

Chemosynthetic microbial processes in glacier outflows in Southern Greenland

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The Earth's surface has been dominated by cycles of glacial advance and retreat for more than two million years. Interestingly, microbial life has likely been a part of these movements from the on set of glaciation, as microbial life evolved mechanisms to thrive in the cryospheric environment. We now recognize that an active microbial biome (Bacteria, Archaea and Eukaryotes) is present in the snow, cryocoonites and supraglacial lakes (surface), englacial (within the ice), and in the subglacial environment. Recent work indicates that in addition to aiding mineral weathering in the subglacial environment, microbes are integral components of the glacial carbon cycle. Currently Earth's glaciers are retreating at unprecedented rates, thus releasing microorganisms, stored bio-active carbon and minerals to downstream ecosystems.

Here we present results from a coupled microbiology and geochemical survey from four glaciers in the southern Greenland Ice Sheet (GIS). 16S rRNA gene amplicon sequencing reveals that microbial phylogenetic diversity and coverage were similar across all glaciers sampled, despite differences in outflow pH. NMDS ordination of all samples collected show that all GIS terminal samples were more similar to each other, despite physical separation, than to downstream coastal outlet samples, fjords, and proglacial lakes. Chemolithoautotrophic sulfur and iron oxidizing-like microorganisms were abundant in three of the glaciers. Additionally, dissolved organic carbon from the glacier's terminal outflow has a distinct microbial signature that decreases with distance from the glacier, suggesting that microbial autotrophic processes, in part, are likely an import source of DOM in glacial outflows.