

Novel microbial communities in subglacial (dark) permafrost

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At Bird Brain Cave, a subglacial conduit network allows access to permafrost sediment below Bird Glacier (Fuglebreen, Svalbard, Norway). In order to understand microbial processes in the subglacial permafrost, we sequenced 16S rRNA gene tags in sediments from the cave entrance to the most distal cave passages along the water flow path. Whereas fluvial sediments are rapidly transported through the passage network, permafrost exposed in the subglacial conduit walls has been buried for several thousands of years and exposed to the cave atmosphere for less than a year. The microbial community composition of the sediments had two contrasting patterns. In fluvial sediments, the most abundant OTUs reflect an origin in the surface environment, including strains of the cosmopolitan periglacial cyanobacterium *Leptolyngbya* (17-21%), globally wind-distributed *Polaromonas* spp. (10-18%), and novel genera and species of Actinobacteria (12-20%) and Bacteroidetes (5-35%) common in soil and known for complex organic polymer degradation. In contrast, subglacial permafrost sediments had extremely high taxonomic novelty and a low abundance of the surface-derived taxa named above. They contained primarily members of novel Chloroflexi (16-31%), WS3 (0-17%) and Gemmatimonadetes (10-12%) orders and representatives of a novel Acidimicrobiales family (0-7%). Based on the assumption that the subglacial sediments have only recently been exposed to oxygen or organic matter inputs from the surface, we hypothesized that autotrophic pyrite oxidation is likely one of the primary microbial metabolisms. This is consistent with our observation that *Gallionella* spp. were major populations (1-16%) in both fluvial and permafrost sediments. We retrieved little to no evidence for a methane cycle. Based on the high degree of taxonomic novelty in the dark permafrost sediments, additional inferences about metabolic processes beneath the glacier await, and will be informed by both geochemical analyses and omics approaches.