Microbial communities correlate with Lemon Creek Glacier meltwater discharge

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Mineral weathering has long been recognized as an important ecological process that is mediated in part by microorganisms. Recently, microorganisms have been implicated in the weathering of rock in the interstitial waters between bedrock and overlying glaciers (1,2), a process which may directly impact carbon cycling in the the northern Atlantic Ocean (3). Here we surveyed microbial communities associated with sub-glacial meltwaters and mixed sediments over the course of four months as they were discharged from the Lemon Creek Glacier located near Juneau Alaska, USA. Utilizing a high throughput small subunit ribosmal RNA gene sequencing approach, the diversity and structure of microbial communities was quantified and correlated to changes in the water geochemistry.

Microbial communities were consistently dominated by *Proteobacteria* classes *Beta, Alpha, Gamma* and *Delta* (in decending order of abundance), which accounted for 40-70% of the total community). Many sequences from uncultured groups often associated with anoxic environments were also recovered, including candidate divisions BD1-5, OD1 and TM7 (1-5%) and novel methanogenic Archaea (<0.1%). Phylogenetic richness was high in most samples (15-85 unique lineages) and resemebled typical sediment community diversity. Community structure was distinct in each sample and was signifcantly correlated with time of discharge and sampling location (*e.g*. lower glacial fed lake, glacial outflow channel, and sub-glacial interstitial waters).

Our results suggest that interstitial microbial weathering supports diverse microbial communities that resemble those from anoxic environments, are highly dynamic with respect to time of discharge, yet retain a consistant phylum level taxonomic structure. Furthermore this work highlights ice-water-sediment interfaces as important microbial habitats that are potential analogs for other low temperature geochemically active environmets such as the deep subsrface.

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Causes and consequences of low atmospheric pCO_2 in the Late Mesoproterozoic

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Based upon various proxy, theoretical, and model constraints, Paleoproterozoic atmospheric pCO_2 [1] was much higher than Phanerozoic levels [e.g., 2]. However, relatively little is known about the transition between the two climate states. Here, geochemical mass-balance from ~1.1 Ga old Midcontinent Rift System (USA) paleosols is used to reconstruct atmospheric pCO_2 during the Mesoproterozoic. The calculations robustly indicate low atmospheric pCO_2 (<10 times Preindustrial levels). Results are consistent between seven paleosols at one site, between paleosols at different Midcontinental Rift sites, and between the new results and previously published penecontemporaneous paleosol [3] and microfossil reconstructions [4-5]. In spite of the lower than expected pCO_2 values, climate models driven by the reconstructed pCO_2 levels predict equable conditions [6]. The newly recognized Mesoproterozoic pCO_2 minimum is best explained as the culmination of a long-term C burial event by the biosphere that is also indicated by marine carbonate $\delta^{13}C$ changes during the Mesoproterozoic, and which is consistent with changes in the biosphere including increased stromatolite abundance and diversity, evolution of sulfur-utilizing bacteria, and the spread of microbial mats into continental environments. One potential testable consequence of this hypothesis is that it should be accompanied by a gradual rise in atmospheric pO_2 throughout the "boring billion."

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