Mapping genetic variation in *Microcystis* to improve Great Lakes harmful algal bloom models

CORE QUESTION:
How do genetic differences influence *Microcystis*' ability to survive predators in harmful algal blooms?

A BLOOMING PROBLEM

In Lake Erie, Saginaw Bay, and other areas of the Great Lakes, harmful algal blooms (HABs) have become an annual challenge. HABs are population explosions of microscopic organisms called cyanobacteria, which can generate toxins that threaten recreation, ecosystem health, and drinking water supplies.

A genetically diverse species called *Microcystis* typically dominates Great Lakes HABs. *Microcystis* has many traits that help free-floating cells and colonies get nutrients and defend against predators. However, a genetic advantage against one kind of predator may come with a trade-off or vulnerability toward another. This suggests that *Microcystis* with different genotypes, or genetic profiles, may play different roles within the food web.

Understanding the implications of diverse *Microcystis* genotypes could help shape better strategies for predicting, tracking, and assessing the effects of HABs in the Great Lakes.

MAKING A MICROCYSTIS MAP

Vincent Denef, an associate professor in the Department of Ecology and Evolutionary Biology at the University of Michigan, and Melissa Duhaime, an assistant professor in the same department, are leading a project that will link *Microcystis* genetic variation with its ability to defend against predators and viruses. Denef and his team will focus on two predators that play major roles in Great Lakes food webs: filter-feeding quagga mussels and zooplankton *Daphnia*. They will introduce these predators to *Microcystis* samples taken from Lake Erie. Then they will map genotypes of *Microcystis* populations against their traits for resistance or vulnerability toward predation. Duhaime's team will focus on genetic analysis that will give insights into *Microcystis*' ability to withstand viruses.

The team will also study the *Microcystis* microbiome, or the community of bacteria that live alongside *Microcystis* cells and colonies, to gauge how the microbiome affects survival against predation.

Incorporating these insights into decision-making models could help improve HABs predictions and tracking, as well as illuminating the effects of *Microcystis* on Great Lakes food webs.

CONTACT

PRINCIPAL INVESTIGATOR

Vincent Denef
Associate Professor, Department of Ecology and Evolutionary Biology, University of Michigan
vdenef@umich.edu

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