Case Studies: Application of DNA-based tools for cyanobacterial monitoring

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Abstract

Cyanobacterial blooms are a common feature in many North American lakes and reservoirs during the summer and fall months. Many monitoring programs utilize a tiered management approach whereby potentially toxic cyanobacterial cells in excess of a given threshold illicit a beach closure or trigger toxin testing. Under this framework, toxin analyses are informed by knowledge of the genus of cyanobacteria present and their recognized potential to produce a given toxin. However, many strains of cyanobacteria are nontoxic, so this approach often wastes resources by screening for toxins when they are not present. Research indicates that cyanobacteria tend to produce toxins if they have the ability to do so; those that do not produce toxins physically lack the genes necessary to produce these compounds. DNA-based tools that target toxin genes can be used to improve monitoring efforts by more directly predicting which samples are likely to contain toxins. This presentation will provide an overview of the real-time quantitative PCR (QPCR) methodology—including its Pros and Cons, and these data will be compared with traditional metrics such as cell counts and toxin measurements using peer-reviewed and published data sets (Otten et al., 2012; Otten et al., 2015; Otten et al., 2016). In addition to predicting toxins, we provide additional data showing that QPCR can be used to predict taste-and-odor compounds such as geosmin. Additional topics to be covered include: sample collection/processing/storage, data interpretation, relative costs, turnaround times, and broader applications (e.g., sediment analysis).

Data to be presented can be found in the following publications and Supplementary Material:

Otten TG, Xu B, Qin B, Zhu G, Paerl HW. 2012. Spatiotemporal Patterns and Ecophysiology of Toxigenic *Microcystis* Blooms in Lake Taihu, China: Implications for Water Quality Management. Environmental Science & Technology 46:3480-3488.

Otten TG, Mackey S, Crosswell JR, Dreher TG. 2015. Application of molecular tools for microbial source tracking and public health risk assessment of a *Microcystis* bloom traversing 300 km of the Klamath River. Harmful Algae 46:71-81.

Otten TG, Graham JL, Harris TD, Dreher TW. 2016. Elucidation of Taste- and Odor-Producing Bacteria and Toxigenic Cyanobacteria in a Midwestern Drinking Water Supply Reservoir by Shotgun Metagenomic Analysis. Applied and Environmental Microbiology 82(17):5410-5420.