

DEPARTMENT OF CHEMISTRY AND ENVIRONMENTAL SCIENCE
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1:00PM-2:20PM

GUEST SPEAKER

Dr. Sarah P. Preheim
Associate Professor
Environmental Health and Engineering
Johns Hopkins University

TOPIC

Major trends and environmental correlates of spatiotemporal shifts in the distribution of genes compared to a biogeochemical model simulation in the Chesapeake Bay

ABSTRACT

The Chesapeake Bay is an important ecosystem, characterized as a national treasure by President Obama in 2009. Efforts to protect this important ecosystem have resulted in some improvements to hypoxic volume, a key indicator of ecosystem health, but more work is needed to better understand environmental factors impacting oxygen. Nutrient reductions have resulted in less hypoxia (oxygen concentrations < 62.5 mM) and stronger resilience to the impacts of climate change. However, the hypoxic volume generated per unit nitrogen doubled between 1965-1980 and 1985-2007. Although causes for this change may include increased stratification and changes in wind direction, increases in ammonia and phosphate released from sediments likely play a major role. This release and subsequent fate of ammonia, whether it was denitrified or used to fuel additional phytoplankton growth, partially depend on microbial processes, such as nitrification, denitrification and nutrient uptake rates. Thus, microbial processes could be the key to understand how changes in nitrogen levels will impact oxygen concentrations long-term. We used DNA sequencing of water samples (metagenomics) from the Chesapeake Bay at multiple sites, depths, and times of year to identify the most abundant populations and genes in the Bay. Our metagenomic analysis suggests that springtime denitrification, and summertime autotrophic denitrification and nitrogen fixation could be important but under-appreciated nitrogen cycle

pathways in the Chesapeake Bay. We also found genes involved in these processes to be persistent and active, as they were found in a meta-transcriptomic dataset at one site within the

Bay made several years before our study. We compared our results to a biogeochemical model of the Bay to identify similarities and large discrepancies. We found that sulfide oxidizing organisms with genes for denitrification are strongly associated with hypoxia and transcriptionally active in low oxygen environments. Denitrification genes are abundant and expressed in oxic waters in the spring. We hypothesize microenvironments on particles provide low oxygen conditions favoring denitrifying organisms under high oxygen conditions. Nitrogen fixation genes were found and expressed in deep, hypoxic or anoxic water with relative abundance highly correlated with phosphate. Building on this data, we hypothesize that these processes are important sources and sinks of nitrogen that may explain changes to the total hypoxic volume generated per unit nitrogen and may impact predictions of oxygen concentrations in long-term forecasts.

BIO



Sarah Preheim

Associate Professor

Johns Hopkins University

The Preheim Lab seeks to understand the microbial processes impacting water quality to aid remediation efforts and protect the environment and public health. She has expertise in microbial ecology and bioinformatics and uses computational techniques to develop a mechanistic understanding of microbial community structure and function.

Dr. Preheim received her PhD from a Joint Program with Woods Hole Oceanographic Institution and Massachusetts Institute of Technology (MIT) in Biological Oceanography and did a postdoc in the Biological Engineering Department at MIT. She has been faculty in the Environmental Health and Engineering Department at Johns Hopkins University since 2015.

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