McGill

The impact of an active soil microbial community on greenhouse gas emissions in arctic cryosols.

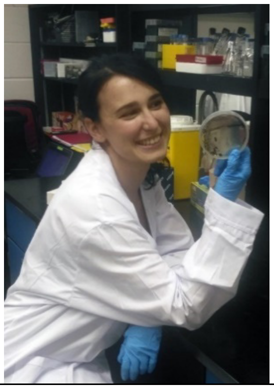
Oral Defence by PhD Candidate Ianina Altshuler

Natural Resource Sciences

March 22nd, 2019 @ 13:15 — Raymond Building, Room R4-047

Abstract

Anthropogenic climate change is thought to have a disproportionately larger impact on polar regions, resulting in permafrost thaw and microorganism mediated greenhouse gas (GHG) emission. Permafrost soils contain between 25-50 % of the total soil organic carbon pool and as permafrost thaws, this carbon will become accessible to microbial degradation. Carbon dioxide (CO_2), methane (CH_4), and nitrous oxide (N_2O) are the most important GHGs and their flux from permafrost affected soils contributes to a positive feedback loop of climatic warming. However, our understanding of how microorganisms contribute to the biogeochemical cycling and flux of these gases in Arctic soils remains limited. Topology of the Arctic landscape has a significant impact on GHG emissions as evidenced by the flux at the ice-wedge polygon (IWP) terrain. The wetter tough soils exhibited higher emissions of CO_2 and N_2O, but lower uptake of CH_4, compared to the drier polygon interior soils. Topology also affected the composition of the overall microbial community, with the trough soils having a higher proportion of Betaproteobacteria, Deltaproteobacteria, and Bacterioidetes but a lower proportion of Acidobacteria compared to polygon interior soils. The community of nitrogen fixers, methanotrophs, and denitrifiers was also affected by the topology with all three groups showing unique structure. Moreover, these organisms appear to be active in the soils, as evidenced by metatranscriptomic RNA analysis. Based on stable isotope probing (SIP) the active methanotrophs in these soils are likely part of the USCα cluster of currently uncultured high-affinity methanotrophs. SIP analysis coupled with metagenome binning lead to the identification of an Alphaproteobacterial MAG that contained many of the methane cycling genes including a soluble methane monooxygenase. In addition to topology affecting the microbial community structure, key microbial members across the IWP terrain also appear to have positive and negative impacts on other microbial species. This was determined by developing a novel hybrid network analysis to determine species interactions within the microbial community. Overall members of Proteobacteria, Candidatus Rokubacteria, and Actinobacteria phyla tended to have a positive impact, while members of Verrucomicrobia and Acidobacteria had a negative impact on other microbials members. These results indicate that both environmental abiotic parameters and biotic interactions impact the microbial community structure and possibly GHG fluxes from soils.



About the Candidate

Ianina Altshuler holds a Honours BSc. in Biological Sciences from York University and an MSc. in Environmental Sciences from Windsor University. She joined the Whyte lab in 2013 as a PhD student working on Arctic biogeochemical cycles.