



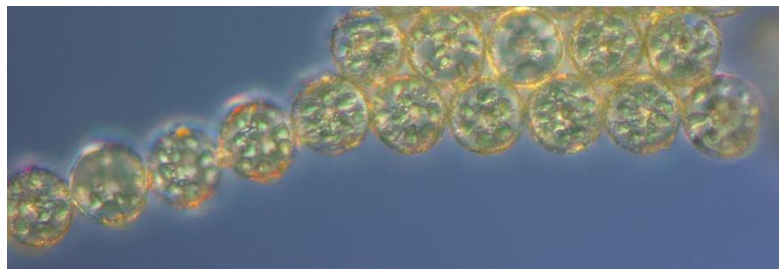
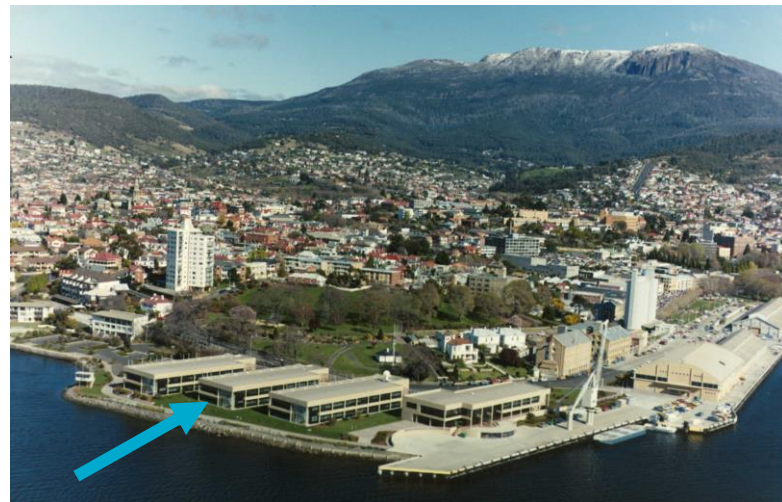
Genome evolution and long-term stress exposure increases toxin production in *Raphidiopsis raciborskii*

Anusuya Willis & Laurence Clarke
Australian National Algae Culture
Collection



Australian National Algae Culture Collection

Our collection is a significant resource holding living cultures of >1000 micro- and macro-algae strains. The collection supports research and is accessed by industry, universities and researchers.





Australian National Algae Culture Collection



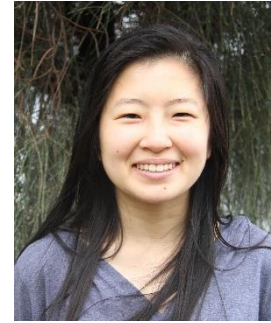
Anusuya Willis
Director

Cyanobacteria genomics
Adaptation
Algae Physiology



Ros Watson
Collection Manager

Algae Culture
Cryopreservation



Eileen Lee
Technician
Algae culture



Laurence Clarke
Cyanobacteria
Metabolic regulation
eDNA



Diane Purcell
Applied algal Characterisation
Industrial applications



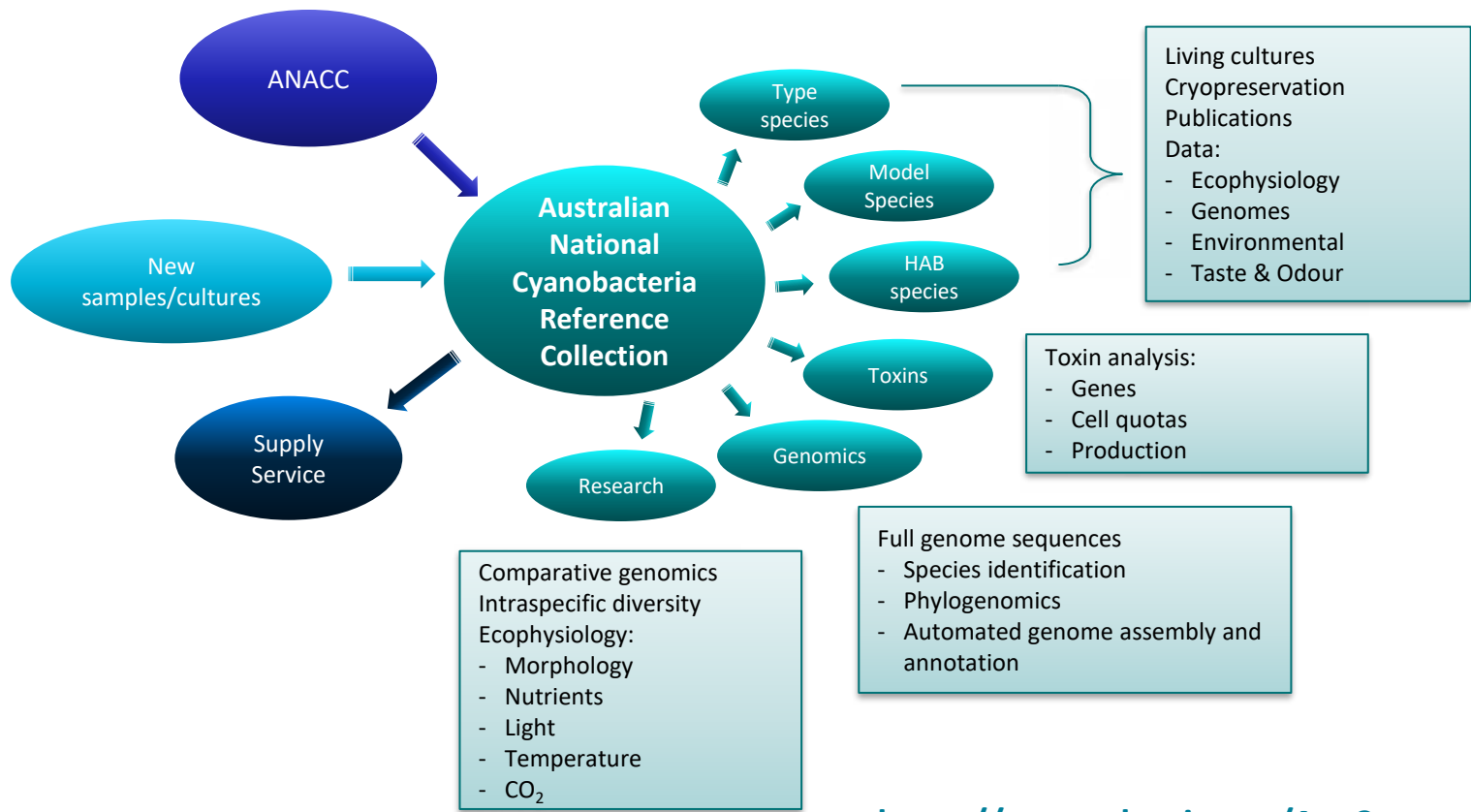
Cintia Iha
Seaweed Taxonomy
Genomics
Bioprospecting

Students

Kaya Baxter - PhD
Isis Londono - Masters
Josh Platt - Masters



Australian National Cyanobacteria Reference Collection



Cyanobacteria Diversity

Diverse

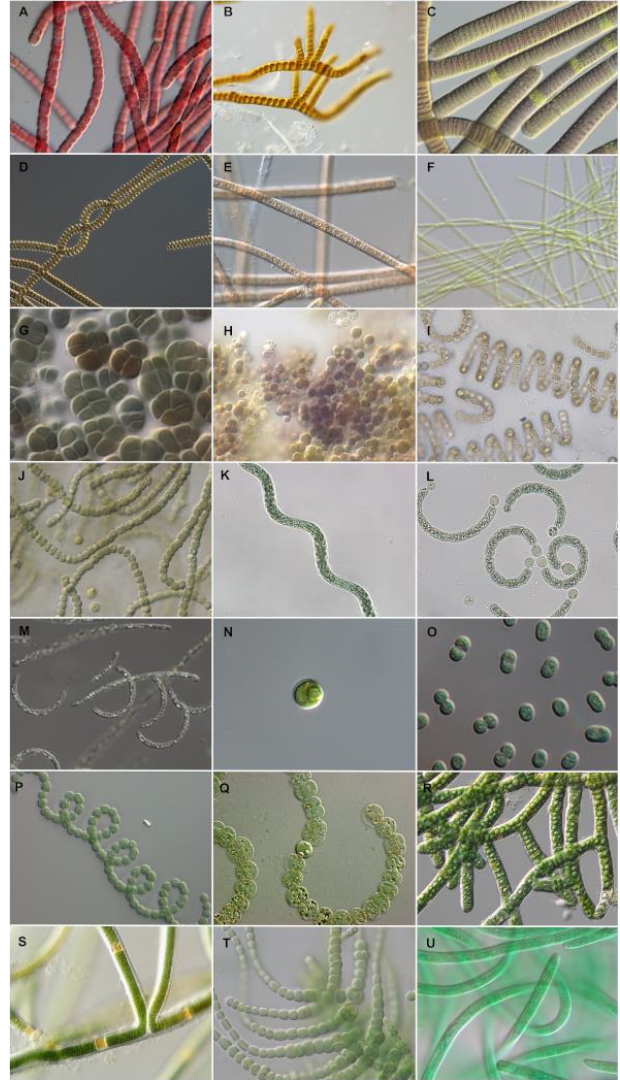
- Interspecific and intraspecific

Plastic

- Phenotypic plasticity
- Resilient to disturbances

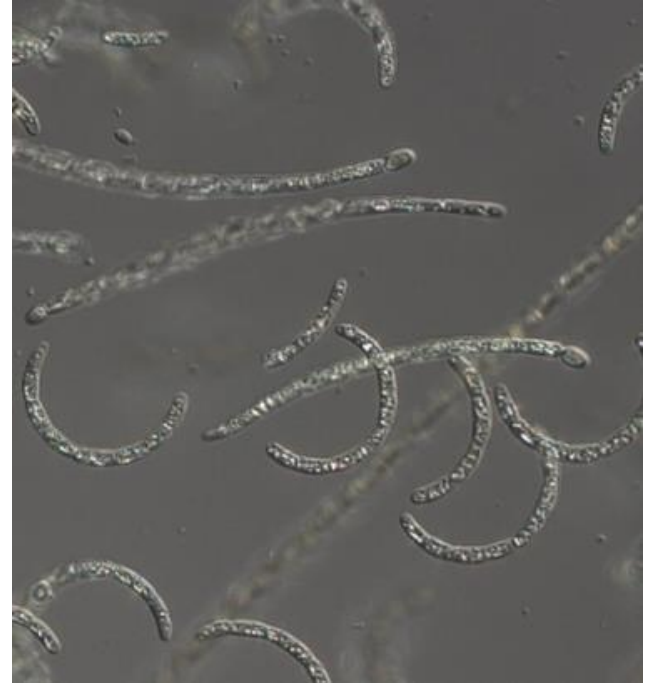
Adaptive

- Genome evolution
- Promotes speciation



Raphidiopsis raciborskii

- Freshwater
- Summer blooms
- Filamentous
- Coiled and straight trichomes
- \pm toxins
- Nitrogen fixing
- Small genomes: \sim 3.5 Mbp



Raphidiopsis raciborskii CS-506



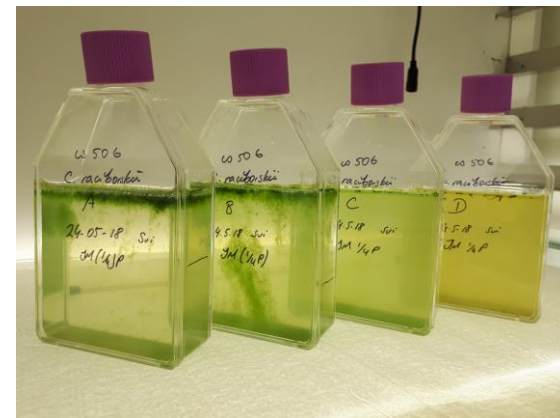
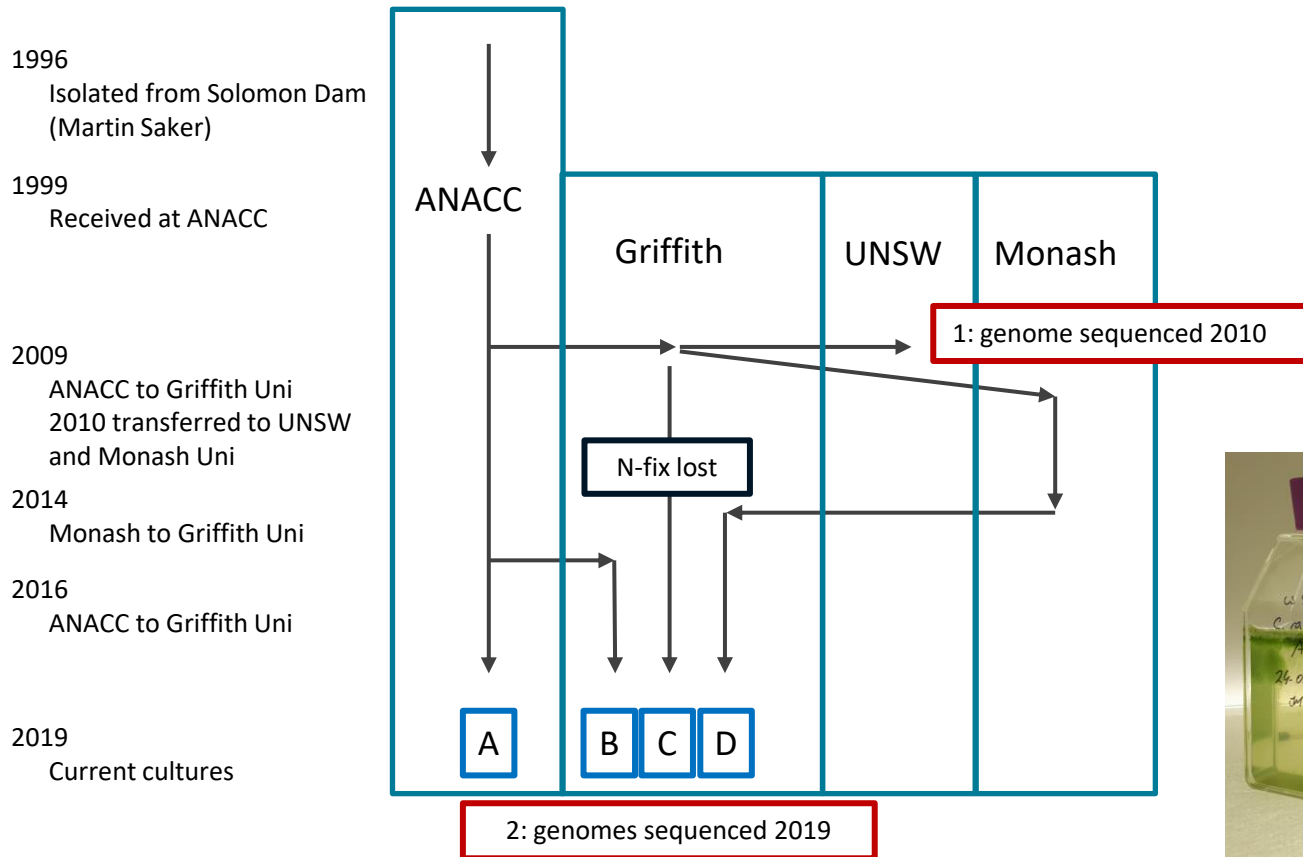
Living strains in collection

- Cyanobacteria are continually adapting to their conditions.





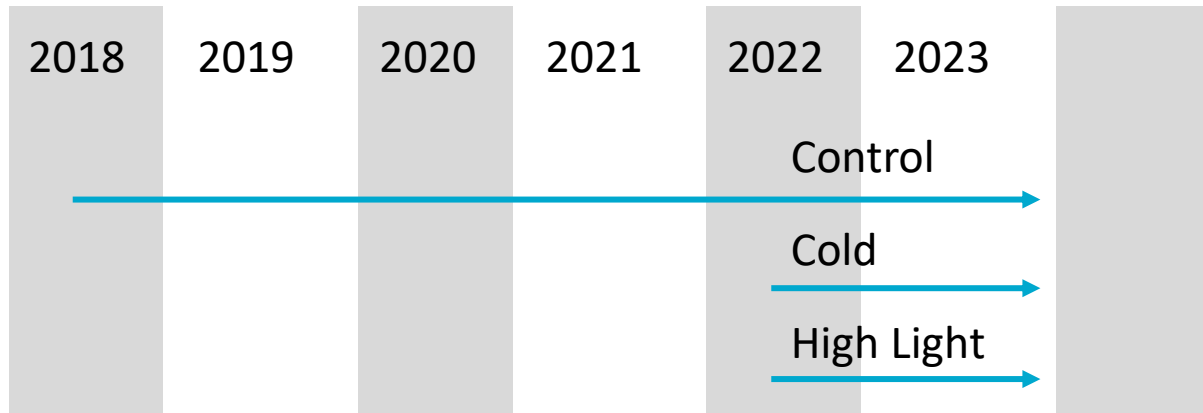
Culture History: *R. raciborskii* CS-506





Culture History: 2018 - present

- Four sister strains



Control:
Temp: 25°C,
Light: 10 $\mu\text{Mol photons m}^{-2} \text{s}^{-1}$

High Light
Temp: 25°C,
Light: 50 $\mu\text{Mol photons m}^{-2} \text{s}^{-1}$

Cold
Temp: 20°C,
Light: 10 $\mu\text{Mol photons m}^{-2} \text{s}^{-1}$



Long read: control

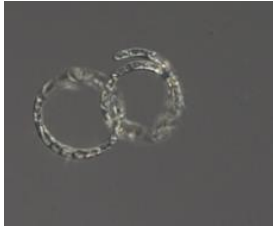
Short read: control + cold + HL

Transcriptome: control + cold + HL

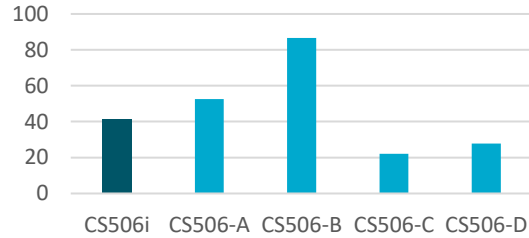
Epigenome: control + cold + HL

2018: morphology

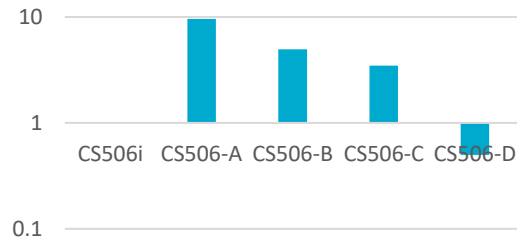
Shape



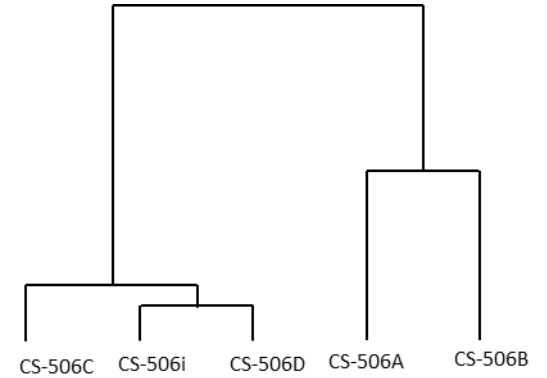
cell volume (um³)



change in toxin cell quota



Euclidean distance





Genetic Drift

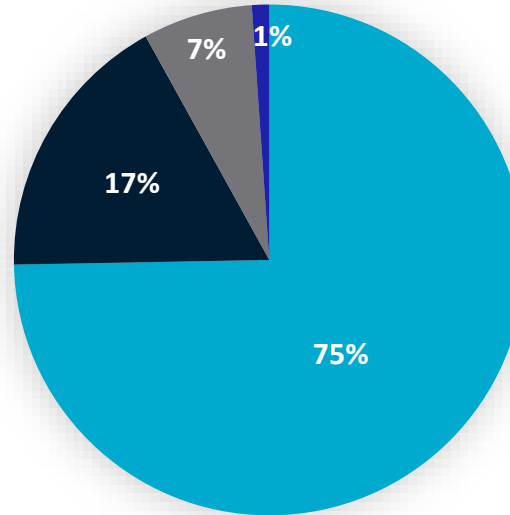
Variable+SNPs = 249 genes (8%)

- 92% = hypothetical protein
- CRISPR-Cmr
- Iron sulfur cluster regulator
- High-affinity carbon uptake
- Phospholipid ABC transporter

SNPs = 536 genes (17%)

- 55% = hypothetical protein
- 28 unknown function
- Transposase, mobile element, CRISPR
- Carbon dioxide concentrating mechanism
- Polyketide synthase

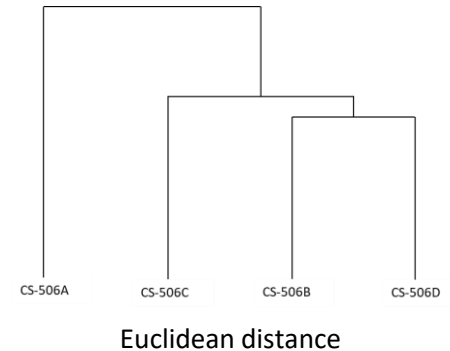
Genome comparison



■ CORE ■ COREwSNPs ■ Variable ■ VariablewSNPs

CORE = 3213 genes

- 33% = hypothetical protein
- Toxin biosynthesis cluster
- Nitrogen fixation
- Carbon metabolism



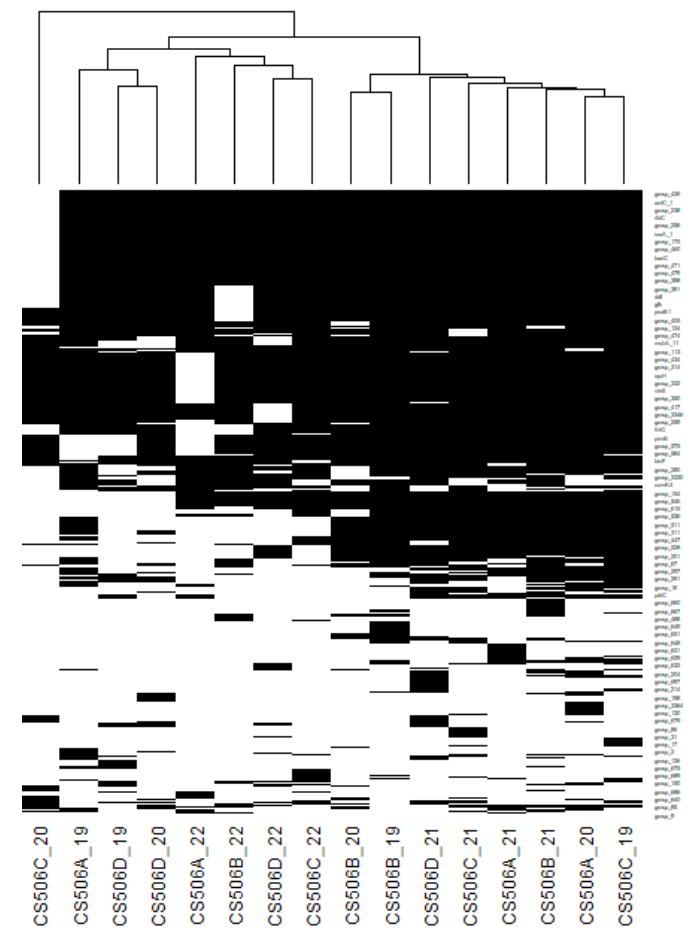


2018 - 2022

- Core genes 2673
- Shell genes 545
- Total genes 3387

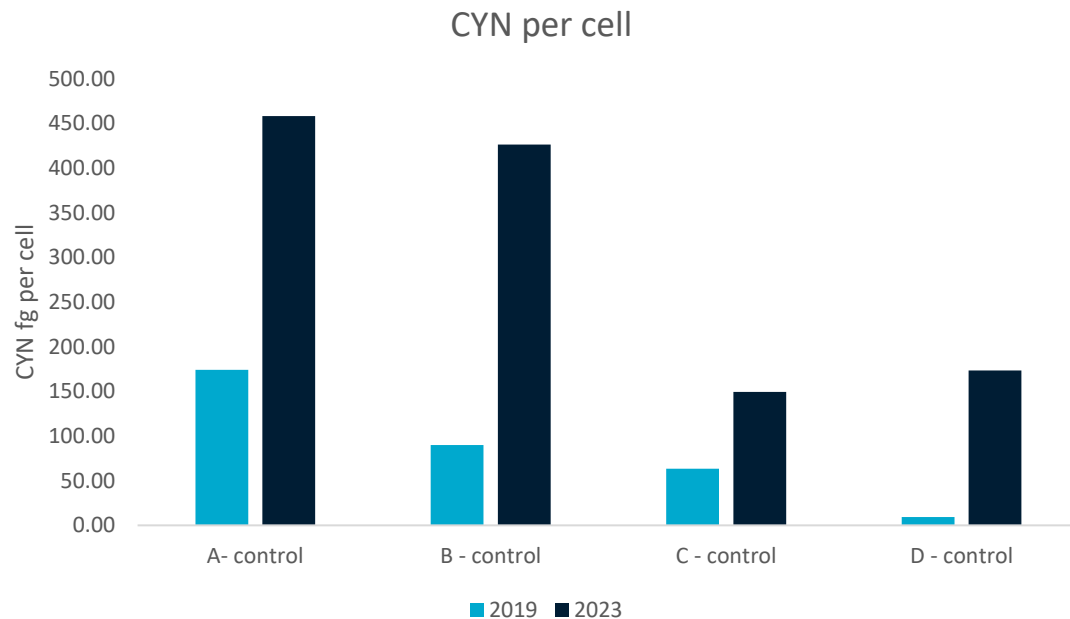
Control:
Temp: 25°C,
Light: 10 $\mu\text{Mol photons m}^{-2} \text{s}^{-1}$

variable genome of 2018-2023 strains



Gene presence/absence heatmap

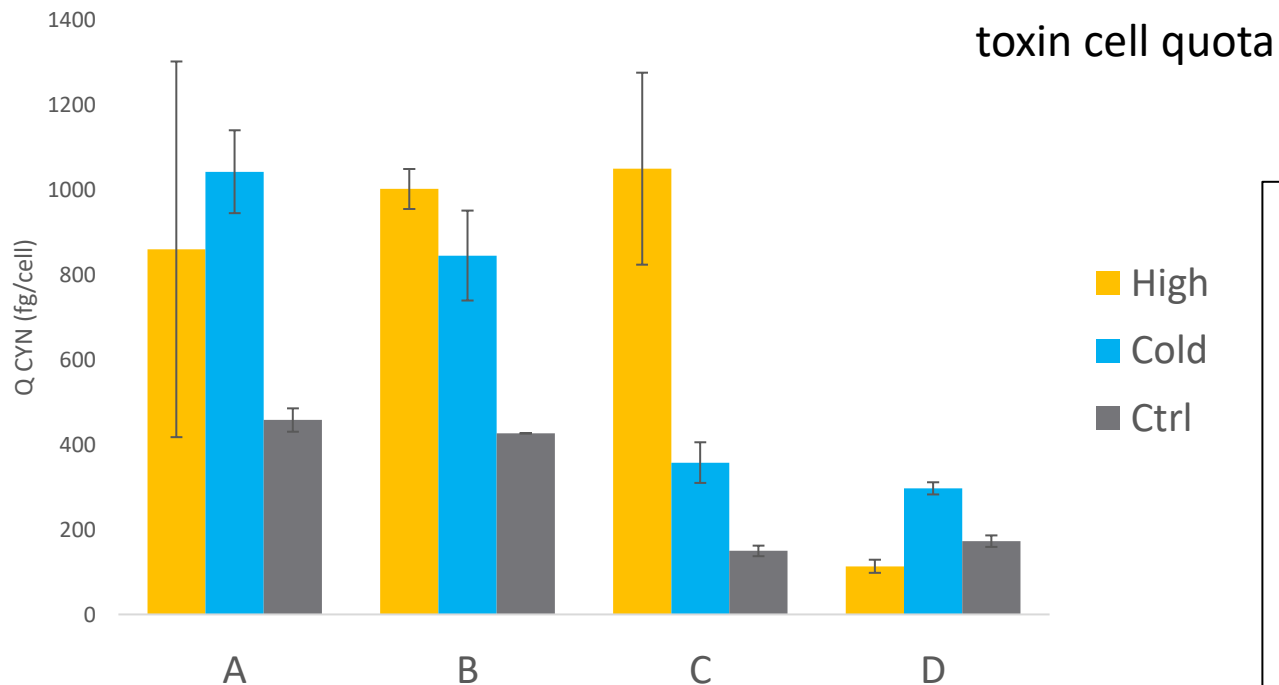
2018 – 2023: toxin per cell



Control:
Temp: 25°C,
Light: 10 $\mu\text{Mol photons m}^{-2} \text{s}^{-1}$



2023: High Light, Cold (12 months)



Control:
Temp: 25°C,
Light: 10 $\mu\text{Mol photons m}^{-2} \text{s}^{-1}$

High Light
Temp: 25°C,
Light: 50 $\mu\text{Mol photons m}^{-2} \text{s}^{-1}$

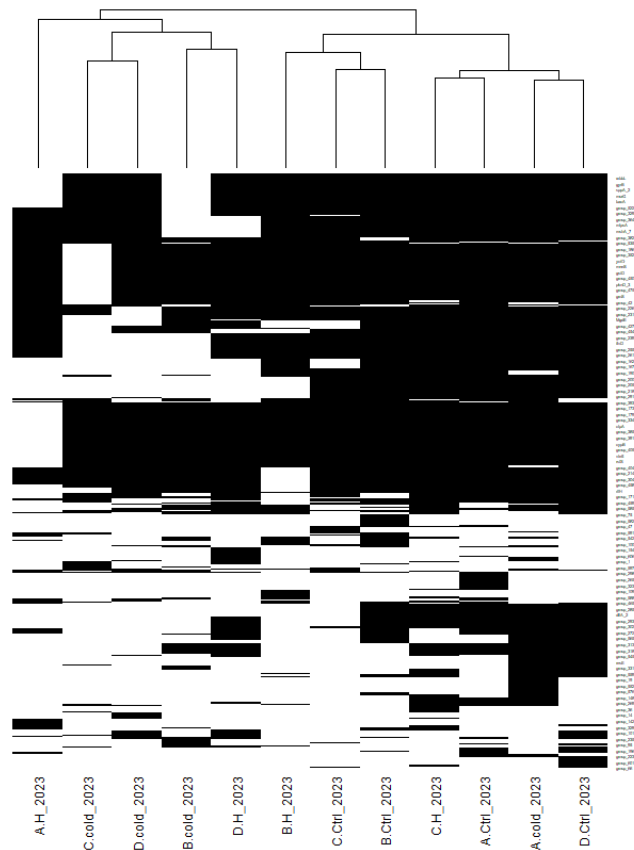
Cold
Temp: 20°C,
Light: 10 $\mu\text{Mol photons m}^{-2} \text{s}^{-1}$



Genome changes: 2023

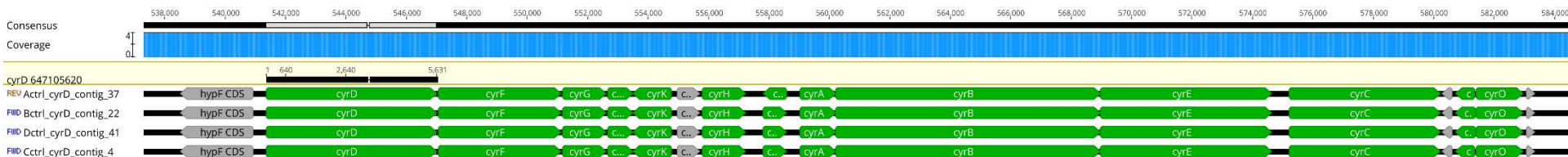
- Core genes 2713
- Shell genes 604
- Total genes 3317

variable genome of 2023 strains



Gene presence/absence heatmap

2023: long-read sequence



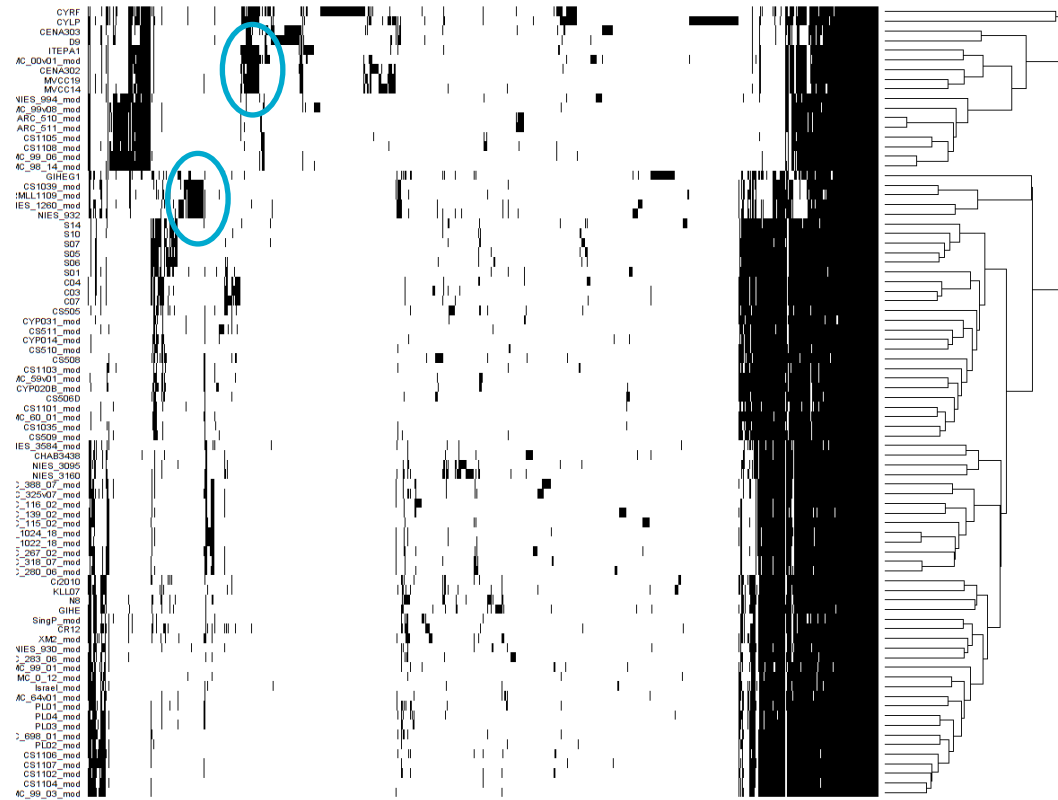
- CYN gene cluster: identical between strains

- Core genes 3293
- Shell genes 615
- Total genes 3908

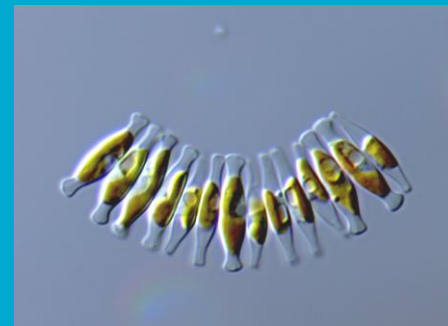
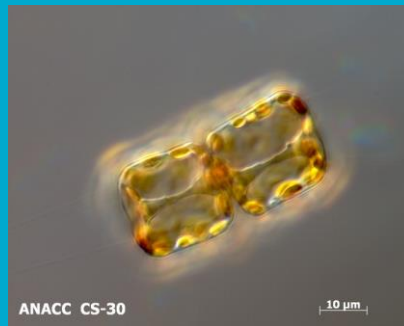
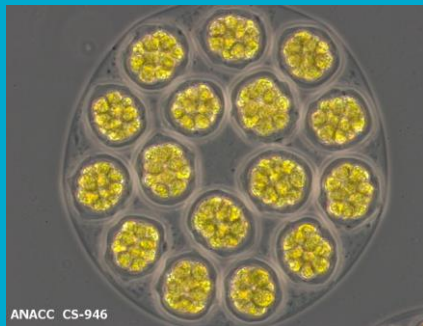
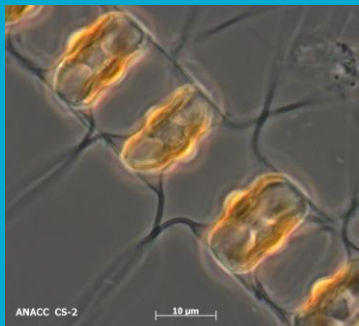


Conclusion

- No link to toxin cell quota from genome
- Stable core genome
 - High genome variability
- Cannot predict phenotype from genotype (yet)
- Genomes provide useful overview of physiological features
 - Less useful on fine scale intraspecific diversity.



Gene presence/absence heatmap



Thank you

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Environomics Future Science Platform
Advanced Engineering Biology Future Science Platform

