

Diversity and seasonal variation in arctic marine eukaryotic microbes

AIMS

- To investigate the abundance and diversity of marine eukaryotic microbes throughout the arctic winter and spring
- To compare the communities and seasonal variation of marine eukaryotic microbes in an advective fiord with no sea ice to a semi-closed fiord with winter sea ice

SUMMARY

The diversity and ecosystem functioning of marine picoeukaryotes (single-celled organisms $< 3 \mu\text{m}$) is poorly known in general, and in the Arctic in particular. Recent investigations have shown an amazing biodiversity among these tiny cells, but little is yet known about e.g. their role in the microbial food web. In this study, we use molecular tools to investigate the diversity and functioning of picoplanktonic eukaryotes in two arctic fiord systems.

PROJECT DESCRIPTION

Although their presence is not always obvious, microscopic organisms thrive in the seemingly most inhospitable places (e.g., Behnke *et al.* 2006). Recent developments in molecular genomics have revolutionized our view of microbial life on earth showing the existence of numerous new lineages in the tree of life as well as new proteins and transcripts of unknown function (e.g., Diez *et al.* 2001; Not *et al.* 2005; Dinsdale *et al.* 2008). The seemingly inhospitable Arctic with its extreme annual light variation and cold climate is no exception; in recent genomic studies of picoplanktonic eukaryotes in the Arctic, several new lineages representing various classes were discovered (Lovejoy *et al.* 2006, 2007).

Marine microbes are fundamental regulators of the Earth's biogeochemical cycles (Falkowski *et al.* 2008). Although they represent only 0.2% of the global primary producer biomass, marine phytoplankton is responsible for one-half of the global primary production (Falkowski *et al.* 1998; Field *et al.* 1998), and in the Arctic Ocean Survey of 1994, picophytoplankton (defined as cells $< 2 \mu\text{m}$) were shown to contribute 36% to total phytoplankton biomass (Booth & Horner 1997). In spite of their importance in terms of global ecology and ecosystem functioning, marine picoeukaryotes are among the least understood biodiversity component on Earth.

Arctic regions are predicted to experience amplified climatic change, and arctic ecosystems are thus among our first warning systems towards the effect of climatic change (IPCC 2007). Knowledge about picoeukaryote biodiversity and function in the Arctic is scarce, and for this metagenome component we are in need of baseline data that can be used to assess ecosystem changes in response to e.g. climatic warming. The data that are available on arctic picoeukaryotic diversity so far (Sharr *et al.* 2003, Not *et al.* 2005, Lovejoy *et al.* 2006, 2007), suggest that there is a consistent change in the picoplanktonic communities when moving from temperate to arctic waters (e.g., Not *et al.* 2005). One main difference is that the important cyanobacterial primary producers *Synechococcus* and *Prochlorococcus* are virtually absent from arctic waters. Instead, a dominant primary producer seems to be the small prasinophyte *Micromonas pusilla* (e.g., Lovejoy *et al.* 2007). In addition, small ubiquitous haptophytes from more temperate waters seem to disappear in arctic waters (Not *et al.* 2005; except the ice algae *Phaeocystis pouchetii*). These changes impose highly interesting questions regarding the arctic microbial food web, its impact on heterotrophic protists and small zooplankton, as well as the potential to adapt to future climate change. The investigations performed so far, have only scratched the surface of this important ecosystem element.

In this project, we will use molecular tools in combination with epifluorescence microscopy to investigate the diversity, abundance and seasonal variation in picoeukaryote plankton in the Isfjorden area, Spitsbergen. We will address questions such as: How does the picoeukaryotic species composition vary throughout the arctic spring? Are the photoautotrophs present also throughout the winter, or are they recruited from spores/resting stages in the spring? What is the succession of picoeukaryote species throughout the arctic spring? What are the differences in the species composition and timing of spring bloom between an open, advective fiord and a semi-closed fiord with winter sea ice?

Methods

The sampling locality Karlskronadjupet in Isfjorden, Spitsbergen will be sampled 3 times in January/February, and every week from March to mid May. In addition, we will sample every 2nd-3rd week in Adolfbukta in Billefjorden. The Billefjorden sampling will be coordinated with two other master projects (by Allison Bailey and Lilith Kuckero).

From each locality and sampling date, a CTD with fluorometer will be used to determine sampling depth. We will take one water sample at the *Chl a* maximum depth and one sample closer to the bottom (150 m at Adolfbukta and 250 m at Karlskronadjupet). In addition, we will take sediment samples to investigate to what degree the picoeukaryotes may be recruited from the sediments. The water samples will be prefiltered first using a 200 µm nylon net, and then using 3 µm polycarbonate filters to remove larger microalgae and zooplankton. The picoplankton in the filtrate will then be collected on 0.7 µm polycarbonate filters. These filters will be used for molecular genetic analyses of the species composition of picoeukaryotes by sequencing of the small subunit nuclear ribosomal DNA.

Water samples will also be collected from each depth and filtered for biomass estimates. 0.5-2L sea water will be filtered to 3 µm filters and to GF/F (0.7 µm) filters, and the amount of *Chl a* in these fractions will be measured using a Turner fluorometer. The amount of picoeukaryotes in the fraction 3-0.7 µm will be calculated.

For total picoplankton counts and estimates of heterotrophic vs autotrophic cells, approximately 100 ml of sea water will be fixed in glutaraldehyde stained with DAPI (4',6-diamidino-2-phenylindol) and prepared for fluorescence microscopy.

References

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