Bacteria Form Distinct Ecological Groups That May Impact Nutrient Cycling and Dead Zone Formation in the Chesapeake Bay

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Abstract

The Chesapeake Bay is vital habitat for numerous fish and invertebrate species but is subject to anoxic conditions and dead zone formation during the summer that can result in mass mortalities of these organisms. The development of these dead zones is intimately tied to bacterial metabolism and nutrient cycling, fueled largely by nitrogen and phosphorous pollution. High-resolution characterizations of the spatiotemporal distributions of bacterial communities can help to delineate their role in nutrient cycling and dead zone formation in the Bay. In this study, bacterial communities were characterized by 16S rRNA amplification and sequencing at a single site in the Chesapeake Bay known to experience anoxia in the summer. Water samples were collected at 1m intervals from surface to bottom in June, July, and August 2015 to capture bacterial communities before and during anoxia formation. To determine the factors that shape bacterial community structure, we also measured water chemistry to compare community structure to chemical concentrations and physical parameters. Overall, bacterial communities segregated by sample month and depth and formed 11 clusters by hierarchical clustering (4 June clustes, 3 July clusters, 4 August clusters). The most abundant OTUs were widely distributed across samples, present in all 11 clusters at varying abundances. To identify patterns shaping organism distribution, we found four groups defined by OTUs with correlated relative abundance profiles, suggesting these OTUs may be interacting or influenced by the same environmental conditions. One group consisted of OTUs that were associated with all 4 June clusters where dissolved oxygen remained above 2 mg/L (hypoxy). Two groups were associated with the oxygenated waters in the upper two July and August clusters, respectively, while one group was most abundant in July and August anoxic water clusters. Association with environmental parameters was also reflected in predicted gene content of OTU groups, suggesting their important role in biogeochemical cycling. Ultimately, understanding the impact of specific OTU interactions on community distribution, metabolism, and dead zone development will be crucial to developing better models of dead zone formation and strategies to mitigate their impact in the Chesapeake Bay.

Introduction

The Chesapeake Bay is the largest estuary in the United States and vital habitat to over 3,600 native species. Degradation of algal biomass by bacteria reduces dissolved oxygen levels in the water, which can result in high mortality levels for aquatic species (Fig. 1).

The Chesapeake Bay displays oxygen (Fig. 2A) and salinity (Fig. 2B) stratification during the summer. Stratified lakes can display distinct bacterial communities between layers. However, bacterial communities are poorly represented in models simulating hydrodynamic and biogeochemical processes during Chesapeake Bay dead zone formation. This study sought to characterize bacterial communities prior to and during dead zone formation to better understand how bacterial communities impact biogeochemical cycling and dead zone formation in the Chesapeake Bay.

Fig. 1. Dissolved oxygen levels in the Chesapeake Bay during the summer of 2005. Source: Chesapeake Bay Foundation.

Fig. 2. Dissolved oxygen and salinity gradients in the Chesapeake Bay. A) Dissolved oxygen gradient in the Chesapeake Bay from June 2015 to August 2015. Measurements were taken at the sample site. B) Depth profile of salinity at the sample site in July 2015.

Materials and Methods

Collect water at 1m intervals from surface to bottom in June, July, and August 2015

Isolate bacterial DNA and amplify the 16S rRNA gene

Sequence 16S rRNA amplicons on the Illumina MiSeq

Characterize water chemistry

Perform community analyses in QIIME

Pick operational taxonomic units (OTUs) by Cluster Free Filtering (2)

Ecological Groups are Associated with Different Physiochemical Variables and May Impact Biogeochemical Cycling

Fig. 5 Mean OTU correlations with measured physicochemical variables within each ecological group. Temp.; Temperature, Cond.; Conductivity, ORP; Oxidation-Reduction Potential, DO; Dissolved Oxygen.

Different Predicted Metabolic Potentials Between Ecological Groups May Impact Nutrient Cycles

Fig. 6. Predicted gene and corresponding pathway abundances for nitrogen and sulfur metabolism in each ecological group. Metabolic predictions were made with PICRUSt (4) based on taxonomic composition.

Conclusions

The Chesapeake Bay experiences dead zone formation during the summer months that produces oxygen and salinity stratification within the water column (Fig. 2). However, an abundant core bacterial community was present throughout the water column prior to and during anoxia formation (Fig. 3), suggesting mixing between water layers. More work is needed to understand how mixing within the water column impacts biogeochemical cycling. Bacterial communities formed ecological groups (Fig. 4) that were often more strongly associated with physiochemical variables other than dissolved oxygen and salinity, including the presence of nitrogen and sulfur electron acceptors (Fig. 5). Different metabolic potentials, including nitrogen and sulfur reduction, were also predicted between ecological groups (Fig. 6). This suggests that mechanical mixing of water and water chemistry may play a more important role in bacterial community composition than physical stratification in the Chesapeake Bay.

Linking individual community members to specific metabolic pathways by shotgun metagenomics will be crucial to improving modeling efforts of biogeochemical processes in the Chesapeake Bay during dead zone formation.

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References

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