

Dolichospermum evolution during cyanobacterial bloom: insights from metatranscriptomics.

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seb951.github.io/atrapp/evol_RI2019.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 **harmful 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.

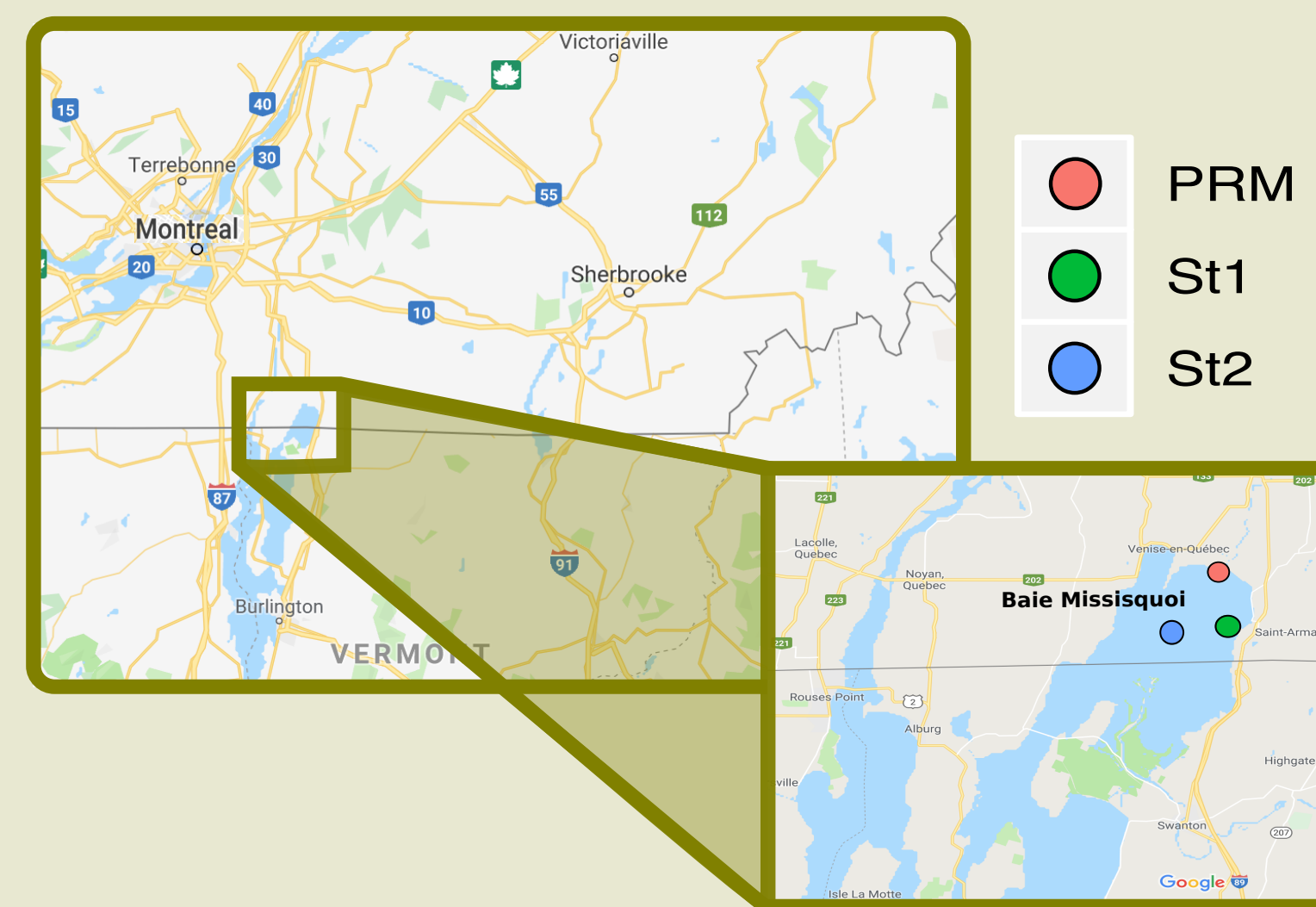
Big sciencey questions

- 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.

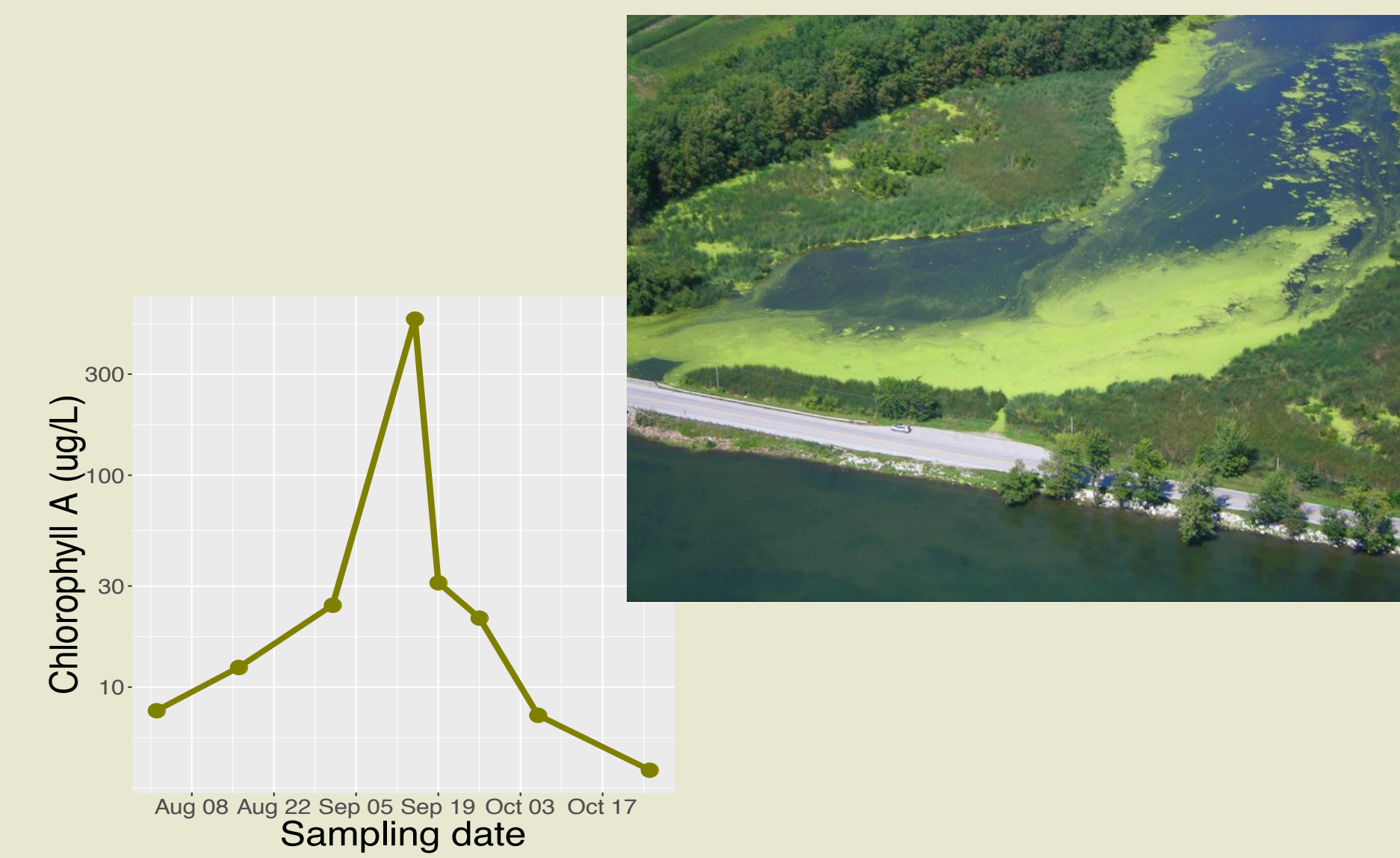
Fancy tools and analyses

- Water sampled at three location in Lake Champlain (Baie Missisquoi) during the cyanobacterial bloom (June 1st – October 6th 2016).
- RNA extracted, followed by High Throughput sequencing (100bp paired end Illumina HiSeq).
- Metatranscriptomes processed using SAMSA2 pipeline (trimming, merging, removal of rRNA, annotation)^[1].
- Sequences specifically annotated to Dolichospermum (the main cyanobacteria responsible for the bloom) used to produce a de novo reference transcriptome assembly using Trinity².
- Dolichospermum sequences aligned to transcriptome using bowtie³. SNP called using SAMtools⁴.
- Changes in allele frequency quantified using regressions (logistic for St1 & St2, linear for PRM).
- Candidate genes showing significant changes (q -value < 0.05) in allele frequency BLASTed to reference database.

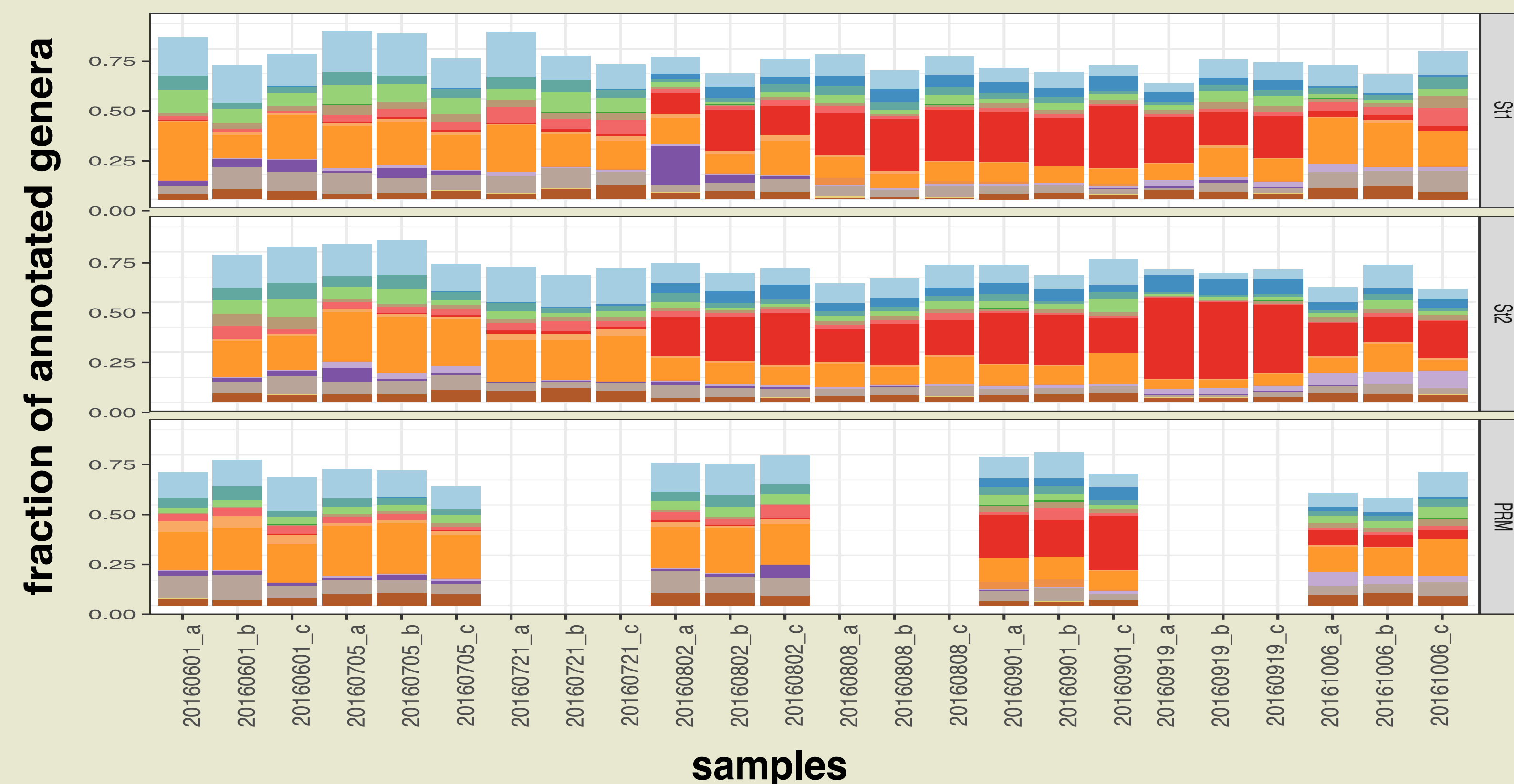
Things we find in the lake



Sampling sites

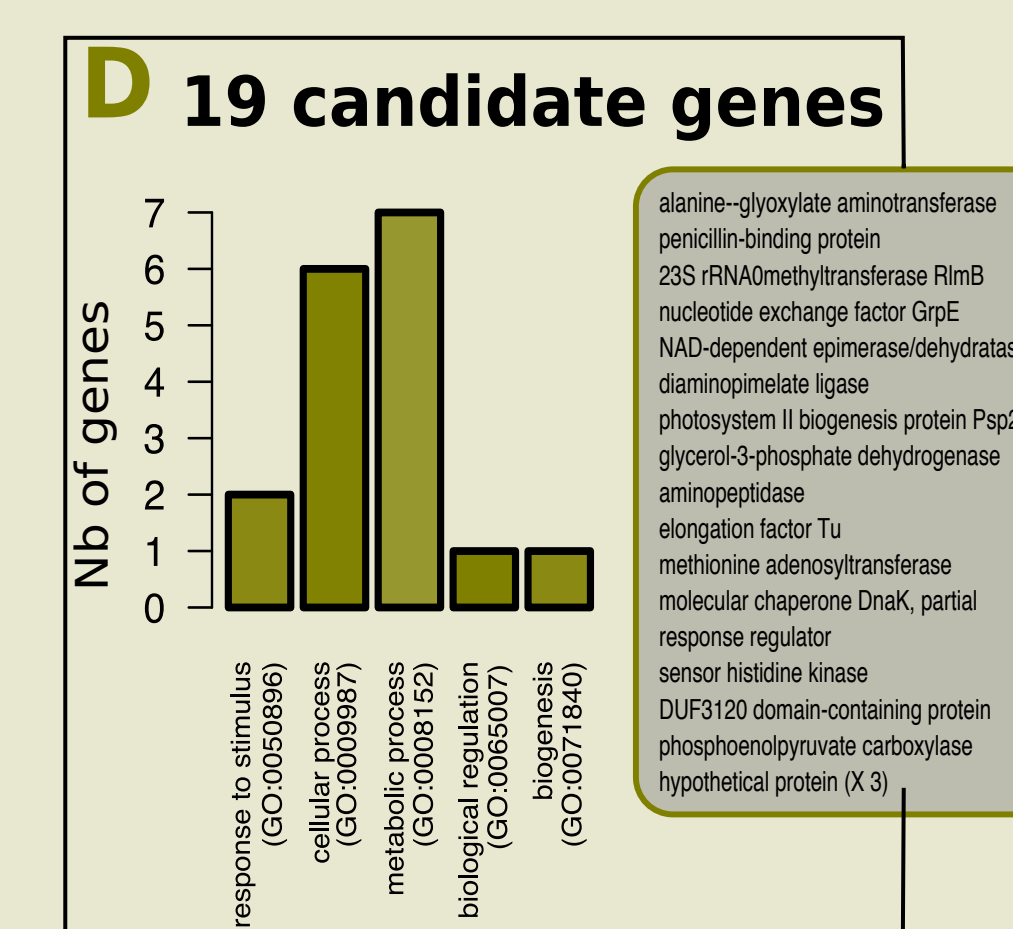
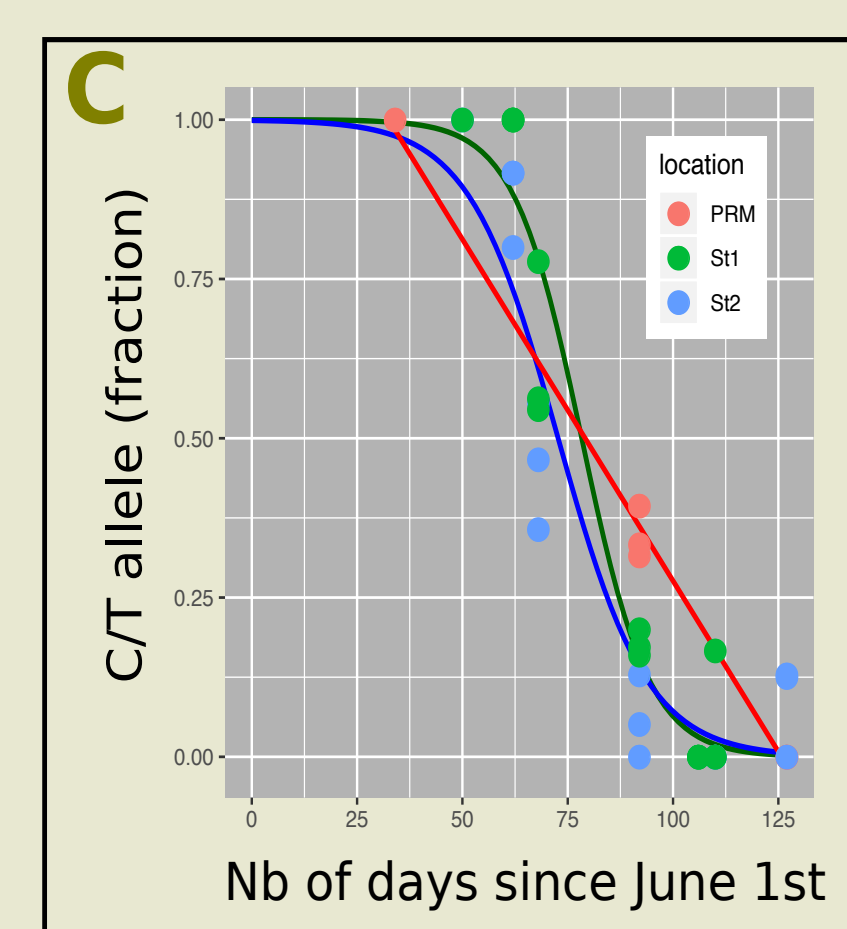
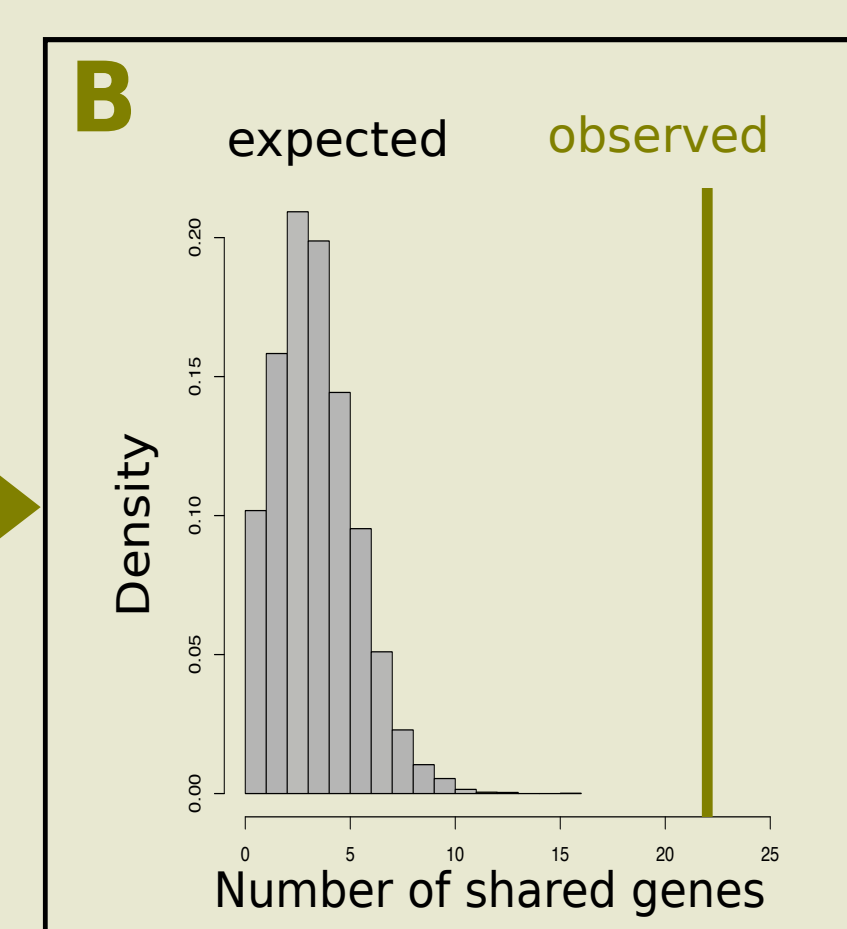
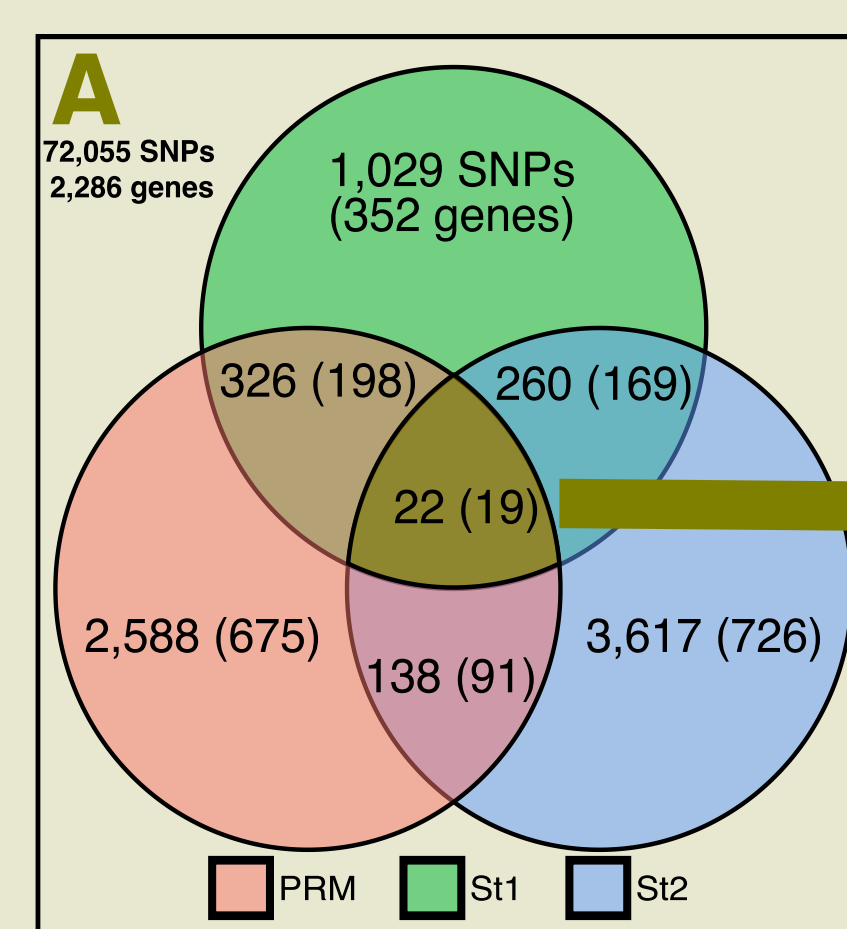
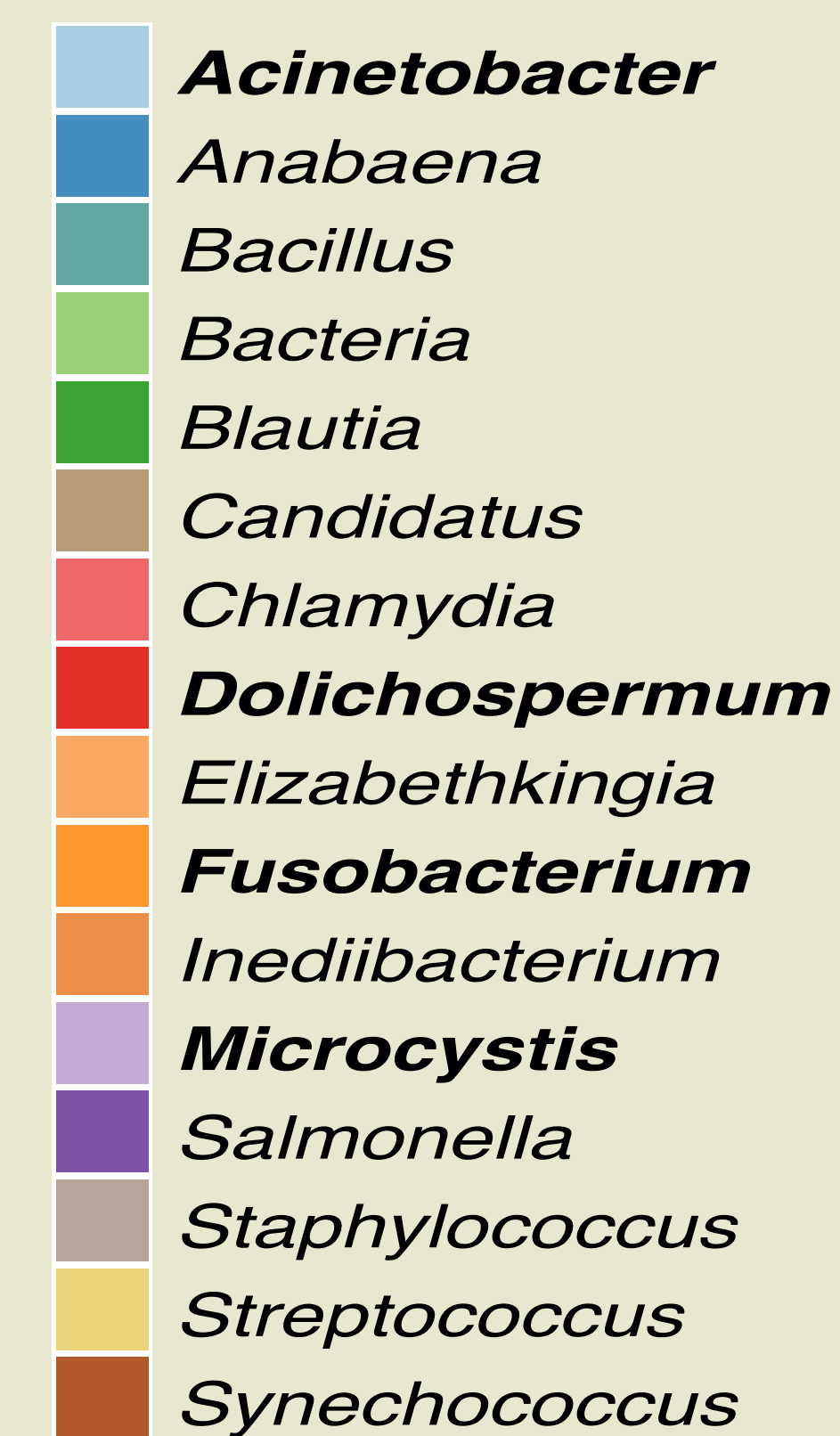


[Chlorophyll] peaked in mid-September resulting in a cyanobacterial bloom



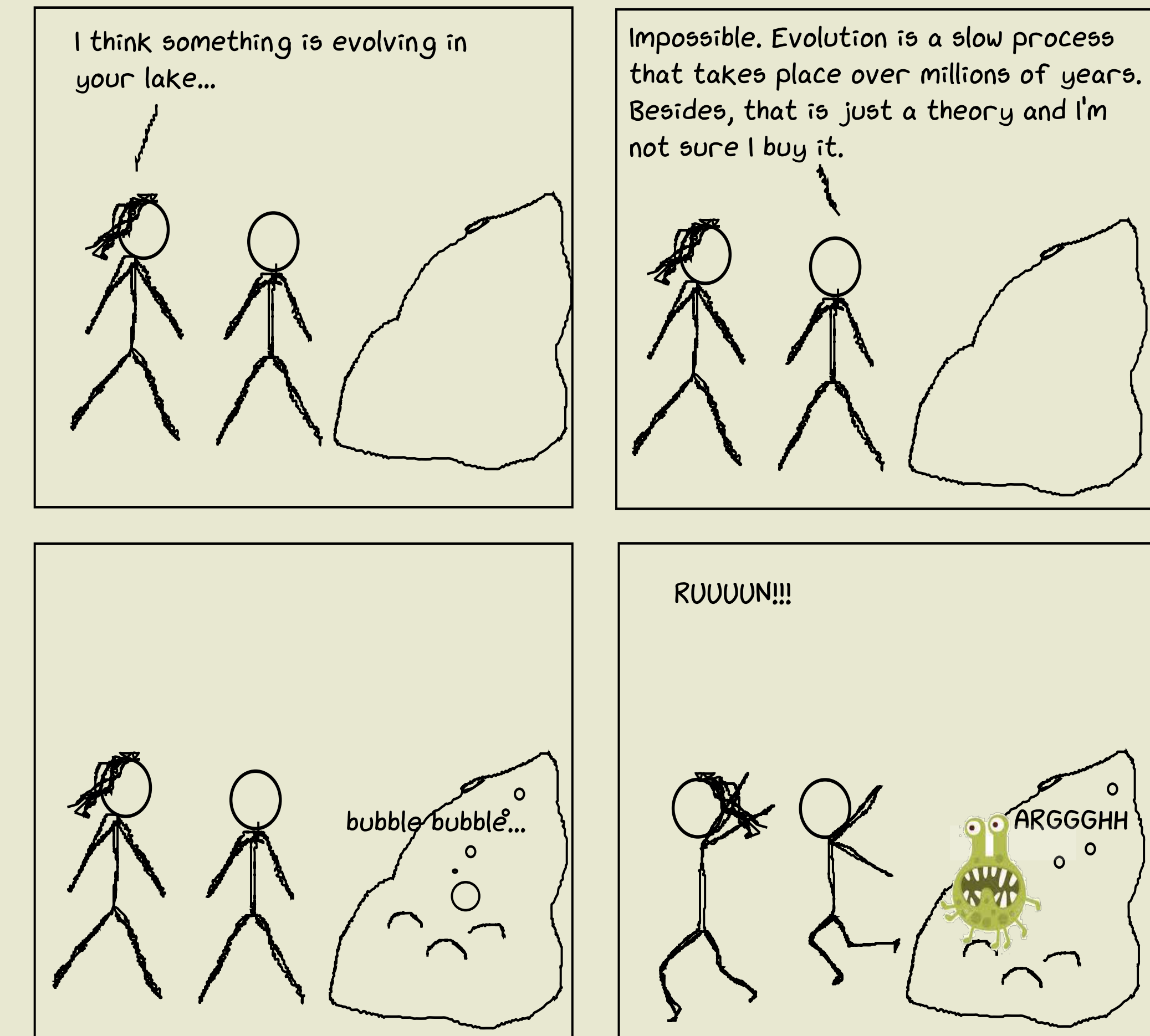
Communities dominated by Gram negative *Fusobacterium* & *Acinetobacter* prior to bloom. During bloom, *Dolichospermum circinale* rose in frequency, followed to a lesser extent by *Microcystis aeruginosa* in September.

Taxonomy



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

People paying for the science

