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Stress-Induced Shifts in Endometabolome Composition Reveal Microbial Adaptations on Glacier Surfaces

Annika Morische[1], Marie Bolander Jensen[1], Yrsa Larsson[1], Kai Bester[1], Liane G. Benning[2], Martyn Tranter[1], and Alexandre M. Anesio[1]

[1]Aarhus University, Department of Environmental Science, Denmark
[2]GFZ Helmholtz Centre for Geosciences, Interface Geochemistry Section, Germany

Surface microbial communities on the Greenland Ice Sheet play a vital role in modulating glacier surface melt by altering surface albedo through extensive algal blooms. The potential for extended melt season through a changing climate bears the fuel for microbial bloom expansion. However, the mechanisms governing bloom density and distribution, including the roles of microbially produced signalling and defensive compounds, remain poorly understood. This study investigates intracellular metabolic changes in supraglacial microbial communities under environmental stress to uncover factors regulating bloom dynamics and cell-to-cell communication. We employed high-resolution mass spectrometry (HRMS) to identify intracellular microbial secondary metabolites with ecological functions. The endometabolome composition was analysed to assess its response to abiotic stressors such as different light, pH, salinity and temperature conditions and its role in modulating bloom dynamics. Results indicate that light intensity strongly impacts supraglacial microbial communities' metabolic profiles, highlighting light conditions as a key driver of their ecological fitness. Our findings contribute to an expanding database of microbial metabolites and offer insights into the chemical diversity of glacier ecosystems in oligotrophic extreme environments.