

Seasonal hypoxia impacts nutrient fluxes and microbial communities in Narragansett Bay sediments

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Hypoxia, the force behind aquatic dead zones, has become widespread in coastal areas over the past several decades. These regions are impacted concurrently by rising global temperatures and high nutrient inputs. In Narragansett Bay, RI, a recent reduction in discharged wastewater nutrients has reduced previously seen dramatic events such as large-scale fish kills, but intermittent hypoxia still persists and may still cause impactful changes in bottom waters and surface sediments. Sediment microbial communities significantly impact sedimentary nutrient fluxes, which in turn influence nutrient concentrations in overlying water. Decreasing oxygen concentrations can shift sedimentary nitrogen cycling and favor processes with additional nitrogen outputs, leading to changes in water column nutrient availability and potential risks to fisheries. To investigate how coastal seasonal hypoxia is impacting sediment bacterial communities and associated nutrient cycling, we collected sediment cores from Greenwich Bay, Rhode Island, USA in Fall 2020 both during and after onset of hypoxia. We profiled cores to 3 cm using Unisense microsensors, subsampled for microbial DNA, and collected porewaters for nutrient analysis. We determined bacterial community composition by amplifying and using high-throughput sequencing to compare the V4 region of the highly-conserved 16S rRNA gene for overall community composition and the *nifH* gene to identify potential nitrogen fixers. Comparisons between porewater nutrient concentrations and overlying water oxygen revealed a decrease in ammonium flux under transiently hypoxic conditions in opposition to observed trends in other coastal systems, and negligible nitrate flux regardless of hypoxia. Preliminary DNA analysis revealed closer relationships between bacterial communities in samples collected on the same date than those collected at the same depth over time. Our combination of nutrient analyses and amplicon sequencing provides unique insights into the relationships between sediment microbial communities and water column conditions, helping to inform predictions of how increasing coastal hypoxia will impact estuarine chemistry.