

Bacterial 16S diversity of basal ice, sediment, and the forefront of Svínafellsjökull glacier via isolation chips and classical culturing techniques

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Sub-glacial microbes are receiving increased attention due to their central roles in storage and release of greenhouse gases, such as methane and CO₂. Climate change driven warming and resulting glacier retreat exposes bedrock that can contribute to soil formation in which subglacial-released microorganisms may play a crucial role. Basal ice, which forms in the lowermost part of glaciers in the absence of light is characterised by a high debris concentration that can be regarded as a glacier niche that must be sustained by the utilisation of overridden organic matter or primary production based on chemolithotrophic metabolism. Compared to other glacial ecosystems, subglacial microbial ecology remains poorly understood, due to limited accessibility and difficulties associated with low microbial occupancy. In this study, different defined types of basal ice (cryofacies) were targeted, namely stratified cryofacies (highest sediment content, fine-grained), debris bands (intermediate debris content, coarse-grained) and dispersed cryofacies (low sediment content, polymodal). Debris bands have been suggested to form by the entrainment of sediment due to shearing forces near the bedrock. Internal glacial processes proceed to modify debris bands leading to the formation of dispersed cryofacies. Stratified cryofacies, result from a range of processes that confers high debris content with a characteristically layered appearance. Basal ice is involved in the creation of subglacial tills and therefore in moraine formation. Elemental analysis, using a portable X-ray fluorescence portable analyser (Olympus Delta), confirmed that debris bands and dispersed cryofacies were highly similar, and distinct from stratified cryofacies, which support the dispersed cryofacies formation hypothesis. Bacteria from basal ice, sediment and forefront soil were cultured via inserted isolation chips (ichips) and traditional extraction/dilution plating. Isolated bacteria were subsequently identified following 16S rRNA gene sequencing and phylogenetics. Basal ice communities comprised a mix of soil and glacial bacteria, with higher proportion of ice-related bacteria in dispersed cryofacies (*Polaromonas* sp, *Flavobacterium xinjiangense*) and a water (*Arthrobacter agilis*) and soil-related microorganisms (*Pseudomonas* sp) in the debris bands, similar to sub-glacial sediment. During debris band formation, microorganisms from bedrock and overridden soils can be entrained into the ice matrix and those which have adapted to icy conditions can proliferate, explaining the higher viable bacterial counts on dispersed ice as well as higher proportions of glacial isolated-related microorganisms. Once the subglacial sediment and basal ice are released from the glacier and as soil age increases, increased representation of soil-related microbiota (*Arthrobacter alpinus*, *Stenotrophomonas rhizophila*) were identified. The results in this study suggest cultivable communities shift in two directions: firstly, within the basal ice layer from subglacial sediment, dominated by soil and water communities towards dispersed ice with a high proportion of glacial communities. The other shift occurs when subglacial sediment is released into the forefront, where the composition changes towards a soil-like microbiota with increase in soil age.