

# 12<sup>TH</sup> U.S. SYMPOSIUM ON HARMFUL ALGAE

## TRANSCRIPTOMIC INSIGHTS INTO MARGALEFIDINIUM POLYKRIKOIDES BLOOMS ACROSS VARYING NUTRIENT, SALINITY, TEMPERATURE, LIGHT, AND PHYTOPLANKTON COMMUNITY DIVERSITY REGIMES

### SESSION: POSTER SESSION, TUESDAY

**ABSTRACT:** In the lower Chesapeake Bay and its tributaries, blooms of the harmful dinoflagellate *Margalefinidium* (previously *Cochlodinium*) *polykrikoides* are observed almost annually. Live populations of *M. polykrikoides* have been shown to increase larval shellfish and finfish mortality. *M. polykrikoides* is a mixotroph known to graze on smaller plankton and take up organic compounds. Modeling studies of *M. polykrikoides* blooms in the Lafayette River have suggested that heterotrophic growth is required to reach the high cell abundances observed during blooms that coincide with nutrient depleted conditions. However, mixotrophic growth is notoriously difficult to measure in field populations. Studying the expression of genes related to mixotrophy (those associated with photoautotrophy, phagotrophy, and osmotrophy) via a transcriptomic approach can provide insight into when and under what conditions *M. polykrikoides* employs its heterotrophic capabilities.

The purpose of this study was to investigate the relationships between nutrient concentrations, salinity, temperature, and phytoplankton community composition and the up- and down-regulation of gene expression related to a mixotrophic metabolism. During the months of July and August of 2021 and 2022, molecular samples were collected during *M. polykrikoides* blooms from the Lafayette River, Norfolk, VA at mid-day and mid-night from the surface or chlorophyll max depth. Nutrient concentrations, salinity, temperature, and phytoplankton community composition were measured in concurrently collected samples. Extracted RNA was QC checked using Qubit fluorometry and Agilent Bioanalyzer before CLONTECH library preparation and sequencing on an Aviti Element Sequencer. Sequences were used for de novo transcriptome assembly and read mapping against existing *M. polykrikoides* transcriptomes. We hypothesize that genes associated with heterotrophic metabolism will be upregulated when there are low nutrients, high temperatures, and at night when it is dark.

**SPEAKER:** Katherine Crider, Old Dominion University | [kcrid001@odu.edu](mailto:kcrid001@odu.edu)

**SPEAKER BIO:** Katherine (Katie) Crider is a PhD candidate in the Oceanography program at Old Dominion University's Department of Ocean & Earth Sciences. She received her MS in Ocean & Earth Sciences in 2022 from ODU, and her BS in Biology from James Madison University in 2020. At JMU, Katie conducted co-culture experiments in the Steffen/Wurch lab studying microbial interactions in *Microcystis aeruginosa* and *Aureococcus anophagefferens* grown with their associated bacteria. At ODU, Katie was a member of the Chappell Marine Molecular Ecology Laboratory and is currently a member of the Mulholland Nitrogen & Carbon Biogeochemistry Laboratory. Katie's dissertation focuses on the understudied processes of nitrogen fixation and mixotrophy in coastal ocean and estuarine environments, including the Outer Banks, North Carolina and the lower Chesapeake Bay, Virginia, respectively. Her research specifically investigates the variability of nitrogen fixation rates and cyanobacterial diazotroph community abundance, and the metabolic shifts between photoautotrophic and heterotrophic metabolisms in the harmful bloom species *Margalefidinium polykrikoides* across the life of a bloom and changing nutrient, temperature, light, and community regimes. Katie is also employed at General Dynamics Information Technology (GDIT) as a Scientist conducting data curation and quality assessment under an Environmental Protection Agency (EPA) contract for the Great Lakes National Program Office (GLNPO).

### CO-AUTHORS:

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