Geological controls on desert spring microbiomes

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Desert springs are aquatic oases that provide critical habitat for aquatic and riparian species in an otherwise arid landscape. Yet, our knowledge of the microorganisms in these ecosystems is limited in both scope and scale. To address this gap, we conducted a 16S rRNA gene amplicon survey of 683 samples collected from 73 springs across the southern hydrographic Great Basin, USA, along with several shotgun metagenomes and analyzed the ecological patterns within an extensive ecohydrogeological framework. Our study revealed a strong differentiation between the microbiomes of (i) local springs characterized by cold, young, and dilute waters, (ii) regional springs characterized by warmer, older, and more evolved waters, and (iii) saline springs. Local spring microbiomes were diverse, resembled soil and rhizosphere communities, and hosted predominantly aerobic, saprophytic microbial communities. Regional spring microbiomes were less diverse, more unique, and hosted abundant Cyanobacteria. Regional and saline springs first evolved on the landscape during the Late Miocene (11.63 to 5.333 Ma) during which the southern hydrographic Great Basin underwent rapid tectonic extension; we are currently modeling the spaciotemporal evolution of these two spring types on the landscape to tie tectonics to the diversification of spring microbiomes. We also documented subtle geochemical differences imparted by metamorphosed Paleozoic (538.8 to 251.9 Ma) roof pendant weathering in the source area of some springs in the Owens Valley kilometers above the springs sources. Relative to other springs, roof pendant-recharged springs were characterized by elevated: (i) Ca²⁺/Na⁺, Ca²⁺/Mg²⁺, and divalent/monovalent cation ratios, (ii) relative abundance of taxa inferred to be benthic aerobes and prosthecate/stalked bacteria, and (iii) abundance and diversity of shredder and collectorgatherer benthic macroinvertebrates. Our study identifies key geological controls over tens to hundreds of millions of years on extant desert microbiomes.