

The metabolic potential of freshwater Bathyarchaeota

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Microorganisms catalyze fluxes of matter and energy at global scales, yet the vast majority of microorganisms on Earth remain intractable to laboratory studies since they have not yet been cultivated. This intractability confounds efforts to create predictive biogeochemical models informed with the metabolic potential and physiological capacity of the relevant microbial catalysts. Subsurface sediments comprise one of the largest biomes on the planet, and these sediments are rife with microbial phyla lacking cultured representatives—so called Microbial Dark Matter. Members of the recently defined archaeal candidate phylum, the Bathyarchaeota, are numerically abundant members of marine subsurface microbial communities that have recently been implicated in fermentative carbon metabolisms and methanogenesis. The Bathyarchaeota also feature prominently in the terrestrial and lacustrine subsurface, but their role in these settings remains mostly speculative. To explore the metabolic potential of freshwater Bathyarchaeota we sequenced DNA recovered from sediments of the ferruginous (Fe-rich) Malili Lakes system on Sulawesi Island, Indonesia. Amplicon-based 16S rRNA gene community profiling revealed the microbial communities in anoxic sediments from lakes Matano and Towuti comprised up to 60% Bathyarchaeota. Shotgun-based metagenomic sequencing yielded population pangenomes from the former sub-phylum MCG-A. Within the MCG-A sub-phylum, Malili lake pangenomes cluster into a new and distinct subclade. Pathway based metabolic reconstructions from these pangenomes reveal that these freshwater Bathyarchaeota have the genomic potential for carbon transformations likely integral to the biogeochemistry of anoxic sediments.