



Insight into biogeochemical inputs and composition of Greenland Ice Sheet surface snow and glacial forefield river catchment environments.

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The volume of freshwater transported from Greenland to surrounding marine waters has tended to increase annually over the past four decades as a result of warmer surface air temperatures (Bamber et al 2012, Hanna et al 2008). Ice sheet run off is estimated to make up approximately of third of this volume (Bamber et al 2012). However, the biogeochemical composition and seeding sources of the Greenland Ice Sheet supraglacial landscape is largely unknown. In this study, the structure and diversity of surface snow microbial assemblages from two regions of the western Greenland Ice Sheet ice-margin was investigated through the sequencing of small subunit rRNA genes. Furthermore, the origins of microbiota were investigated by examining correlations to molecular data obtained from marine, soil, freshwater and atmospheric environments and to geochemical analytes measured in the snow. Snow was found to contain a diverse assemblage of bacteria (Alphaproteobacteria, Betaproteobacteria and Gammaproteobacteria) and eukarya (Alveolata, Fungi, Stramenopiles and Viridiplantae). Phylotypes related to archaeal Thaumarchaeota and Euryarchaeota phyla were also identified. The structure of microbial assemblages was found to have strong similarities to communities sampled from marine and air environments, and sequences obtained from the South-West region, near Kangerlussuaq, which is bordered by an extensive periglacial expanse, had additional resemblances to soil originating communities. Strong correlations were found between bacterial beta diversity and Na⁺ and Cl⁻ concentrations. These data suggest that surface snow from western regions of Greenland contain microbiota that are most likely derived from exogenous, wind transported sources.

Downstream of the supraglacial environment, Greenland's rivers likely influence the ecology of localized estuary and marine systems. Here we characterize the geochemical and biotic composition of a glacial and glacial forefield fed river catchment in the northern region of Pituffik, near Thule, throughout the 2011 melt season. Betaproteobacteria dominated all DNA and RT-rRNA assemblage libraries (mean abundance 38.0 ± 10.5 %), and a further 21 classes were identified with > 0.5 % mean abundance. Rhodospirillum related operational taxonomic units featured as the most abundant assemblages in both DNA and RT-rRNA sequence libraries (6.61 % and 8.35 % respectively). Correlations of bacterial assemblages to both dissolved and particulate chemistries were calculated, and comparisons of assemblages to sequence libraries from likely seeding environments were utilized to suggest the functionality and predominant sources of biota. Together, these studies look to address the biogeochemical sources and composition of samples from hydrological entry and exits points of the Greenland Ice Sheet.