

Abstract

In polar regions, green microalgae (Chlorophyta) are an important group of primary producers. However, little attention has been paid to them in comparison with other primary producers such as diatoms and cyanobacteria. The aim of this thesis was to describe the diversity of Chlorophyta in Arctic and Antarctic lakes, and to gain new insights into their taxonomic composition and biogeographic patterns.

Microbial mat samples were collected from the littoral zones of 137 Arctic and Antarctic lakes from various regions (Svalbard, North Greenland, South Greenland, Antarctic Peninsula, and Continental Antarctica) during expeditions performed between 1993 and 2018. We combined Sanger sequencing of isolated strains and amplicon sequencing of environmental samples. The 18S rDNA and ITS2 rDNA regions were analysed using both molecular methods.

In total, 65 laboratory cultures were established from Svalbard and Antarctic Peninsula samples. Sanger sequencing of strains revealed 15 taxa belonging to classes Chlorophyceae and Trebouxiophyceae. The most abundant were for instance *Chlorella* spp. and *Micractinium* spp. Amplicon sequencing of 18S rDNA yielded 202 OTUs in total, of which 61.4% of OTUs were present in both polar regions. The use of ITS2 rDNA revealed 1,104 OTUs in total, with 53.2% being present in both the Arctic and Antarctica. The alpha diversity (OTU richness) was much higher in the Arctic (average 106 OTUs/sample) than in Antarctica (average 72). However, this trend was absent when 18S rDNA data were considered. 18S rDNA data showed that the most abundant class in the Arctic was Ulvophyceae (56% of OTUs), while in Antarctica Chlorophyceae prevailed (49%). There was a very low amount of unclassified Chlorophyta in contrast to ITS2 rDNA (roughly 60% in both polar regions). Canonical analysis revealed high separation of samples from particular biogeographic regions. Among the most frequent OTUs with bipolar distribution (e.g., *Chloromonas* sp., *Ulothrix zonata*) there were also species which were previously considered as presumably endemic (e.g., *Chodatodesmus australis*, *Hazenia broadyi*). Several species of snow algae were also abundant (*Sanguina* spp., *Raphidonema nivale*). Number of taxa detected by both culture dependent and independent methods was quite low (13 taxa). This shows that both approaches complement each other. To our knowledge, this is the first study that used amplicon sequencing with group specific primers to uncover green microalgae diversity in polar lakes.

Key words: polar regions, Antarctica, Arctic, Chlorophyta, biogeography, amplicon sequencing