Phytoplankton Ecology in an Oilsands End Pit Lake

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Abstract

Alberta oilsands mining and extraction have produced over 1 trillion litres of tailings wastewater (AER 2021) containing several compounds of concern (Cossey et al. 2021). End-pit lakes are a low-cost, long-term proposed strategy of tailings reclamation that sequester tailings in a mined-out pit under a freshwater cap. Through dilution and biogeochemical processes, the water cap should over time develop into a functional ecosystem integrable with the local watershed (Cossey et al. 2021, Saborimanesh 2021). Established in 2012, Base Mine Lake is currently the only full-scale pilot end pit lake developed by the Alberta oilsands industry and requires further investigation to validate end pit lakes as a tailings reclamation technology (Cossey et al. 2021). The first stage of reclamation requires the development of a phytoplankton community, which serves as the base of the aquatic food web (CEMA 2012).

The primary objective of this study was to characterize the phytoplanktxon community over time in BML from 2016 to 2021 to determine how community composition and abundances shift over seasons and years. Characterization used Illumina gene sequencing targeting 16S rRNA, 18S rRNA, and 23S rRNA gene amplicons, giving relative abundance data over time for phytoplankton. Cell count data was used to verify gene sequencing results. The phytoplankton community composition and diversity in Base Mine Lake was compared to those of a freshwater reservoir and a tailings pond.

Analysis of gene sequencing data revealed that major genera of phytoplankton included *Cryptomonas* (*Cryptophyceae*), *Choricystis* (*Trebouxiophyceae*), *Euglena* (*Euglenales*), and *Synechococcus* (*Synechococcales*), all of which appear to exhibit seasonal blooms during 2016-2021 (Fig. 1). Sequencing analysis also indicated that Base Mine Lake and its freshwater input source Beaver Creek Reservoir shared many of the same genera but different strains/species of those genera. This suggested that the distinct conditions in each aquatic site may have selected for distinct strains. Diversity analyses of gene sequencing data revealed that phytoplankton diversity in Base Mine Lake was intermediate between that of its freshwater input reservoir and a tailings pond.

There currently exists no low-cost, large-scale treatment method that fully reclaims tailings water (Cossey et al. 2021, Saborimanesh 2021). End-pit lakes retain tailings until recalcitrant compounds are degraded to near-environmental levels (Saborimanesh 2021, CEMA 2012), but further research is required before end-pit lakes can be approved as a viable reclamation technology (Cossey et al. 2021). Although research is available now on native microbial communities in tailings waters, knowledge on their contributions to an aquatic microbial food web is limited (Saborimanesh 2021). This proposed research is the first of its kind to examine the contribution of phytoplankton to end pit lake food web ecology. This will advance knowledge of end-pit lakes as a reclamation strategy in effort to reduce the environmental footprint of tailings water.

Keywords

mine reclamation, community analysis, gene sequencing

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Ethics and security

Not applicable.

Author contributions

CCF and PFD were responsible for project conception, project funding, and experimental design. CCF and AVS were responsible for rRNA gene sequencing. CCF, AVS, and PFD

were responsible for analysing and interpreting the data. CCF and PFD wrote the paper, with comments from AVS. All authors read and approved the final manuscript.

Conflicts of interest

The authors have declared that no competing interests exist.

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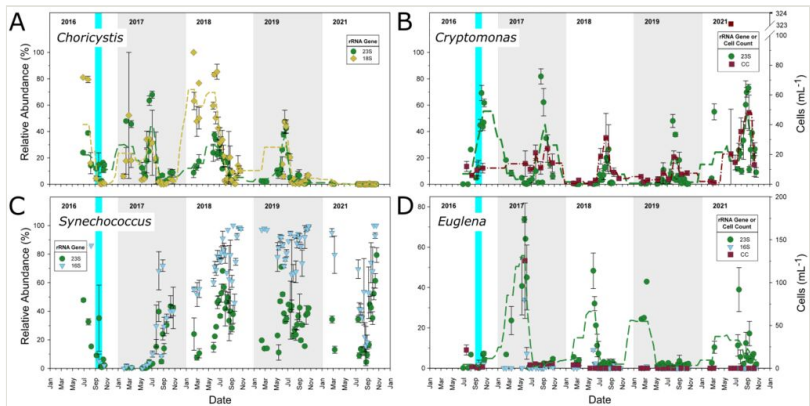- Saborimanesh N (2021) Toward sustainable remediation of oil sands fine Tailings - A review. Journal of Environmental Management 288 (112418): 1-10. [In English]. https://doi.org/10.1016/j.jenvman.2021.112418

Figure 1.

Relative abundances of the four major algal genera in BML surface waters: (**A**) *Choricystis*, (**B**) *Cryptomonas*, (**C**) *Synechococcus*, and (**D**) *Euglena*, based on 23S, 16S and/or 18S rRNA gene amplicon sequencing Also included for B) and D) are microscopic cell count data. Data points are means of three platforms ± 1 SEM. Where error bars are not seen they are contained within the symbol. The blue bar indicates alum addition. Dashed lines indicate running averages calculated based on sequential segments of the full dataset.