

PhD Dissertation
Department of Environmental Science and Policy
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Title: Bacterioplankton Communities In Relation to Environmental Variables in Four Mid-Atlantic Estuaries (Potomac, Delaware, Neuse and Chowan)

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ABSTRACT

Research suggests that concentrations of dissolved carbohydrates and amino acids, “microbially-labile organic carbon (DiMLOC)”, in the Potomac River Estuary (PO) are unusually high and correlated with high abundance of free-living, phenotypically similar bacterioplankton. These microbial communities play a pivotal role in seasonal anoxia/hypoxia during summer when primary production is not at its peak, suggesting that typically monitored bulk indicators alone, like phytoplankton, are not sensitive and reliable predictors of ecosystems conditions. We hypothesized that a combination of hydrographic parameters, measures of preferred bacterioplankton substrates and bacterioplankton community diversity are inextricably linked to eutrophication in the PO, and that this may be in contrast to other regional estuaries. To our knowledge, the composition of these communities in relation to these phenomenon and direct comparison to other regional estuaries with consistent methods has not been documented.

In a 2013 study, water samples and hydrographic data were collected from four estuaries, the Delaware (DE), Neuse (NE), Chowan (CH) and PO, once in each of the months April, July, August and October. Samples were collected from cross-river transects and multiple depths (7 samples per transect per estuary) within the closest time frame possible. In addition to chlorophyll and phaeophytin concentration, bacteria were enumerated by direct count and several forms of organic carbon, including total organic carbon (dissolved and particulate), dissolved monosaccharides and polysaccharides, dissolved free amino acids and biochemical

oxygen demand, were measured. Total genomic DNA was extracted to assess microbial biodiversity in these systems.

The most compelling result from our analysis was that the relationship of bacterioplankton abundance (BA), dissolved oxygen (DO), phytoplankton, DiMLOC and bacterioplankton assemblages were not unique to the PO, but may be similar in other eutrophic estuaries. Across all the estuaries, DiMLOC components were the best variables (best fit model) explaining bacterioplankton assemblages. The data indicate that the PO and NE were the most similar of the four estuaries. Both the PO and NE were eutrophic, but possibly at different stages — the NE seemed to be like the PO of two decades ago, having very high BA, high DiMLOC and low DO. In addition, their diversity profiles were also similar and they were much lower diversity than either the DE or CH that did not have critically low DO concentrations or high BA conditions. In terms of BA, DO, DiMLOC, and diversity (Operational Taxonomic Unit (OTU) composition, alpha and beta diversity measures) the PO and Neuse (NE) estuaries were found to be similar, particularly in summer when both estuaries were at times anoxic and hypoxic. In bottom water, where low oxygen was most severe, the communities were very similar. In contrast, the mesotrophic DE and CH estuaries were dissimilar to the PO and NE. The DE was consistently the most dissimilar overall to the other estuaries. The PO and NE had lower bacterioplankton community diversity and the most similar community composition. The DE was the most diverse with the CH between. Many of the specific OTUs identified (at the Order/Family level) in the DE were unique and the DE had higher relative abundance of Archaea OTUs than any of the other estuaries.