

## Contamination of the Arctic reflected in microbial metagenomes from the Greenland ice sheet

Globally emitted contaminants accumulate in the Arctic and are stored in the frozen environments of the cryosphere. Climate change influences the release of these contaminants through elevated melt rates, resulting in increased contamination locally. Our understanding of how biological processes interact with contamination in the Arctic is limited. Through shotgun metagenomic data and binned genomes from metagenomes we show that microbial communities, sampled from multiple surface ice locations on the Greenland ice sheet, have the potential for resistance to and degradation of contaminants. The microbial potential to degrade anthropogenic contaminants, such as toxic and persistent polychlorinated biphenyls, was found to be spatially variable and not limited to regions close to human activities. Binned genomes showed close resemblance to microorganisms isolated from contaminated habitats. These results indicate that, from a microbiological perspective, the Greenland ice sheet cannot be seen as a pristine environment.

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### [Åben publikation](#)

## Upstream freshwater and terrestrial sources are differentially reflected in the bacterial community structure along a small Arctic river and its estuary

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## Bacterial diversity in snow on North Pole ice floes

The microbial abundance and diversity in snow on ice floes at three sites near the North Pole was assessed using quantitative PCR and 454 pyrosequencing. Abundance of 16S rRNA genes in the samples ranged between 43 and 248 gene copies per millilitre of melted snow. A total of 291,331 sequences were obtained through 454 pyrosequencing of 16S rRNA genes, resulting in 984 OTUs at 97 % identity. Two sites were dominated by Cyanobacteria (72 and 61 %, respectively), including chloroplasts. The third site differed by consisting of 95 % Proteobacteria. Principal component analysis showed that the three sites clustered together when compared to the underlying environments of sea ice and ocean water. The Shannon indices ranged from 2.226 to 3.758, and the Chao1 indices showed species richness between 293 and 353 for the three samples. The relatively low abundances and diversity found in the samples indicate a lower rate of microbial input to this snow habitat compared to snow in the proximity of terrestrial and anthropogenic sources of microorganisms. The differences in species composition and diversity between the sites show that apparently similar snow habitats contain a large variation in biodiversity, although the differences were smaller than the differences to the underlying environment. The results support the idea that a globally distributed community exists in snow and that the global snow community can in part be attributed to microbial input from the atmosphere.

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