Virginia Harmful Algal Bloom Task Force Annual Meeting: 2022 Freshwater Recap

Leah Anne Gibala-Smith February 24, 2023 Virginia Institute of Marine Science, College of William and Mary, Gloucester, VA



20 nm

The Phytoplankton Analysis Laboratory at Old Dominion University



Leah Anne Gibala-Smith Laboratory Manager

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The Phytoplankton Analysis Laboratory at Old Dominion University



The Phytoplankton Analysis Laboratory at Old Dominion University has been a **Primary Task Force member** of the Virginia Harmful Algae Bloom Task Force (HABTF) for over 30 years, and along with the Virginia Institute of Marine Science at the College of William and Mary, works with members of the VA HABTF **Rapid Response Team to** provide taxonomic, molecular, and toxin analyses used to identify and describe Harmful Algal Blooms in marine, tidal, and freshwaters of Virginia.

Holsinger and Everton 2016



Algae blooms 101

The term <u>algae bloom</u> is inexact and subjective:

- a large population of phytoplankton
- extremely high cell densities of phytoplankton (greater than 20,000 to 100,000 cells per mL)
- a proliferation of phytoplankton dominated by a single or a few species
- a visible accumulation of phytoplankton at the water surface

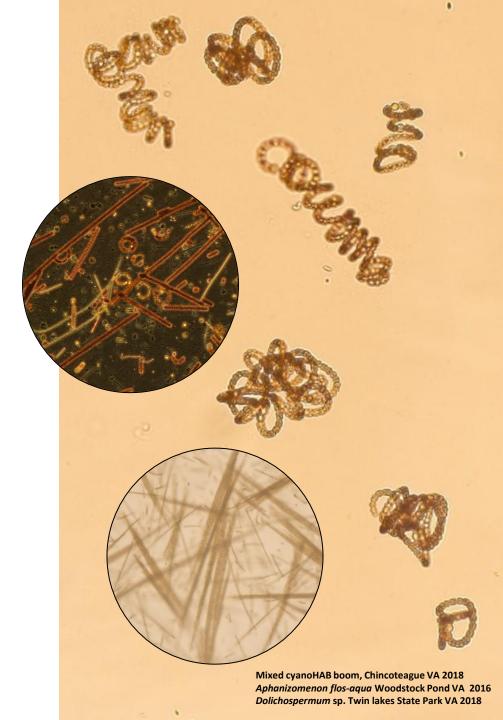
2022



What are harmful algae blooms (HAB)?

An algal bloom may be called harmful because of:

- reductions in dissolved oxygen concentrations
- alterations in aquatic food webs
- unsightly scums along shorelines
- production of taste-and-odor compounds that cause unpalatable drinking water and fish flesh
- the production of toxins potent enough to poison aquatic and terrestrial organisms

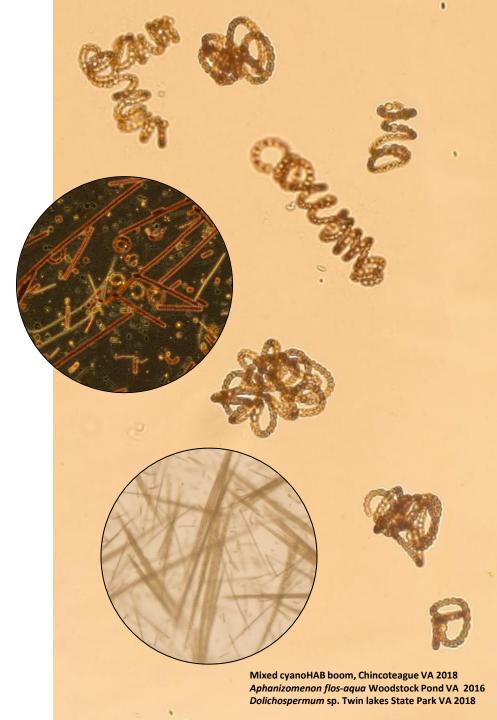




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What are cyanobacterial harmful algae blooms (CyanoHAB)?

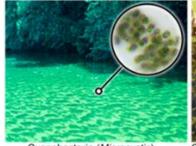
Many different types of algae can cause harmful algal blooms in marine, tidal, and freshwater ecosystems.

The most frequent and severe blooms in non-tidal surface freshwaters in Virginia are caused by <u>cyanobacteria</u>, an organism with the potential for the production of toxins potent enough to adversely affect human health.

Cyanobacteria:

- are naturally occurring
- are true bacteria with a prokaryotic cell structure (cells that lack membrane-bound nuclei)
- have photosynthetic pigments like eukaryotes (cells with membrane-bound nuclei)

Because cyanobacteria are functionally algae-like (primary producers) in aquatic ecosystems, they are considered to be part of algal communities.





Cyanobacteria (Microcystis)

Chlorophytes (filamentous green algae)





Cyanobacteria (Nodularia)

Dinoflagellates (Noctiluca)





Dinoflagellates (Prorocentrum)

Cryptophytes (Cryptomonads)





Diatoms (Pseudo-nitzschia)

Prymnesiophytes (Prymnesium parvum)

Figure 2. Harmful algal bloom species representative of major taxonomic algal groups along the freshwater-to-marine continuum.



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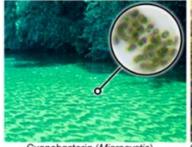
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Figure 2. Harmful algal bloom species representative of major taxonomic algal groups along the freshwater-to-marine continuum.





Pennate diatom

Filamentous green algae

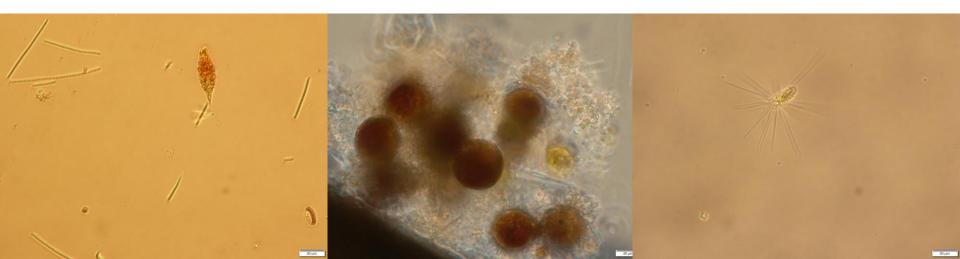
Filamentous green algae

Not all freshwater HAB events are caused by cyanobacteria!

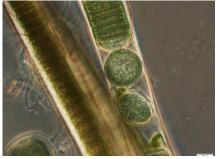
Euglena – motile stage

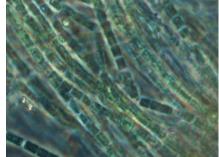
Euglena – palmella stage

Mallomonas



Cyanobacteria taxa groups







Potentially toxigenic (PTOX) filamentous and colonial cyanobacteria genera observed in Virginia

<u>PTOX</u> - not all cyanobacteria taxa produce toxins, different toxins may be produced by multiple taxa, and some taxa may produce multiple toxins over the course of a bloom

Toxin categories associated with select filamentous and colonial cyanobacteria genera observed in fresh and tidal waters of Virginia (2017-2022).

	Dermatoxins			Hepatotoxins			Neurotoxins				Taste and odor	
	LYN	APL	LPS	CYL ^{2,3}	MC ^{2,3}	NOD ²	ATX ^{2,3}	BMMA	NEO	SAX ^{2,3}	GEOS	MIIB
Anabaena ¹			Х	x	Х		х	х	Х	Х	х	х
Anabaenopsis ¹			Х		Х							
Aphanizomenon ¹			Х	x			х	х	Х	х	x	
Arthrospira ¹					Х		x					
Chrysosporum ¹				x			x					
Cuspidothrix ¹							x			х		
Cylindrospermum			Х				x	х				
Dolichospermum ¹			Х	x	Х		x			х		х
Limnothrix				x	х		?	х				
Lyngbya	x	х	Х				x	х		х		
Microcystis ¹			Х		Х	х	x	х				
Microseira	x		Х	x	х					х		
Oscillatoria ¹	x	Х	Х	x	Х		x	х		х	x	х
Phormidium ¹					х		x			х		
Planktolyngbya ¹							x			х		
Planktothrix ¹		х	Х		Х		x	х		х	x	х
Pseudanabaena ¹			Х		Х		x				x	х
Raphidiopsis ¹			Х	x			x	х		х		
Snowella			Х		х							
Sphaerospermopsis ¹					?		x					
Woronchinia			х		х		x			?		

1 Taxa which have been observed in samples collected at Lake Anna during rapid responses for Harmful Algal Bloom (HAB) reports.

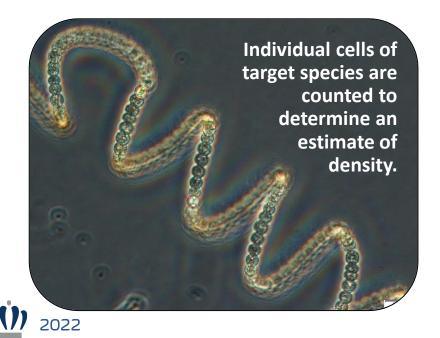
2 Toxin categories analyzed by ELISA during rapid responses for HAB reports (MC & NOD by ADDA since 2015, CYL since 2017, and ATX & SAX since 2020). 3 Toxins with an action threshold (CYL 15ppb, MC 8ppb, ATX 8ppb, and SAX 4ppb) in VA.

Toxin data included in this table are based on documented production in laboratory cultures and data based on circumstantial evidence, such as co-occurrence of genera and toxin or taste-and-odor compounds in environmental samples. LYN, lyngbyatoxin-a; APL, aplysiatoxins; LPS, lipopolysaccharides; CYL, cylindrospermopsins; MC, microcystins; NOD, nodularins; ATX, anatoxins; BMAA, β-N-methylamino-L-alanine; NEO, neosaxitoxins; SAX, saxitoxins; GEOS, geosmin; MIB, 2-methylisoborneol.



Taxonomic enumeration

Scan is conducted to identify dominant species





Abraxis microcystins (ADDA) ELISA

8.0 ppb

0.15ppb - 5.0ppb (higher w/dilution)

Abraxis cylindrospermopsin ELISA

15.0 ppb > 0.05ppb - 2.0ppb (higher w/dilution)

Abraxis anatoxin-a ELISA



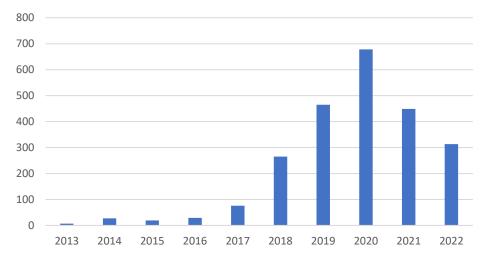
> 0.15ppb - 5.0ppb (higher w/dilution)

Abraxis saxitoxin ELISA

4.0 ppb

0.02ppb - 0.4ppb (higher w/dilution)

2017 – 2022 HAB TF Overview



Number of freshwater analyses per year



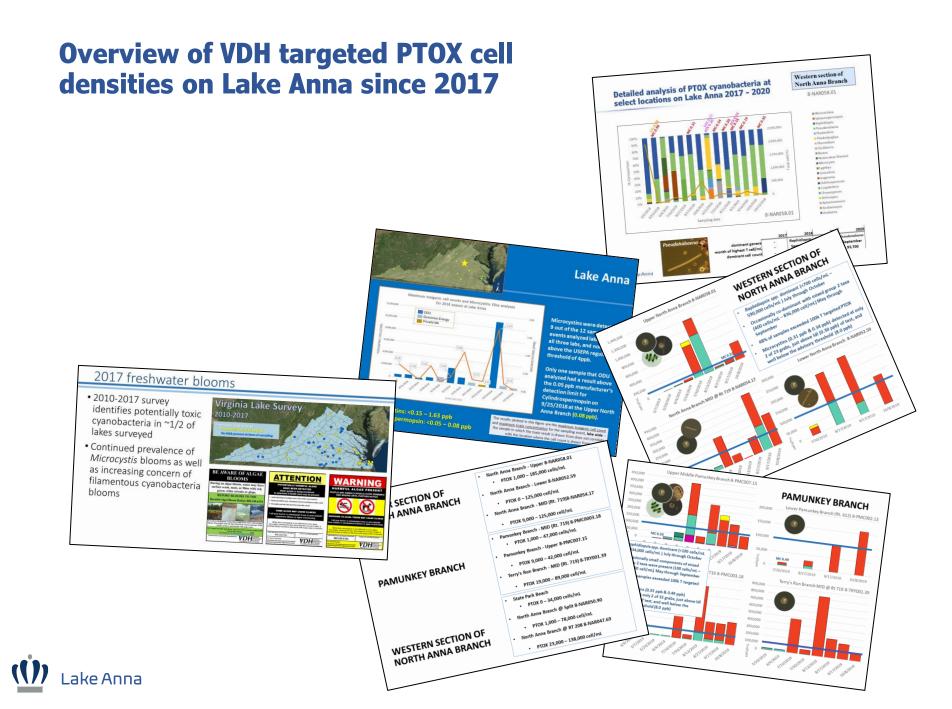


2022 Freshwater Overview

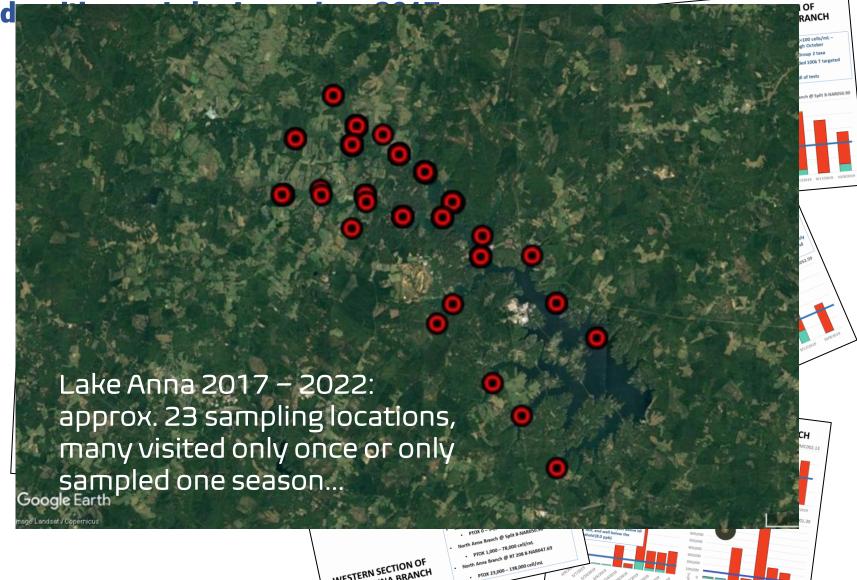
- 549 samples under our VDH contract
 - 484 estuarine samples
 - 65 inland freshwater samples
 - 77 of these were associated with a rapid HAB response
 - 12 samples from tidal waters
 - 65 inland freshwater samples
- Freshwater breakdown
 - 65 samples received
 - 313 analyses conducted
 - 65 taxonomic enumerations
 - 62 microcystins by ELISA
 - 62 cylindrospermopsin by ELISA
 - 62 anatoxin-a by ELISA
 - 62 saxitoxin by ELISA





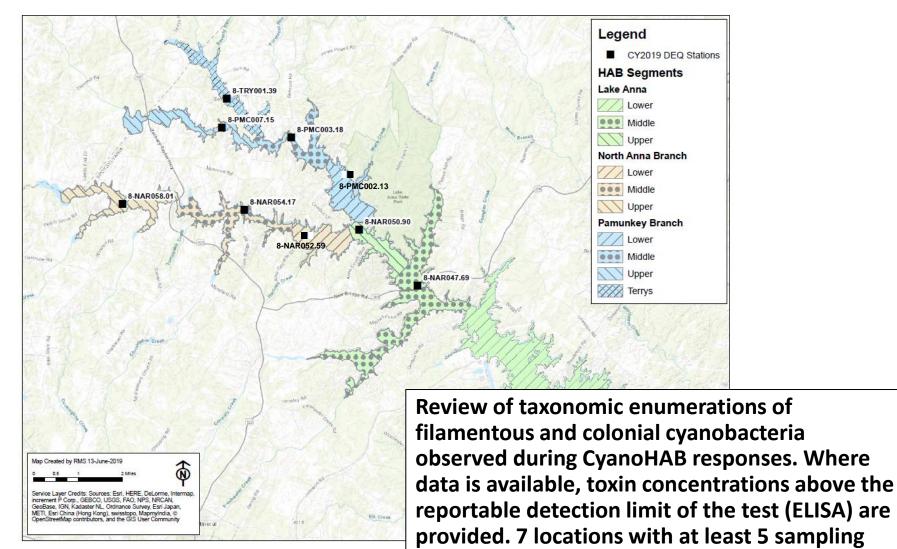


Overview of VDH targeted PTOX cell





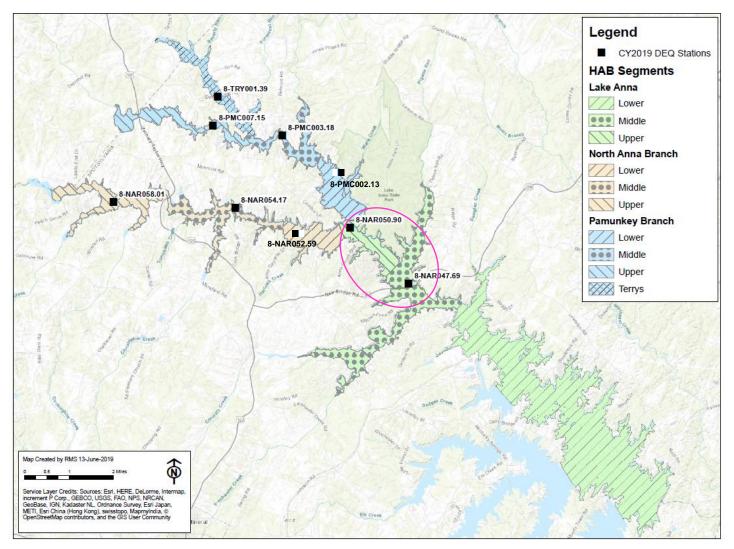
WESTERN SECTION OF NORTH ANNA BRANCH



events over a minimum of 2 seasons.

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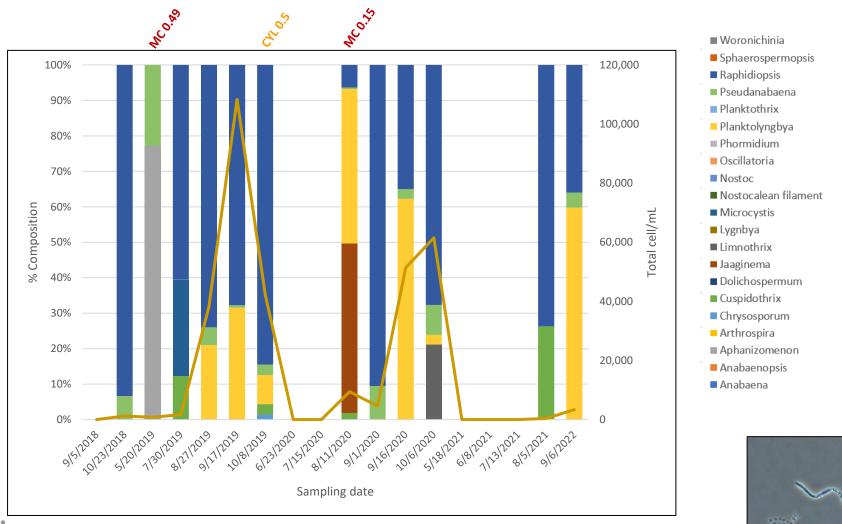
Lower section of North Anna Branch





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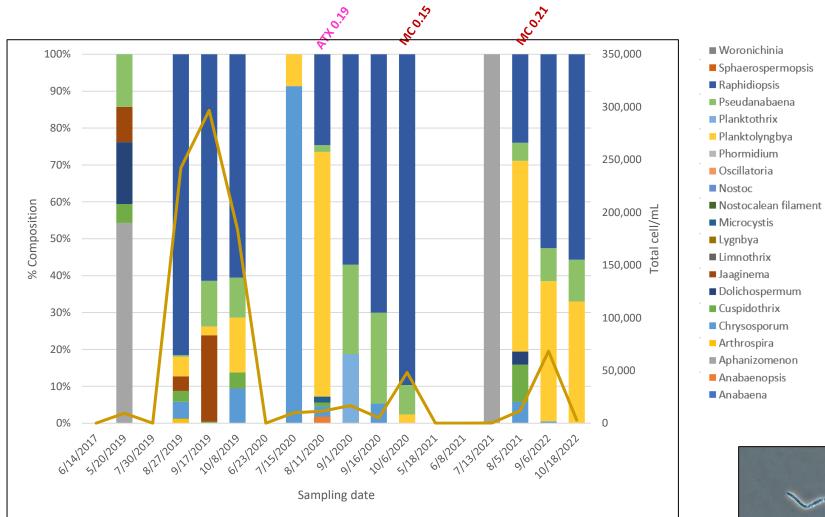
8-NAR047.69



🕐 Lake Anna

Lower section of North Anna Branch

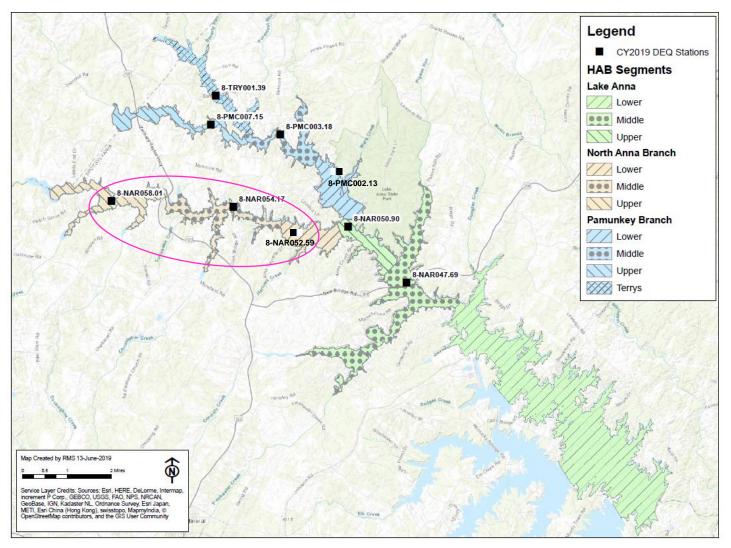
8-NAR050.90



Lake Anna



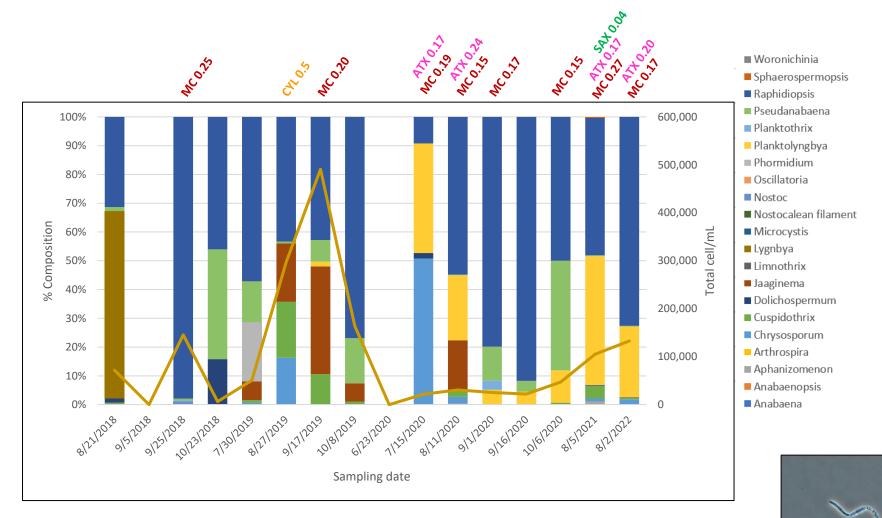
Western section of North Anna Branch



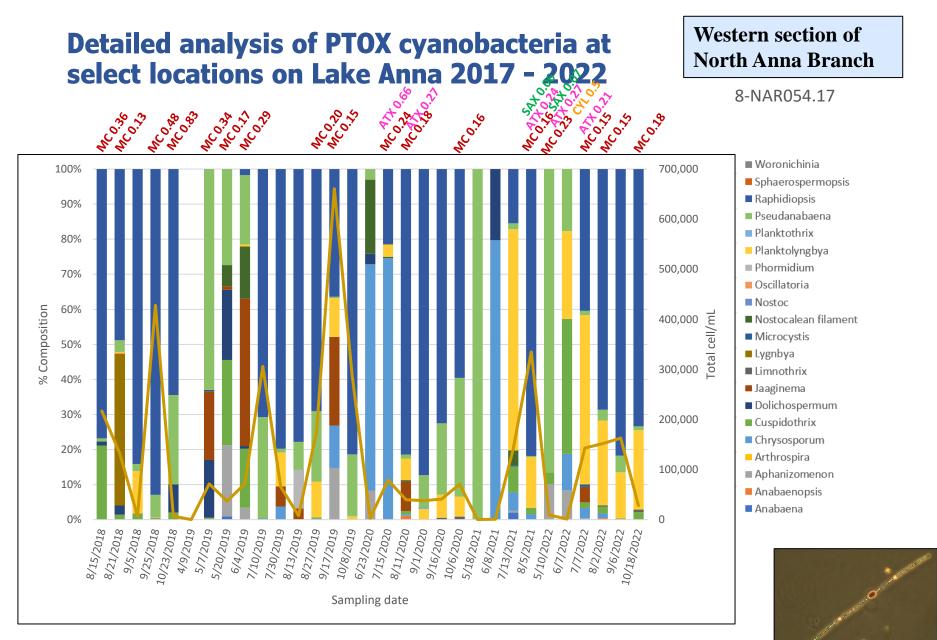
<u>(()</u>)

Western section of North Anna Branch

8-NAR052.59



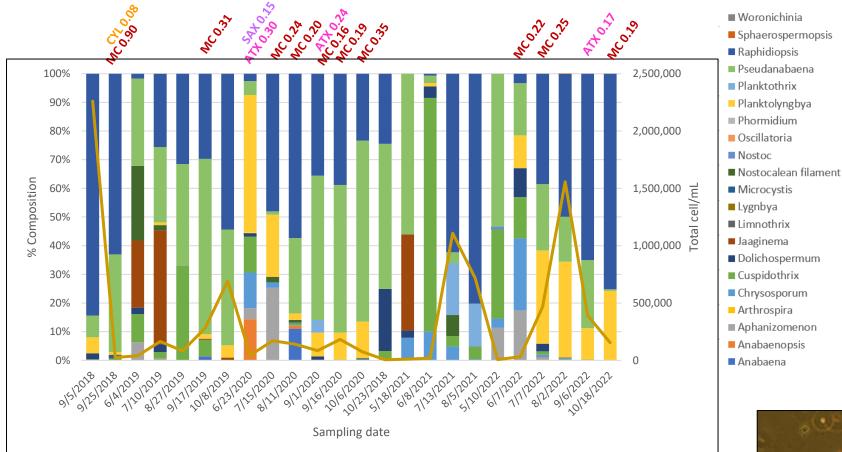






Western section of North Anna Branch

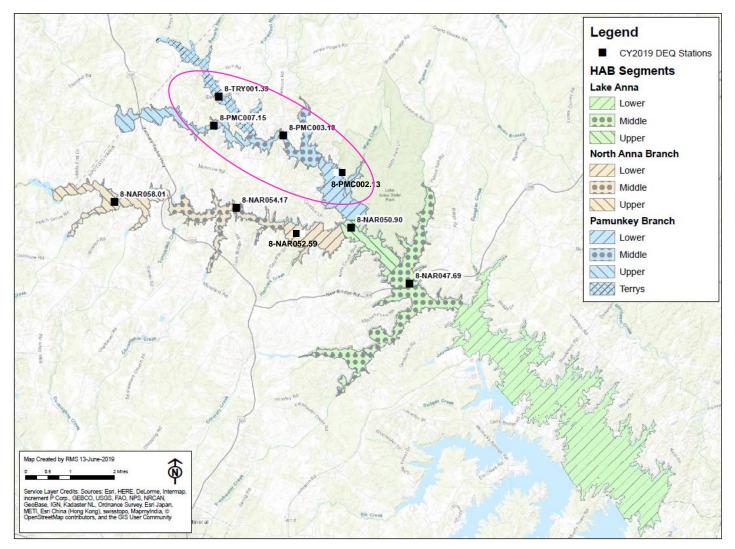
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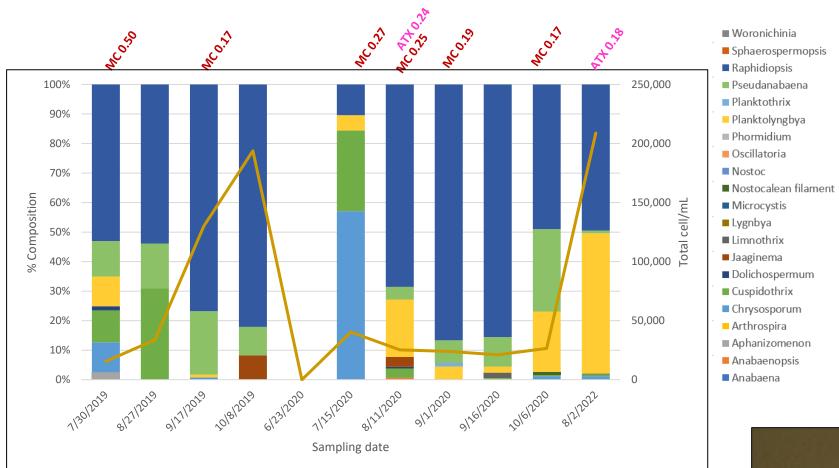
Pamunkey Branch





Pamunkey Branch

8-PMC002.13

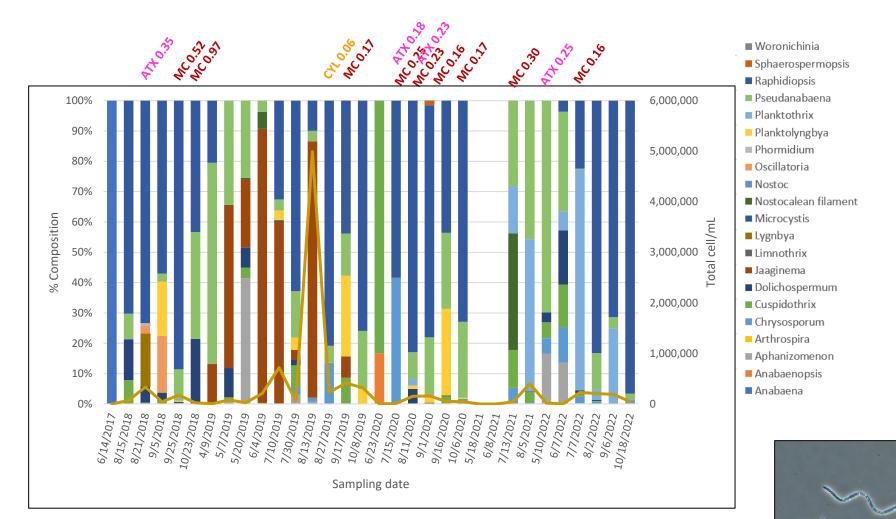






Pamunkey Branch

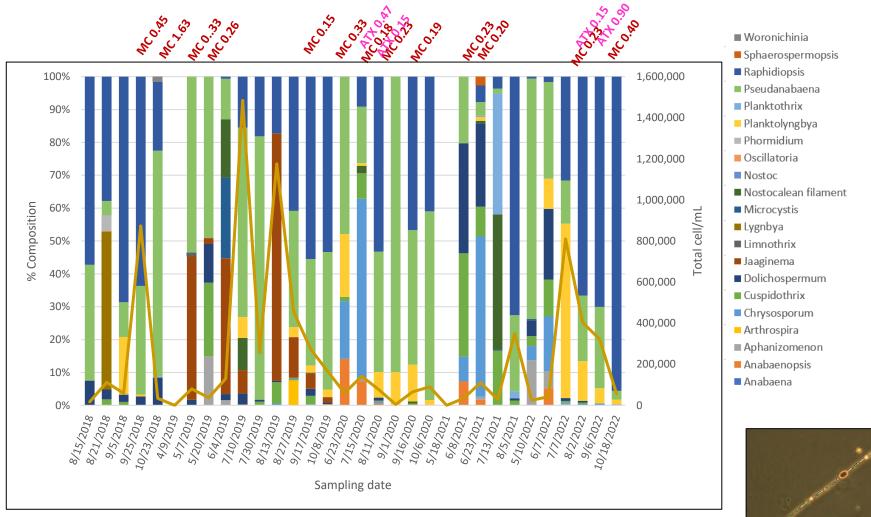
8-PMC003.18





Pamunkey Branch

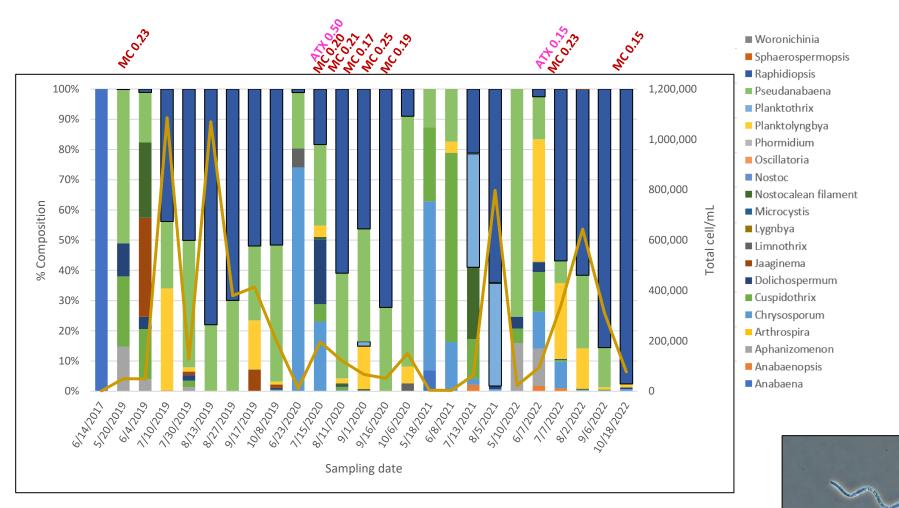
8-PMC007.15



Lake Anna

Pamunkey Branch

8-TRY001.39





Lake Anna toxin concentrations 2017 - 2022

- toxins generally remain below or just above reportable detection limits at regularly monitored locations
- the presence or absence of hepatotoxins is not a predictor of the presence or absence of neurotoxins
- *Raphidiopsis* is usually a major component of the community when MC is present
- Pseudanabaena, Planktolyngbya, Chrysosporum, Cuspidothrix, and Dolichospermum are also associated with the presence of MC and other toxins







Understanding the Lake Anna phytoplankton community and potential for toxin production is complicated

Lines of inquiry being explored to complement current projects by LACA and DEQ :

- Full algal taxonomy on Lake Anna to better understand the relationship between the cyanobacteria community within the greater phytoplankton community, and how it may be influenced by environmental conditions and/or mitigation practices (treatments)
- Joint QA/QC with LACA and NOAA for clarity of taxonomic nomenclature
- Developing qPCR methods to determine the presence of cyanotoxin producing genes
- Mapping akinete seed banks to identify potential bloom initiation sites
- Isolation of cyanobacterial cultures to examine growth kinetics (Aliyah Downing, PhD candidate)











Thank you.

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