

Land use and Environmental Drivers of Harmful Algal Bloom Formation and Cyanotoxin Production to Inform Lake Management Practices

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INTRODUCTION

- Formation of toxic cyanobacteria harmful algal blooms (cHABs) are difficult to predict due to complex dynamics
- Factors that influence cyanobacteria biovolume: water temp, TP, N:P ratio - cyanobacteria genera respond differently to environmental drivers
- How has cyanobacteria community and toxicity changed over time in sample lakes? How do these changes relate to land use and environmental drivers?

SAMPLE SITES

- Sampled 6 inland MN Sentinel Lakes (White Iron, Tait, Portage, Hill, Carrie, Peltier)
- Various latitude, land use, watershed characteristics and lake morphometry (FIG 1)

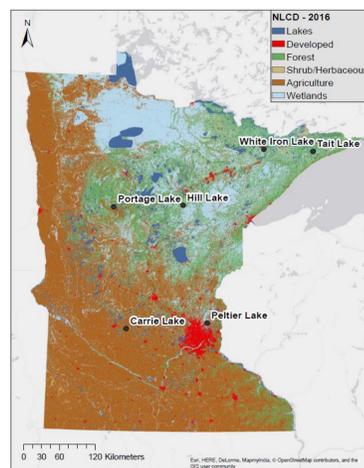


FIG 1. Land use of sample lakes (lakes, developed, forest, shrub/herbaceous, agriculture, wetlands)

METHODS

- Conducted biweekly ecological surveys from June – Oct.
- Collected water samples (FIG 2) for nutrients, phytoplankton counts, limnology data, pigments, and genomic analyses
- Further genomic analyses conducted on Peltier Lk, *Dolichospermum sp.* and *Microcystis sp.* genomes analyzed for Microcystin toxin genes, chosen based on dominate genera present from phytoplankton counts



FIG 2. (A) Peltier Lk 9/10/2020; (B, C) Peltier Lk 8/19/2021

RESULTS

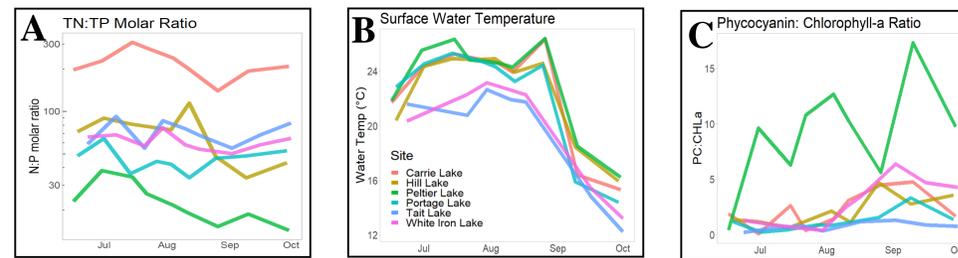


FIG 3. (A) Total nitrogen: total phosphorus molar ratio (log transformed y-axis); (B) Surface water temperature (°C); (C) Phycocyanin: Chlorophyll-a ratio (PC: Chla)

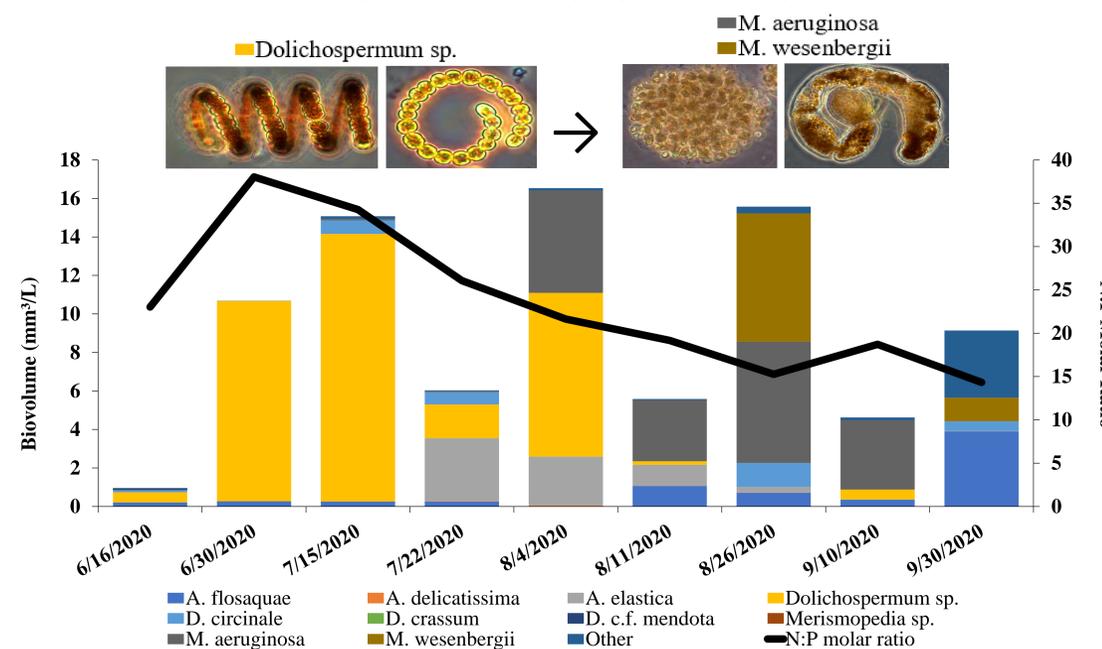


FIG 4. Peltier Lk cyanobacteria species biovolume (mm³/L) based on phytoplankton counts across 9 sample rounds; N:P molar ratio (black line). *Other* category includes: Pseudanabaena spp, Woronichinia spp, Planktothrix sp, Synechococcus sp, Oscillatoria sp. Phytoplankton counts of remaining lakes - in progress.

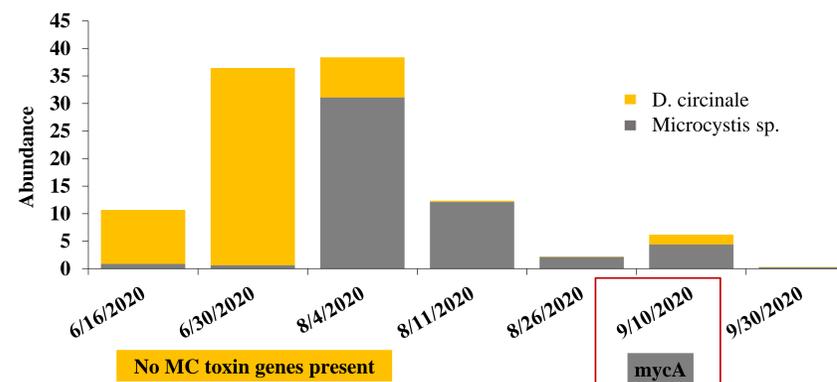


FIG 5. Peltier Lk cyanobacteria species abundances based on Metagenome Assembled Genomes across 7 sample rounds (incomplete analyses for 7/15/20 & 7/22/20), *D. circinale* and *Microcystis sp.* genomes analyzed for Microcystin (*mcxA*) toxin gene.

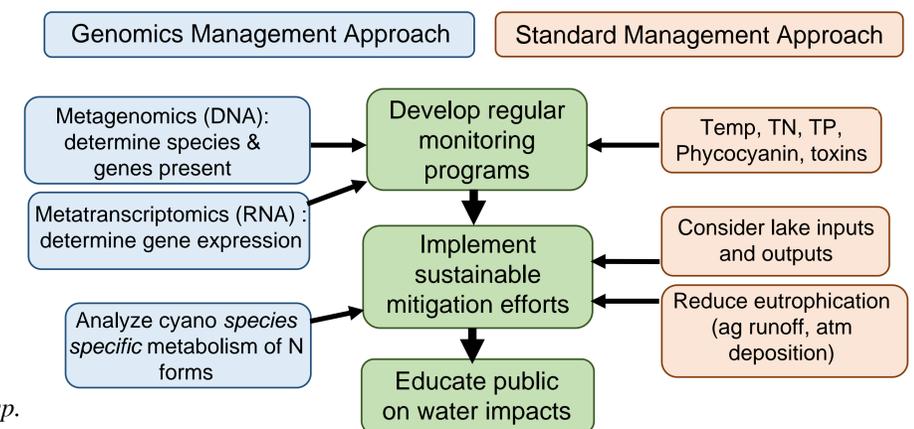
RESULTS

- N:P molar ratio highest in Carrie Lk; lowest in Peltier Lk (FIG 3A)
- Surface water temperature unimodal shaped, highest temperature in southern lakes (FIG 3B)
- PC: Chla ratio greatest in Peltier Lk, high ratio indicates phytoplankton community dominated by cyanobacteria (FIG 3C), further analyzed Peltier Lk
- Shift from N-fixing (*Dolichospermum sp.*) to non-N-fixing (*Microcystis sp.*) cyanobacteria in Peltier Lk (FIG 4)
- No toxin genes present in *D. circinale* genome, *mcxA* gene present in *Microcystin sp.* genome during 9/10/20 sample event (FIG 5)

DISCUSSION

- Bloom species composition and biovolume varies across time
- N-fixers dominant during high N condition, not as anticipated because of *Dolichospermum sp.* ability to fix atmospheric N during N limitation
- Cyano community does not follow nutrient limitation expectations because: (1) we do not have complete understanding of metabolic N demands (species specific N uptake), or (2) other factors influencing late season community composition, such as water temperature
- *D. circinale* genome not toxic, *Microcystis sp.* genome able to produce toxins
 - conducting further genomic analyses of *Microcystis sp.* genome
 - Metatranscriptomic analyses – in progress
- Results suggest that surrounding land use, temperature, and nutrient dynamics contribute to cyanobacteria community composition and toxicity of cHABs

MANAGEMENT PRACTICES



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