



## FALL 2017 SEMINAR SERIES

DEPARTMENT OF OCEAN, EARTH, AND ATMOSPHERIC SCIENCES

3:00 PM – ROOM 200 IN THE OCEANOGRAPHY/PHYSICS BUILDING

THURSDAY, OCTOBER 12, 2017

### **Dynamics of Microbial Populations and Biogeochemical Processes in Aquatic Dead-Zones**

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Run-off from agricultural and urban areas pollutes many water bodies in the US, such as in the Chesapeake Bay, creating oxygen-free (anoxic) or reduced oxygen (hypoxic) dead-zones. This deteriorates the habitat of many aquatic animals and drives microbial processes that alter nutrient cycling and generate potent greenhouse gases, such as methane and nitrous oxide. Understanding the dynamic chemical and microbial changes that occur in dead-zones are vital to improving computational modeling efforts that guide remediation strategies. To investigate the relationship between microbial genes and biogeochemical model predictions, we began with a simple aquatic ecosystem, Upper Mystic Lake. Samples were collected approximately every meter from the surface to 22 meters depth from spring to summer in 2013. The distribution in the water column of genes known to be involved biogeochemical processes was explained by biogeochemical process rates predicted by the model, suggesting genes may be a useful proxy for biogeochemical rates under certain circumstances. By looking at co-occurrence patterns of dominant microbes and reconstructing microbial genomes from complex assemblages of microorganisms, we identified additional biogeochemical processes that, if active, would significantly alter the predicted biogeochemistry of the lake. We are also investigating the relationship between microbes, their genes and model predictions in a more complex ecosystem, the Chesapeake Bay. Samples were collected in the Chesapeake Bay at one site for monthly for 3 months during the period of anoxia from 2015-2017. We also collected water samples from the bottom of the Bay throughout the dead-zone in 2016 and 2017. By analyzing the microbial community within the water samples, we found that many microorganisms are present throughout

the water column, but that their relative abundance changes based on chemistry and oxygen. We also found genes involved in anoxic processes are more abundant in the water column where oxygen is depleted. We will analyze whether microbial activity, assessed through gene transcription, is more informative than gene abundance in complex ecosystems like the Chesapeake Bay. We will also use genome reconstruction to identify biogeochemical processes not currently included in models and assess whether including them would significantly change predictions of dead-zone biogeochemistry. With these observations, we hope to improve predictions of how size and duration of the dead-zone will respond to environmental changes.

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