

**THE MICROBIOLOGY OF SERPENTINIZING ULTRAMAFIC INTRUSIONS: INSIGHTS FROM THE KIRKLAND LAKE KIMBERLITES** M.O. Schrenk<sup>1</sup>, S. Hamilton<sup>2</sup>, G. Lacrampe-Couloume<sup>3</sup>, B. Sherwood Lollar<sup>3</sup> <sup>1</sup>Michigan State University, 288 Farm Lane, East Lansing, MI 48824 (schrenkm@msu.edu), <sup>2</sup>Ontario Geological Survey, Sudbury, ON, Canada <sup>3</sup>University of Toronto, Toronto, ON, Canada

To date, a majority of studies relating serpentinization to microbial activities have focused upon the aqueous alteration of ophiolites, or upon hydrothermal systems near mid-ocean ridges. The alteration of ultramafic intrusions in continental settings represents an additional, distinct type of environment that may sustain biogeochemical processes related to serpentinization and play important roles in controlling the exchange of carbon and reducing power between the deep Earth and the surface biosphere. Serpentinizing diamondiferous kimberlite intrusions represent a geographically and contextually distinct system to explore the relationship between serpentinization, carbon, and life. A series of deep, ultrabasic wells were sampled near Kirkland Lake, Ontario, Canada in 2012 and 2013 for coupled geochemical and microbiological analyses. The wells were high pH (between 9 and 12) and contained elevated concentrations of H<sub>2</sub> and hydrocarbon gases. However, the wells exhibited methane isotopic signatures distinct from one another, which reflect different sources and/or processing mechanisms for the resulting gas. Parallel analyses of microbial abundances and community composition provided insight into the biogeochemistry of these ecosystems. While hydrogen-driven chemolithoautotrophy appeared to be common across all of the wells based upon the predominance of Betaproteobacteria in tag sequencing analyses of 16S rRNA genes, sequences associated with known methanogens were partitioned between the wells. Shotgun metagenomics data from 4 of the wells allowed us to document the potential substrates utilized for microbial methanogenesis, and highlighted relationships between putative acetogens and methanogens in the groundwater ecosystem. These results are in stark contrast to existing data on continental serpentinites, which have provided relatively scant evidence for biological methane cycling. Putative biogeochemical roles for the subsurface microbial communities will be discussed and compared to other known serpentinizing ecosystems. These data are significant in that they provide insight into microbial activities and biogeochemical signatures in serpentinizing environments associated with ultramafic intrusions, which may be a prominent setting in extraterrestrial environments without active plate tectonics.