

# Abstract

Snow algae cause blooms in slowly melting snowfields in mountain and polar regions. Although they are excellent models for the study of life in extremely cold environments, their taxonomical diversity, geographical distribution and variety of physiological strategies used to cope with their harsh environment are only partially understood.

This work was focused on green algae from the order Chlamydomonadales and in one case on golden algae from the order Hibberdiales. An integrative approach was applied to characterise species, including the sequencing of several molecular markers (18S rDNA, ITS2 rDNA, *rbcl*) to reveal genotypes and infer phylogenetic positions. Light and electron microscopy were conducted to describe the detailed structure of cell wall surfaces and intracellular compartments. Moreover, fatty acid and pigment profiling were carried out to provide new insights into the adjustments of metabolic pathways in these algae. Rapid light curve measurements were used as a proxy of light preferences of photosystem II.

Firstly, one of the main algae responsible for causing the phenomenon of red snow was shown to represent a single, monophyletic lineage, independent from other algae within the Chlamydomonadales (**paper I**). Therefore, the new genus *Sanguina* (S.) was described, with two closely-related species, *S. nivaloides* and *S. aurantia*. Using molecular methods, a cosmopolitan distribution of *S. nivaloides* in polar and alpine regions was demonstrated. Secondly, the physiology of *Sanguina nivaloides* was compared to another red snow forming species (*Chlainomonas* sp.) thriving at ice-covered high alpine lakes, the former exhibited high photophysiological plasticity and had significantly lower polyunsaturated fatty content (**paper II**). Furthermore, a new species *Chloromonas* (C.) *hindakii* causing orange snow blooms was described (**paper III**). Multiple populations were collected over a wide altitudinal gradient, and the exploration of light preferences of field samples and a laboratory strain showed a high intraspecific ability to adapt their photosynthesis to different light conditions. Additionally, the old taxon *Scotiella tatrae* was transferred to *C. nivalis* and reduced to a subspecies as *C. nivalis* subsp. *tatrae* (**paper IV**), likely representing a variation of a common cryoflora species with distinct cell wall morphology until now known only from the Tatra Mts (Slovakia/Poland). Next, *Scotiella cryophila* is considered to be the asexual cyst of *C. rosae* var. *psychrophila*; however, field-collected cysts identifiable as *S. cryophila* originating from the Austrian Alps were phylogenetically separated from the authentic strain of *C. rosae* var. *psychrophila* from North America and thus probably represent a new species (**paper V**). Two new species of golden algae were described; *Kremastochryopsis austriaca* causing yellow snow, and *K. americana* from a pond (**paper VI**). The application of high throughput amplicon sequencing was evaluated for the characterization of snow algal communities. An optimized workflow was proposed for such projects to assist in accurate biodiversity analyses (**paper VII**). A strain of *C. reticulata* isolated from red snow exhibited a range of unusual physiological characteristics: invariant high growth over a broad range of temperatures, high electron transfer rates between the quinon Q<sub>A</sub> and Q<sub>B</sub>, and the dominance of phosphatidylglycerol in thylakoid membranes in its chloroplasts (**paper VIII**). In the first lipidomic study of snow algae (**paper IX**), *Chloromonas* snow species accumulated various triacylglycerols with fatty acid chains in various stereospecific positions. Raman spectra of carotenoids of various snow algae communities were detected and interpreted (**paper X**).

The presented thesis contributes to our understanding of the taxonomical and physiological diversity of microalgae in mountain and polar snow fields. It shows that the biodiversity of these extreme environments is underestimated, and provides new insights into the biogeography of snow algae. Furthermore, the results reflect the species-specific dynamic nature of responses of metabolic profiles and photosynthesis in the changeable snow environment.