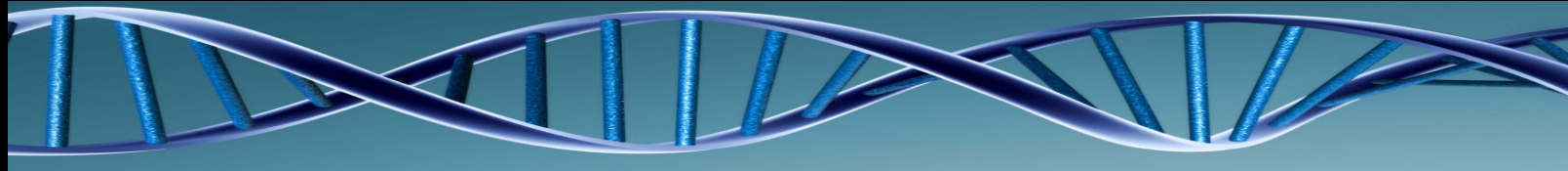


Application of molecular tools for routine water quality monitoring



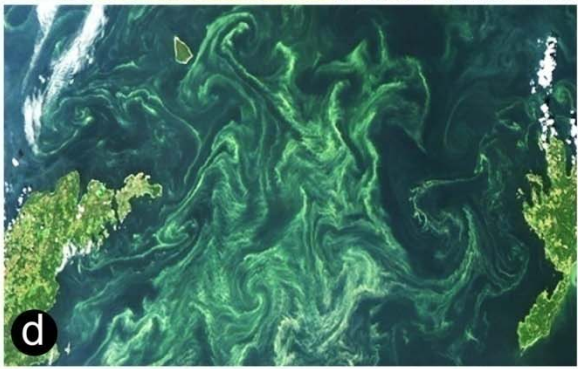
MWQI Technical Meeting - May 27, 2015

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Bend Genetics, LLC
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Overview of presentation contents

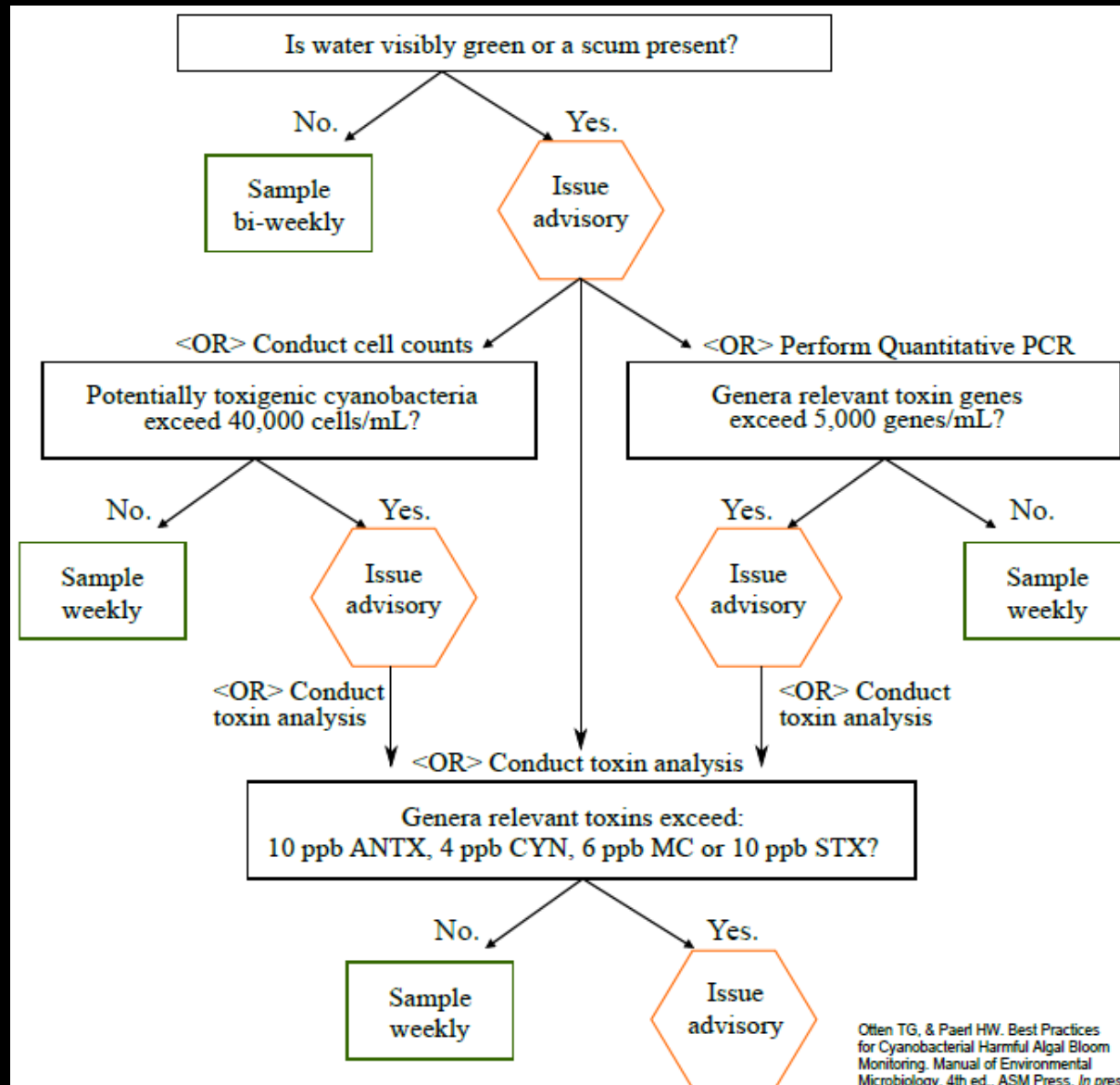
- Brief background on CyanoHABs, sample collection/processing and genetic tools for their study
- Application of each method (case studies):
 - Comparison of QPCR vs. microscopy for routine monitoring
 - Metagenomics as a roadmap for lake monitoring
 - Elucidate microbial community structure & function
 - Development and validation of a geosmin QPCR assay
- Goal is to be able to use this information to more effectively manage our aquatic resources and to protect human and environmental health



Sample collection

- Collection method varies by need
 - Public health - collect scum from most impacted site
 - Environmental - off-shore, depth integrated (1-2 SD)
 - Collect 0.5L in sterile plastic bottles (HDPE-2 is best)
 - Store on wet ice in the dark until processing
 - Don't want it to freeze which will lyse the cells
- Goal is to identify harmful/nuisance organisms before they reach problematic concentrations
- Adaptive management guides sampling frequency

Development of a tiered management approach to CyanoHAB monitoring



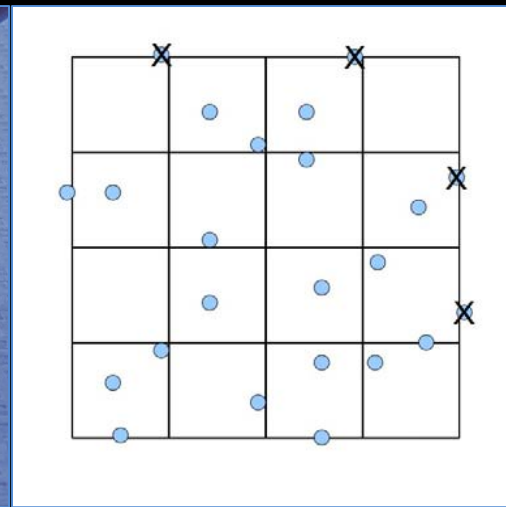
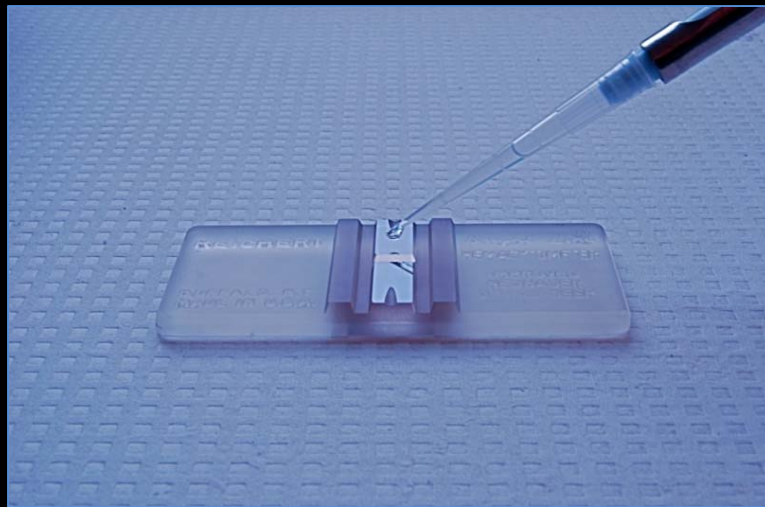
WHO guidelines

Experimentally derived

Varies by state

Offen TG, & Paerl HW. Best Practices for Cyanobacterial Harmful Algal Bloom Monitoring. Manual of Environmental Microbiology, 4th ed., ASM Press. In press.

Phytoplankton enumeration by microscopy



Pros: Can inventory all phytoplankton, equipment/materials costs are low

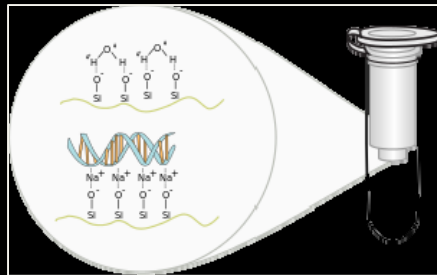
Cons: Hard to accurately count amorphous colonies, cannot distinguish toxic from nontoxic cells, relatively expensive and slow

~\$125-\$350/sample

DNA extraction and processing

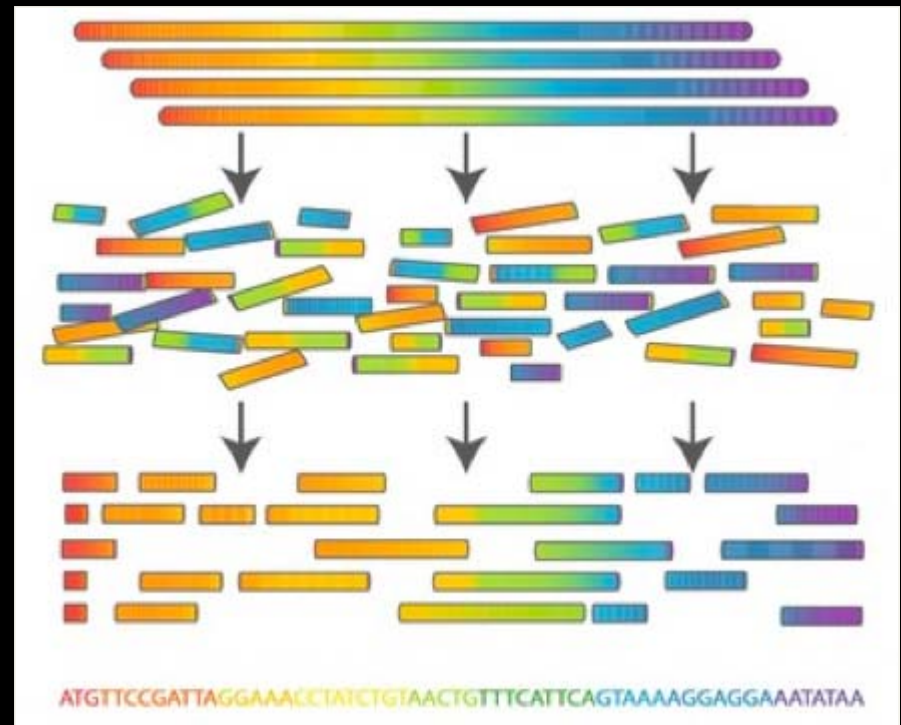


1. Concentrate sample



2. Extract DNA

3. DNA is now ready for downstream applications such as PCR/QPCR or sequencing



*Store filters at $\leq -20^{\circ}\text{C}$ until DNA extraction

Descent from common *mcy*⁺ ancestor

Mom



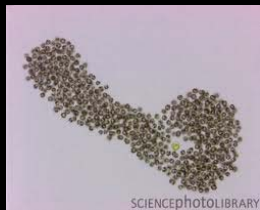
Gloeotrichia



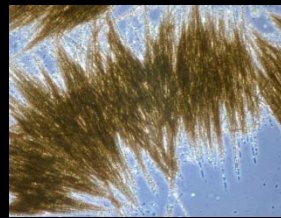
Hapalosiphon



Nostoc



Microcystis



Aphanizomenon

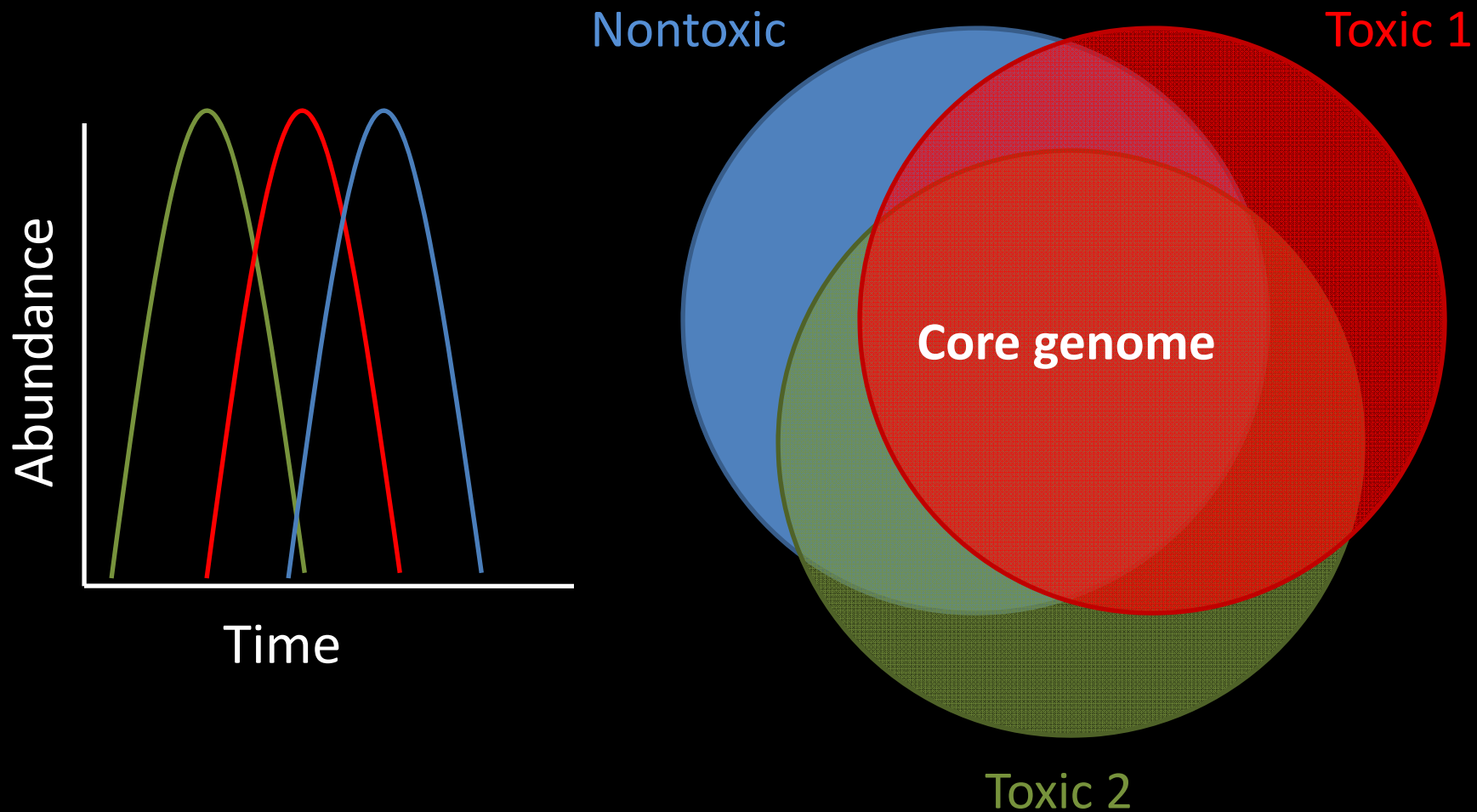


Anabaena

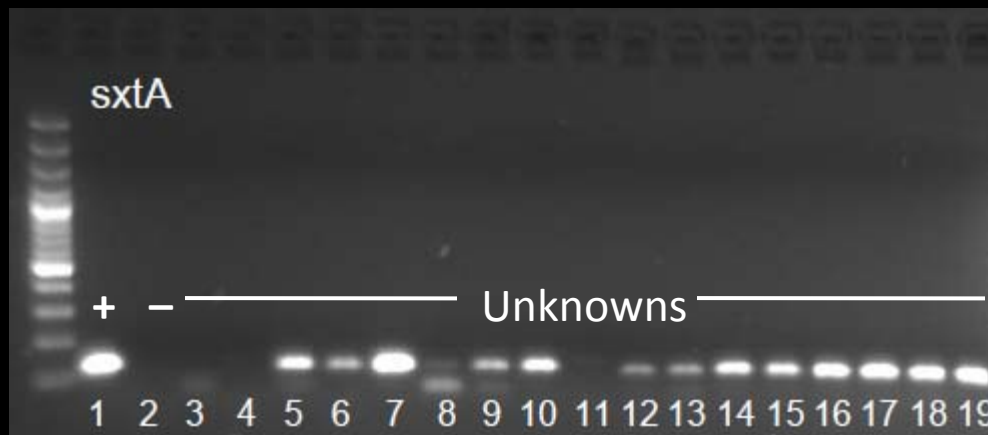
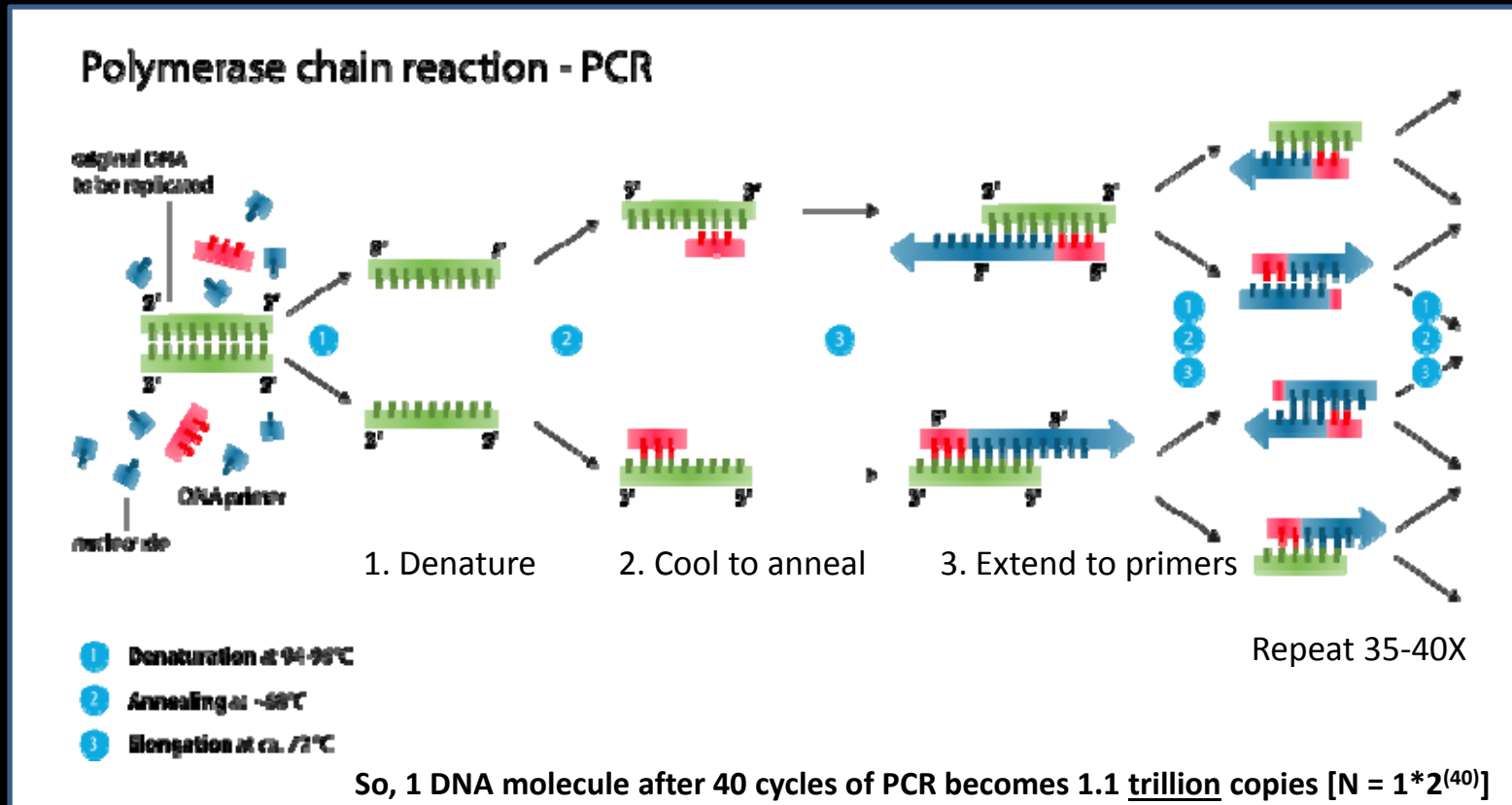


Planktothrix

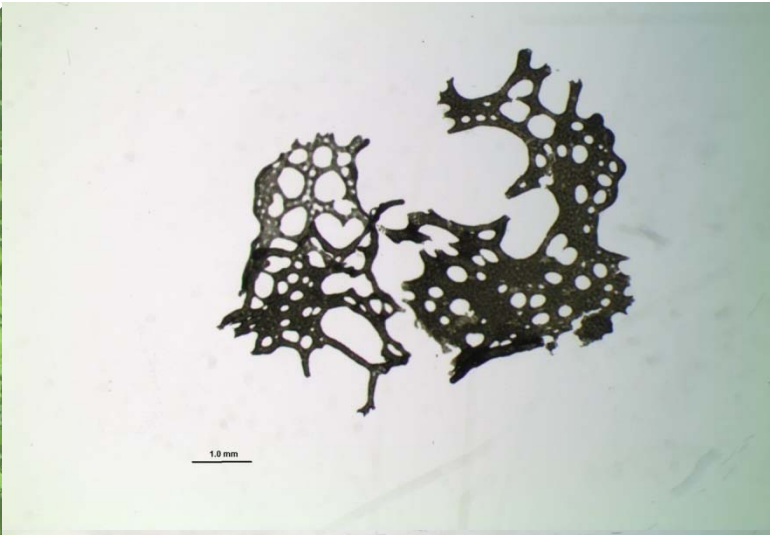
Like many genes, toxicity and T&O are strain specific traits (not genus/species)



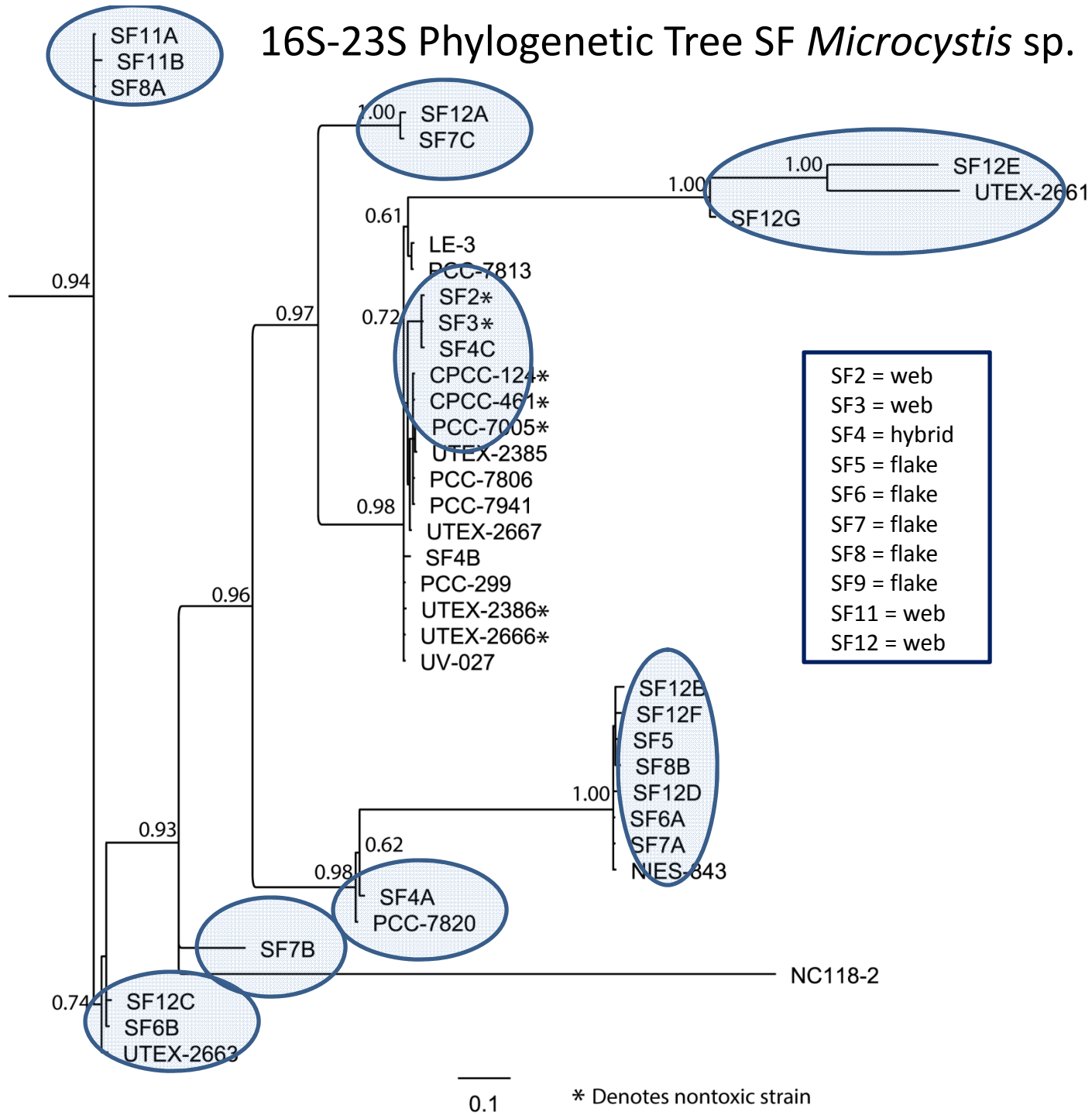
Polymerase Chain Reaction (PCR)



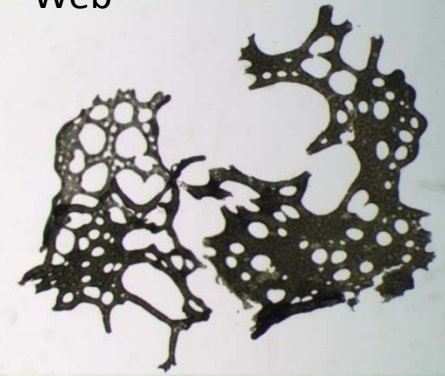
Amplification products can be visualized under UV light after gel electrophoresis



16S-23S Phylogenetic Tree SF *Microcystis* sp.



"Web"



"Flake"



"Hybrid"



Overview of real-time quantitative PCR (QPCR)

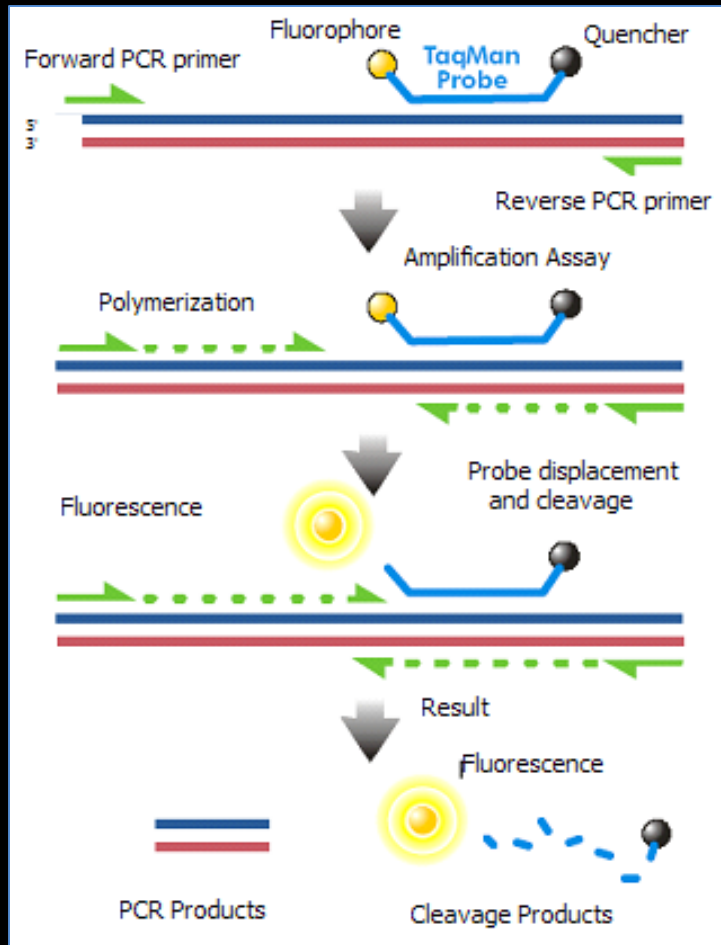
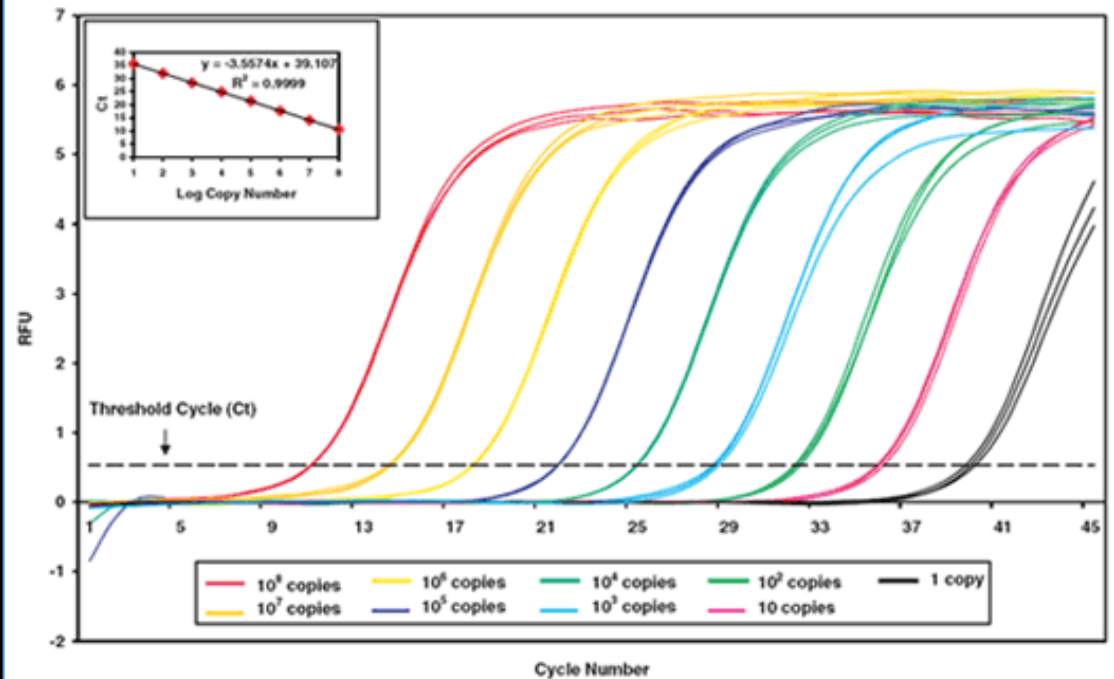


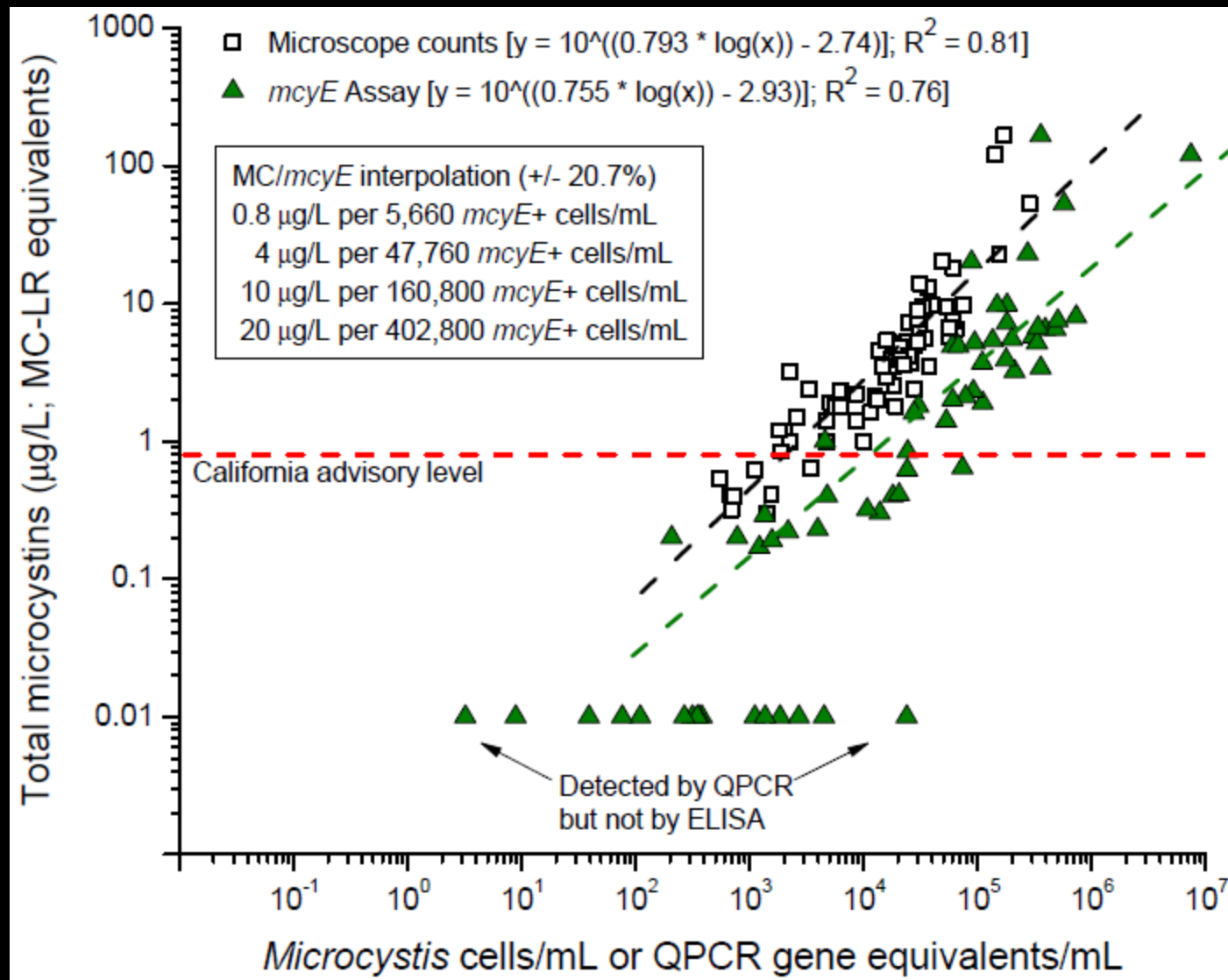
Fig. 2. Real-time PCR Amplification using HotStart-IT™ Probe qPCR Master Mix with UDG (PN 75764).



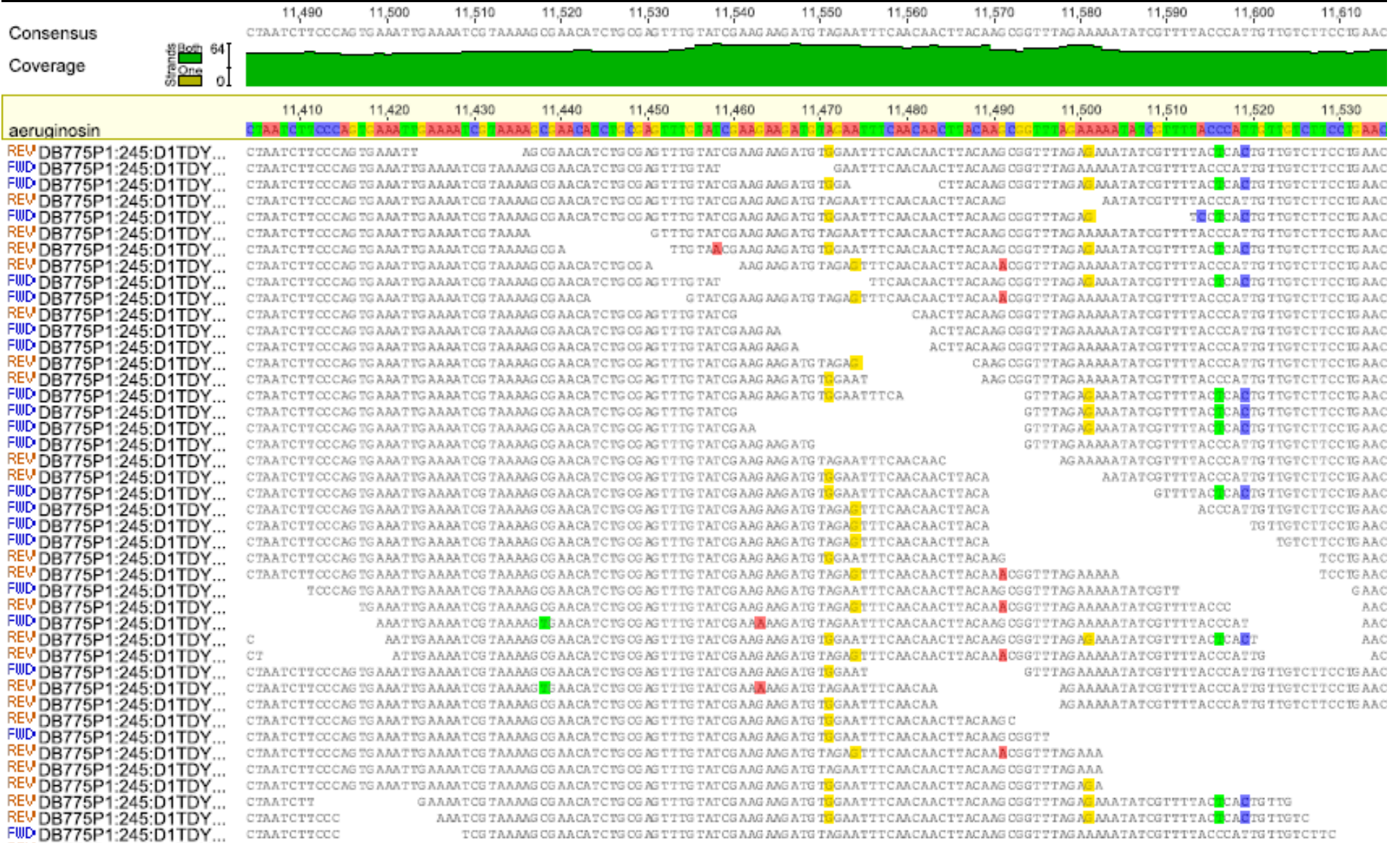
DNA extraction = \$20
QPCR/sample/assay = \$30

Pros: Provides earlier warning detection of nuisance organisms than direct measurements of toxins or cell counting, robust predictor of toxicity and T&O, no user objectivity as in cell counting and facilitates high throughput sample processing.
Cons: Relatively expensive equipment and relatively technical to conduct

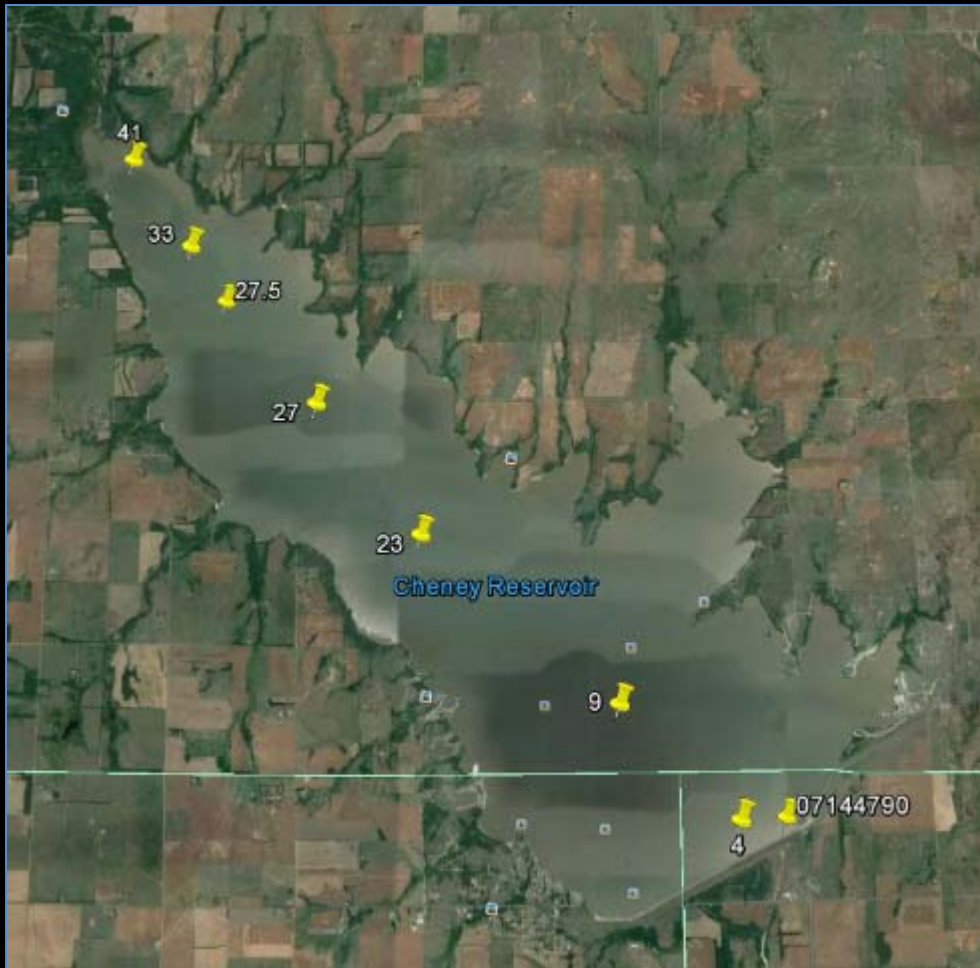
Comparison of microscopy and QPCR for estimating cyanotoxin risks



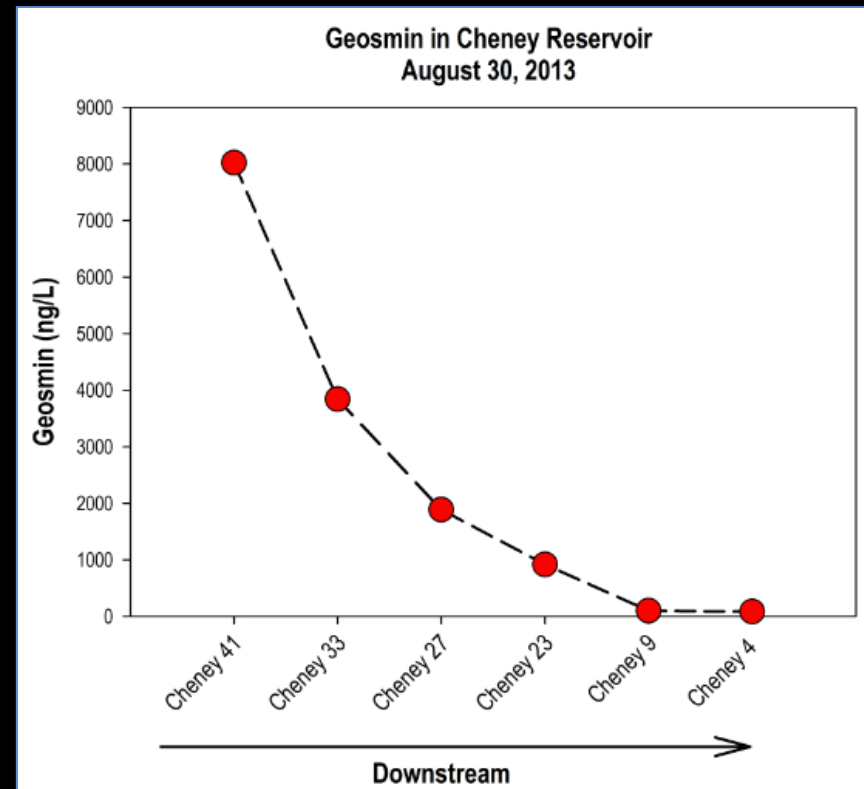
Shotgun metagenomics for assessing microbial community structure and physiological potential



2013 transect caught a major geosmin event

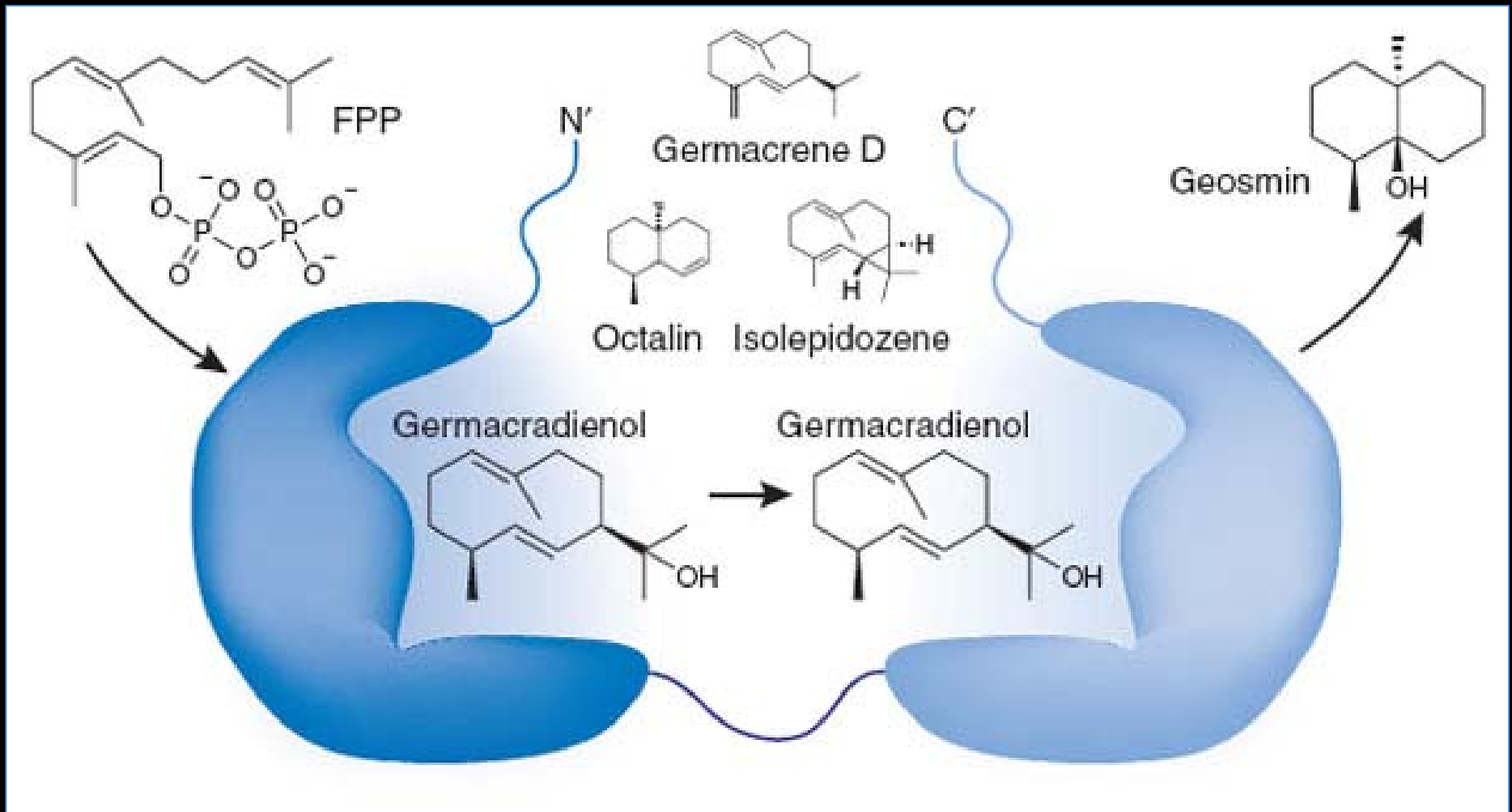


Cheney Reservoir: Wichita, Kansas

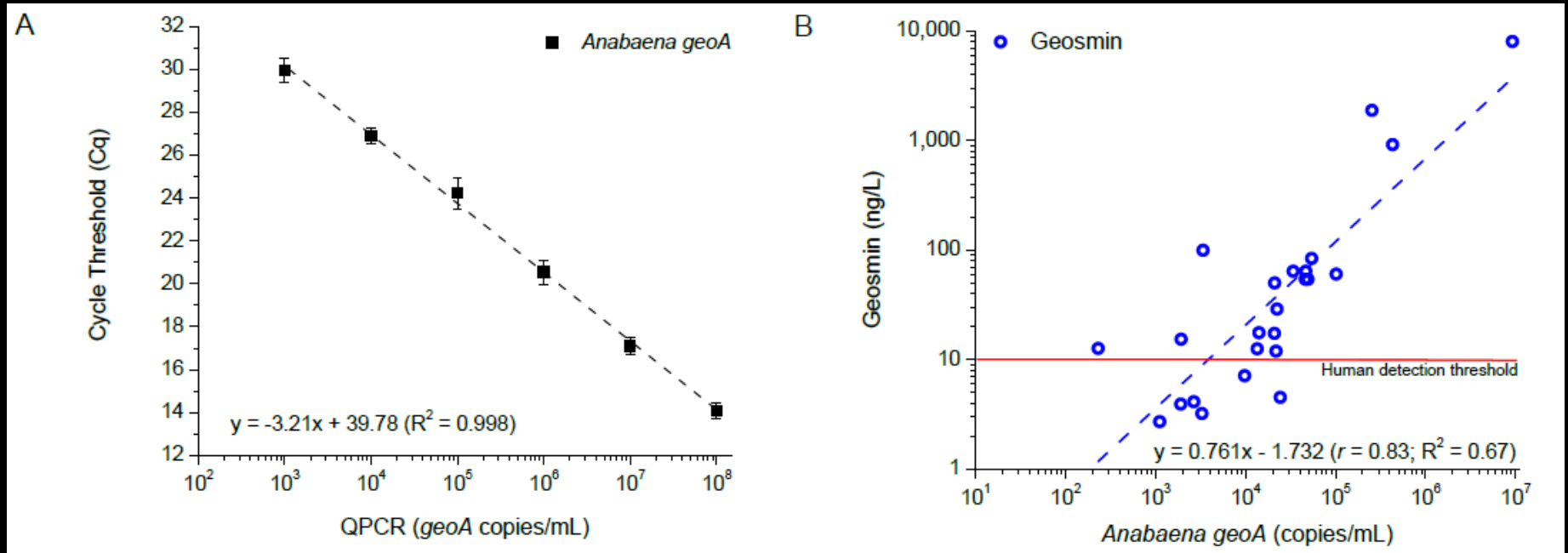
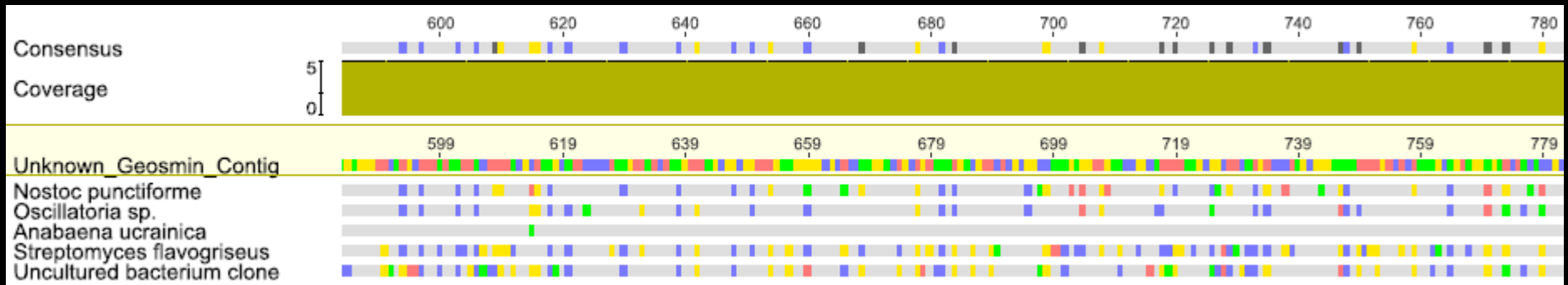


Human perception of geosmin is 4-10 ng/L

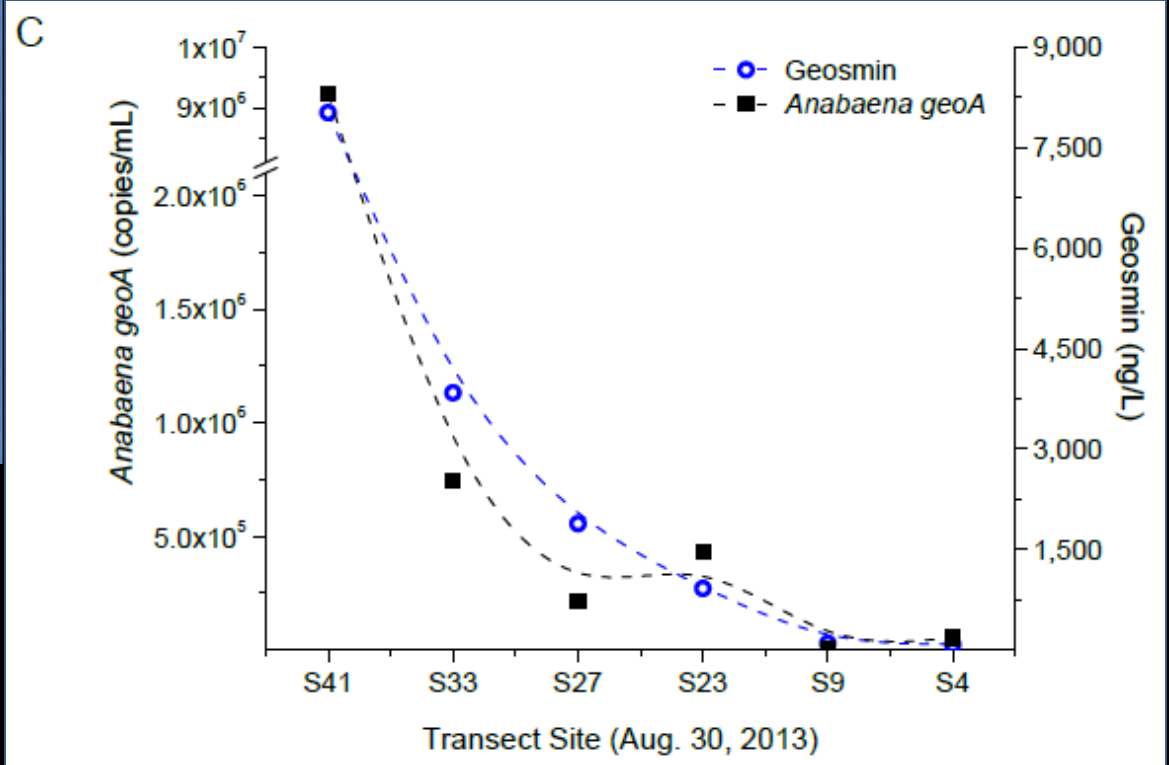
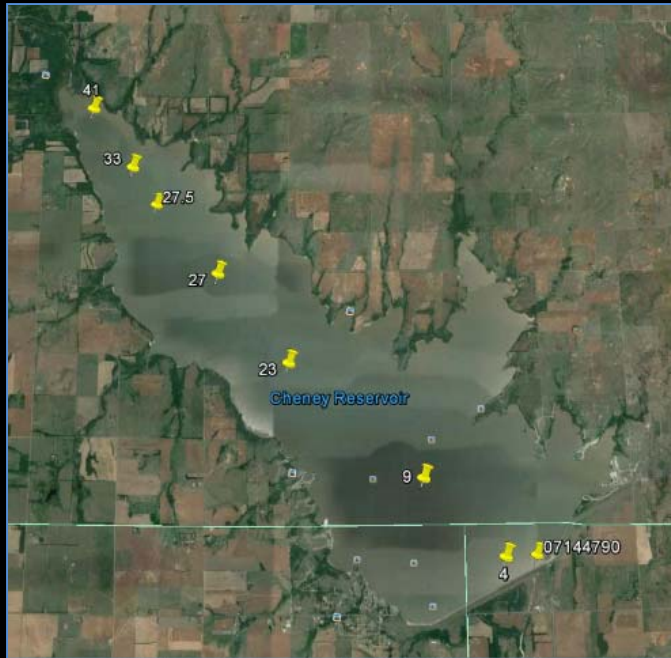
Geosmin synthase



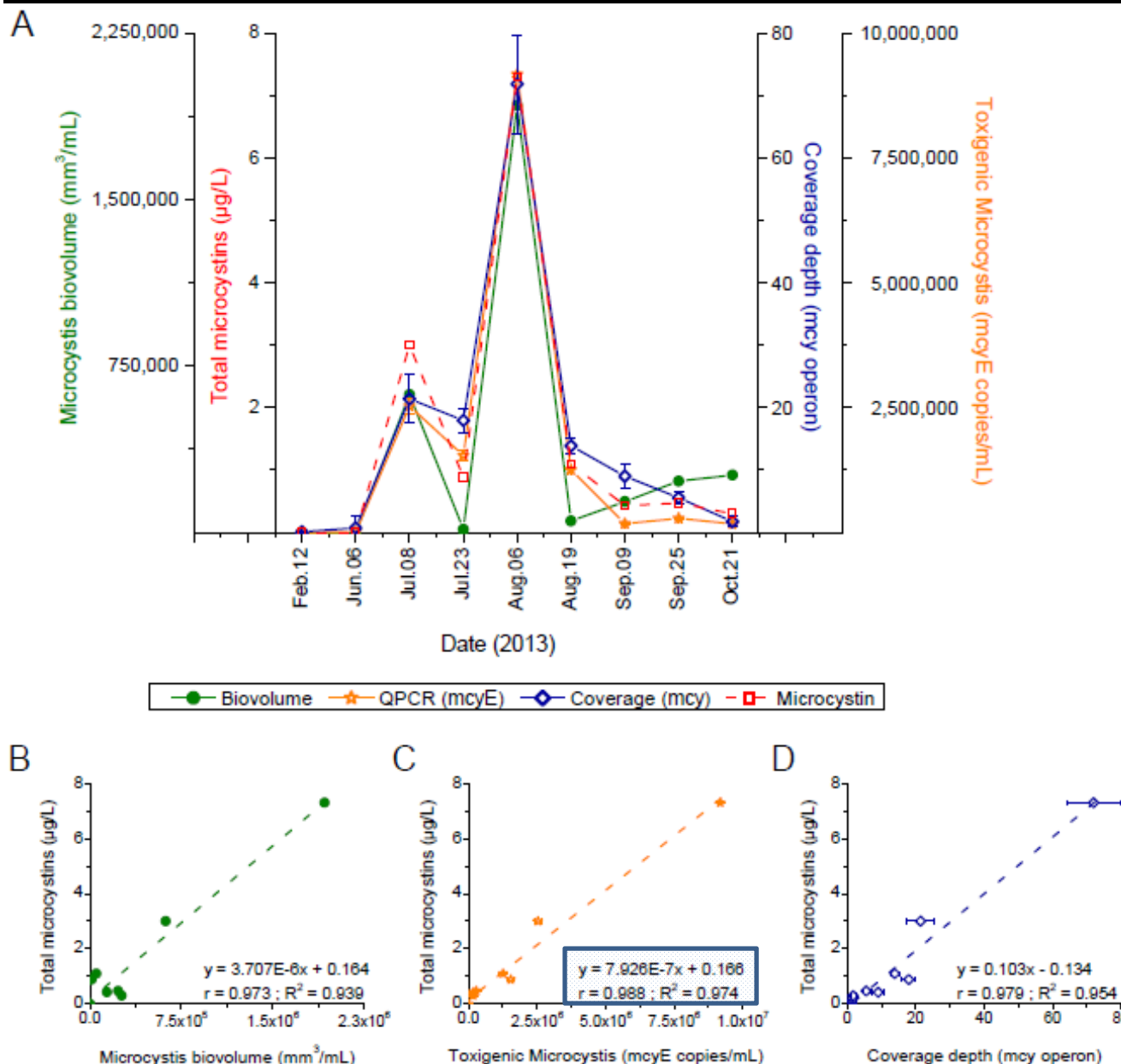
Development of a QPCR assay for geosmin detection



Application of the new QPCR assay to the 2013 geosmin event



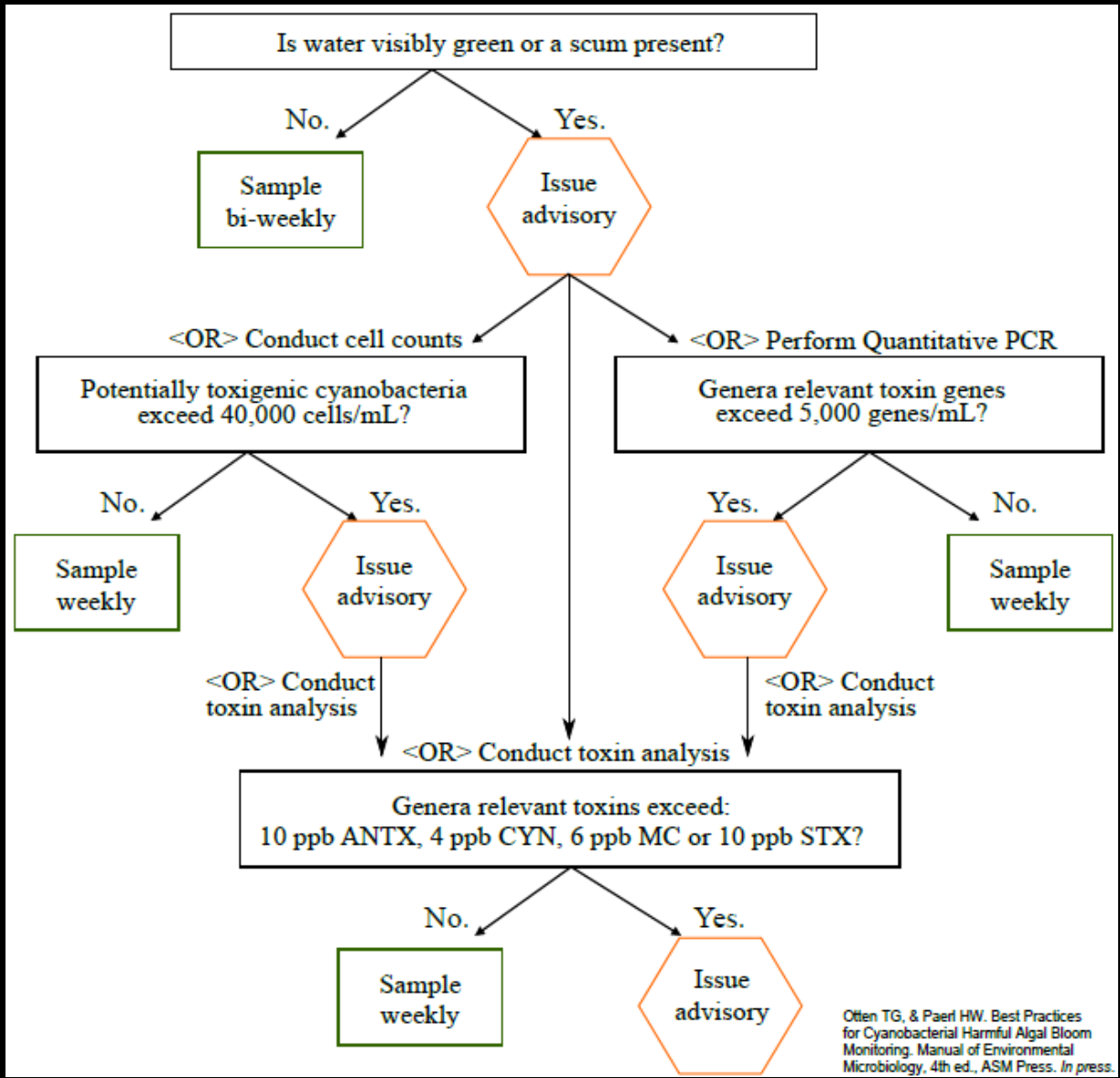
Inference of MCs by microscopy, QPCR and metagenomics



A) Time-series of a Midwestern reservoir showing **microcystin** (MC-LR eq.), *Microcystis* biovolume, toxigenic *Microcystis* by **QPCR** and shotgun metagenomics.

B-D) Linear regressions for each method relative to total microcystin.

Proposed method for CyanoHAB monitoring

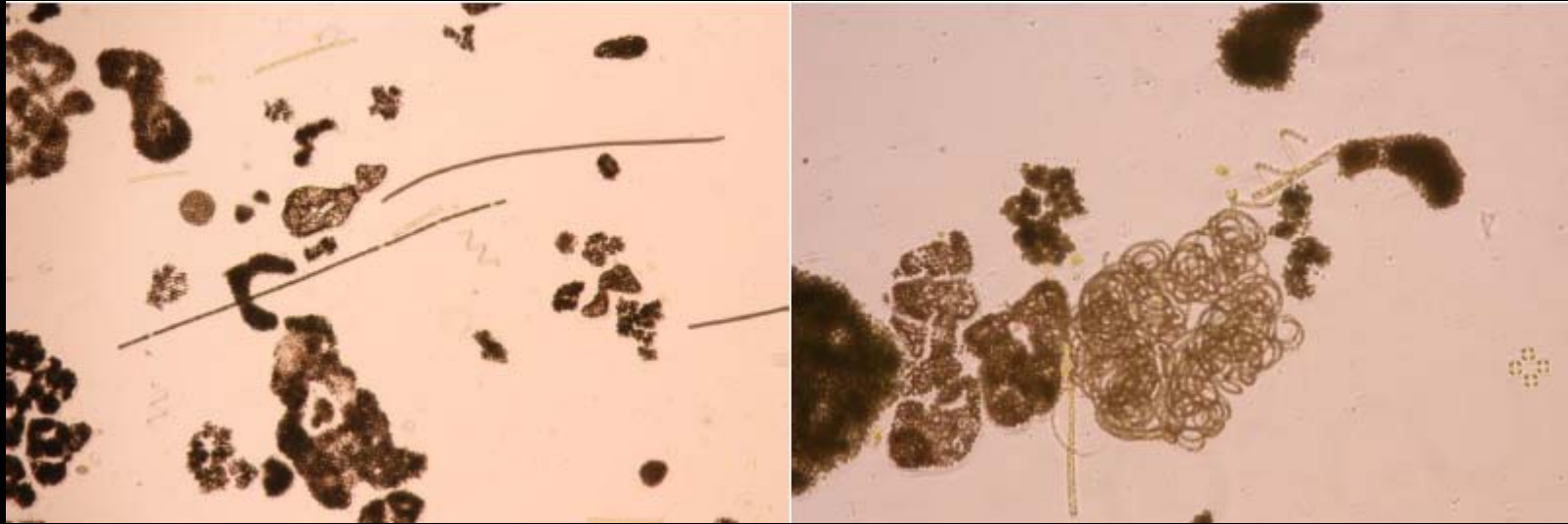


1. Conduct bi-weekly visual assessments of water.
2. Collect samples when algae becomes visible or bi-weekly during peak months (e.g., May – Oct)
3. Use QPCR to quantify potential toxin producers, if these > ~5,000 toxin genes/mL conduct appropriate ELISA

Rationale: DNA based methods are cheaper (\$50/sample/assay) and higher throughput than direct measurements of toxins (\$75/sample/assay) and because most samples may contain low/no toxicity.

Offen TG, & Paerl HW. Best Practices for Cyanobacterial Harmful Algal Bloom Monitoring. Manual of Environmental Microbiology, 4th ed., ASM Press. In press.

Thanks for your attention!



Please feel free to contact me with any questions.

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