Pan-Arctic drivers of glacial microbial community structure and function

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Glaciers are important components of Earth's climate and water system. Physical and chemical aspects of glaciers have been studied intensively; however, glacial microbiology is still in its infancy. Glacial surfaces have been considered barren for a long time, yet distinct habitats can be found to harbour species from all three domains of life. We recently showed that snow and ice algae are critical and prolific primary colonisers and producers in these environments [1]. Furthermore, due to the development of pigmentantion they have a significant effect on surface albedo. However, the relationships between environmental conditions and microbial abundance, diversity and function on snow and ice surfaces in the Arctic are still poorly understood.

Here we present the first comprehensive metagenomic study of various snow, slush and ice habitats from 21 glaciers spanning the European Arctic (Svalbard, Sweden, Iceland, Greenland) sampled during the 2012-2014 melting seasons. The biome composition and function and the geochemical parameters that affect their growth have been characterized. Our results reveal a cosmopolitan distribution of snow and ice algae and that our habitat classification is valid across all studied Arctic glaciers. Algal composition within a single habitat is more similar than within a geographic location. On the other hand, the bacterial composition shows a more endemic distribution. Archaea were also detected in all samples. Overall functionality (e.g., metabolic fingerprints, pigments, fatty acids) seems to be controlled by nutrient availability and trends for C/N/P ratios could be established.

[1] Lutz et al. (2014). *FEMS Microbial Ecology* ***89***(**2**), 402-414.