

Metagenomic analyses reveal the role of organosulfur in deep subsurface biogeochemical sulfur cycling

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It is well documented that subsurface microorganisms fuel their metabolisms through inorganic sulfur reduction and oxidation reactions. However, organic forms of sulfur are historically overlooked in these settings, despite their abundance in biomass and the range of oxidation states they can occupy. Mineralization of organosulfur compounds is an important source of inorganic sulfur species in surface systems; therefore, we hypothesize that it may also play a significant role in biogeochemical sulfur cycling in the deep biosphere. Here, we used metagenomic and genome-level investigation of 164 unique microbial communities collected through the Census of Deep Life to probe the importance of organic sulfur cycling across deep-subsurface systems. This robust dataset contains 467 metagenome assembled genomes (MAGs) and spans both marine and terrestrial systems, allowing for a comparison of the metabolic capacity of communities in these two distinct biomes. Assimilatory and dissimilatory inorganic sulfur metabolisms as well as organosulfur assimilation, production, and utilization were prevalent in both marine and terrestrial deep subsurface environments. However, the frequency and proportion of occurrences varied by gene and pathway across the marine and terrestrial divide. While both marine and terrestrial genomes have key organosulfur pathways, terrestrial MAGs have a greater variety of genes, including several that were not detected in marine MAGs. Continued exploration into the scope and scale of microbially driven organosulfur transformation will refine our understanding of deep subsurface biogeochemical sulfur cycling and inform how this impacts broader Earth systems.