

# 東ブレッガー氷河-氷河後退域におけるバクテリア群集の変化

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## Bacterial community change between glacier and glacier foreland around Austre Brøggerbreen, Svalbard

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Tundra soil covered most of high arctic terrestrial area and slightly little change of material cycles caused by climate change affect their biodiversity. After glacier retreat, microbial structure called Biological Soil Crust (BSC) is developed on glacier foreland soil surface and these will supply nutrient and water to moss and vascular plant. On the upstream glacier ice surface, cryoconite granule (CG), which are around 1mm diameter granule formed by filamentous cyanobacteria, are widely spread over the bare ice are of glacier. Rapid retreat of glacier terminus and increase of supraglacial melt water flow transfer CG to glacier foreland soil and ecological interaction may be occurred between glacier foreland soil (including BSC) and CG connects together. Despite of ecological importance of primary succession caused by these interactions, microbial connection was not studied well. In order to understand these connections, we analyzed bacterial 16S rDNA diversity and community structure of both BSC and CG.

DNA concentration and  $\alpha$  diversity of BSC is higher than that of CG and may show higher bacterial activities. *Cyanobacteria* is most major phylum (more than 60% of total abundance) in CG, but less in BSC (Fig. 1). Instead of lower relative abundance of cyanobacteria, *Planctomycetes*, *Verrucomicrobia* increase in BSC. Genus level taxonomy comparison shows *Leptolyngbya* and *Nostoc* in phylum *Cyanobacteria* are common in both. Otherwise, more detail OUT level taxonomy shows most of OTUs are not common in both. These results suggest bacterial community structures are largely different in BSC and CG.

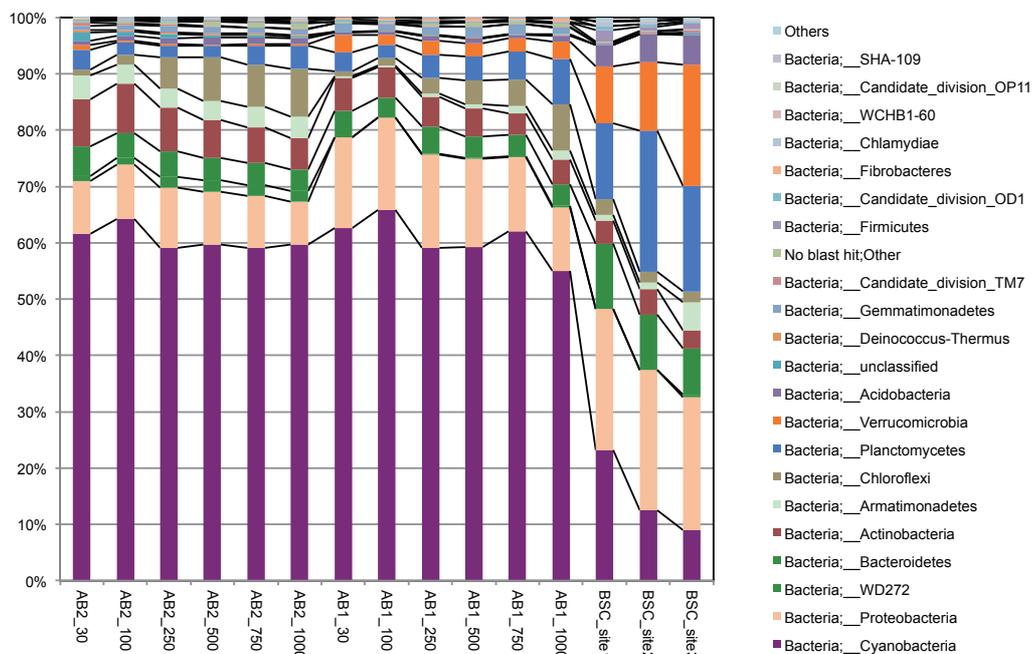


Figure 1. Phylum level taxonomy