

3) One-page abstract/project summary

ECOHAB: Resolving the effects of resource availability, predation, and competition on brown tide dynamics via metatranscriptomics

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Total proposed cost: \$723,870

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Abstract: *Aureococcus anophagefferens* is a pelagophyte that causes harmful brown tides that have decimated multiple fisheries and seagrass beds in mid-Atlantic US estuaries for three decades. The recent sequencing of the *Aureococcus* genome, combined with comparative genomic studies, *in situ* ecosystem observations, and experimental studies have collectively evidenced the importance of multiple bottom-up and top-down controls of brown tides. While advances have been made in understanding how nitrogen impacts the occurrence of brown tides, the relative importance of other factors that strongly influence the onset of these HABs is unclear. Taking advantage of the *Aureococcus* genome sequence, on-going gene expression studies by the PIs, and advances in both high throughput sequencing and informatics technology, we propose a combined field and laboratory study using eco-transcriptomics to address the question: ***what are the precise environmental factors that drive the initiation, persistence, and demise of brown tides?*** We will generate transcriptomes (global gene expression patterns) for *Aureococcus* cultures exposed to a suite of environmentally conditions relevant to bloom formation including growth on multiple sources of organic matter, exposure to multiple types of zooplankton, selenium limitation, and ideal conditions. These transcriptomes will be used in conjunction with others the PIs have generated during prior projects (low nitrogen, low phosphorus, low light) to define precise transcriptomic signatures elicited by these factors. In the field, we will perform metatranscriptomic profiling of *Aureococcus* and competing phytoplankton populations in a chronically brown tide-prone embayment during the initiation, persistence, and decline of blooms while concurrently measuring pertinent environmental variables. We will perform incubation experiments during which we will perturb existing environmental conditions (nutrients, organic matter, light, grazing) to affirm factors that drive patterns of gene expression in, and dominance among, *Aureococcus* and competing phytoplankton species. The ability to quantitatively compare the specific transcriptomic profile of *Aureococcus* under multiple controlled laboratory conditions to the profiles of brown tides as they develop will identify the environmental factors that have the strongest influence on the growth and physiology of *Aureococcus* and competing phytoplankton during blooms. Assessing environmental conditions in concert with meta-transcriptomes over the course of brown tides will be the crux of our eco-transcriptomic approach: linking of expression of genes by a HAB and competing phytoplankton to specific environmental conditions to define the precise niche of each algal species. This approach will, therefore, provide a comprehensive understanding of the interaction of brown tides and their environment. Since most of the environmental conditions we will explore have been anthropogenically created (e.g. high N, high P, high organic matter, high metals, low light), our findings will support managerial actions to ameliorate blooms via the improvement of specific environmental conditions. Towards this end, we will host local and regional workshops with managers from NY State and the mid-Atlantic region to communicate the results of this project with the ultimate goal of providing information regarding environmental conditions that should be improved to manage and mitigate brown tides.