From Biodiversity to Biomarker Variability: Sampling Strategy in Planetary Analogue Missions

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Life and habitability detection in planetary exploration relies on a combination of low-resolution remote sensing and infrequent *in situ* robotic missions limited in the number and geographical range of samples that can be analyzed. Knowing the expected spatial variability in the target biomarkers and related biogeochemical parameters is key to efficient planetary exploration sampling.

Though terrestrial soil microbial biodiversity is well-studied, many of its major controlling factors are not relevant to planetary exploration (*e.g.* effects of land use or tree and bush root effects). Further, results from biomass-rich environments may not generalize to low-biomass sites dominated by non-typical nutrient or other survival constraints; lower microbial abundance may be correlated with more spatially-diverse communities.

Five simulated expeditions to Icelandic Mars analogue environments have been used to establish a baseline for biomarker diversity and to test sampling strategy [1]. Multiple classes of biomarker (cell counts, ATP, and nucleic acids) and mineralogical data (moisture content, grain size, Vis/NIR/SWIR reflectance spectra, and X-ray fluorescence spectra) were taken at different spatial scales. Nested sampling grids, a technique adapted from landscape ecology, were effective in establishing that biomarker types may vary independently down to <10 cm scales even when enviroments appear homogeneous.

The results indicate that sampling based on coarse remote sensing data requires an infeasible number of replicates (>10) for accurate biomarker characterization [2]. The extension of these biomarker diversity maps to include geochemical correlation is in progress. The continued adaptation of statistical tools from terrestrial biodiversity and ecological studies will help to develop an improved sample site selection pipeline as well as to add context to astrobiological data from past and current missions.

[1] Amador *et al.* (2015), *Planetary & Space Science* 106, 1-10
[2] Gentry *at al*. (2017), *Astrobiology* 17(10), 1009-21