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Microbial abundance, presence, and function in Gulf of Maine coastal sediment

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Maine has an extensive coastline along the Gulf of Maine, one of the fastest-warming bodies of water on Earth. Shallow coastal sediments help to control the flow of energy and carbon from land to ocean. However, the geochemistry of coastal sediments can vary widely, based on local inputs and different physical factors. Ecology in these sediments have been characterized at few localities, but studies include recent investigations into the seasonal dynamics of the iron biogeochemical cycle, bioturbation impacts, and rate measurements of active microbial redox metabolisms in an intertidal mudflat. However, the larger sediment expanse of this important Gulf system remains largely uncharacterized, with regards to both chemistry and ecology. Sediments at deeper depths (>10 cm below seafloor; cmbsf) have also remained unsampled due to sampling constraints. The diversity and abundance of ocean sediment microbes is generally much greater than in overlying waters, but we know far less about their encoded functions and possible metabolic activities. In addition to developing methods to quantify microbial activity and identify function metabolic abilities, we have developed sampling abilities for near shore sediment coring of up to 2 meters in the Gulf of Maine. Recently, we have recovered sediment cored up to 150 cmbsf, at a water depth of over 100 m. Using flow cytometry, we have quantified microbial cells in Gulf of Maine sediment to be as high as ~10^7 cells cm^{-3} in shallow sediments, and as low as ~10^5 at depths of 150 cmbsf. Using metagenomics on the same samples we quantified biomass in, we are able to characterize the relative abundance, metabolic functions, and distribution of microbial species across multiple riverine, dynamic cove, and ocean sediment ecosystems at different sediment depths. In this presentation, we will explore how available chemistry influences (and is influenced by) microbial metabolic functions within sediment carbon, iron, and sulfur cycles, integrating chemical and genomic analyses across a range of spatial and depth scales.