Contrasting Microbial Communities in Cave Ferromanganese Deposits With Overlying Surface Soils

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Arid-land carbonate caves, such as Fort Stanton Cave, receive limited surface input; hence, critical constituents required for microbial communities are often limited. We hypothesized that the microbial communities residing in surface soils would differ from their subsurface counterparts found throughout the Snowy River passage on walls and ceilings in soil-like material (speleosol) rich in Fe- and Mn-oxides. Also referred to as ferromanganese deposits (FMDs), these secondary mineral deposits represent low nutrient environments that would likely select for organisms with metabolisms that favor low-nutrient local conditions and may be chemolithotrophic (“rock eaters”). We examined archaeal and bacterial makeup of low-nutrient ferromanganese deposits occurring in Fort Stanton Cave, NM, USA, and in corresponding overlying surface soils. Results of 16S rRNA gene sequencing indicate that bacterial and archaeal communities in the cave are taxonomically significantly dissimilar to their corresponding surface soils. Core microbial constituents of these communities, representing operational taxonomic units (OTUs) occurring in >80% of all samples, determined that there were only 19 and 17 archaeal and bacterial OTUs shared between surface and cave samples, respectively out of the total 1,639 archaeal and 12,051 bacterial OTUs. Surface archaeal communities were primarily represented by the Thaumarchaeota class Soil Crenarchaeotic Group (SCG), which play important roles in nitrogen cycling. Dominant archaeal groups in the subsurface included the Euryarchaeota class Thermoplasmata and Thaumarchaeota classes South African Gold Mine Gp 1 (SAGMCG-1), Marine Group I, and AK31. Bacterial cave OTUs significantly different from surface bacteria included Nitrospirae, GAL15, Omnitrophica, Zixibacteria, Latescibacteria, SBR1093, and Ignavibacteria. Results suggest Fort Stanton Cave provides a biological niche for low nutrient/chemolithotrophic bacterial/archaeal groups, several of which are players in critical nutrient cycling (e.g. nitrogen). Community composition is likely driven by depth below the surface and rock geochemistry, which is supported by the high number of reads shared amongst cave core OTUs.