PROGRESSING FROM EXPLORATORY STUDIES TO HYPOTHESIS TESTING

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Harnessing the power of -omics tools to
understand cyanobacterial harmful algal blooms

The -omics haven't just revolutionized our understanding of the breadth of the microbial biodiversity of our planet, but they've also pushed many fields toward a more comprehensive and holistic approach to biological questions. Rather than a traditional, reductionist approach studying a single model organism, the -omics have helped us recognize that biological interactions are the foundation of biodiversity and even ecosystem function. We've seen this shift in research on cyanobacteria in the last few years, with a renewed focus on interactions between cyanobacteria and the members of their broader microbial community that span all three domains of life (and viruses).

My talk will focus on how we can apply the various -omics tools to our research questions about cyanobacteria in the context of interactions and exchanges that occur between microbes in cyanobacterial harmful algal blooms. These exchanges leave molecular signals in the expression profiles of the participants. We can use these signals as clues in -omics style data to deconstruct the physiological mechanisms that shape community dynamics in the various cHAB communities. In my lab, we've transitioned from using an exploratory approach, using genomics and transcriptomics to generate hypotheses about bloom communities to testing those hypotheses both in the field and in the lab. I'll share examples that range from genome sequencing of individual constituents of bloom microbiomes, to co-culture expression studies, to experiments in field populations to highlight the various ways the -omics have allowed us to grow our understanding of bloom dynamics. These data can eventually be harnessed to develop a more comprehensive suite of mitigations strategies that consider both biotic and abiotic drivers of cyanobacterial harmful algal blooms.