Picoplankton: The successful spreading over the Arctic Ocean

Estelle Silvia Kilias[1], Christian Wolf[1], Ilka Peeken[1,2], Katja Metfies[1]
[1]Alfred Wegner Institute for Polar and Marine Research, Bremerhaven, Germany
[2]MARUM - Center for Marine Environmental Science, Bremen, Germany

Introduction

Why?
The Arctic Ocean is a threatened environment. Hence, evaluations of the impact on the base of the food web, on local phytoplankton communities, are required. Prerequisite of such an evaluation is comprehensive information about the present phytoplankton diversity and distribution. Recent investigations indicate that rising temperatures as well as freshening of surface waters in the marine environment promote a shift towards picoeukaryotes. In such a scenario, picoplankton can comprise a large pool of biomass by attaining high abundances.
The **objective** of this study is to deliver a framework for better understanding the interactions between environmental conditions and corresponding pico- & nanoplankton communities by assessing the presence of biogeographic patterns.

Where?
In order to comprehend how environmental variables influence picoplankton diversity, occurrence and distribution sampling has taken place in areas of divers hydrodynamic conditions like I) the Fram Strait & II) the central Arctic Ocean.

Fig.1. Map of the study area **I)** presents the "Hausgarten" long-term observatory and **II)** the stations along the transect. In this respect T1-T5 are located within the East Greenland Current (EGC), T6 & T7 within the transition zone and T9 & the Hausgarten samples within the West-Spitzbergen Current (WSC).

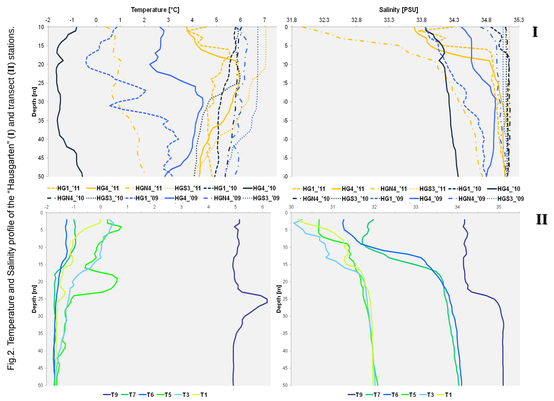

Fig.2. Temperature and Salinity profile of the "Hausgarten" (**I**) and transect (**II**) stations.

How?
The analysis has been carried out by the application of ribosomal fingerprinting technology (ARISA) to assess the community structure and of Next Generation Sequencing to analyze the diversity assessment.

Results

I "Hausgarten" (0.4-3.0 µm)

- The meta MDS plot (ARISA) shows a similar community structure within the years **2010** (ArkXXV/2) and **2011** (ArkXXVI/2)

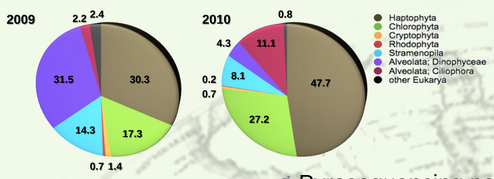

Fig.4. Pyrosequencing - relative abundance of the picoeukaryotes at HG4 in 2009 and 2010

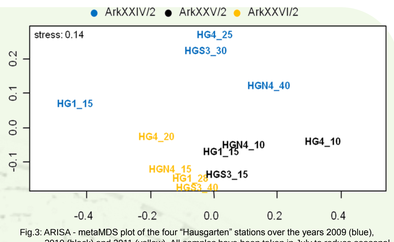

Fig.3: ARISA - metaMDS plot of the four "Hausgarten" stations over the years 2009 (blue), 2010 (black) and 2011 (yellow). All samples have been taken in July to reduce seasonal variation. The back number refers to the sampling depth (chlorophyll max.).

- Pyrosequencing points to a higher proportion of dinoflagellates in 2009 whereat 2010 displays a higher proportion of ciliates, hapto- & chlorophytes

II Greenland Transect (whole size class)

- The meta MDS plot shows a similar community structure of T3, T5 & T6, while T1, T7 & T9 are plotted as outliers

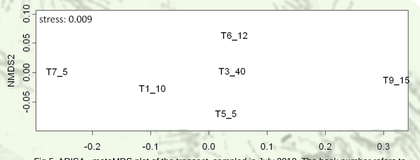

Fig.5. ARISA - metaMDS plot of the transect, sampled in July 2010. The back number refers to the sampling depth (chlorophyll max.).

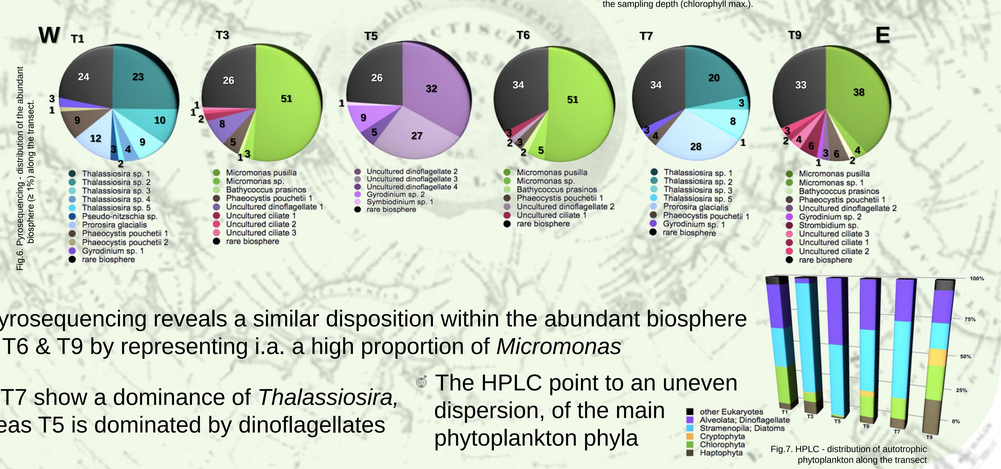

Fig.6. Pyrosequencing - distribution of the abundant biosphere (≥ 1%) along the transect.

- The pyrosequencing reveals a similar disposition within the abundant biosphere of T3, T6 & T9 by representing i.a. a high proportion of *Micromonas*
- T1 & T7 show a dominance of *Thalassiosira*, whereas T5 is dominated by dinoflagellates
- The HPLC point to an uneven dispersion, of the main phytoplankton phyla

Fig.7. HPLC - distribution of autotrophic phytoplankton along the transect

III Central Arctic Ocean

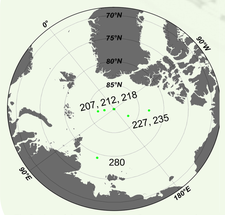

Fig.8: Map of the central Arctic Ocean presenting samples of further pyrosequencing analysis

- The water samples cluster according to the water mass in which the Laptev Sea shows the highest spreading
- Subsequent pyrosequencing of CTD station 207, 212, 218, 227, 235 & 280

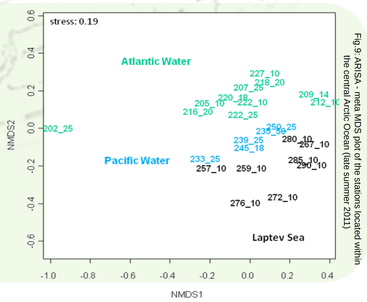

Fig.9: ARISA - meta MDS plot of the stations located within the central Arctic Ocean (late summer 2011)

Discussion

Précis

- The analysis of the three locations confirms the hypothesis that water masses are the driving force in picoplankton dispersal
- Temperature seems to have a strong emphasis by showing higher diversity within warmer water masses
- Bloom situation as well as ice coverage need to be considered during the evaluation process

I

- The comparison of the community structure at the **"Hausgarten"** over a period of three years point to a different phytoplankton composition in 2009.This strong deviance in 2009 can be explained by a low annual average temperature and limited irradiance due to an ice coverage of 50%. Ice floes have the potential to impair the diversity by releasing implicit phytoplankton species during the melt process. A closer insight into the genetic diversity of the picoeukaryotes at HG4 confirms the previous results of the ARISA approach by presenting more dinoflagellates and less autotrophs like chloro- and haptophytes in 2009.

II

- During the study, the area of the EGC was characterized by a Polynya undergoing dynamic freezing processes. This mirrors the different species distribution at T1,T3 & T5. While the formation of a stable melt water layer promote the growth of diatoms at T1 we have a post-bloom situation at T5 which has been located along the ice edge for weeks and thus presents a dominance of dinoflagellates. T3, T6 & T9 display similar species distributions which can be explained i.a. by the hydrodynamic conditions. Some of the inflowing Atlantic Water directly recirculates within the Fram Strait due to the strong topographic steering and thus can lead to similar phytoplankton distribution patterns. The deeper sampling depth at T3 and the high ice coverage at T6 further display harsh conditions that favour picoplankton species like *Micromonas pusilla*. Altogether the highest diversity was observed in the Atlantic Water.

III

- The ARISA approach of the central **Arctic Ocean** displays a clustering of the stations according to the different water masses. In this regard the water samples of the Laptev Sea present the highest variation which could be due to varying nutrient supply caused by river and offshore input.

Estelle.Kilias@awi.de