

Microbial Drivers of Methane Emissions from Unrestored Industrial Salt Ponds [†]

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Abstract: Wetlands are important carbon sinks, yet many have been destroyed and converted to other uses over the past few centuries, including industrial salt making. A renewed focus on wetland ecosystem services (e.g., flood control, habitat) has resulted in numerous restoration efforts whose effect on microbial communities is largely unexplored. We investigated the impact of restoration on microbial community composition, metabolic functional potential, and methane flux by analyzing sediment cores from two unrestored former industrial salt ponds, a restored former industrial salt pond, and a historic wetland. We observed elevated methane emissions from unrestored salt ponds compared to the restored and historic wetlands, which was positively correlated with salinity and sulfate. 16S amplicon and shotgun metagenomic data revealed that the restored salt pond harbored communities more phylogenetically and functionally similar to the historic wetland than to unrestored ponds. Archaeal methanogenesis genes were positively correlated with methane flux, as were genes encoding enzymes for bacterial methylphosphonate degradation, suggesting methane is generated both from bacterial methylphosphonate degradation and archaeal methanogenesis in these sites. These observations demonstrate that restoration effectively converted industrial salt pond microbial communities back to compositions more similar to historic wetlands and lowered salinities, sulfate concentrations and methane emissions.

Keywords: metagenomics; hypersaline; methane; wetlands

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