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

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INTRODUCTION

Microbial communities on glacier ice, dominated by ice algae *Ancylonema alaskanum* and *A. nordenskiöldii,* darken the surface and accelerate melt rates.

- Bloom intensity and spread depend on microbes' adaption strategies.
- Environmental stress likely affects intracellular metabolism driving bloom dynamics.
- We used high-resolution mass spectrometry (HRMS) to identify key secondary metabolites linked to microbial stress responses.

Goal: **Improve understanding of glacier algae metabolism and their role in melt feedbacks.**

Shining a light on glacier microbes Jensen et al. (2024)

- Higher photosynthetic efficiency occurs under lower light conditions
- Algae tolerate wide range of physicochemical conditions

METHODS

The metabolomic stress response of microbial glacier communities (Greenland, 2021) was tested for four environmental parameters (Fig. 1).

Metabolite samples were filtered, quenched, and reconstituted in 50% MeOH for polar metabolite extraction (Fig 1).

LC–MS analysis was performed via Agilent UHPLC system with a Sciex TripleTOF 6600 mass spectrometer.

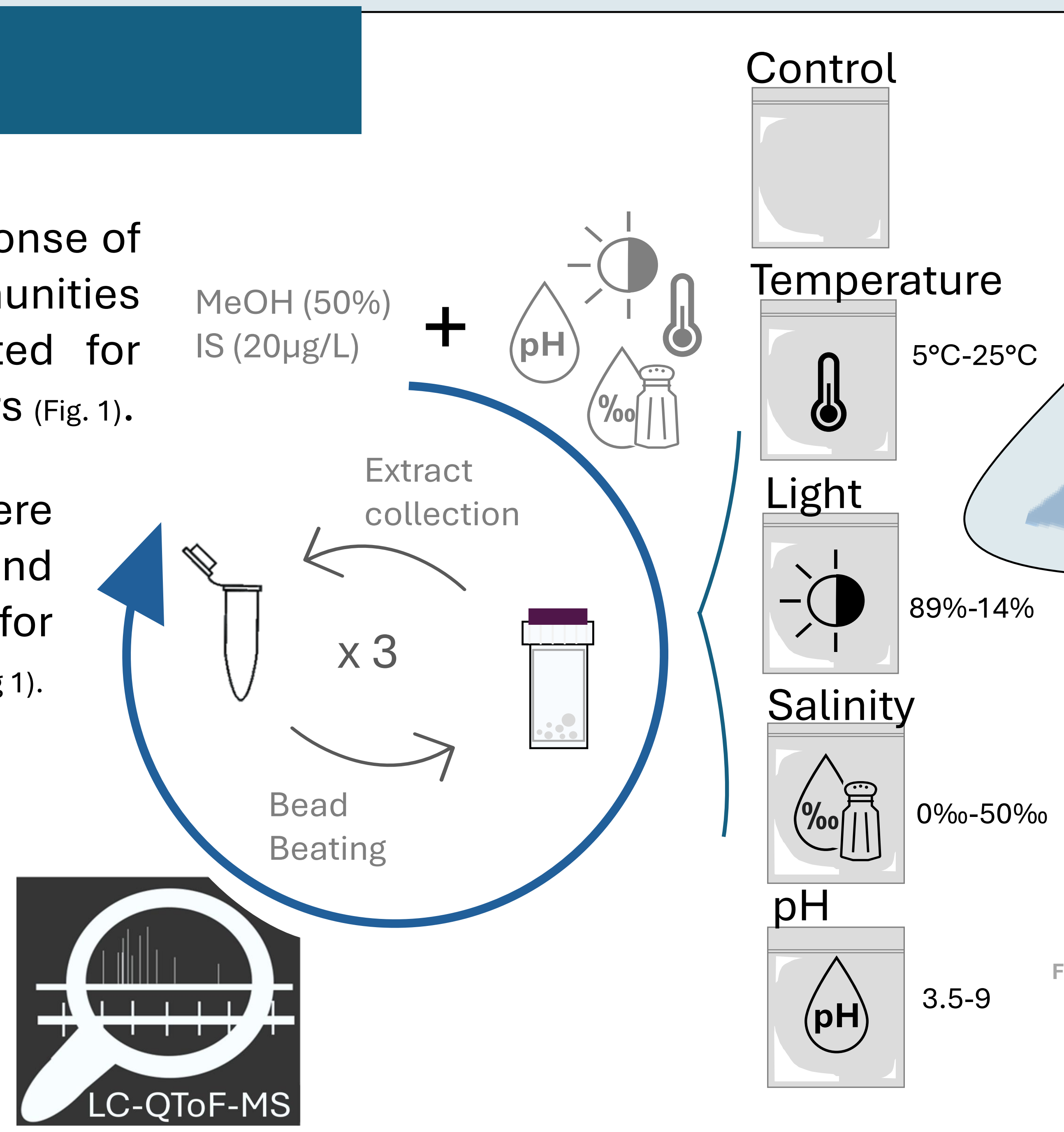
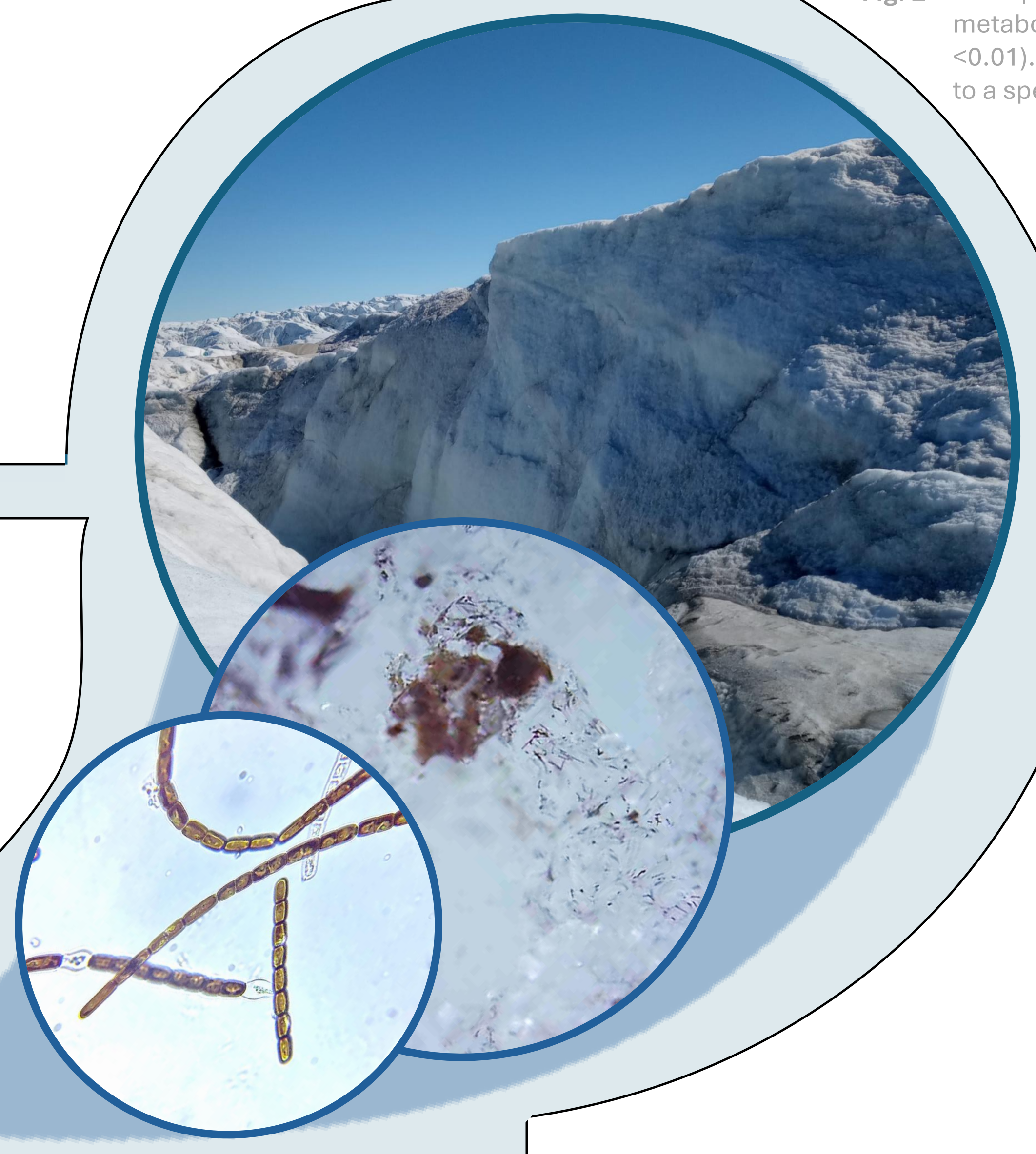


Fig.1 Experimental Design for testing glacier microbial communities' intracellular metabolic response to abiotic stressors



RESULTS

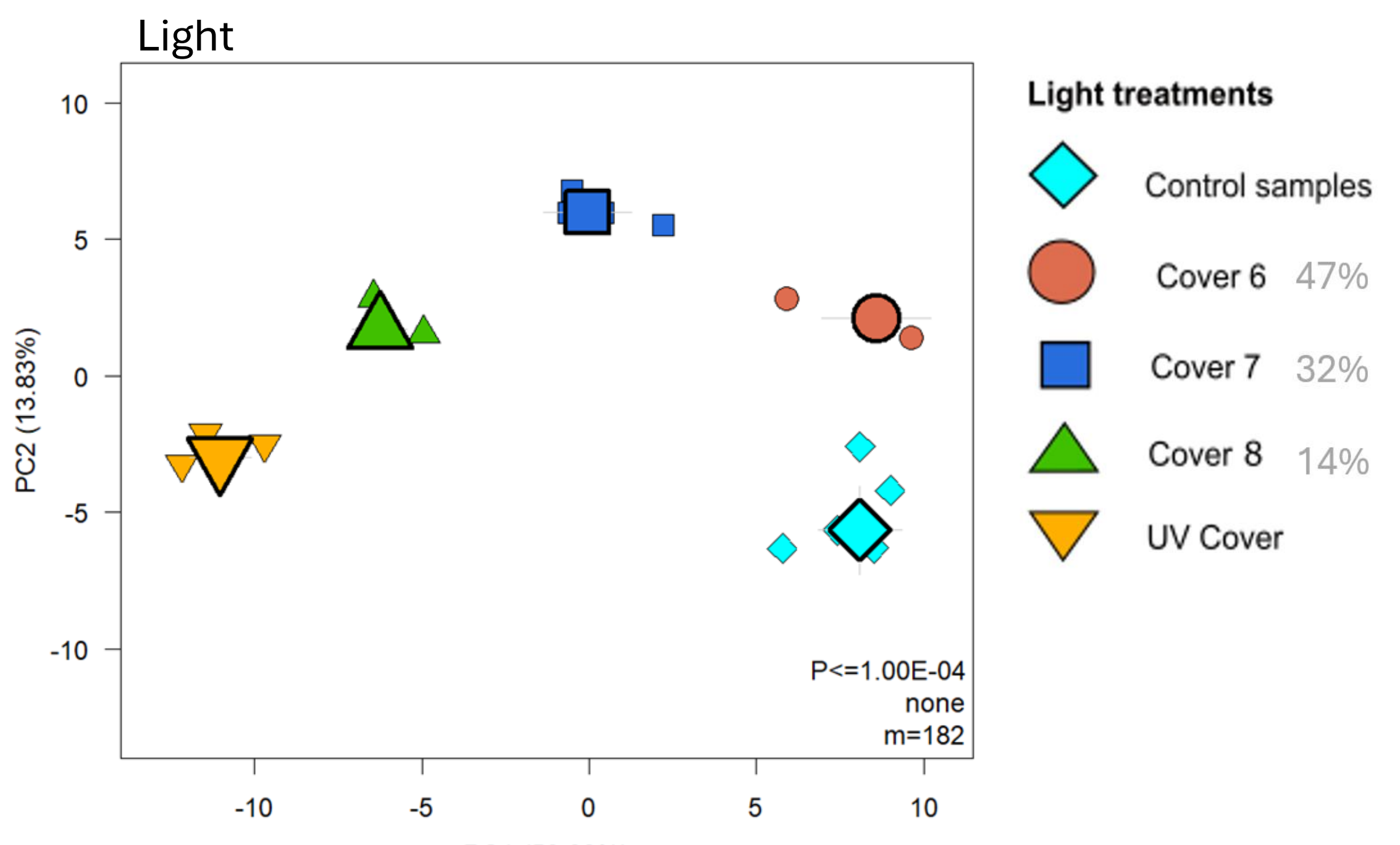


Fig. 2 Principal component analysis (PCA) restricted to putatively annotated metabolites significantly differentiating samples' treatments (p-value <0.01). Each light condition represents a cover reducing ambient light to a specific percentage, as indicated.

Marked differences in metabolite features after 48-hour incubations across light treatments indicate a rapid metabolic response of glacier microbial communities to solar irradiance (Fig 2).

- Solar irradiance changes likely trigger metabolic reprogramming (Fig. 3)
- Shifts pathways toward stress defense, bioactive compound production

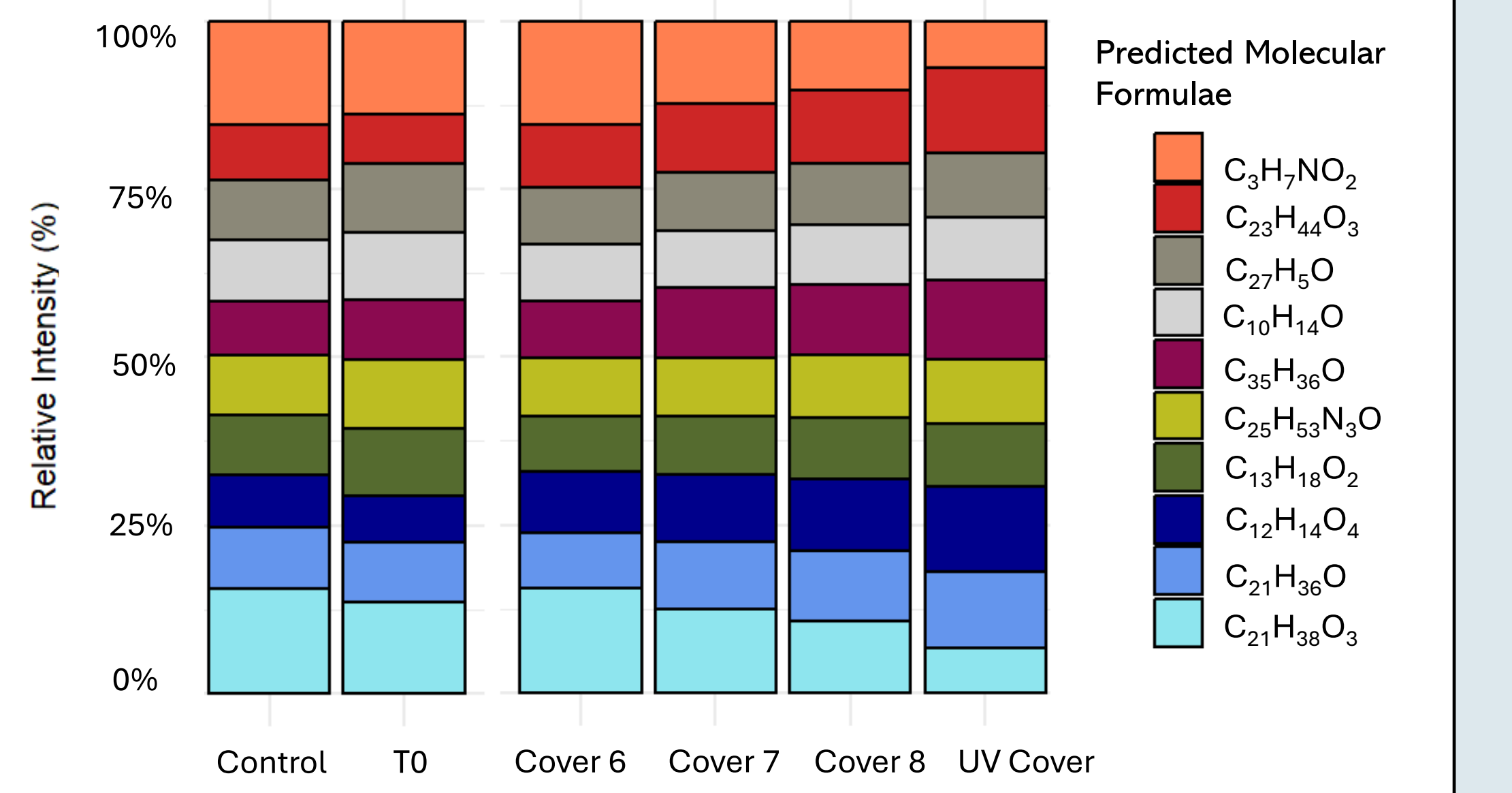


Fig. 3 Relative signal contribution of key metabolite features driving group separation along PC1 in light treatments, annotated with predicted molecular formulae.

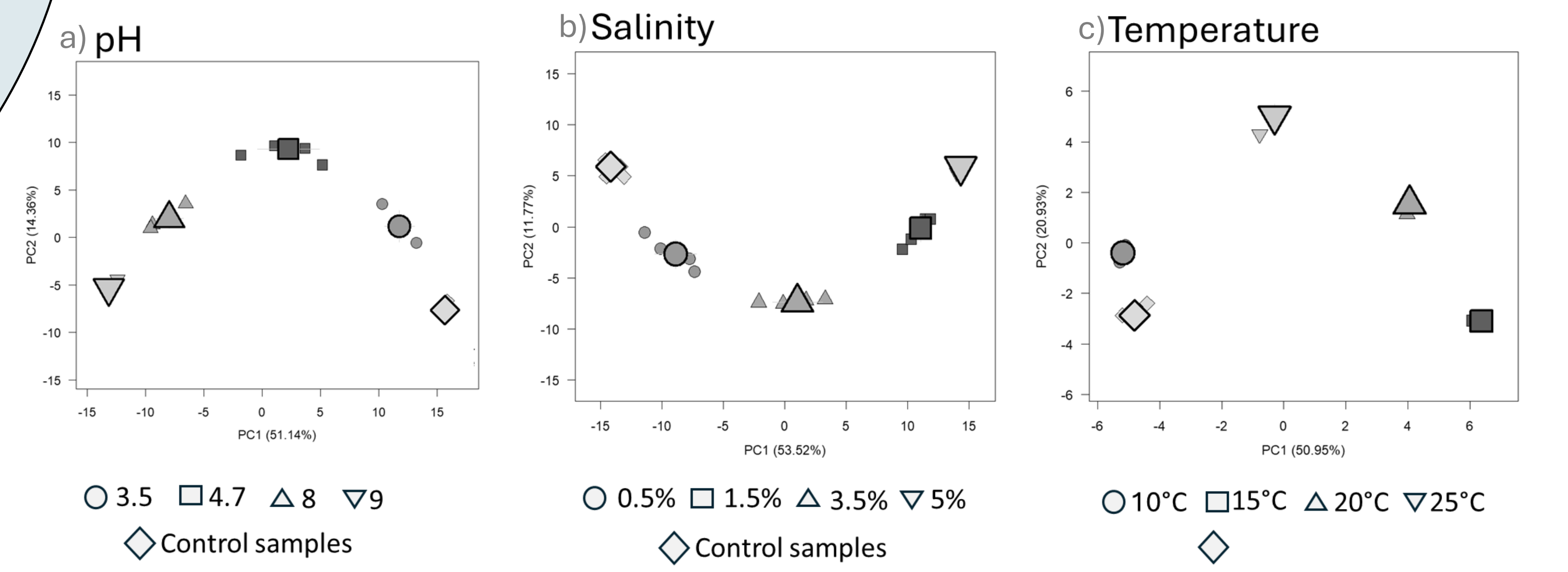


Fig. 4 Principal component analysis (PCA) of putatively annotated metabolites (p < 0.01), showing treatment-specific separation for each abiotic stressor: (a) pH, (b) salinity, and (c) temperature.

pH, salinity, temperature, and light each likely induce rapid metabolic changes (Fig.4). Together, these stressors reshape the endometabolome composition.

Abiotic stress rapidly reshapes the endometabolome, highlighting its key role in adaptive bloom responses and associated ice melt.

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