

Life in the Lava Tubes: Bacterial, Archaeal and Eukaryotic Communities in a Mars Analog Environment

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Lava caves are prime targets of interest in the search for extant or past life on rocky planets. Here on Earth, they harbor diverse and abundant microbial communities, which are often associated with secondary minerals formed on host basalt rock. Here, we will present results from an ongoing NASA planetary analog project, Biological and Resource Analog Investigation in Low Light Environments (BRAILLE), underway at Lava Beds National Monument (Northern CA, USA). Using 16S and 18S rRNA gene sequencing, we characterized the distribution, diversity, and putative metabolic capabilities of microbial and eukaryotic communities within several caves with a variety of physical parameters such as length, depth, number of entrances, and human visitation. We sampled distinct morphologies in the caves, ranging from soft sticky “ooze”, to microbial films, secondary mineral features (“speleothems”), and what appeared to be bare basalt. The soft-material samples, ooze and microbial biofilms, had lower relative abundances of Actinobacteria and higher relative abundances of Proteobacteria than mineral features. The bacterial community structure did not differ significantly between features, but the community in soft features was higher than in mineral features. The three unclassified archaeal genera, from the families *Nitrosotaleaceae*, *Nitrosopumilaceae*, and *Woesarchaeales*, tend to co-occur and correlate inversely with the genus *Candidatus Nitrosocomicus*. These taxa and abundant bacterial genera, such as *Nitrospira*, are likely involved in nitrogen cycling, and the presence of nitrogen metabolism is further supported with metagenomic data. Our study provides insight into an essential nutrient cycle in a relevant Mars analog environment and may inform future sample collection in the search for life on other planets.