

# Microbial Community Dynamics in Base Mine Lake, the First End-Pit Lake in the Alberta Oil sands Industry

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## Abstract

Oil extraction from bitumen in the Athabasca region of northeastern Alberta, comprises a large segment of the Canadian economy. However, the process of oil extraction from surface mined oil sands ores results in diverse environmental issues including disturbance of land areas and habitats for wildlife, as well as production of large volumes of fluid tailings containing many compounds of concern for the environment. Land reclamation strategies of most oilsands operations propose the construction of end-pit lakes (EPL) to contain and biodegrade tailings, eventually becoming integrated into local watersheds. We used 16S/18S rRNA gene amplicon and metagenome sequencing to monitor prokaryotic and eukaryotic communities in the first full-scale pilot EPL of the Canadian oilsands, Base Mine Lake (BML) Fig. 1, over 6 years from 2015-2021, and compared them with communities from two active tailings ponds, Mildred Lake Setting Basin (MLSB) and Southwest in-Pit (SWIP), as well as with communities from a more natural freshwater body, Beaver Creek Reservoir (BCR). Alpha diversity in BML is intermediate to diversities in active tailings ponds and a natural lake, although highly variable with time, depth, and season. Microbial communities in BML resemble neither freshwater lake nor active tailings communities, although a structural shift of either microbial community occurred every year, and 2021 was a year of the most profound effect. Moreover, metabolic functions in BML also shifted every year, with the most dramatic shift for photosynthesis-related genes. Temporal changes among protists identified in BML were characterized by enrichment of species designated as picophytoplankton: *Cryptomonas*, *Mychonastes*, *Trebouxiophyceae*, and *Dinobryon*, and among bacterial genera by enrichment of common freshwater lake species or bacterioplankton: *Ca. Fonsibacter*, *Sporichthyaceae*, *Ca. Planktophila*, *Microbacteriaceae* ML602J-51, *Ilumatobacteraceae* CL500-29 group. Network analysis identified a potential microbial consortium between newly enriched species of picophytoplankton and bacterioplankton. Heterotrophic bacteria with streamlined

genomes may overcome auxotrophic limitations by scavenging metabolites and other compounds produced by phototrophs presumably via chemotaxis behaviour. We propose that the formation of the consortium might serve as a biomarker for reclamation process of an oil sands tailings pond.

## **Keywords**

End-pit Lake, oil sands, oilsands, fine fluid tailings, consolidated tailings, mine reclamation, bioremediation, water cap technology, alum, community analysis, 16S/18S rRNA gene amplicon sequencing, microbial consortium.

## **Presenting author**

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## **Conflicts of interest**

The authors have declared that no competing interests exist.

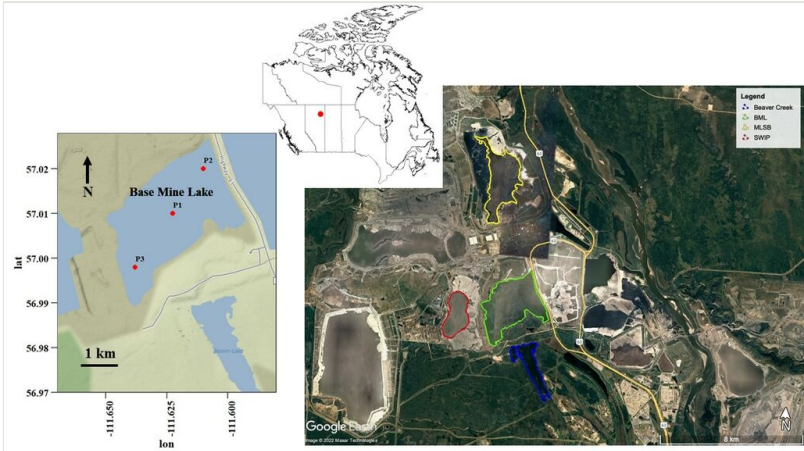


Figure 1.

Geographical location of BML on the map of Canada, coordinates of BML and three sampling platforms by latitude and longitude, a satellite image of the oil sands operation area with sampling sites highlighted by color: BML, MLSB, SWIP, and BCR.