Evidence for Iron and Sulfur-driven Chemosynthesis below Antarctic Ice

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Community structure and metabolic function in subglacial environments are strongly influenced by the interfaces between ice, subglacial water, basal sediments, and bedrock. Here we present evidence for the importance of S and Fe driven chemosynthesis from two distinct Antarctic subglacial environments. Blood Falls (BF) is a hypersaline, Antarctic subglacial brine. Previous work using isotope geochemistry and molecular analysis of functional genes from BF suggested that a catalytic sulfur cycle was linked to Fe reduction. Recent metagenomic analysis confirms the presence of numerous genes involved in oxidative and reductive S transformations including genes that code for pyridine nucleotide disulfide oxidoreductase (DsrE-like), which transfers electrons from H₂S to Fe(III). These genomic data support linked S and Fe cycles in the subglacial environment and provide a possible biological mechanism for the re-oxidation of S. Cultured representatives of organisms involved in many of the above-described S and Fe transformations are known chemolithoautotrophs. The metagenomic data analyzed from Blood Falls samples show the occurrence of diverse pathways for dark CO₂ fixation pathways including novel genes encoding for RuBisCo, a key enzyme in the Calvin Benson Basham cycle, the reductive acetyl CoA pathway and reductive tricarboxylate cycle. These results will be discussed in light of recent analyses of samples collected from Subglacial Lake Whillans, which was recently sampled as part of the WISSARD Project. Subglacial environments provide important insight into the function of the cryosphere and allow for the development of relevant tools for exploration of geomicrobiological other subglacial environments on Earth as well as icy extraterrestrial targets.