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Methane-cycling microbial communities across changing environments

Methane is a potent greenhouse gas with a global warming potential approximately 28 times greater than carbon dioxide over a 100-year period. Biological processes are responsible for ~60% of global methane emissions, most of which are produced by archaeal methanogens. Wetlands and lakes are known to contain robust methane-cycling microbial communities and represent significant sources of methane. As anthropogenic influences, including climate change, alter these ecosystems, their microbial communities are consequently affected. These communities feed back into the climate through changes in their production and consumption of methane, yet the magnitude and direction of change are unclear. Constraining methane emissions in these rapidly changing environments is therefore critical to our understanding and predictions of climate change. In this research, we examine methane-producing microbial communities in two dynamic and high-methane environments. Arctic permafrosts store approximately twice as much carbon as is currently present in the atmosphere, and their thaw is predicted to result in substantial methane emissions. These emissions are typically modeled using surface environmental characteristics such as soil temperature and moisture; however, in Alaskan permafrost we found that sites with the highest methane flux (hotspots) were outliers and contained very low relative abundances of near-surface methanogens. The Great Salt Lake is another environment experiencing rapid anthropogenic change, as increased water usage has resulted in higher salinity. In contrast to previous studies, we document extreme methane emissions from Great Salt Lake soils containing novel methanogens. In this work we cultured and characterized a new species of the halophilic methanogen genus, *Methanohalophilus*. While we hypothesized it would be specifically adapted to changes in salinity, genomic and proteomic data suggest that community interactions may have larger impacts on its physiology. Overall, this dissertation utilizes a combination of microbiology and microbial ecological techniques in conjunction with measurements of methane flux to determine how methane-cycling microbial community composition and physiology change under anthropogenic influence. The work presented highlights the impact of community dynamics on methanogen physiology and methane flux in changing environments.

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