Dolichospermum evolution during during cyanobacterial bloom: insights from metatranscriptomics.

Sébastien Renaut[1,2], Nathalie Fortin[3], ,Charles W. Greer[3], B. Jesse Shapiro[2]

[1]Institut de Recherche en Biologie Végétale, Université de Montréal, Montréal, Québec, Canada. [2]Department of Biological Sciences, Université de Montréal, Montreal, Quebec, H3T 1J4, Canada. [3]Energy Mining and Environment, National Research Council Canada, Montreal, QC, Canada

sebastien.renaut@umontreal.ca   @seb_renaut   seb951.github.io/atrapp/RENAUT_evol_R12019.pdf

ATRAPP - Algal Blooms, Treatment, Risk Assessment, Prediction and Prevention Through Genomics

Stuff you need to know

• Specific environmental conditions, such as elevated levels of nutrients from human activities, warmer temperatures, still water, and sunlight promote the growth of cyanobacteria. At high density, they form **harmfull algae blooms.**

• Each summer, cyanobacteria make an appearance in **Lake Champlain** and pose health risks to humans and animals due to the production of cyanotoxins.

Big sciency questions

• Use a **metatranscriptomics** approach that targets genes expressed in the water to identify changes in the bacterial community during the summer.

• **Identify cyanobacteria genes** that change in allele (SNPs) frequency during the bloom.

Fancy tools and analyses

1. Water sampled at three location in Lake Champlain (Baie Missisquoi) during the cyanobacterial bloom (June 1st – October 6th 2016).

2. RNA extracted, followed by High Throughput sequencing (100bp paired end Illumina HiSeq).

3. Metatranscriptomes processed using SAMSA2 pipeline (trimming, merging, removal of rRNA, annotation)[1].

4. Sequences specifically annotated to Dolichospermum (the main cyanobacteria responsible for the bloom) used to produce a de novo reference transcriptome assembly using Trinity[2].

5. Dolichospermum sequences aligned to transcriptome using bowtie2[3]. SNP called using SAMtools[4].

6. Changes in allele frequency quantified using regressions (logistic for St1 & St2, linear for PRM).

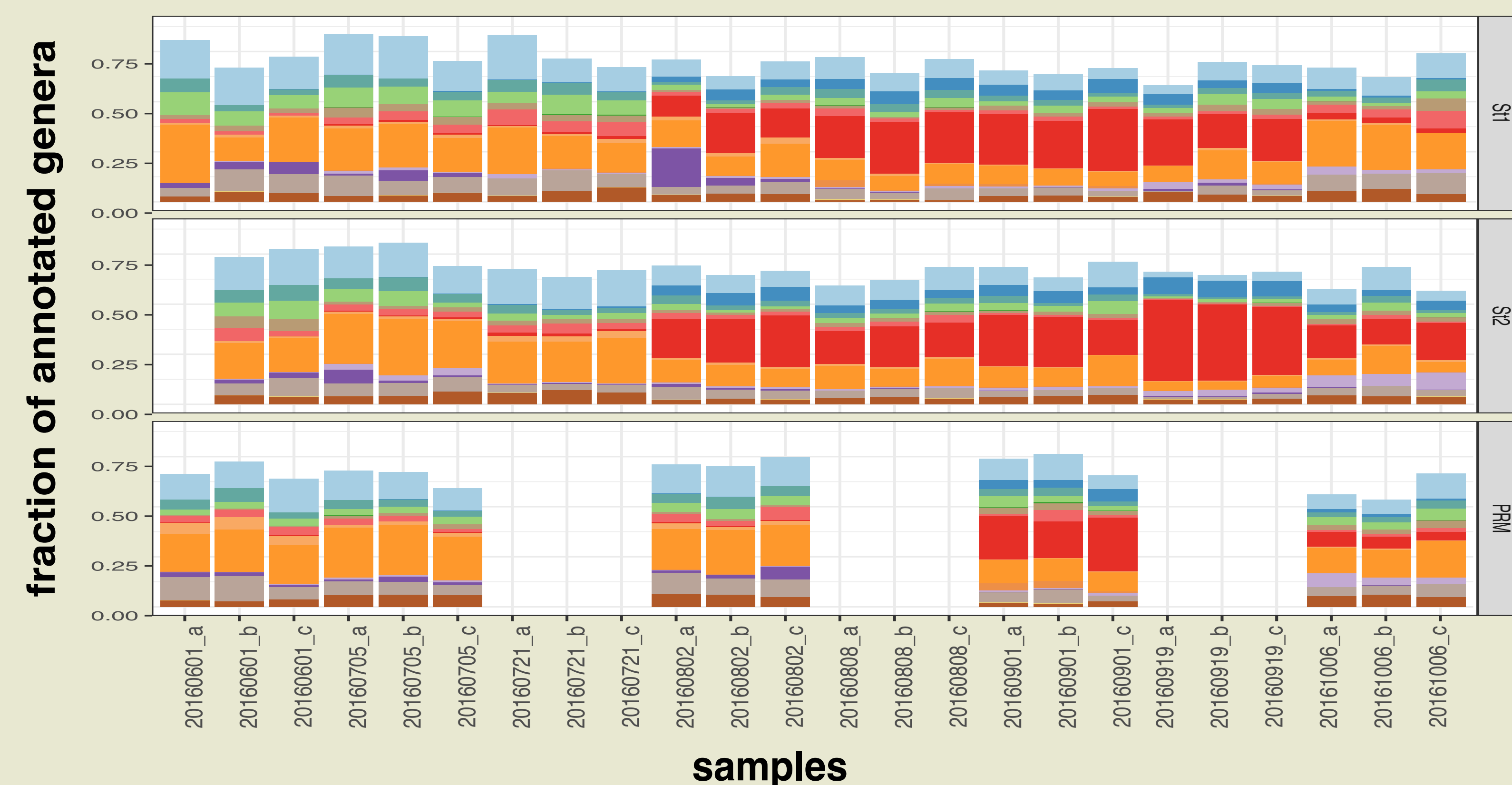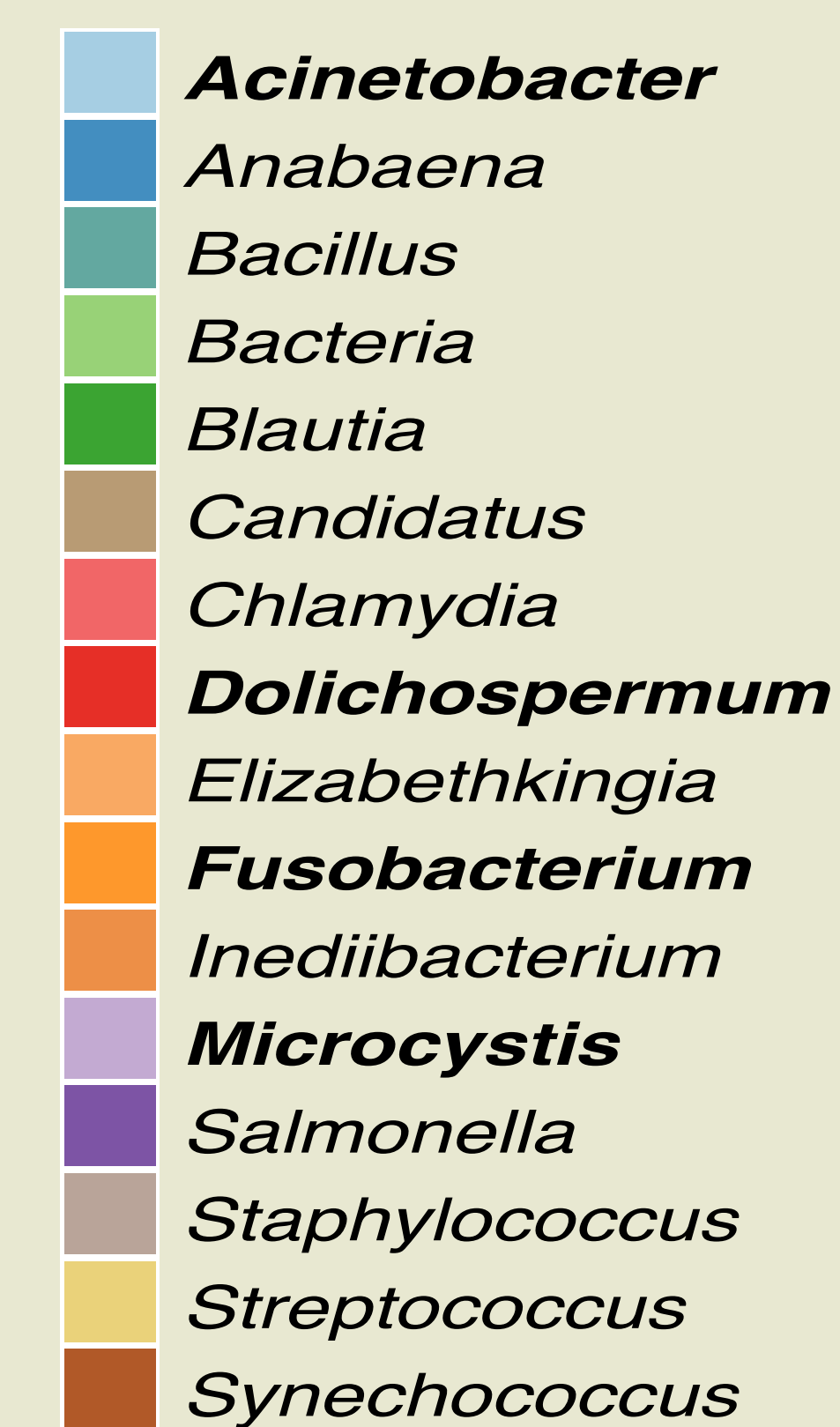7. Candidate genes showing significant changes (q-value < 0.05) in allele frequency BLASTxed to reference database.

## Things we find in the lake
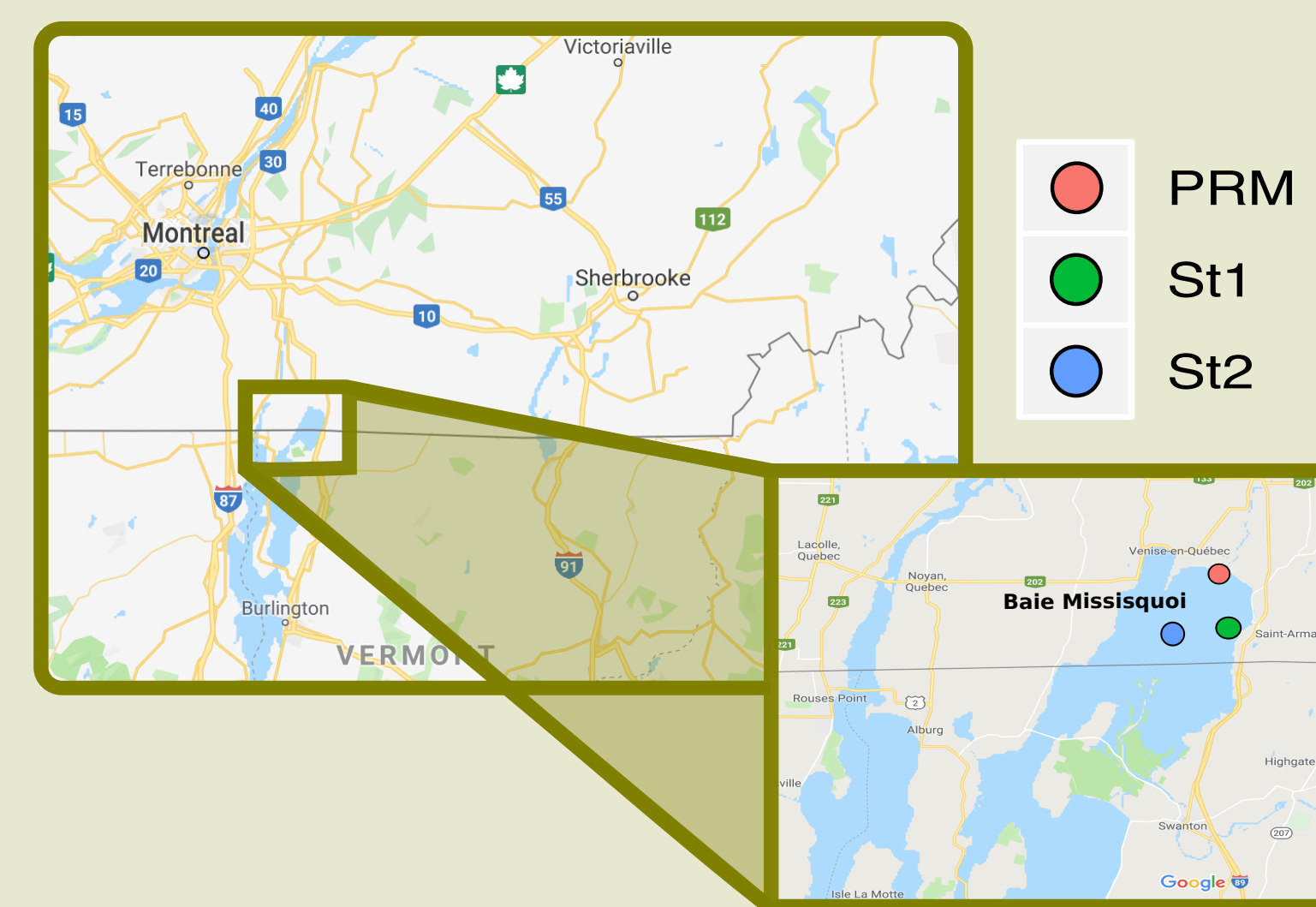
Sampling sites
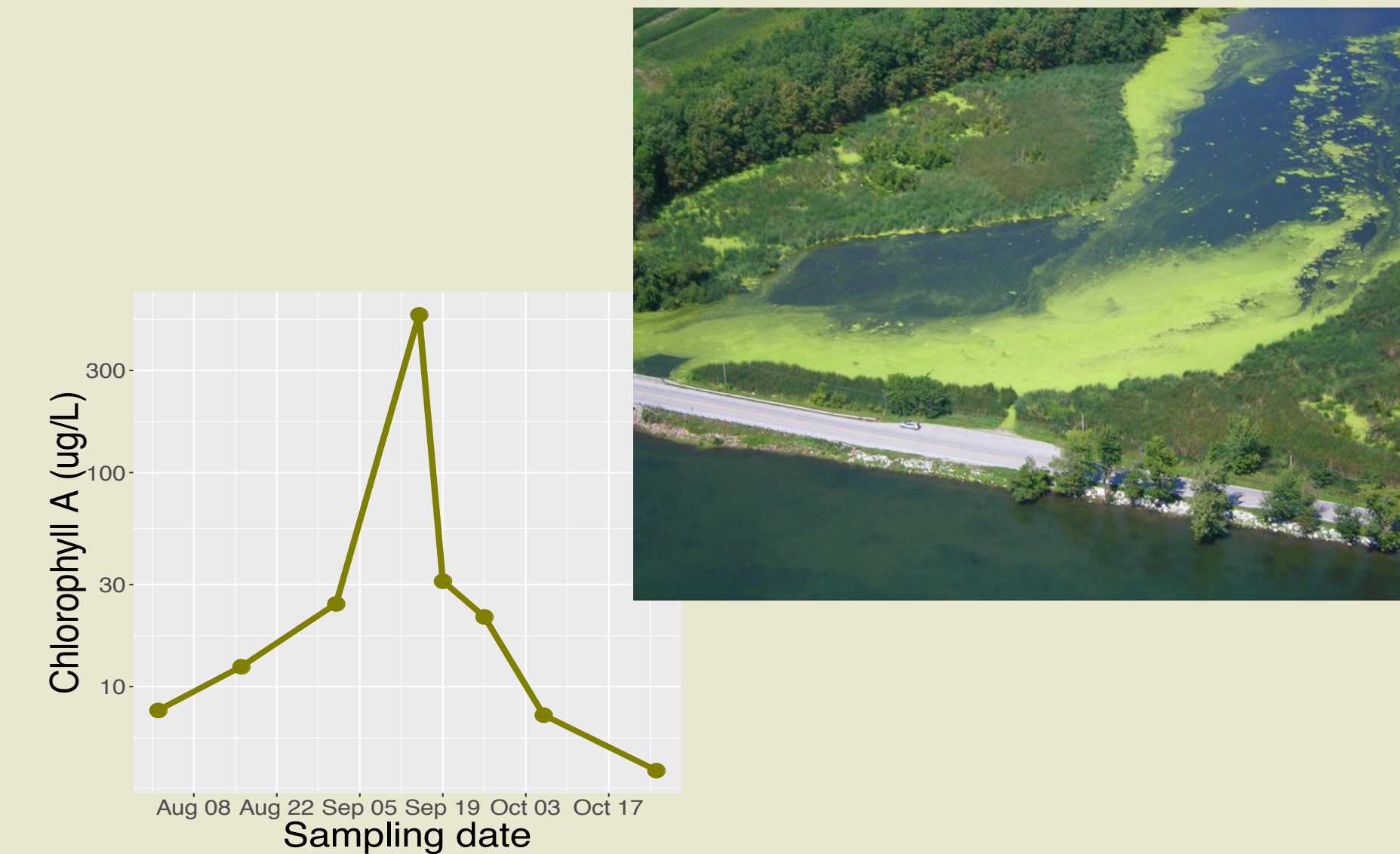
[Chlorophyll] peaked in mid-September resulting in a cyanobacterial bloom

Taxonomy

- ***Acinetobacter***
- *Anabaena*
- *Bacillus*
- *Bacteria*
- *Blautia*
- *Candidatus*
- *Chlamydia*
- ***Dolichospermum***
- *Elizabethkingia*
- ***Fusobacterium***
- *Inediibacterium*
- ***Microcystis***
- *Salmonella*
- *Staphylococcus*
- *Streptococcus*
- *Synechococcus*

Communities dominated by Gram negative Fusobacterium & Acinetobacter prior to bloom. During bloom, Dolichospermum circinale rose in frequency, followed to a lesser extent by Microcystis aeruginosa in September.
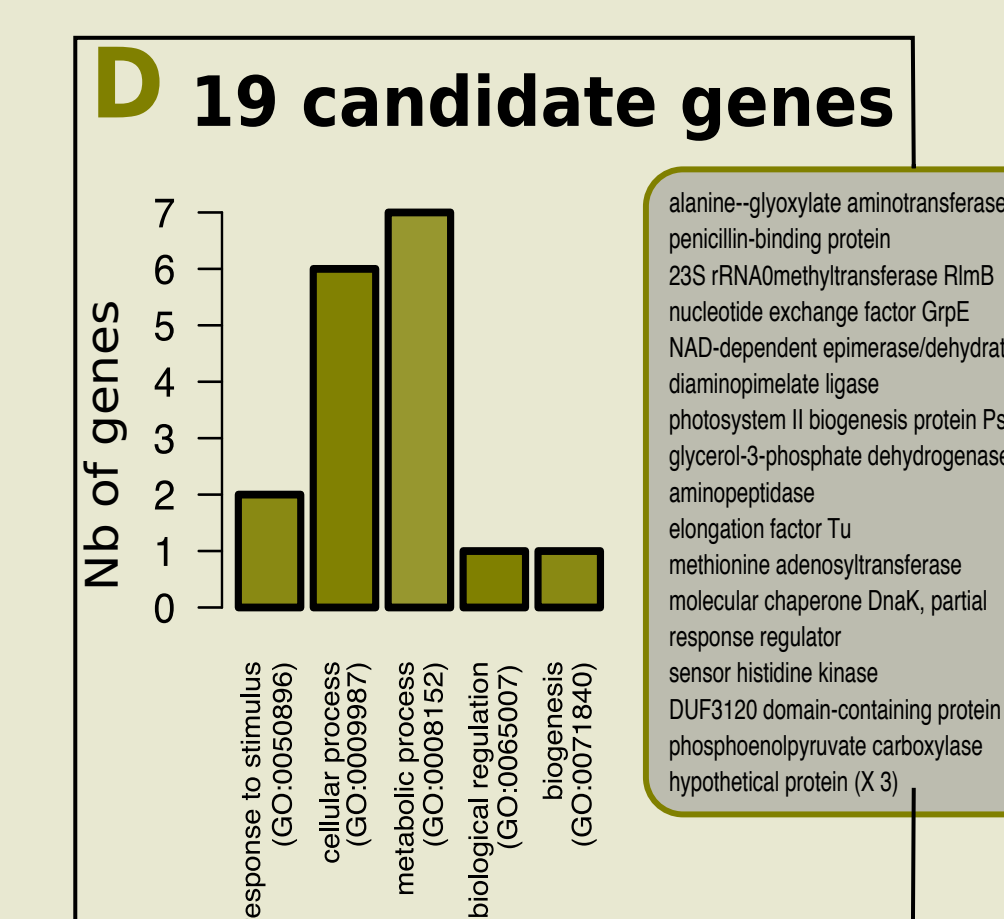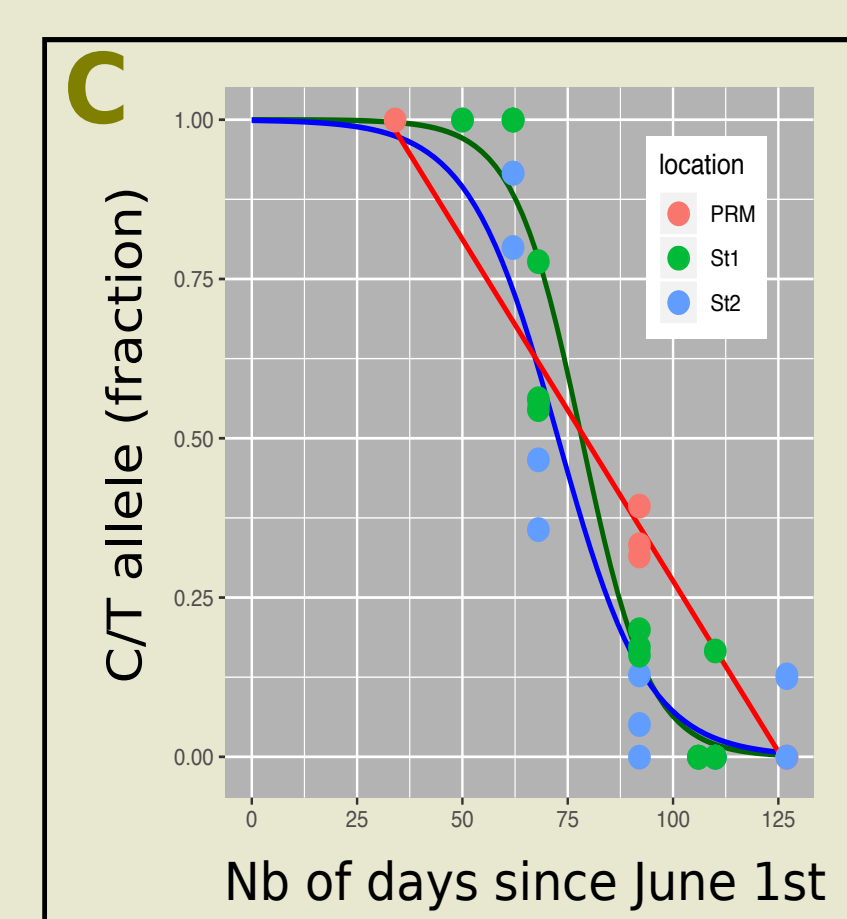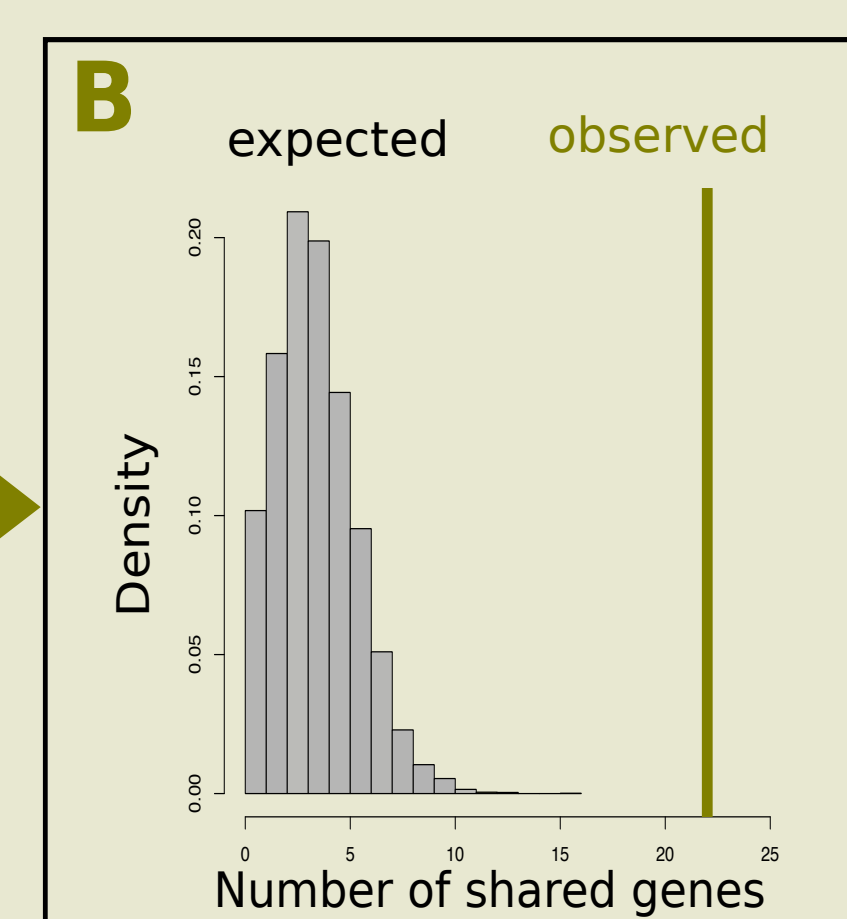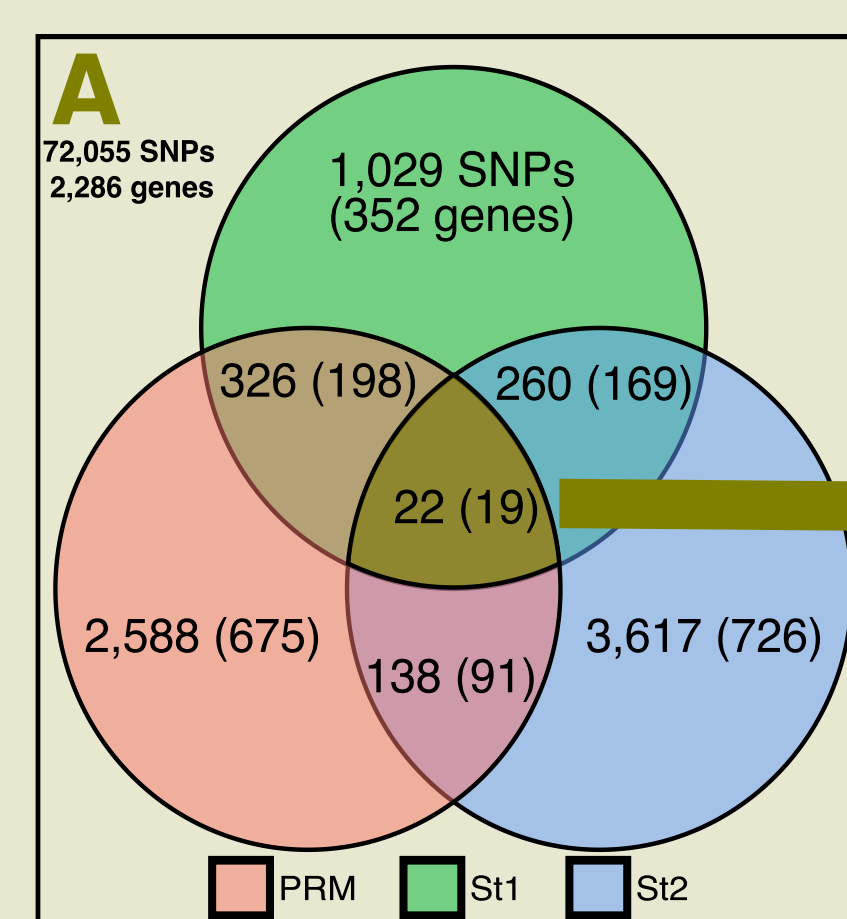
A. 72k SNPs identified in 2,286 Dolichospermum genes. Venn: Number of SNPs (genes) showing significant changes in allele frequency from beginning (June 1st) to end of bloom (October 6th). **B.** Example of a SNP showing a change from C to T allele in both St1, St2 (logistic regressions) and PRM (linear regression). **C. 22 SNPs showed significant changes in allele frequency in all three sites compared to three expected (p-value < 0.0001). D.** Gene ontology and list of candidate genes.

Possible outcomes

• **Metatranscriptomics is highly effective** in identifying bloom causing cyanobacteria.

• **Dynamic evolution of the system:** ~7,000 SNPs (10% of all SNPs) changed in allele frequencies during the bloom in at least one of the sampling site.

• **Nineteen genes showed repeatable changes in allele frequencies in all sampling sites.** These represent **candidate genes which may help to predict blooms.**

• **Further sampling in other lakes** will confirm patterns observed here.

Papers I read

[1] Samuel T Westreich et al. SAMSA2: a standalone meta transcriptome analysis pipeline. BMC bioinformatics 19 (2018)

[2] Manfred G Grabherr et al. Trinity: reconstructing a full-length transcriptome without a genome from RNA-Seq data. Nature biotechnology 29 (2011)

[3] Ben Langmead and Steven L Salzberg. Fast gapped-read alignment with Bowtie2 Nature methods 9 (2012)

[4] Heng Li et al. The sequence alignment / map format and SAM-tools. Bioinformatics 25 (2009)

[∞] A bunch more paper and fancy methods I read & used, but not cited here

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