

Metagenomic analysis of microbial communities along the Mackay Glacier 'ecotone' reveals soils with diverse functional potentials

Van Goethem MW^{1,2}, Makhalanyane TP^{1,2}, Vikram S^{1,2}, Hall G³, Woodborne S^{3,4}, Van de Peer Y^{2,5,6,7}, Hogg ID⁸, Cowan DA^{1,2*}

¹ Centre for Microbial Ecology and Genomics, University of Pretoria, Pretoria, South Africa

² Genomics Research Institute, University of Pretoria, Pretoria, South Africa;

³ Mammal Research Institute, University of Pretoria, Pretoria 0028, South Africa;

⁴ iThemba LABS, Private Bag 11, Wits 2050, South Africa;

⁵ Department of Plant Systems Biology, VIB, 9000 Ghent, Belgium;

⁶ Department of Biotechnology and Bioinformatics, Ghent University, 9000 Ghent, Belgium;

⁷ Bioinformatics Institute Ghent, 9000 Ghent, Belgium;

⁸ School of Science, The University of Waikato, Private Bag 3105, Hamilton, New Zealand

mwvangoethem@gmail.com

'Ecotones' are defined as transitional zones between two or more distinct ecosystems. These regions are often the sites of the most rapid change and can therefore provide extremely sensitive indicators of climatic changes (1). Understanding the abiotic factors which shape soil microbial diversity and functional capacity along ecotones may provide a valid model for deciphering the effects of climate change. Here we applied shotgun metagenomic sequencing and isotopic analysis to 19 soil communities representing transitional sites within and adjacent to the Mackay Glacier 'ecotone' that lies between northern and southern Victoria Land, Antarctica. Metagenomic analysis revealed extensive bacterial colonisation (94.6% of sequences), with lower numbers of Viruses (3.38%), Eukaryotes (1.64%) and Archaea (0.34%). *Bacteroidetes*, *Proteobacteria*, *Cyanobacteria* and *Acidobacteria* were the dominant phyla in all soil communities and represented ~80% of metagenomic sequences between them, which is consistent with hyperarid Dry Valley soil surveys (2).

Annotated functional genes related to important soil carbon cycles were assigned primarily to these dominant bacterial phyla. Carbon cycling pathways include aerobic respiration, aerobic and anaerobic carbon fixation and carbon monoxide oxidation. Isotopic data showed that soil carbon is likely cycled via the Calvin-Benson cycle (C3), which was complete in most metagenomes. Soil nitrogen was extremely low in all soils (<0.04%). Isotopic analysis suggested that soil nitrogen is heavily recycled and is supported by the prevalence of nitrogen cycling genes in the metagenomes, including those involved in nitrogen assimilation, denitrification and nitrogen mineralization. Assimilatory sulphate reduction and sulphur mineralisation genes were found in all metagenomes with major assignments belonging to the phylum *Bacteroidetes*. Viral populations were dominated by the bacteria-infecting families *Siphoviridae* and *Myoviridae* of the order Caudovirales.

Network analysis showed that viruses exhibit positive co-occurrences with their hosts as well as a predominance of positive interactions between autotrophic community members. Subtle changes in microbial community structure resulted from differences in soil pH and phosphorous content, although the best predictor of differences in community structure was altitude. Overall this study provides insights into the microbial biodiversity patterns along the Mackay Glacier ecotone, which is a system that harbours diverse soil microbial communities with the capacity for driving multiple nutrient cycling pathways in spite of extreme environmental constraints imposed by cold.

1. Kupfer JA, Cairns DM. The suitability of montane ecotones as indicators of global climatic change. *Progress in Physical Geography*. 1996;20(3):253-72.
2. Cowan DA, Makhalyane TP, Dennis PG, Hopkins DW. Microbial ecology and biogeochemistry of continental Antarctic soils. *Front Microbiol*. 2014;5:154.