



Genetic variation of the noxious cyanobacterium, *Microcystis aeruginosa*, within and among lakes: implications for harmful algal blooms.

Abstract

Harmful algal blooms endanger aquatic and marine systems across the globe, however a thorough understanding of the genetic composition of harmful algal species both among and, especially, within water bodies is lacking. To better predict future HAB events, we suggest that more studies should determine the genetic diversity of natural populations of harmful algal bloom species in space and time and use these data in existing models.

In this study, we show that isolate survivorship of the noxious cyanobacterium, *Microcystis aeruginosa*, from lakes that range in productivity (total phosphorus concentrations $\approx 10 - 100 \text{ ug L}^{-1}$) is typically low (i.e., mean = 7% and maximum = 30%) and is positively related to total phosphorus concentration ($P = 0.012$, $R^2 = 0.424$, $N = 14$). Additionally, individual colonies of *M. aeruginosa* collected from an oligotrophic lake (total phosphorus $\approx 20 \text{ ug L}^{-1}$ and DIN:TP ratio = 12.75), Gull Lake (Kalamazoo County, Michigan), exhibited substantially higher survival (WC media types vs BG media types; $P < 0.000$) in less-rich algal media with a higher N:P ratio (28 – 37 % survival) than lower N:P ratio media (0 – 4% survival).

Even with relatively low isolate survivorship, most populations of *M. aeruginosa* were shown to be genetically diverse with most clones being distantly related to clones collected from lakes directly attached to the Laurentian Great Lake, Lake Michigan, and culture collection strains collected from Canada, Scotland, and South Africa. Additionally, analysis of molecular variance (AMOVA) indicated that within-lake genetic variation (70%) was significantly greater than the among-lake variation (30%) for the *M. aeruginosa* populations ($\Phi_{pt} = 0.283$; $P < 0.001$). Subsequently, 93% of the *M. aeruginosa* clones contained the microcystin toxin gene (*mcyA*), however five clones from four lakes lacked the toxin gene. Thus, four of the *M. aeruginosa* populations were comprised of mixed assemblages containing clones that both lacked or contained the toxin gene. If microcystins are considered to be grazing deterrents, our population genetic data suggest that natural selection toward grazing resistant *M. aeruginosa* strains is possible in these habitats given the high genetic variability observed in these water bodies. Additionally, such genetic variation at the local and regional scale could aid in explaining conflicting results regarding important ecological phenomena, such as, dramatic seasonal variation in toxin content of lakes and the response of *M. aeruginosa* to the invasive bivalve, *Dreissena polymorpha*.

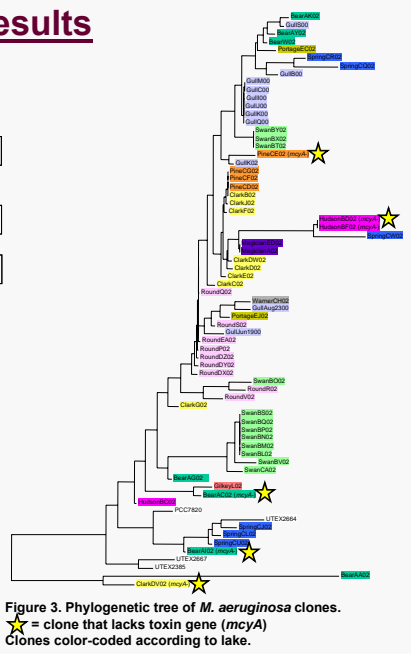
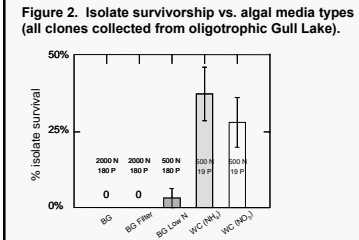
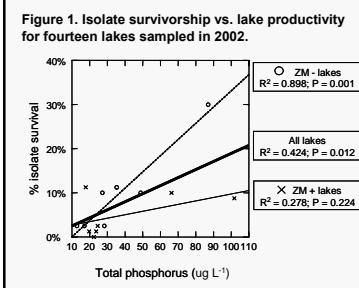
Questions

- In this project, we addressed the following questions.
- (1) Do phytoplankter isolate survival rates relate to lake total phosphorus concentration?
 - (1) Are populations of *M. aeruginosa* comprised of one or many genotypes within and among lakes?
 - (3) If within-population genetic variation exists for *M. aeruginosa*, do sympatric genotypes vary in the presence of the microcystin producing gene (*mcyA*)?
 - (4) Does the presence of the zebra mussel (*Dreissena polymorpha*) affect any of the above relationships?

Methods

During the summers of 2000 and 2002, fourteen lakes that varied in phosphorus content were sampled for *M. aeruginosa* with a standard 100um mesh zooplankton net. Samples were returned to the lab where individual *M. aeruginosa* colonies were isolated, rinsed, and inoculated into sterile test tubes filled with algal medium. Isolates were monitored for several months to determine isolate survivorship. Survivorship was shown to be positively correlated with lake phosphorus concentration (Fig. 1). Thus, additional isolates from an oligotrophic lake were inoculated into five different media that varied in nitrogen and phosphorus content to determine if these clones would fare better in less rich media (Fig. 2). Once clones were established in the lab, samples from each clone were lyophilized and analyzed via HIP-PCR (highly iterated palindromic polymerase chain reaction) to differentiate among distinct genotypes. To create the phylogenetic tree (Fig. 3), the banding patterns produced by the respective HIPCA and HIPCT PCRs were scored for the presence/absence of bands in 20 discrete positions for all samples and these scores were analyzed via BANDAIID (Tim Salmon – UNSW). The clones were also analyzed for the presence/absence of the microcystin toxin gene (*mcyA*) using specific *mcyA* primers.

Results



Results

AMOVA data output for population genetic comparisons of *M. aeruginosa* clones from nine of the fourteen study lakes. In the analysis, only unique genotypes from each lake (i.e., no duplicate genotypes were included) and clones from the 2000 and 2002 collections were included. P-values below diagonal. P-values based on 999 permutations above diagonal. Φ_{pt} values below diagonal. P-values < 0.05 bolded and in red.

Source	df	SS	MS	Estimated variance	% variance explained	Φ_{pt} value	P-value
Among Pops.	8	46.122	5.765	0.745	30%	0.298	0.001
Within Pops.	41	71.998	1.756	1.756	70%		

	Bear	Clark	Gull	Hudson	Pine	Portage	Round	Spring	Swan
Bear	-	0.008	0.006	0.475	0.379	0.509	0.001	0.348	0.006
Clark	0.237	-	0.005	0.231	0.235	0.252	0.001	0.011	0.003
Gull	0.211	0.261	-	0.023	0.047	0.068	0.001	0.014	0.003
Hudson	0.000	0.075	0.299	-	0.348	0.338	0.022	0.366	0.102
Pine	0.039	0.000	0.304	0.000	-	0.661	0.001	0.306	0.031
Portage	0.000	0.059	0.304	0.000	0.000	-	0.036	0.334	0.105
Round	0.528	0.355	0.564	0.543	0.591	0.557	-	0.002	0.002
Spring	0.011	0.296	0.305	0.001	0.114	0.000	0.475	-	0.045
Swan	0.263	0.364	0.461	0.247	0.406	0.363	0.611	0.240	-

Summary

Survivorship of *M. aeruginosa* isolates from a suite of lakes throughout southern Michigan was positively related to total phosphorus content. Additionally, isolates from an oligotrophic lake exhibited greater survivorship in less rich media (lower phosphorus content) vs. more rich media.

Although overall isolate survivorship was relatively low (7% average), we found huge genetic diversity within and among populations of *M. aeruginosa*. Also, four populations contained sympatric clones that lacked or contained the microcystin toxin gene (*mcyA*).

Thus, lake managers should not assume that harmful algal bloom species are genetically homogenous. Instead managers should understand that algal populations maintain incredible levels of genetic diversity and this information should be considered when deciding on bloom prevention, identification, and mitigation plans.

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