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Metabolic Characterization of Glacier Surface Autotrophs via ^{13}C Labelling

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Ice algae inhabiting glacier surfaces are key primary producers that influence surface albedo and are integral for glacial microbial community structures. Ice surface species such as *Ancylonema nordenskiöldii* are central to carbon cycling in the supraglacial environment, yet their metabolic potential and ecological roles have not been fully characterised. Experiments using metabolic labelling by supplying and tracing $^{13}\text{CO}_3^{2-}$ with fluxomics techniques offer a powerful strategy for probing microbial metabolism. In this study, we apply $^{13}\text{CO}_3^{2-}$ based labelling and fluxomic analyses to glacier surface communities to assess their metabolism and carbon utilization strategies. High-resolution mass spectrometry (HRMS) is employed to accurately detect and identify labelled intracellular metabolites, including secondary metabolites, providing detailed insight into the metabolic pathways active in the autotrophic community. By tracking ^{13}C incorporation into intracellular metabolites, we aim to resolve active carbon assimilation pathways and secondary metabolite production with potential relevance to microbial community dynamics. Our results represent the first use of fluxomics in glacier environments targeted at surface ice-associated autotrophs. Understanding metabolic strategies is essential in light of accelerating glacier melt, which alters environmental conditions and may reshape microbial activity on glacier surfaces. As glacier surface conditions are highly vulnerable to climate-driven alterations in melt dynamics, identifying the metabolic strategies of ice surface-dominating ice algae and other autotrophs is essential for anticipating shifts in ecosystem function.

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