

The Undiscovered Biosynthetic Potential of the Greenland Ice Sheet Microbiome

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Abstract

The Greenland Ice Sheet is a biome primarily driven by microbial activity. Despite the harsh conditions, such as cold temperatures, low nutrient levels, high UV radiation in summer, and long dark winters, various niches can be found on the ice sheet that can support organisms capable of withstanding these challenges. During the summer, eukaryotic glacier ice algae grow in large quantities on the ice surface, accompanied by a community of bacteria, fungi, and viruses. Additionally, cryoconite holes and snow serve as habitats with their own distinct microbial communities. Nevertheless, the microbiome of supraglacial habitats remains poorly studied, leading to a lack of representative genomes from these environments. In this study, we conducted a comprehensive investigation of the supraglacial microbiome using both culturing-dependent and -independent methods. We compared genomes obtained through metagenomic sequencing (133 high-quality metagenome-assembled genomes or MAGs) and whole genome sequencing (73 bacterial isolates) to the metagenome assemblies to determine their abundance within the total environmental DNA. Interestingly, the isolates obtained in this study were not dominant taxa in their respective habitats, unlike the MAGs.

Under-investigated extremophiles, such as those inhabiting the Greenland Ice Sheet, may offer an untapped reservoir of undiscovered chemical diversity. We cataloged the biosynthetic potential of these organisms by examining the presence of biosynthetic gene clusters (BGCs) in the obtained genomes. To accomplish this, we utilized tools like the Antibiotics and Secondary Metabolites Analysis Shell (AntiSMASH) and the Biosynthetic Gene Similarity Clustering and Prospecting Engine (BiG-SCAPE) to mine these genomes and subsequently analyze the resulting predicted BGCs. We identified a total of 849 BGCs, which were organized into 411 gene cluster families (GCFs). Notably, the MAGs and isolate genomes exhibited distinct pools of biosynthetic diversity, with only 5 GCFs shared between the two groups. The cryoconite genomes yielded the most unique GCFs. Furthermore, we found evidence for the capacity of these microbes to produce

antimicrobials, carotenoids, and osmoprotectants. However, many of the obtained BGCs could not be matched to similar, previously described BGCs, highlighting the vastness of the undescribed biosynthetic potential present in microbes from the Greenland Ice Sheet.

Keywords

supraglacial habitats, extremophiles, metagenomic sequencing, biosynthetic gene clusters

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Conflicts of interest

The authors have declared that no competing interests exist.