Sympagic-pelagic coupling and succession of phytoplankton in a High-Arctic fiord

AIMS

- To identify the source and succession of the ice algal assemblages that are formed in one-year sea ice in Billefjorden, Spitsbergen
- To investigate to what degree ice algae assemblages seed the spring phytoplankton bloom in Billefjorden, Spitsbergen
- To investigate the timing of the sympagic and planktonic algal blooms in relation to physical (nutrients and light) properties

SUMMARY

Ice algae form an important basis for the life of sympagic (ice-associated) as well as pelagic arctic organisms. The timing of the sympagic and pelagic spring blooms is important for the zooplankton grazers and thus for the arctic marine food web. We study the source, succession and timing of the ice algal and phytoplanktonic spring blooms in a High-Arctic fiord aiming to investigate the coupling of these communities.

PROJECT DESCRIPTION

The arctic sea ice sustains a wide range of organisms from bacteria to the polar bear. Ice algae are single-celled protists that are connected to the sea ice at some point in their life cycle. Ice algae form an important basis for life in the ice. An investigation from the European arctic recently showed that ice algae represents the primary food source for sympagic zooplankton, and can represent a substantial carbon source (up to 50%) also for pelagic zooplankton (Søreide at al. 2006).

In areas with no summer sea ice, the ice algal assemblages are reformed every year. The origin of ice algae depends on where the ice is situated, i.e. how deep the area is, and how far it is from the shore. Three main types of ice algae can be discerned (cf. Ratkova & Wassmann 2005); 1) <u>Ice specialists</u> are found exclusively in the ice, and probably develop resting spores through which they probably survive in the sediments between seasons. Although resting spores are known from some of the ice specialists, other species including the enigmatic *Nitzschia frigida* have not yet been observed with spores or resting stages. 2) <u>Ice-plankton</u> species also occur in the plankton, and are possibly incorporated during the ice formation. Ice crystals on the bottom of the ice can filter and trap planktonic species from the underlying water. 3) <u>Ice-benthic</u> species are also found in the nearby sediments as active cells, and these are more important in ice formed close to shallow shores (Ratkova & Wassmann 2005). The species composition of ice algae varies depending on geographic position, distance from shore, and age of the ice. The diversity and succession of larger ice algae such as diatoms are to some degree known from other Arctic areas (e.g., von Quillfeldt 1996), but the abundance and diversity of small flagellates in the sea ice has yet been very little studied (but see Ikävalko & Gradinger, 1997).

In this study, we will use a multipronged approach with regular field sampling in combination with microscopic analyses, culturing and molecular techniques to investigate the coupling between sympagic and pelagic algae, their succession and timing of the spring bloom. Using molecular tools will enable us to keep a focus on the least known element of the ice algae, the nanoflagellates.

Methods

Samples will be taken in Adolfbukta, Billefjorden every 2nd-3rd week from December 2008 to May 2009. We will take water samples from different depths (0m, 5m, 35 m, 75 m, 150 m, and *Chl a* max) for analyses of nutrients, microalgae communities, and molecular analyses. In addition, we will measure the photosynthetic active irradiation down to 40 m depth. The water samples from 5-150 m will be integrated for the molecular analyses to represent the planktonic fraction. Additional samples for microscopic analyses will be taken using net hauls from 30-0m using a 20 μm net. When the ice has formed (usually in February), ice cores will be taken in three parallells using an ice drill. Samples will be collected representing the bottom, middle and top of the ice. Algal biomass will be estimated from sea water filtered using a GF/F filter (0.7 μm pore size) and measuring the *Chl a* biomass.

The algal species occurring in sediments, as plankton, and in the sea ice will be identified by microscopic analyses and by sequencing the small subunit nuclear ribosomal DNA gene (18S nrDNA). This gene has previously proved to be extremely useful for identification of various groups of organisms from environmental samples (e.g. Lovejoy et al. 2006). For the molecular analyses, we will fractionate the water samples and focus at species in the size range 40-0.7μm. This size range includes the smaller flagellates, and thus includes a new dimension to the study of ice algal and phytoplankton communities.

This project is done in collaboration with another master project (by Allison Bailey) who will study the seasonal dynamics of zooplankton, *Calanus* in particular. We will thus be able to compare the algal bloom dynamics with that of the grazers.

The main part of the field work will be performed from February/March to May, with sampling by boat or snowmobile every 2nd-3rd week. Sampling in December, January and February will be done from the UNIS Research Vessel "Viking Explorer". Sampling from March onwards will be done by snowmobile.

References

Ikävalko J, Gradinger R (1997). Flagellates and heliozoans in the Greenland Sea ice studied alive using light microscopy. *Polar Biology*, **17**, 473-481.

Ratkova TN, Wassmann P (2005) Sea ice algae in the White and Barents seas: composition and origin. *Polar Research*, **24**, 95-110.

Søreide JE, Hop H, Carroll ML, Falk-Petersen S, Hegseth EN (2007), Seasonal food web structures and sympagic-pelagic coupling in the European Arctic revealed by stable isotopes and a two-source food web model. *Progress in Oceanography*, **71**, 59-87.

von Quillfeldt CH (1996) *Ice algae and phytoplankton in North Norwegian and Arctic waters: Species composition, succession and distribution*. Dr. scient. thesis, Norges Fiskerihøgskole, Universitetet i Tromsø, Tromsø.