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Rapid ^{13}C enrichment indicates preferential channelling of newly fixed carbon into photoprotective pigmentation in glacier ice algae

ANNIKA MORISCHE[1], JAN LISEC[2], CARSTEN JAEGER[2], ALEXANDER ERBAN[3], JOACHIM KOPKA[3], KAI BESTER[1], LIANE G. BENNING[4,5], MARTYN TRANTER[1] AND ALEXANDRE M. ANESIO[1]

[1]Aarhus University
[2]Federal Institute for Materials Research and Testing (BAM)
[3]Max Planck Institute of Molecular Plant Physiology
[4]GFZ Helmholtz Centre for Geosciences
[5]Freie Universität Berlin

Glacier ice algae, such as *Ancylonema nordenskiöldii*, are key primary producers that inhabit bare ice surfaces, influencing surface albedo and affecting the dynamics of supraglacial microbial communities. Yet, their metabolic range has not been fully characterised. We applied ^{13}C labelling, in combination with high-resolution mass spectrometry-based fluxomic analyses, to characterise metabolites in supraglacial autotrophic communities. Surface ice samples were incubated *in situ* on the ice in Greenland with labelled sodium bicarbonate (^{13}C, 99%) in four biological replicates per time point, alongside unlabelled control treatments, and sampled after 24 and 48 hours. Post incubations and biphasic metabolite extractions, we performed isotopologue analysis using LC-MS and GC-MS-based methods. By identifying compound-specific ^{13}C enrichment patterns, we aimed to resolve active carbon fixation routes and downstream biosynthetic pathways. Labelling patterns indicate active incorporation into purpurogallin-related compounds, suggesting fast channelling of newly fixed carbon into secondary pigment-associated pathways. Rapid production of purpurogallin-related compounds reflects active carbon allocation toward photoprotective pigmentation, highlighting the metabolic plasticity of glacier ice algae. Our study represents a novel approach to investigating carbon redistribution in supraglacial autotrophic communities on the Greenland Ice Sheet via isotope-based fluxomics. As glacier melt accelerates and supraglacial habitats undergo rapid environmental change, resolving carbon allocation strategies is essential for understanding shifts in microbial ecosystem function and biogeochemical feedback at the ice surface.