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Constraining Extreme Environment Adaptation Pathways: Tracing Genetic Divergence within Halophilic Microorganisms

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Jet Propulsion Laboratory
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Introduction

Abstract

The adaptations of life to survive in extreme saline and hypersaline ecologies yield survival pathways that in its beginning phases completely eradicate any evidence of the majority of microbial species and lower the diversity of biological communities significantly compared to typical marine environments.

- How can the utilized adaptations of halophilic microorganisms (“halophiles”) to their extreme environments be used to understand their evolution over geologic time?
- How can halophilic microbial communities residing in hypersaline environments on Earth tell us about biosignature detection for extant life in Martian and Europa in their respective analogue geochemical environments?

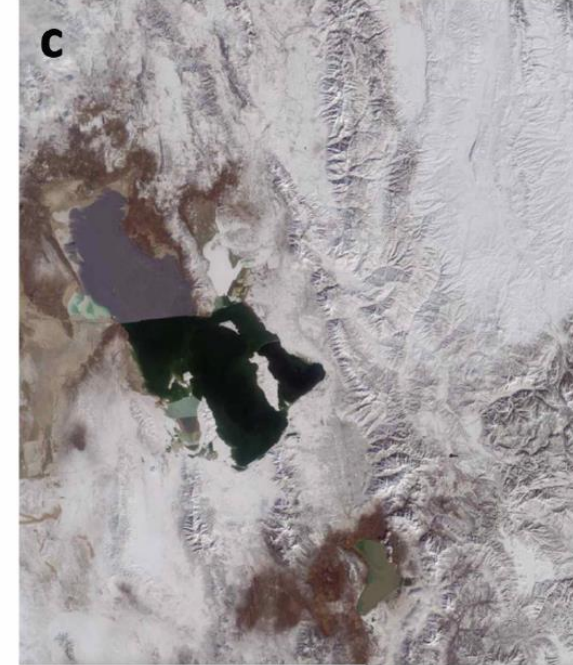
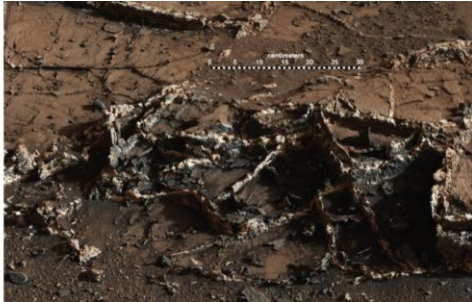


Fig 1. (Adopted from Fig. 1c from Perl & Baxter, 2020). Aerial view of the salinity gradients of the Great Salt Lake, Utah, United States.

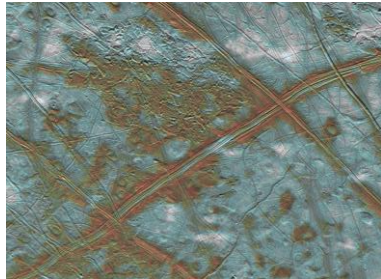


Problem Description

How can we understand the adaptations of life “as we don’t know it” without a evolutionary baseline? What adaptations are needed for extreme life on Earth that we can build a baseline for? What gene expressions are needed for biology outside of Earth?



- New interest in extant life on Mars as well as continued searches for life on the ocean worlds need a context for how adaptative that biology would need to be in order for it to be detected. Discovering a second sign of biology is equally important to understanding it's point in evolution.
- SOA: This is a novel methodology that has never been used in a planetary context. We are applying what we consider “early” evolutionary adaptation pathways for microbial survival to how biology could indeed survive during the loss of surface water on Mars and in the ocean-ice interface on Europa.
- This is relevant to NASA and JPL due to the impacts for life detection and biological validation work
- Results will enable recommendations for in-situ sample analyses, “taxis-driven” experiments (in-situ and laboratory), and validation experiments.
- Strengthens JPL’s broad expertise in astrobiology, life detection, state-of-the-art laboratory SOPs, and new tools for genomics and microbiology investigations.
- Provides NASA with a biology-driven approach to future payload designs and mission formulation



We will investigate the active and non-active gene expressions of halophilic bacteria from the genomic metadata from previous field investigations to understand these adaptations for planetary insight.

Results 2/3



- From the species-level data, the taxonomic units are compared against our databases for filtering of only genes that correspond to specific adaptations (Na-buffering for halophiles are shown here).
- These genes then are matched to other 16S rRNA sequences for metabolism overlaps, then filtered again for what is not present in our sites.
- Expressed genes for Na-buffering also include arsenic resistance expressions even though the original in-situ site does not contain these chemistries

Enzyme Code Distribution [glimmer_sequences_seqs_BLAsted]

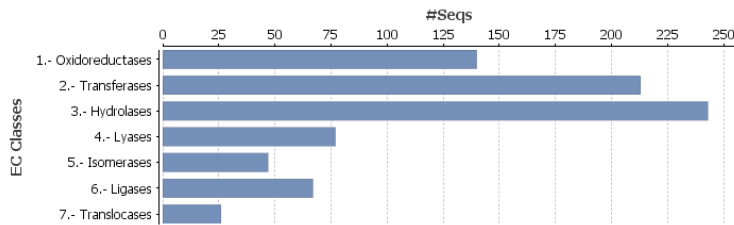


Fig 4. EC distributions for chosen OTU sequences

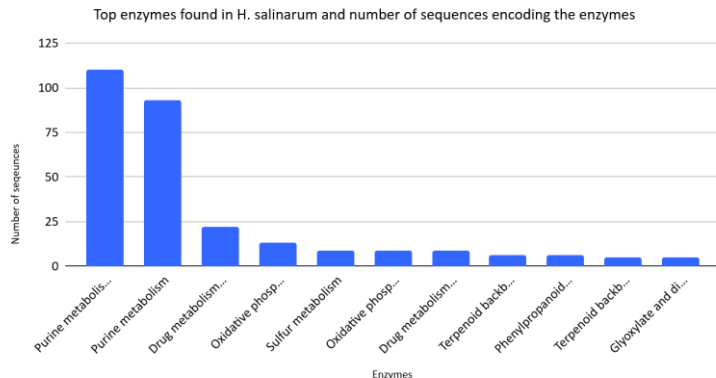


Fig 6. Final filtered metabolisms from Fig. 5 expressed genes

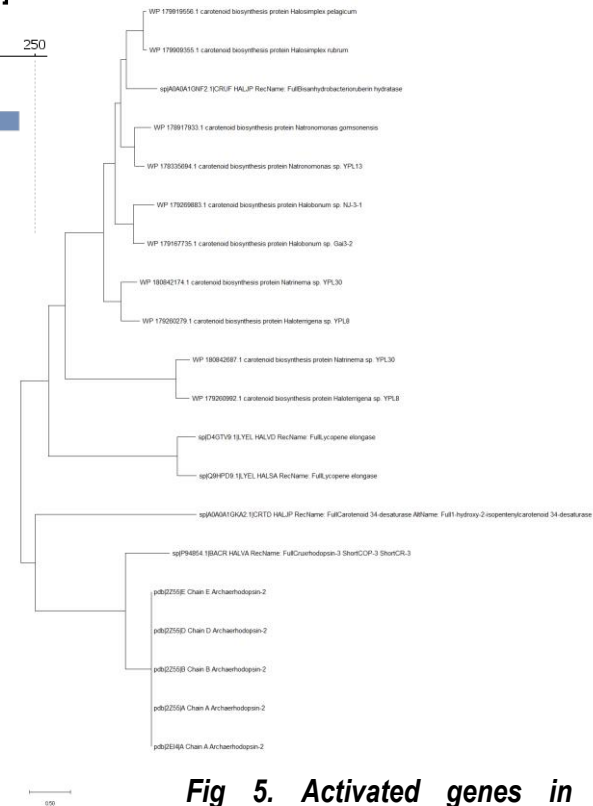


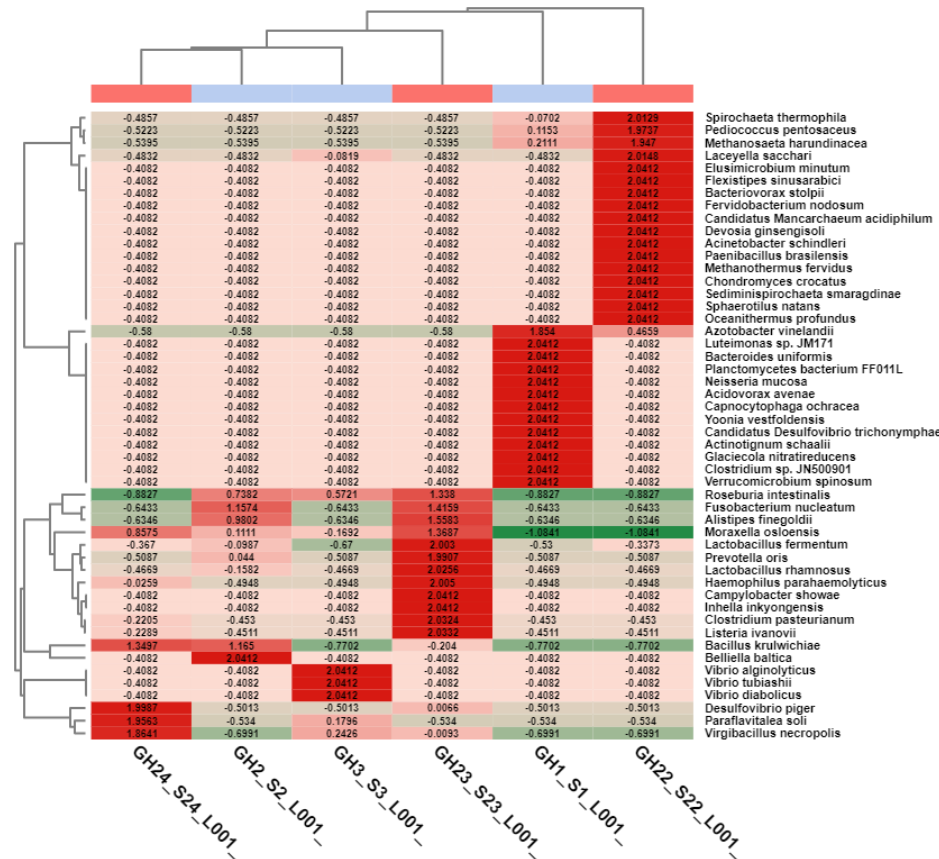
Fig 5. Activated genes in halophiles for photoprotection (UV) ability

Results 3/3

- Our final heat map from our in-situ samples show which halophilic microorganism genes are activated (expressed) in the matrix compared to BLAST and KEGG databases. This gives us an idea about how commonplace some genomic expressions are.
- Our future proposals will expand on this database from new in-situ samples and allow us to create a library of extreme environment microorganisms, and their genes that would need to be activated in order to survive on ancient or modern Mars as well as Europa's frozen climate.



Fig 7. Total heat map of the top halophilic species with respect to our samples. Upregulated genes (red bars indicative of high relative expression) show which species contain this active gene. Downregulated genes (green bars = low expression) are present and likely used for other processes but not halophilic-driven ones.



Publications

- Perl, S.M. & Basu, C. (in-prep) Using Genomic Expression a Biomarker for Adaptation and Survivability. *To be submitted to Astrobiology*
- Perl, S.M., Basu, C., Baxter, B.K., Celestian, A.J. (in-prep for AbSciCon) Constraining Halophilic Gene Expression for Ancient Mars Surviveability *To be submitted to the Mars Habitability session for the 2021 Astrobiology Science Conference*

References

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- Jones, D.L., Baxter, B.K. DNA (2017) Repair and Photoprotection: Mechanisms of Overcoming Environmental Ultraviolet Radiation Exposure in Halophilic Archaea *Frontiers in Microbiology*. 8: 1882
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