have generated a new online database on *Halobacteria*, compiling phenotypic