Bipolar distribution and dispersal pattern of snow algae

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Red snows are a worldwide springtime phenomenon caused by blooms of red-pigmented green algae in thawing snow and historically have been recorded in the daily logs of polar and alpine explores such as Captain John Ross and Charles Darwin. The red pigments are carotenoids that serve as antioxidants, as an energy sink, and as a light shield for algal cells exposed to the intense ultraviolet radiation on the snow surface. The algae photosynthetically produce organic matter, which can reduce the snow-surface albedo and accelerate the melt rate of snow, and thus algae have an impact on cryospheric environments.

Several taxa of red-snow algae have been recognized in snow fields worldwide, mainly based on light microscopic features of the cells. Spherical red-snow cells have often been identified as *Chlamydomonas* cf. *nivalis* and can be regarded as a cosmopolitan cryophilic species. On the other hand, several studies have used next-generation sequencing technology to elucidate the geographic distribution of red-snow algae based on molecular data. Recently, red-snow algae collected from different regions of the Arctic have been reported to be cosmopolitans based on 18S rRNA gene analysis. However, this gene resides within a relatively slow-evolving region and thus is frequently used for establishing algal taxonomy at the species level. Therefore, this gene is considered unsuitable for elucidating the distribution pattern of algae, especially the interpretation of global distribution, because the resolution of any phylogeographical analysis depends on evolutionary rates of focusing genes.

In this study, we describe the biogeographical distribution of snow algae on red snows collected from the Arctic and Antarctica using the sequences of the nuclear rDNA internal transcribed spacer 2 (ITS2) region, which has a high evolutionary rate and is thus suitable for revealing fine-scale genetic structures. We addressed the issue of whether snow algal species on red snows have a bipolar distribution or are distributed in limited areas of the world. We found that limited numbers of the phylotypes exist in both polar regions and that most of them are present only in the Arctic or Antarctic. The bipolar phylotypes account for the majority (37%) of the entire sequences, suggesting that red-algal blooms observed worldwide are caused by only a few phylotypes of algae that are globally dispersed via the atmosphere across both polar regions.

Whether microorganisms are distributed globally or locally remains a hot topic of discussion. The microbial cosmopolitan dispersion hypothesis of Baas Becking ("Everything is everywhere, but the environment selects") is often invoked to explain the observed patterns of global algae distribution driven by the capacity for widespread dispersal. In the present study that a few cosmopolitan species of green algae dominate red-snow habitats, but indeed much endemism was detected. Thus, it seems unlikely that the Baas Becking hypothesis holds for snow algae. Our findings underscore the importance of understanding the ecology of snow algae as well as improving the population analyses and taxonomic classification methods that utilize environmental samples.