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Geochemical controls on biological N_2 fixation within Mars analogue systems

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Noachian-age (4.1-3.7Ga) terrestrial hot spring deposits have been identified on Mars [1,2] along with fixed nitrogen compounds [3]. We investigated the geochemical controls on biological nitrogen cycling at four analogue geothermal systems in Iceland, and how these influence resulting geochemical biosignatures.

We find all sites have little abiotic nitrogen input, with $D^{15}N$ values of biomass, sediment and rocks consistent with expected fractionation effects of biological nitrogen fixation and ammonium uptake pathways [4] (Figure 1). Metagenomic data supports this, with nitrogen-fixing and uptake genes being the most abundant nitrogen-cycling genes in every site (Figure 2). Communities with the most negative $D^{15}N$ values are hypothesised to be switching to alternative nitrogenase enzymes [4] and genes encoding these enzymes were also identified within metagenomic data. These sites exhibited limited molybdenum solubility, thus geochemically inhibiting conventional nitrogen fixation via the Mo-dependent nitrogenase, instead favouring the alternative enzymes which rely on available iron and vanadium.

The geochemical and biological parameters which regulate biological nitrogen fixation are crucial to these communities and impact the isotopic biosignatures produced. Mo-limitation in these sites caused unusually low $D^{15}N$ values that are more likely to be identified in the rock record. Martian meteorites are molybdenum-poor, similar to the basaltic bedrock of many Icelandic hot springs [5]. Hence, the search for life on Mars and definitions of isotopic biosignatures should therefore account for feasible Martian biochemistry operating under basalt-buffered nutrient supplies, characterized by high levels of Fe, V, and P relative to Mo and N.

References

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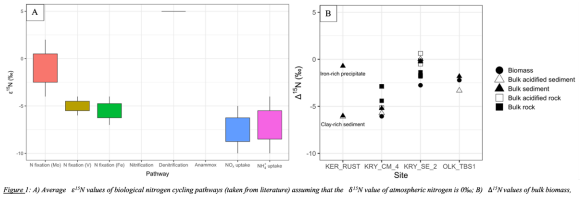

Figure 1: A) Average $\varepsilon^{15}N$ values of biological nitrogen cycling pathways (taken from literature) assuming that the $\delta^{15}N$ value of atmospheric nitrogen is 0‰. B) $\Delta^{15}N$ values of bulk biomass, sediment, and rock from hot spring sites. $\delta^{15}N$ values of dissolved N_2 were used to calculate $\Delta^{15}N$ values in each site, assuming that the biomass is derived from fixation of N_2. Bulk sediment and rock samples were acidified and remeasured where sufficient material was collected (see legend) to remove any inorganic nitrogen. No visible biomass (mat or streamers) was observed in KER_RUST site, although two different substrates were sampled (iron-rich precipitate and clay-rich sediment beneath). Standard deviations were calculated using at least 6 replicates of USGS-62 standard and are included but hidden by datapoints (SD = 0.06).

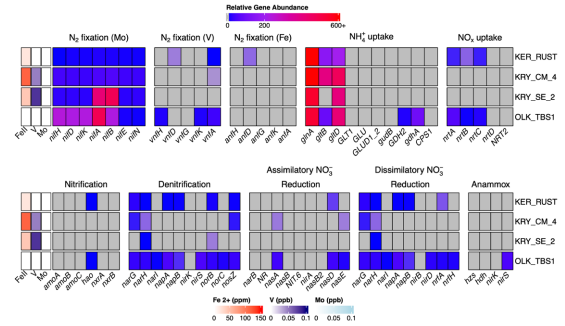

Figure 2: Relative gene abundance of nitrogen-cycling pathways. All genes involved in these pathways are included at the bottom of heatmaps. Genes for each nitrogenase enzyme are highlighted. Genes which were not identified by Prokka/BLAST are in grey. Metal concentrations of Fe^{2+}, V and Mo are included to the left of the plot for each sample.