

Current questions on snow and glacial algae

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Keywords: cryoflora, psychrophilic, microalgae

Snow algae are unique organisms specialized to thrive in melting mountainous and polar snow fields. Likewise, glacial algae are found to grow exclusively at certain glacier surfaces. During the melting season, both can cause blooms with striking discolorations in green, yellow, red or dark purple. Green Algae (Chlorophyta) are the dominating phototrophs in these extremophilic habitats, and they build up an ecosystem including bacteria, fungi and small animals like ciliates. The algae have to cope with low temperatures, freeze-thaw-cycles and extreme irradiation conditions at the surface. Due to their pigmentation, they can reduce surface albedo and thus blooms of cryoflora are believed to foster snow and ice melt during summer. This is currently especially the case at the western margin of the Greenland Ice Sheet.

Snow and glacial algae are promising candidates to explore the biodiversity of polar and alpine cold ecosystems, to understand fundamental strategies of cellular stress response and for screening of metabolites of nutritional or biotechnological interest.

In a traditional way, the focus of research is on occurrence, morphology, photosynthesis and taxonomy of virtually monospecific blooms. With the onset of sophisticated molecular and analytical methods, the trend has shifted to the description of whole snow communities (metagenomics) or prevailing biocompounds, respectively dominating biosynthetic pathways (metabolomics).

The fact that many of these species abundantly contain valuable molecules like polyunsaturated fatty acids, carotenoids, polyols or vitamins made snow and glacial algae interesting for biotechnology, however many of them have not been cultured successfully yet, *e.g.* strains of *Sanguina nivaloides* (the main global causer of red snow) or *Mesotaelium berggrenii* (a very common glacial alga) are unknown.

Lack of sampling in difficult to access regions like the Andes, tropical equatorial glaciers or Continental Antarctica evokes expectations that still many new species can be found. High-throughput-amplicon sequencing of field samples indicated that cryoflora is made of both cosmopolite taxa on the one side and local ones on the other side. Enhanced techniques like optimized primer designs, the use of more than one molecular marker sequence (*e.g.* 18S rDNA, *rbcL* and ITS2 rDNA together) will improve the species assignment of Operational Taxonomic Units.

Metabolomic protocols applied to different cellular stages in the life cycle of a species or at different abiotic conditions will provide insights to biochemical strategies.