

Combining high resolution organic matter characterization and microbial meta-omics to assess the effects of nutrient loading on salt marsh carbon sequestration

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Abstract: Salt marshes sequester an order of magnitude more carbon in their sediments than their terrestrial counterparts because rates of decomposition are inhibited by anoxic, water-logged soils. Once easily degradable organic matter is preferentially used by microbes, the less labile fraction is buried vertically within the sediments, and is thought to remain stable. Recent work, however, suggests that the addition of nitrogen in its oxidized form (nitrate) may stimulate decomposition of this organic matter by providing an energetically favorable electron acceptor for heterotrophic metabolisms. In controlled experiments we found that the addition of nitrate at 25 cm depth fundamentally altered the microbial community, and stimulated organic matter decomposition. By providing more energy to the system, the added nitrate allowed microbes to oxidize a pool of organic matter otherwise left untouched. This degradation not only lessens the ability of salt marshes to store carbon, but may also release this carbon as CO₂, contributing to greenhouse gas release and climate change in unknown ways. The question that remains is, can the addition of nitrate in deep salt marsh sediments that capture 3000 years of stored carbon, also stimulate decomposition, or is the organic matter simply too recalcitrant for microbes to use, even with the increased energy supplied by the enhanced electron acceptor? We hypothesize that some portion of the highly recalcitrant stored carbon that is thousands of years old will be decomposed when exposed to elevated nitrate concentrations and there will be a concomitant shift in the structure and function of the microbial community, providing a mechanistic basis for this carbon loss.

We will test this hypothesis by sequencing salt marsh sediment microbial metagenomes and metatranscriptomes in parallel with high resolution characterization of recalcitrant organic matter from sediments exposed to long term nitrate enrichment. We will analyze sediment samples from three-meter-deep cores, where deepest sediments are approximately 3000 years old, that we already collected as part of a multi-investigator team studying the long-term nutrient enrichment of salt marshes at the Plum Island Ecosystem LTER. This experiment, supported by ongoing funding from the National Science Foundation, involves experimental nitrate enrichment of duplicate salt marsh creeks since 2004. We have documented the dramatic effect of added nitrate on surface microbial processes but, have not yet examined how deep into the marsh this influence propagates. It is, however, essential to understand how nitrate enrichment alters sediments at depth, as that is where the preponderance of carbon storage takes place. We therefore propose to link changes in genetic potential and expression to the high-resolution characterization of organic matter using solid state ¹³NMR, which can resolve components of complex organic matter, from samples collected at depth in nitrate enriched and unenriched marshes. With parallel deep sequencing of the metagenomes and metatranscriptomes of these sediments, we can 1) identify genomes of novel microbial players that are able to decompose recalcitrant organic matter in the presence of nitrate, 2) determine which metabolic pathways are differentially expressed as a result of nitrate addition, and 3) link differential expression of these genes to the decomposition of organic matter in salt marsh sediments. Taken together this work will provide novel insights into the forces that control carbon storage in salt marsh sediments and it will shed light on how exposure of those sediments to a critical global change driver, nitrate enrichment, alters carbon storage capacity, a critical ecosystem service.