BACTERIAL DIVERSITY OF Fe/Mn & WHITE ROCK COATINGS IN KÄRKEVAGGE: A POTENTIAL MARS ANALOGUE

Ryan C. Sheehan[1,2], Cassandra L. Marnocha[2], & John C. Dixon[2,3], [1]Central Connecticut State University, sheehanryc@my.ccsu.edu, [2]Arkansas Center for Space and Planetary Sciences, University of Arkansas, [3]Department of Geosciences, University of Arkansas

INTRODUCTION

Kärkevagge- a region in the Swedish lapland defined by a 5km valley created by glacial processes. Kärkevagge exhibits low mean annual temperature (-2°C average), low precipitation (<900mm), an acidic environment, and a mineralogy dominated by sulfate and iron- all aspects which make the region a good analogue for the Martian landscape. [1]

Mineralogy- the region is host to a variety of rock coatings and weathering rinds. Iron-rich weathering rinds, Fe/Mn films, silica and alumina glazes, sulfate crusts, and heavy metal skins are found in the valley [2].

Biosignature Potential- microbial activity is capable of influencing geological formations [3]. Through cataloguing the microbial diversity in the rock coatings and understanding the relationship between microbes and the mineralogy on rock coatings, the potential application of rock coatings as biosignals for life on the Martian landscape can be advanced.

Figure 1. Rock coatings from the Kärkevagge region. Top left- sufate crust. Bottom left- Fe/Mn skin. Right- white coating.

RESULTS

- The microbial diversities of samples L2 (Fe/Mn skin) and H1 (white coating- a rock coating of alumina glaze with silicon and iron) were analyzed
- Gene sequences were compared to sequences of cultured organisms and (separately) to uncultured and environmental submissions in the BLAST nucleotide database
- Sample H1 displayed a Simpson Diversity Index of 0.36, sample L2 displayed an index of 0.84 (previously analyzed sulfate crust K2 displayed an index of 0.22)
- Bacteria from sample H1 display isolate matches with 15 unique organisms
- Bacteria from sample L2 display isolate matches with 3 unique organisms from 4 different environments

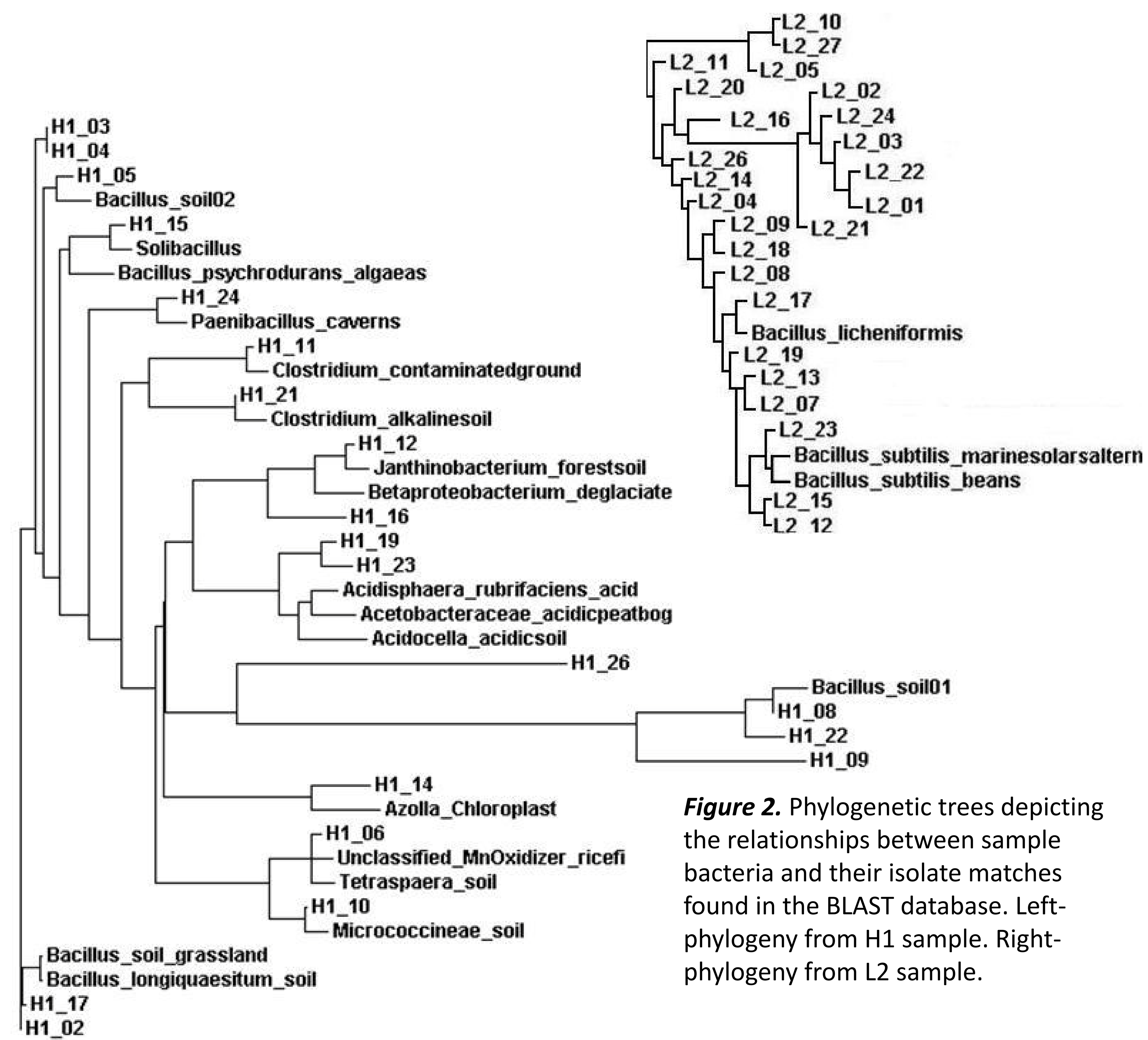

Figure 2. Phylogenetic trees depicting the relationships between sample bacteria and their isolate matches found in the BLAST database. Left- phylogeny from H1 sample. Right- phylogeny from L2 sample.

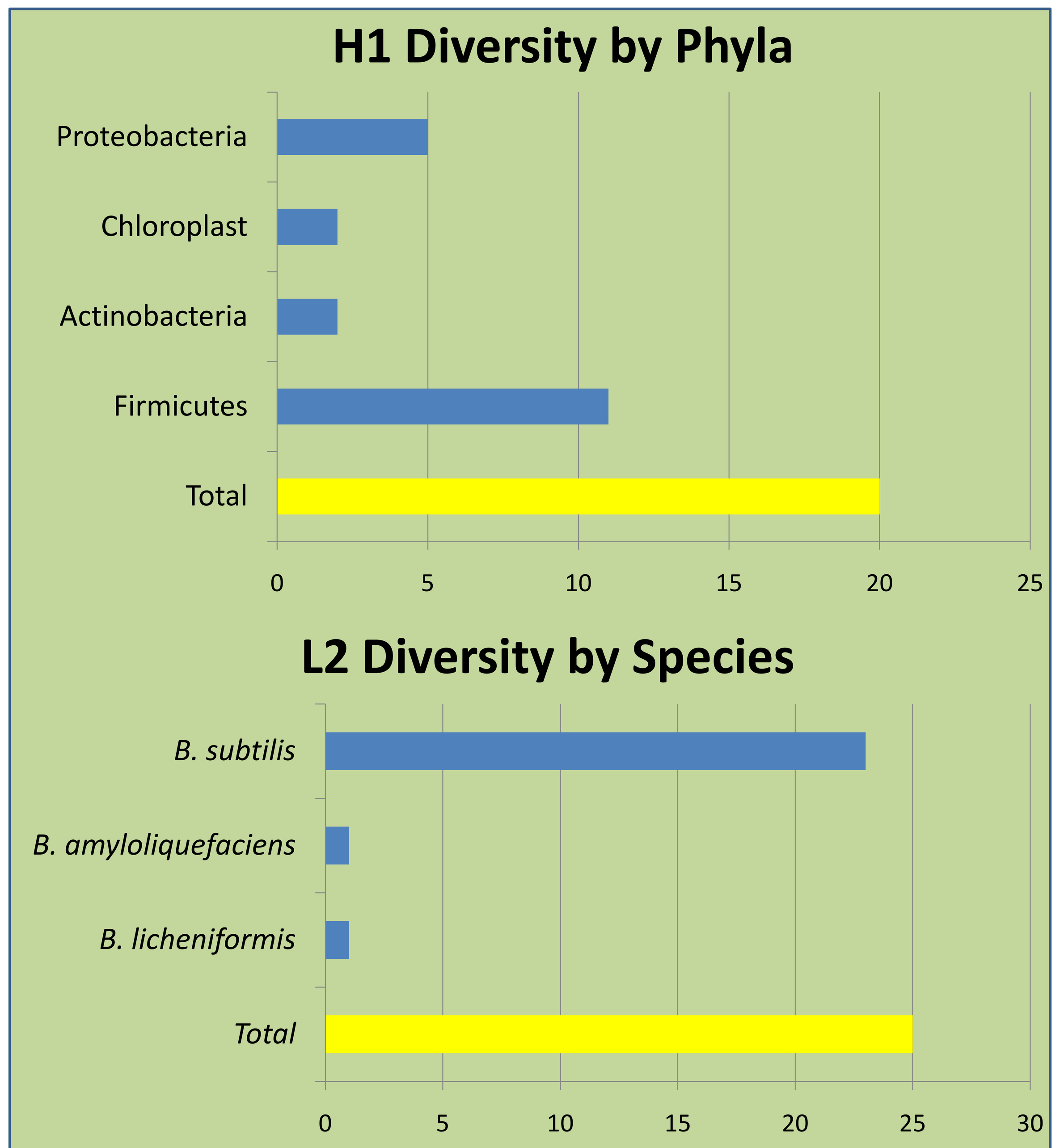

Figure 3. Bacterial diversity in the isolate matches of H1 & L2 samples, as described by the amount of highest identity isolate matches per taxa. Isolate matches in H1 are distributed between three separate phyla in addition to bacteria matching chloroplasts found in organisms within the kingdom Plantae. Every isolate match in L2 belonged to the phylum Firmicutes, and were divided by species.

METHODS

1. Isolation of DNA from fragmented rock coatings
2. Amplification of Bacterial 16S rDNA fragments via PCR
3. Transformation of fragments into *E. Coli* cells
4. Incubation of transformed *E. coli* cells
5. Selection of positive colonies, amplification of DNA fragments again via PCR
6. Sequencing of gene fragments
7. Comparison of gene sequences to BLAST database
8. Analysis of isolate matches from BLAST database

CONCLUSIONS

- Rock coatings of different morphologies provide distinct bacterial phylogenies, providing evidence for influence of bacterial diversity on variable rock coating evolution
- Isolate matches provide a range of environmental tolerations and physiologies as reference for the organisms of the samples
  - Common soil, groundwater, and cavern-dwelling
  - Ubiquitous *Bacillus* genus is known to facilitate iron-cycling [4]
  - Acid tolerant
  - Alkaline tolerant
  - Psycrophiles
  - Endoliths
  - Thermophiles
  - Mn-oxidizing [5]
  - Heavy metal-reducing
- These characteristics lend evidence to microbiota as potential analogues to organisms which would survive in the Martian landscape
  - Survivability in such a range of environments provide relevance for astrobiology on Mars
  - Bacterial heavy metal interaction may be involved in the genesis of rock coatings

REFERENCES

[1] Thorn, C. E., Dixon, J. C., Darmody, R. G., & Allen, C. E., 2005. A 10-year record of the weathering rinds of surficial pebbles in Kärkevagge, Swedish Lapland. *Catena* **65**, 272-278.
[2] Marnocha, C. L. & Dixon, J. C., 2011. Bacterial diversity of sulfate rock coatings in Kärkevagge, Swedish lapland: a potential Mars analog. *LPSC XXXXII*, Abstract #1598.
[3] Fortin, D., 2004. What biogenic minerals tell us. *Science* **303**, 1618-1619.
[4] Johnson, D. B. & McGinness, S., 1991. Ferric iron reduction by acidophilic heterotrophic bacteria. *App. Env. Microbiology* **57**, 207-211.
[5] Cahyani, V. R., Murase, J., Ishibashi, E., Asakawa, S., & Kimura, M., 2009. Phylogenetic positions of Mn-oxidizing bacteria and fungi isolated from Mn nodules in rice field subsoils. *Bio. & Fertility of Soils* **45**, 337-346.

ACKNOWLEDGMENTS

Special thanks to Dr. John Dixon for his mentorship and for the opportunities he's afforded me, to Kate Dreier & Dr. Julia Kennefick for coordinating and making possible my REU programme, to Dr. Mack Ivey and Dr. Tim Kral for the gracious provision of their lab materials and space, and to Cassie Marnocha for her dedication, advice, and magnanimous support. Funding for this project was provided by the National Science Foundation, Award Number 0851150.

FUTURE WORK

- Further phylogenetic analysis of bacterial diversity of rock coating samples
- Mineralogical analysis of rock coatings
- Culturing of microbiota to reproduce biomineralization
- Expansion of phylogenetic analyses to include archaeal diversities