

# A New Database on Phenotypic Data on Halophilic Archaea and Insights into their Application in Astrobiology

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**Introduction:** Extremely halophilic archaea are microbes that thrive under very high salinities (>20% NaCl) and are almost exclusively placed in the class *Halobacteria* (Oren, 2014). In addition to their characteristic preference for high salinity and moderately high temperatures, many species of this class are resistant to desiccation, vacuum, and radiation, making them interesting targets for Astrobiological studies as model organisms and particularly relevant for the study of Mars, as highlighted by several authors (e.g., DasSarma et al., 2020). This class has a wide environmental range and includes species that live in salty biotopes such as salterns, salted foods, subterranean halite, lakes, or even in deep-sea brines in a list that includes several analogue sites (e.g., Antunes et al., 2020).

One current bottleneck of research with this group is the dispersed nature of data associated with its species. Our study partly addresses this by compiling phenotypic information and records of astrobiological experiments for all *Halobacteria*. We have established a database (HAPIE- Halophilic Archaea Phenotypic Information Explorer) that allows us to quickly compare different species as well as analyze trends and identify knowledge gaps and research opportunities.

**Setting up the HAPIE Database:** The HAPIE database is structured as Spring MVC application layers which leads to a maintainable and testable application. We configured the development environment with Java Development Kit, Maven build tool, Tomcat web server and Spring Tool Suite.

The collection of phenotypic data relied on information from the original publications of each type species complemented with data from Bergey's Manual

of Systematics of Archaea and Bacteria. Furthermore, a wide-scoped literature search allowed us to collect information on all species within this group that have undergone astrobiological testing. All data was imported into pre-defined templates defined by us.

## Knowledge Gaps and Research Opportunities:

Despite the clear relevance of *Halobacteria*, only a very small fraction of its species has been tested for Astrobiology, so far. As one of the highlights, we found that existing datasets were very scarce with most of the experiments concentrated exclusively in species the order *Halobacteriales*, while the order *Natrialbales* was the least studied (with 3 species only).

Regarding the type of testing reported there were also clear gaps. Radiation exposure was the most common type of dataset available; but also included microgravity or ultragravity tests, effects of vacuum, desiccation, as well as astrobiologically-relevant toxic chemical compounds and utilization of inorganic energy sources. In most cases only one type of experiment was made, so there are clear gaps in our knowledge both on exposure to single and multiple astrobiologically-relevant stress conditions.

Our study identified gaps in coverage and knowledge (both at the level of taxonomy and range of tested parameters) and assisted us in defining new testing priorities.

## References:

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- DasSarma S. et al. (2020) *Extremophiles*, 24, 31.
- Oren A. (2014) The Family Halobacteriaceae. In: *The Prokaryotes – Other Major Lineages of Bacteria and the Archaea*.