

## Comparative metagenomics of Arctic landscapes.

Tatiana Vishnivetskaya<sup>1,2\*</sup> (tvishniv@utk.edu), Xiaofen Wu<sup>1</sup>, Wyatt A. Cyr<sup>1</sup>, Katie Sipes<sup>1</sup>, Andrew Steen<sup>1</sup>, Andrey A. Abramov<sup>2</sup>, Elizaveta Rivkina<sup>2</sup>, **Karen G. Lloyd**<sup>1</sup>

<sup>1</sup>University of Tennessee, Knoxville Tennessee 37996 USA

<sup>2</sup>Institute of Physicochemical and Biological Problems of Soil Science, Pushchino, Russia

With increasing availability of metagenome datasets from different locations in Arctic, we have a unique opportunity to compare the diversity and functionality of microbial communities to better predict microbial responses to climate changes. Samples from the permafrost active layer were collected from three geographic locations, Bayelva, Svalbard (78.92062 N, 11.84158 E), Axel Heiberg Island (AHI), Canada (79.415 N, 90.75833 W), and Bykovsky Peninsula, Russia (71.783167 N, 129.41086 E) and were processed for the total genomic DNA extraction followed by metagenome sequencing. Samples from Bayelva (n=3) and AHI (n=12) were collected in early spring when ground was frozen using portable drill, while samples from Bykovsky (n=5) were collected in late summer from open pit. The amount of DNA was low for Bykovsky (10.7-14.5 ng/g soil) and Bayelva (13.3 ng/g soil), while DNA content was significantly higher for AHI and showed decrease from 8.5 µg/g in upper 5 cm layer to 2.6 µg/g at 35 cm depth to 0.9 µg/g at 65 cm. Bayelva and AHI represent mineral soil with a dominance of pebbles and coarse sands, while the soil in Bykovsky is loam with trace of humus. Analysis of metagenomes showed differences in microbial diversity depending on depth. Integrated analysis of metagenomes showed that upper 5-7 cm layer (n=5) is dominated by Alphaproteobacteria (23.9% vs 12.0%) and Acidobacteria (2.9% vs 0.9%), while Actinobacteria (27.5% vs 20.6%), Bacteroidetes (1.3% vs 0.5%), Clostridiales (4.1% vs 2.4%), Thermotogales (0.2% vs 0.4%) and methanogenic Archaea (1.7% vs 0.9%) were more abundant in deeper layers (n=16). Alphaproteobacteria were represented mostly by aerobic and microaerophilic methanotrophic, methylotrophic, and nitrogen-fixing bacteria. Bacteria identified in metagenomes of the upper active layer were able to metabolize a wide range of organic carbon sources, degrade complex aromatic compounds, obtain energy through photosynthetic reactions or form symbiotic relation with plants during nitrogen fixation. This analysis indicates similarities in microbial community between the low organic carbon mineral soils collected from geographically different locations.

US Department of Energy, Office of Science, Office of Biological and Environmental Research, Genomic Science Program (DE-SC0020369)