12. SEA ICE BIOLOGY AND BIOGEOCHEMISTRY

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Objectives

Sea ice is of major importance in the polar oceans since it affects the solar radiation fluxes due to its reflective properties, and constitutes a habitat and feeding ground for various organisms of the polar ecosystem. The Arctic Ocean is now in a state of rapid transition that is best exemplified by the marked reduction in age, thickness and extent of the sea ice cover. The European Arctic margin is largely influenced by drift ice formed on the Siberian shelves and carried to the Fram Strait via the Transpolar Drift. Sea ice thickness for the various regions of the Transpolar Drift between 1991 and 2007 showed a reduction in modal ice thickness from 2.5 m towards 0.9 m. A long-term trend towards thinner sea ice has profound implications for the timing and position of the Seasonal Sea Ice Zone, and the anticipated ice free summers in the future will have major implications for the entire ecosystem and thus alter current biogeochemical cycles in the Arctic.

Due to the generally low solar elevation and extreme seasonality, light is considered to be the key factor for primary production in the ice covered oceans. Light penetration in the Arctic is generally reduced by the sea ice cover, and additionally snow greatly reduces light transmission through the ice. In the framework of climate warming, the atmospheric moisture budget in the Arctic is forecast to change, resulting in an increasing snow cover and thus reducing the light for primary production. However, the reduction from MYI to seasonal ice and additional increase of melt ponds on FYI will substantially increase light transmission through ice. Additionally, the sea-ice surface topography, i.e. the presence of deformation elements (ridges) and melt ponds, determine the redistribution of snow on the surface. This, together with the above mentioned processes, affects the light transmission and thus affects one of the main limiting factors for algae growth.

Sea-ice physical, chemical and biological properties are highly variable in time and space, thus field sampling and producing representative model output of ice algae are extremely challenging. A big question concerning sea ice sampling is how representative of the surrounding area are the measurements taken at a certain location. Such a problem arises also when trying to upscale these observations, since upscaling always means parameterization, averaging and simplification. Thus, it is fundamental to determine the temporal and spatial scales of variability of sea-ice algae, and even more to determine any relationship of sea ice algae distribution with the variability of physical and chemical sea ice properties. In addition, special environments for algae growth and survival, such as very young ice and deformed ice have not been fully characterized so far. Particular ridges are an under-sampled component of the sea ice environment in terms of their biogeochemical properties. The presence of ridges may offer an inhomogeneous, albeit favorable, environment for sea-ice algae growth. Thus, particular attention should be given to ridged and deformed ice, which is commonly overlooked as potential algae growth site.

Sea ice harbors a distinct community of prokaryotic and eucaryotic photo- and heterotrophs (Hardge et al. 2017). Sea ice algae contribute substantially (5 to ca 60 %) of total Arctic

primary production (Fernández-Méndez et al. 2015), and support not only an ice based food web, but also provide important food pulses to pelagic and benthic communities. Within the ice, newly formed particulate matter is consumed by various protozoa and metazoa, including Acoela, Crustacea and Rotifera. Sea ice algae are also a source of dissolved organic matter, which is channeled through a microbial network back into the particulate food web. All these ice inhabitants have typically sizes of less than 1 mm, to be able to explore the branched network of brine channels within the ice. In addition, ice algae can be directly consumed by under-ice amphipods and migratory zooplankton. Also specialized curtain-like algal mats have been observed under sea ice, mainly consisting of *Melosira arctica*. Vertical export of sea ice-derived organic matter is mainly driven either by organism release due to ice melt, or by fecal pellet production of grazing amphipods and zooplankton. Changes in sea ice habitat structure and ice algal production will affect the trophic transfer of sea ice-derived carbon through the under-ice community into pelagic food webs. A key role in transferring carbon from ice algae to higher trophic levels is taken by species dwelling at the ice-water interface, such as *Calanus* spp., *Apherusa glacialis* and polar cod *Boreogadus saida* (Kohlbach et al. 2016). The decline of the sea ice can alter the composition and biodiversity of the sea ice flora and fauna. Biodiversity in turn plays a vital role for the stability of ecosystem processes, and is positively coupled with the efficiency of important ecosystem functions, e.g. fluxes of energy, nutrients and organic matter. Thus understanding the relationship of the biodiversity of sea-ice biota with ecosystem functions is important for predicting consequences of climate change in an Arctic ecosystem.

Summer sea ice retreat alters water mass formation and convection, which may have profound effects on natural biogeochemical cycles between sea ice and seawater. Especially feedback effects to pathways of climatically relevant trace gases will loom large in the equation of change. Increasing water stratification during sea ice melting is likely to limit nutrient availability in near-surface water, which in turn hampers the enhancement of primary production. A characteristic feature of the Arctic Ocean is distinct post-bloom nutrient limitation. Nutrient limitation may be also a possible regulator of methane (CH_4) production in surface water. Methanogens form CH_4 via various pathways commonly classified with respect to the type of carbon precursor utilized, e.g. the methylothrophic pathway indicates the intact conversion of a methyl group to CH_4. The contribution of methylated substrates is potentially large in sea ice, and methylothrophic methanogenis may be a principal pathway from which CH_4 is readily formed by microbial activity. However, the direct evidence of this role of methylated substrates in sea ice is still lacking. In this context, the degradation of dimethylsulfoniopropionate (DMSP), an abundant methylated substrate in surface water and sea ice becomes pivotal. DMSP is produced by marine phytoplankton and sea ice algae. Cleavage of DMSP can be carried out by bacteria or by phytoplankton, and leads to formation of DMS (dimethylsulfide) or methanethiol. DMS, an important climate-cooling gas, partly escapes to the atmosphere where it is oxidized to sulphuric acid and methanesulfonic acid. Methanethiol is a key reactive intermediate utilized as sulphur and carbon sources for biosynthesis or energy generation. In anaerobic environments methanethiol act also as precursor for CH_4 production. In the ocean, processes producing N_2O are mainly being controlled by organic matter and dissolved oxygen. This trace gas is mainly produced by nitrification or nitrifier denitrification under oxic and also microaerophilic conditions. Conversely, partial denitrification can produce N_2O under suboxic conditions, whereas the complete reduction is the only reaction able to consume N_2O under suboxic/anoxic conditions. The assimilative reduction of N_2O to NH_4^+ (N_2O fixation) may be responsible for a certain amount of consumption, but not much is known so far.

The sea ice ecology group of PS106 aims for the following objectives:

- Studying the importance of spatial scales for estimating physico-chemical sea ice properties, ice algae biomass and primary production;
- Investigating the role of light for the production and biodiversity of sea ice algae;
- Studying the importance of physical and biogeochemical properties of sea ice ridges for the growth conditions of ice algae;
- Analyzing the abundance, biodiversity and community structure of sea ice-associated biota and quantifying ecosystem functions and their relationships with biodiversity;
- Using molecular and isotopic biomarkers to trace sea ice-derived carbon in pelagic food webs;
- Quantifying the vertical export under sea ice;
- Identifying the main triggering processes for climate-relevant compounds (CH4, N2O and DMS) in sea-ice and in the underlying water column and quantifying the fluxes across the water-sea ice-air interfaces following the melting cycles in the Arctic Ocean.

Work at sea

General sea ice work

Sea ice cores will be taken for biological, chemical and biogeochemical analyses every other or every third day during the ice camp of PS106.1 and at individual ice stations during PS106.2. We will further sample sack holes, the water under the ice and if present, melt pond water. The depth of the sampling under the ice will be based on vertical profiles of a CTD and fluorescence probe which will be obtained prior to the water sampling. We will measure environmental parameters, such as sea ice temperature, snow depth, free board and ice thickness. Hyperspectral radiometers will be used to measure the spectral composition of the light under the ice for estimating ice-algae biomass. Spectral measurements will be conducted with sensors mounted on Three different platforms: an L-arm for point measurements and calibration (PS106.1 & 106.2), the Surface and Under-Ice Trawl (PS 106.2), and the ROV of the sea ice physics group (PS 106.1 & 106.2). At L-arm survey sites, ice cores will be extracted and processed for chlorophyll a content in order to validate the relationship of ice algal biomass with the under-ice spectral light properties (Lange et al., 2016).

We aim to collect the following core parameters: salinity, nutrients, coloured dissolved organic matter (CDOM), dissolved inorganic carbon (DIC), and filters for particulate N, P and C. Additionally, algae biomass and taxonomic composition will be determined by size-fractionated chlorophyll, marker pigments, Illumina sequencing and cell counts (microscopy and flow cytometer). Also biogenic silicate, particulate organic carbon and nitrogen (POC, PON) and the isotopic composition of POC and PON (δ13CPOC and δ15NPON) will be determined. Flow cytometer and marker pigments will be sampled from the CTD casts in collaboration with the water column biogeochemistry group. Flow cytometer measurements of the pico- and nanoplankton and fractionated chlorophyll from all habitats will be directly counted or measured, respectively. All other samples will be stored and measured at the AWI, UiT, and WMR.

Primary production measurements of sea ice algae and phytoplankton will be conducted in *in-situ* incubations of ice core segments and water samples with stable isotope tracers (^{13}C, ^{15}N). After incubations, samples will be melted, filtered and stored for later analyses in a

stable isotope lab. In parallel to these measurements, the export of organic matter from the ice will be determined using short-term sediment trap samples in 5 and 20 m water depth. Material from the traps will be used to determine the quantity and quality of the exported material (pigments, stable isotopes, eDNA). These data will be augmented by deployment of gel traps to further determine the size and form spectrums of sinking matter.

To assess the relationship between sea ice habitat properties, food web structure and biodiversity, we will sample the meio- and microfauna and microbial communities in sea ice as well as the microzooplankton composition of the ice-water interface layer. Based on melted sea ice, bacteria, heterotrophic protists and meiofauna will be quantified either in fixed samples (fluorescence microscopy) or alive (meiofauna). Meiofauna will be sorted alive and fixed for later taxonomic and food web analyses (e.g. DNA sequencing, stable isotope analysis).

Insights into food web interactions will be achieved through food web markers and grazing experiments. The trophic significance of ice algae in Arctic pelagic food webs will be investigated with isotopic biomarkers. To sample the trophic baseline needed for the interpretation of biomarker results (ice algae and phytoplankton), melted sea ice cores and seawater samples will be filtered. Ice algae-derived carbon will be traced from the ice-associated community through the pelagic system into the benthos by collecting abundant taxa from all three environments (see chapters 14, 15). A stable isotope turnover experiment will be conducted with one or two meiofauna taxa to address the time it takes for changing food sources to be assimilated by these organisms.

A time series will be performed to determine the climate-relevant compounds variability along the late spring season. We intend to measure dissolved gases (CH4 and N2O), DMS, DMSP and δ13C-CH4 concentrations in sea ice and surface sea water. Water samples will be collected from Niskin bottles mounted on a rosette sampler at discrete depths throughout the water column down to 200 m. The number of sampling depths depends of the fluorescence and tO2- sensor signals. We will sample one-year and multi-year sea ice and brine by taking cores with a standard corer. Sea ice cores will be sectioned and melted at 4°C. Methane concentration will be measured on board by gas chromatography (GC) equipped with a flame ionization detector (FID). Gas samples will be stored for analyses of the d13C values of methane by mass spectrometry in the home laboratory. DMS and DMSP concentrations will be measured on board by GC equipped with a pulsed flame photometer (PFPD) and by GC equipped by a flame photometer (FPD), respectively. N2O will be measured either on board or in the home laboratory by GC.

If possible, sampling will further be carried out on surrounding ice floes by using zodiac and helicopter.

Experiments

A. The role of scales for biological sea ice sampling

At the beginning and toward the end of PS106.1 we want to study the spatial scales of ice algae biomass. We will set up a nested approach (Miller et al., 2015) to extrapolate detailed information to larger scales, based on distinguishing hierarchical layers of detail. In particular, a primary scale corresponding to the ice floe (~100m) will define the study area in all its variation. The secondary scale will serve to determine the representativeness of each site. This scale comprises a finite number of selected sites, separated by a distance of ~ 10m and covering all the possible sea-ice conditions (except for ridges, treated separately). Each of these sites is further divided into a 1 m grid, the tertiary scale. Each point of the grid represents one individual measurement. When possible, further sampling will be carried out by zodiac or helicopter to assess sea ice variability on a larger scale (~500-1,000 m). Bottom

sections for fractionated chlorophyll, POC and flow cytometer will be collected for all samples while Meiofauna and DNA will be collected frequently.

B. Gardening

On three fields of 5x5 m the snow coverage will be manipulated and in collaboration with the sea ice physic team the light conditions under the ice will be monitored every other day and subsamples for flow cytometer, microscopy, DNA and fractionated chlorophyll will be taken. Ideally, twice a day the spectral composition measurement surveys will be performed by ROV to estimate the temporal evolution of ice algae and to investigate the influence of snow on light availability and algae growth. Measurements of sea ice algal and phytoplankton primary productivity will be conducted at each experimental site at three time points. These measurements will be corroborated by regular PHYTO-PAM P/I curve measurements.

C. Ridge study

The aim is to sample at least one large ridge for physical and biogeochemical characterization during PS 106.1. In particular, snow transects crossing the ridge will be conducted to characterize the snow distribution in a deformed environment. Ice thickness probes will be used and light transmitted through the ridge structures will be measured with remotely operated vehicles (ROV; in cooperation with the sea-ice physics group at AWI). Ice cores will be extracted from the ridge(s) to analyze the vertical structure (porosity, presence of entrapped sea water). Samples for nutrients, biodiversity, microscopy, flow cytometer and fractionated chl-*a* will be taken from the ice and the water. Primary productivity measurements will assess the activity of the encountered ice algal communities.

D. Trace gases

We plan to deploy a chamber system connected to an auto analyzer Los Gatos Research for continuous measurements of greenhouse gases fluxes across the sea-ice air interface. The measurements will depend on the logistic plan and sea ice conditions. To gain a better understanding on the possible control/influences of microbial community on CH_4 flux to the atmosphere we will additionally conduct incubation experiments to measure CH_4 oxidation rates in melted sea ice and/or sea water collected with Niskin bottles. Experiments for assimilative N_2O fixation will performed using a stable isotope technique in melted sea ice and sea water. ^{15}N-labeled N_2O gas will be the substrate during the experiments to measure N_2O fixation rates by incubating samples.

Preliminary (expected) results

The aim of this study is to understand the variability and biodiversity of the sea ice-associated biomass with respect to the sea ice conditions and nutrient availability, to assess the role of sea-ice biota for the cryo-pelagic, cryo-benthic coupling under different environmental scenarios from the shelf to the deep sea basin and its temporal development from spring to summer. Linking the various components of the food webs to a joint ice-related ecopath model will improve assessments of the role of climate change on the carbon cycle of the Arctic Ocean.

The chl-*a* data collected will be used to assess the sub-kilometer scales of variability in biological and physical parameters. The development of functions able to represent such variability will improve the parameterization for sea-ice algae modeling that are now used in large-scale global circulation models (e.g., MITgcm, FESOM). The consequences of under-sampling will be assessed with the aim to develop a sampling strategy and protocol that can be used for future field work (e.g., MOSAiC). Investigating the temporal evolution of the biological system will help to identify the timing and length of the spring bloom period, a key process to be represented in numerical simulations. Moreover, a set of conditions and

parameters obtained from these field measurements will be used to feed numerical simulations.

In addition, our goal is to achieve high data resolution by continuous measurements of greenhouse gases fluxes across water-sea ice-air interfaces along the late spring; this will also help us to test the sea ice permeability differences through time. We will be able to know the budget of relevant- climate compounds in both compartments, sea ice and sea water, influenced by a melting cycle and to distinguish how the physical and biogeochemical processes trigger concentration/saturation of trace gases.

Data management

Almost all sample processing, such as chemical measurements, species identifications and quantifications, will be carried out in the home laboratories at AWI, WMR and UiT. As soon as the data are available they will be accessible to other cruise participants and research partners on request. Depending on the finalization of PhD theses and publications, data will be submitted to PANGAEA within 1-2 years. The unrestricted availability from PANGAEA will depend from the progress of related PhD theses based on the data.

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13. INVESTIGATIONS ON THE COMPOSITION OF THE BENTHIC FAUNA DERIVED FROM AN ICE-FLOE DRIFT STATION OFF SVALBARD

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Objectives

There are still large knowledge gaps on the life cycles and several aspects of *B*. *saida* biology, especially with respect to time spend in deeper water layers. However, feeding and

ALFRED-WEGENER-INSTITUT
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EXPEDITION PROGRAMME PS106

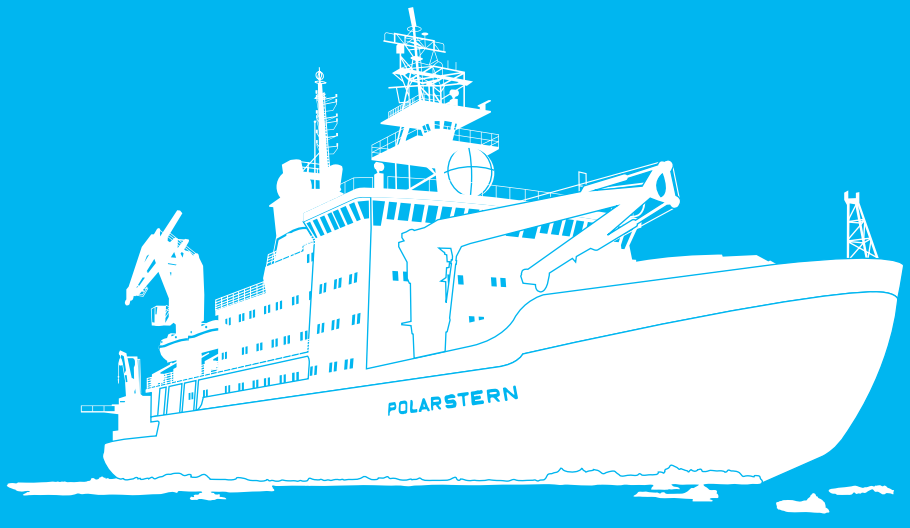
Polarstern

PS106.1
Bremerhaven – Longyearbyen
23 May 2017 - 21 June 2017

PS106.2
Longyearbyen - Tromsø
23 June 2017 - 20 July 2017

Coordinator: Rainer Knust

Chief Scientists: PS106.1 Andreas Macke
PS106.2 Hauke Flores



Bremerhaven, März 2017

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PS106

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