Integrating paleo-16S metagenomics with paleo-variables to infer historical trends of cyanobacterial composition within a freshwater lake

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INTRODUCTION

- Cultural eutrophication of freshwater systems has become a worldwide environmental issue.
- Systematic approaches are frequently initiated only after serious problems have already arisen.
- Long-term monitoring data are often limited or lacking.
- Paleolimnological investigations (e.g. physicochemical and pigment analyses and subfossil remains) can be used to reconstruct historical environmental trends within an aquatic ecosystem.

Study Site - Lake Diefenbaker (LD):
- Large multi-purpose reservoir (built 1967), located in southern Saskatchewan, Canada.
- Provides water for 45% of Saskatchewan residences (SWSA 2012).
- Area residents suggest an increase in algae bloom frequency in recent years.
- Sedimentary pigment analyses suggested an increasing cyanobacterial abundance in the down-reservoir arms (Gardiner and Qu’Appelle arms).

The emergence of problematic cyanobacteria can result in taste-and-odor issues and the production of toxic secondary metabolites (e.g. hepat- and neuro-toxins).

The goal of this project was to reconstruct ecological trends and investigate relationships among the algal/cyanobacterial community, toxin-producing genes, and physicochemical parameters (i.e. environmental proxies).

MATERIALS AND METHODS

- Sediment cores were collected using a Giew Gravity Corer and sectioned at 1-cm increments.
- Genomic DNA (gDNA) was extracted from sediment using E.Z.N.A Soil DNA kits.
- PCR amplification was carried out using two cyanobacterial 16S rRNA primers (renamed Primer-A and -B for simplicity) modified from Nöbel et al. (1997) with illumina recommended overhangs.
- Sequencing was completed using a MiSeq Desktop Sequencer.
- Secondary analysis was completed using a cloud-based microbiome seq analysis workflow in BaseSpace (https://basespace.illumina.com).

RESULTS AND DISCUSSION

Figure 2. Circos plot showing the relative abundance (size of the circles) among cyanobacteria taxa over time, (primer -A and -B) for sediment cores collected from the Gardiner and Qu’Appelle arms of Lake Diefenbaker, Saskatchewan, Canada.

Table 1. Generalized linear model (GLM) of sampling sites, primers and paleo-physicochemical variables for normalized abundance data of Cyanobacteria genera in Lake Diefenbaker, Saskatchewan, Canada.

Figure 3. Alpha diversity of cyanobacterial Operational Taxonomic Units (OTUs) at the two sampling sites over time (years). Linear regressions between alpha diversities (number of observed OTUs; richness, and Shannon-Wiener index; evenness) and time (years) are given. Shaded areas are the 95% confidence intervals for each model. The equation and adjusted r^2 for the specific linear regressions are given in each panel. Alpha diversities are significantly different among years (Observed: ANOVA-year p = 1.93e-06***, site p = 3.3e-07***, primer p = 0.48; Shannon: ANOVA-year p = 0.015, site p = 0.782, primer p = 0.153).

REFERENCES

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