

Exploration of Freshwater Cyanobacteria

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Abstract

Introduction: Various species of single-celled cyanobacteria have the capability to proliferate and aggregate into large masses known as harmful algal blooms (HABs). In some cases, the species that constitute these HABs produce cyclic hepatotoxins, which have been linked to human illness, tumor promotion and even death¹. HABs have detrimental effects on environments and economies as they cause bodies of water to become anoxic and toxic, resulting in losses of biodiversity and billions of dollars in revenue^{3,2}. Anthropogenic sources of phosphorus and nitrogen are a major cause of these blooms². This study focused on the major HAB forming species present in Lake Erie, *Microcystis aeruginosa*. In parallel we also looked for the presence of the marine cyanobacteria *Prochlorococcus* in various samples from Lake Erie since previous studies have suggested it might be present. **Methods:** To discover how HAB forming species proliferate through the metabolism of the anthropogenic nitrogen source urea, a series of molecular techniques (DNA extraction, polymerase chain reaction amplification, gel electrophoresis, and plasmid vector cloning for sequencing) were used. **Results/Conclusion:** This study confirmed both the specificity of *Microcystis* specific *ure-C* primers and the ability of universal *ure-C* primers to amplify the *ure-C* gene in *Microcystis*. This discovery allows these primers to now be used when testing environmental samples for *Microcystis* or other urea metabolizing cyanobacteria. The specificity of the *Prochlorococcus* specific primers was refuted due to their amplification of *Synechococcus*, suggesting that *Prochlorococcus* may not be present in Lake Erie as previously thought. The results from this study will allow for future research in identifying and quantifying freshwater cyanobacteria.

Keywords: Cyanobacteria, Primers, *Prochlorococcus*, *Microcystis aeruginosa*, Harmful Algal Blooms, *ure-C*

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