

The Source and Fate of Microbes on the Greenland Ice Sheet

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Ice sheets and glaciers are important components of Earth's hydrologic system and provide a strong feedback on the climate system. They are being disproportionately affected by global warming and are melting at an unprecedented rate. The key parameter affecting the melt rates is the rapid change in albedo of snow and ice surfaces. Although the physical and chemical components of albedo are relatively well understood, the role that biology plays in changing albedo has been neglected so far. Microbes, in particular snow and ice algae, play a crucial role in decreasing albedo [1], yet, we know very little about the dynamics of microbes or their interactions with the physical and chemical components in changing the albedo on the Greenland Ice sheet (GrIS).

Here we present results from the Black & Bloom field campaign on the GrIS during the 2016 summer melt season. Various snow, ice as well as aerosol samples were collected from 3 separated areas for analysis of the microbial diversity. The bacterial and eukaryotic (e.g., algae, fungi) community compositions were characterized by Illumina sequencing of the 16S rRNA, 18S rRNA and ITS2 genes. Aerosol and surface samples were cross-correlated to evaluate sources and fates of microbes on the GrIS. The algal community compositions of all samples were dominated by the ice algae *Ancylonema nordenskiöldii* with minor contributions of *Chlamydomonadaceae* and *Trebouxiaceae* taxa. In contrast, the bacterial and fungal community compositions were very similar within one habitat (snow vs. ice vs. air), but showed large differences between the habitats.

Our data thus far reveal that eukaryotes in snow and ice were seeded from the air, while bacteria and fungi in the snow were from air inputs, but surface ice showed different microbial dynamics. Combined with non-microbial particulates we aim to derive a bioalbedo parameter for the GrIS. [1] Lutz, S. et al. (2016), Nat. Commun. 7, doi:10.1038/ncomms11968.