**Microbial Analysis of Miocene-Era Bentonite Clay**

Rachel C. Beaver, Josh D. Neufeld

*Department of Biology, University of Waterloo, Waterloo*

To help ensure the long-term integrity of a proposed deep geological repository (DGR) for storage of Canada’s used nuclear fuel, it is essential to characterize microorganisms that may be associated with DGR design components, especially bentonite clay that will surround the used fuel containers (UFCs). Metabolisms of various microorganisms could influence the evolution of a DGR. For example, sulfate-reducing bacteria (SRB) could lead to the corrosion of metal components of UFCs and microorganisms that produce gases could create permeability fissures within the repository. In this study, the microbial communities within four bentonite clay cores from the Tsukinuno clay deposit (Japan), a naturally occurring Miocene-era bentonite deposit, were studied. The goal of this research was to investigate the abundance and composition of microbial communities in these ancient bentonite clay samples as an analogue to future bentonite within a DGR. Our results show low abundances of culturable microorganisms, including SRB. DNA sequencing results demonstrate relatively consistent microbial community compositions dominated primarily by sequences associated with phylum *Proteobacteria*. Low correlations were measured between microbial community composition and concentrations of various metals, non-metals, and clay varieties, suggesting that there may be other factors responsible for the core-dependent variations in microbial community composition observed.