

Comparing the microbial communities in and End-pit lake, active tailings ponds and freshwater bodies from the Athabasca oil sands region

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Abstract

The Athabasca oil sands region in northern Alberta is home to one of the largest bitumen deposits in the world. Oil sands are mostly recovered via surface mining and the oil extraction is achieved with hot caustic water and diluents, a process that produces liquid tailings waste (CEC 2020, Schramm et al. 2000). It is estimated that 1 m³ of bitumen produces around 4 m³ of tailings, which are contained in large tailings ponds (Mikula et al. 1996). End-pit lakes are a potential strategy to reclaim mining pits created by oil sands mining. They may be formed by filling a mined-out pit with tailings and then capping it with a layer of fresh water. With time, tailings undergo a dewatering process in which they become denser and release water to the cap water (Charette et al. 2012).

Base Mine Lake (BML) is the first full-scale demonstration end-pit lake in the Canadian oil sands industry. This former tailings pond was initially capped in 2012 with a 5 m layer of freshwater to allow for consolidation of the tailings and the stimulation of aerobic microbial communities to biodegrade the organic pollutants. Since its establishment, BML has been extensively monitored to assess the improvement in water quality.

The present research focused on determining how the eukaryotic and bacterial communities in BML compare to those in local freshwater bodies and active tailings ponds. Eleven reference sites, including freshwater reservoirs, natural lakes, and 9- to 14-year-old excavated pits filled with water, also known as borrow pits, were sampled along with 5 active tailings ponds and BML during the summer of 2022. Microbial communities were assessed via next-generation sequencing of PCR amplicons of the 16S rRNA gene for bacteria and the 18S rRNA gene for eukaryotes.

Alpha-diversity analysis of the eukaryotic communities showed that BML has greater species richness and evenness than active tailings ponds, but lower than freshwater systems. The bacterial community in both BML and active tailings ponds is dominated by *Proteobacteria*, but the relative abundance of *Actinobacteriota* is similar between BML and freshwater. Beta-diversity analysis revealed that eukaryotic and bacterial

communities in BML cluster distinctly from both the freshwater controls and active tailings ponds, however, the composition of the eukaryotic community shows some overlap with certain freshwater systems (Fig. 1). The results of this research suggest that, 10 years after its formation, the microbial communities in BML are intermediate between an active tailings pond and a freshwater lake.

Keywords

bacterial community, eukaryotic community, alpha diversity, beta diversity

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Conflicts of interest

The authors have declared that no competing interests exist.

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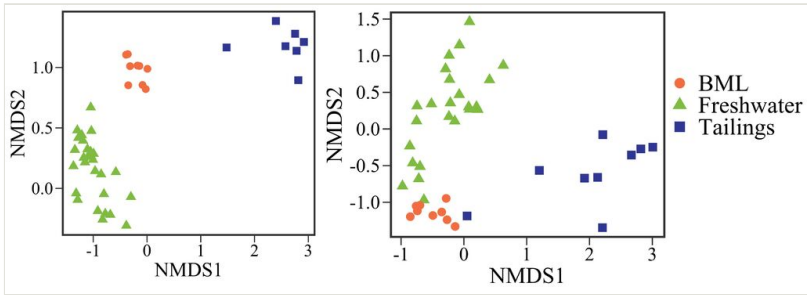


Figure 1.

Nonmetric multidimensional scaling analysis of bacterial (left) and eukaryotic (right) communities in BML (circles), freshwater systems (triangles), and active tailings ponds (squares) from the summer of 2022.