



Molecular diversity and phylogeny of glacial algae from the Greenland ice sheet

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Algae growing on glacier surfaces have recently become a focus of increased scientific attention, for two main reasons. First, they contribute to the darkening of the Greenland ice sheet (GrIS) and other ice masses due to the production of dark protective pigments, thus increasing surface melt rates. Second, their taxonomical affiliation to the family Mesotaeniaceae (Zygnematophyceae, Streptophyta) makes them, according to current knowledge, the phylogenetically closest algal lineage to land plants. Recent dating of different lineages of extant Streptophyta suggests a much deeper origin of lineage splits leading to plants than previous estimates supported by paleontological records and previous molecular-clock-based studies. This timing in fact places the early evolution of terrestrial plants to the cryogenian era (Neoproterozoic, 720-635 million years BP). Hence, the extant glacial algae may be possible inheritors of some ecological or physiological traits, which might reveal new perspectives on the evolution of early land floras. The most challenging aspect of studying these algae is the fact that they are resistant to cultivation attempts, and, according to our knowledge, no pure and sustainable culture of glacial algae is available to date. To circumvent this issue we focused on the molecular diversity of the entire algal (eukaryotic) community. We hypothesize that if the algal population consists of more than one taxon, we will be able to distinguish interspecific variability from the intraspecific (evt. gene homologs) by examination of the ratio of representative sequences among different replicates and by comparison of patterns in different markers. We sampled a starting bloom of glacial algae in the ablation zone of the SW portion of the Greenland Ice Sheet in August 2015 on three localities. Environmental DNA was extracted from replicate samples for each locality, and five markers (rbcL, 23S, cox III and 2 overlapping regions of 18S) were amplified and sequenced using the Illumina MiSeq platform. We then used the sequence data representing the algal community to constrain the molecular intraspecific and interspecific diversity, the phylogenetic position of particular organisms and to link and compare the Greenland ice sheet algal population to related and better-studied organisms from other freshwater environments.