Oilsands contain bitumen, a heavily biodegraded source of oil found in vast quantities within the Athabasca basin of northeastern Alberta, Canada. Surface mining operations of shallow deposits result in large quantities of waste tailings known as oilsands process water (OSPW). OSPW is collected in tailings ponds, where it is acutely toxic to a variety of organisms due to a vast group of organics known as Naphthenic Acids (NAs). Microbial degradation of the NAs is a promising method for remediation, as within OSPW exist microorganisms capable of metabolizing NAs. Here we explore options for harnessing the naturally occurring OSPW communities for potential future use in an ex-situ aerobic bioreactor, hypothesizing that the diverse structure of biofilms suits them to the task. We establish that there are naturally occurring bacteria within the OSPW, capable of forming robust, multispecies biofilms, which are in turn capable of degrading NAs. Multispecies biofilms were compared to multispecies planktonic cultures, and to both biofilm and planktonic single species cultures. Up to 8 different model NAs with various levels of toxicity and recalcitrance were tested, as well as the effect of available nutrients and complementary carbon source. All biofilms were grown using the Calgary Biofilm Device. Gas Chromatography reveals that multispecies cultures are capable of degrading a wider variety of NAs than are single species cultures, highlighting the need for a communal effort. Furthermore, the complementary carbon source has a tangible effect on the ability of the multispecies biofilms to initiate the degradation of the NAs.

Fungal biofilms are applicable to removal of pollutants in biofilters in nonsterile conditions but the bacterial effect is poorly known. Interactions between fungal and bacterial organisms were investigated in preformed or nascent biofilms and the enzyme activities and degradation capacity measured. Different effects of *Escherichia coli* and *Pseudomonas aeruginosa* on degradation of an anthraquinone dye by fungal biofilms colonizing polyurethane foam (PUF) in the presence of bacteria (104-106 CFU) at pH 4.5 and 6 were observed in a 10-day experiment: the former bacterium inhibited degradation whereas the latter not. Production of peroxidases but not of laccase was reduced; the bacteria could not remove the dye. The fungal biomass amount colonizing PUF was unaffected by bacteria, *E. coli* and *P. aeruginosa* increased their respective counts by 1 to 3 and 0 to 2 orders of magnitude. In contrast, the degradation capacity (85-95% decolorization rate at pH 5.5) of preformed 1-week-old fungal biofilms colonizing PUF or pinewood was not affected by the added 106 CFU of *E.coli* in a 4-week experiment. The fungal growth was reduced 1.4-fold and bacterial counts increased up to 2-fold compared to bacterial controls. The results demonstrate a significant resistance of preformed *I. lacteus* biofilms to bacterial stress which is important for practical application. The work was supported by the project IAAX00200901.