

EGU2020-16998

<https://doi.org/10.5194/egusphere-egu2020-16998>

EGU General Assembly 2020

© Author(s) 2021. This work is distributed under the Creative Commons Attribution 4.0 License.



Microbial abundance and transport in glacial near-surface meltwater

Ian Stevens^{1,2}, Tristram Irvine-Fynn², Arwyn Edwards³, Philip Porter⁴, Joseph Cook³, Tom Holt², Brian Moorman⁵, Andy Hodson⁶, and Andrew Mitchell²

¹Geography, Politics and Sociology, Newcastle University, Newcastle upon Tyne, UK (ian.stevens@newcastle.ac.uk)

²Department of Geography and Earth Sciences, Aberystwyth University, Aberystwyth, UK

³Institute of Biological, Environmental and Rural Sciences, Aberystwyth University, Aberystwyth, UK

⁴Geography, Environment and Agriculture, University of Hertfordshire, Hatfield, UK

⁵Department of Geography, University of Calgary, Calgary, Canada

⁶Arctic Geology, The University Centre in Svalbard (UNIS), Longyearbyen, Svalbard

Glacier surfaces are active microbial ecosystems which contribute to melt feedback cycles and biogeochemical processes. Despite this recognition, there is a lack of knowledge regarding the transport dynamics and residence time of microbes in this supraglacial habitat. Throughout the ablation season, meltwater is generated across a glacier's surface and flows through the porous near-surface weathering crust before entering the channelised supraglacial network. Within the weathering crust, solar radiation provides a "photic zone" which, combined with nutrient availability, is conducive for microbial activity. The water flow through this porous near-surface layer provides a transport mechanism for these microbes. However, the nature of controls upon this phenomenon remain unexplored, despite the relevance for cellular export to downstream ecosystems, glacier surface albedo and biogeochemical cycling.

To determine potential controls on microbial transport in the weathering crust, we present 913 measurements of microbial cell abundance in supraglacial meltwaters from 11 glaciers across the northern hemisphere. Each measurement is coupled with weathering crust hydraulic conductivity or stream discharge. These data reveal a mean microbial abundance of 2.2×10^4 cells mL⁻¹ (with a range of $10^3 - 10^6$) in supraglacial meltwaters within the weathering crust and stream channels. Modal microbe size was 1 – 2 μ m (56 % of microbes), with 89 % of microbes smaller than 4 μ m. No substantiated difference in size distributions between weathering crust and stream meltwaters were observed. No correlation between microbial abundance and near-surface hydraulic conductivity or stream discharge were observed, either across the entire dataset or when considered on a glacier-by-glacier basis. At three glaciers, water temperature and electrical conductivity (a proxy measure for ionic load) were also recorded; but we observe no correlation between these two variables and microbial abundance. Our data suggests weathering crust microbe abundance is consistent across differing glacial environments, and the concentrations entrained in the near-surface equal those seen in supraglacial streams. As such, despite the low transfer rate of meltwater, there appears to be limited evidence for substantial storage or

accumulation of biomass in the near-surface weathering crust. Moreover, microbe entrainment does not appear to be driven by primary hydrological controls. Assuming that once liberated within the weathering crust entrained microbes reach channelised supraglacial networks, we estimate a delivery of 1.1×10^9 kg C a⁻¹ to downstream environments globally (excluding Antarctica) to 2100, using existing discharge forecasts. This study represents a crucial first step in examining microbial abundance within, and transport across glacier surfaces and their potential role in biogeochemical process-feedbacks and the inoculation of downstream environments.