

2022 DELTA SCIENCE FELLOW **FINAL REPORT**



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Focus

Identifying environmental conditions driving cyanobacterial multi-species blooms and their toxicity using genome resolved metagenomics

Award \$241,410

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“Exploring the intricate dance of microbial diversity in the Sacramento-San Joaquin Delta not only deepens our understanding of nature but reveals the profound connections between evolving environmental conditions and the emergence of novel cyanotoxins.”

PROJECT

Cyanobacterial Harmful Algal Blooms (cyanoHABS) occur when water conditions foster the growth of algal species that can produce toxins. Recently, there have been more algae in blooms in the Sacramento-San Joaquin Delta, as well as more varied cyanoHABS. Scientists don't yet know what is causing the expanded blooms or how the increased diversity will impact the spread of toxins.

In this study, researchers collected monthly samples of cyanobacteria and co-occurring bacteria in the central and south Delta over eight months in 2023. They analyzed the complete genomes of each species to identify which cyanobacteria are producing toxins and performing other important functions. To confirm actual toxin production, they also used chemical analysis techniques.

RESEARCH CONCLUSIONS

The samples revealed that bloom development in the Delta is a complex process; varied cyanobacterial taxa appear simultaneously, with no single species consistently dominating. Importantly, while one genus, *Microcystis*, is typically considered the dominant harmful cyanobacterium in the region, this research noted the presence of other taxa.

One taxon, *Aphanizomenon/Dolichospermum*, was found to possess genes required to biosynthesize compounds that impart an unpleasant taste to drinking water, which consumers perceive as a sign of poor water quality. Another taxon, *Planktothrix*, was found to produce compounds whose effects on the environment are unknown. A single sample from Discovery Bay included 21 cyanobacterial genomes that contained gene clusters similar to those known to facilitate the production of bioactive compounds; other, as yet understudied gene clusters also appear capable of producing novel, potentially harmful compounds. These results indicate a need to broaden current monitoring practices to include a wider range of harmful cyanobacterial species.

