

Metabolic diversity of hyperalkaliphilic microbial communities associated with serpentinization at The Cedars

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The Cedars, in northern California, is an active site of subsurface serpentinization. The spring waters that emerge from this system feature extremely high pH (pH=11-12), low redox potential (E_h =-600 mV), low salinity, relatively rich in calcium and lack of obvious electron acceptors and carbon sources, making it an exceptionally challenging environment for life. Geochemical studies of The Cedars revealed that the site has two different serpentinizing water sources: a deep source that interacts with the peridotite body as well as the km-deep marine sediments, and a shallow source that interacts only with the overlying peridotite.

Here, we present the analyses of metagenomes, recovered draft genomes and metatranscriptomes from the two different springs GPS1 and BS5. GPS1, fed solely by the deep serpentinizing water source, was dominated by several taxa from the phyla OD1 (“*Parcubacteria*”) and *Chloroflexi*. None of the members in the GPS1 community encoded respiration-related genes and some of those did not encode key biosynthesis-related genes as well. However, both *in situ* replication rates estimated by an index of replication (iRep)* and the gene-expression of cell growth related genes indicated that the OD1s are growing every year, and the estimated growth rate is as fast as the other organisms at The Cedars. Meanwhile, BS5, fed mostly by a shallow source, was populated by hydrogen-driven *Proteobacteria*, in particular *Serpentinomonas* spp. Those findings indicated that harsh highly-alkaline geological settings support diverse microbial metabolic strategies.

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