Phylogeny of Microcystin-Producing Cyanobacteria in Lake Menomin

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OVERVIEW

Habitat: We are studying cyanobacteria that cause green algal blooms in phosphorus-polluted Lake Menomin. Farmland runoff within the Red Cedar Watershed (**Fig. 1**) results in a high phosphorus content, ideal for cyanobacterial growth.

Problem: The resulting algal blooms produce the hepatotoxin microcystin which can be harmful to humans.

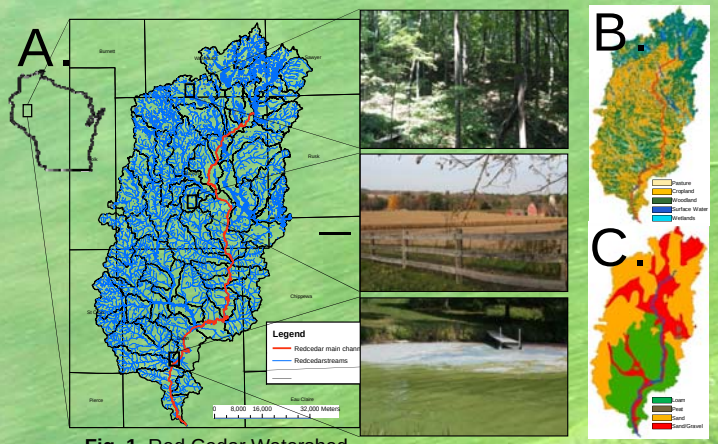

Fig. 1. Red Cedar Watershed

METHODS

Collect water column samples (Fig. 1) → Isolate genomic DNA → Amplify genes using the PCR → Clone, and purify DNA, obtain sequence data → Compile and analyze sequences → Determine closest relatives in GenBank

Assemble phylogenetic trees (Figs. 2, 3, 4, 5)

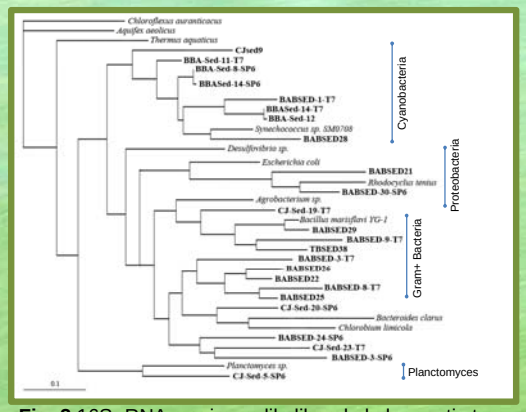

Fig. 2 16S rRNA maximum likelihood phylogenetic tree based on nucleotides from **sediment** clone sequences

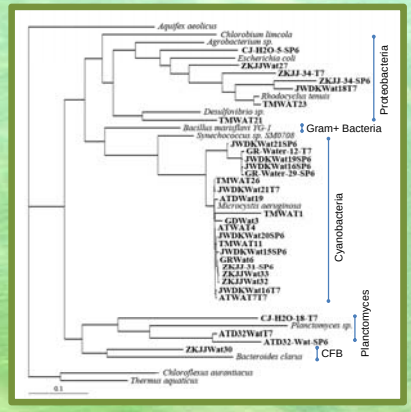

Fig. 3 16S rRNA maximum likelihood phylogenetic tree based on nucleotides from **water** clone sequences

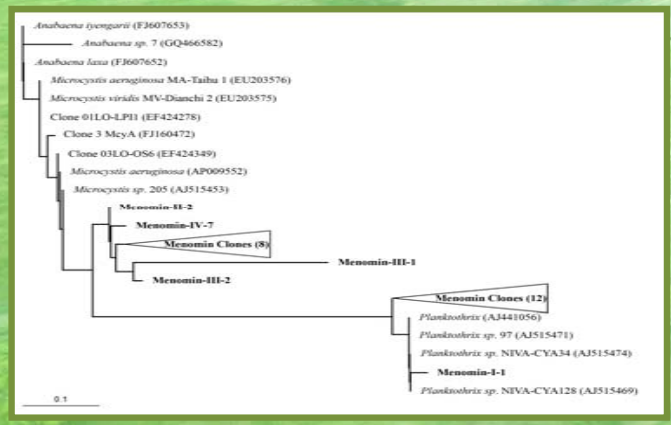

Fig. 4. Microcystin synthetase gene A maximum likelihood phylogenetic tree based on amino acid sequences.

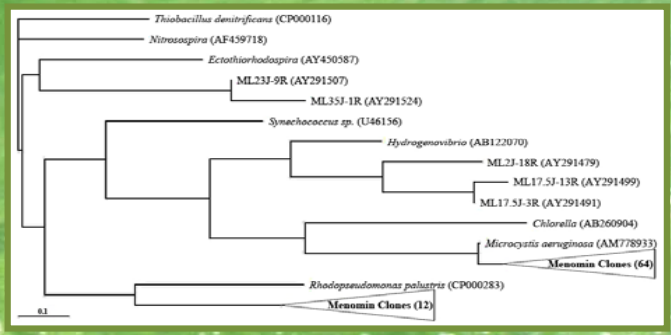

Fig. 5. Ribulose-1,5-bisphosphate carboxylase oxygenase maximum likelihood phylogenetic tree based on amino acid sequences.

CONCLUSIONS

- Sediment microbial diversity appears greater than the water column, which is dominated by *Microcystis aeruginosa* (**Figs. 2,3**).
- Functional genes confirm 16S rRNA data, suggesting *Microcystis aeruginosa* dominates the microcystin synthesis (**Fig. 4**) and carbon fixation (**Fig. 5**) functional guilds.

References

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- Frangeul *et al. BMC Genomics* 2008, **9**:274
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