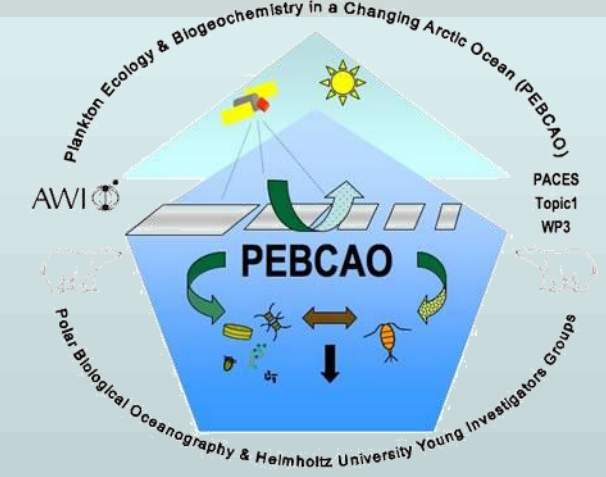


Genetic Diversity of Eukaryotic Picoplankton in the Arctic Ocean (Fram Strait)

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Introduction

Climate change is expected to be particularly intense in the Arctic Ocean having as well extensive consequences on Arctic pelagic ecosystems. Thus evaluations of the impact 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 in the phytoplankton community towards a dominance of smaller cells. In such a scenario, picoplankton can attain high abundances. Understanding the impact of climate related environmental change for picoeukaryotes demands that we understand how environmental parameters influence their diversity and distribution. In this perspective, samples have been taken in the area of the “deep-sea long-term observatory HAUSGARTEN” of the Alfred-Wegener-Institute in July 2009. Samples have been analyzed by the application of ribosomal fingerprinting technology (ARISA), 18S rDNA clone libraries and Pyrosequencing.

Results

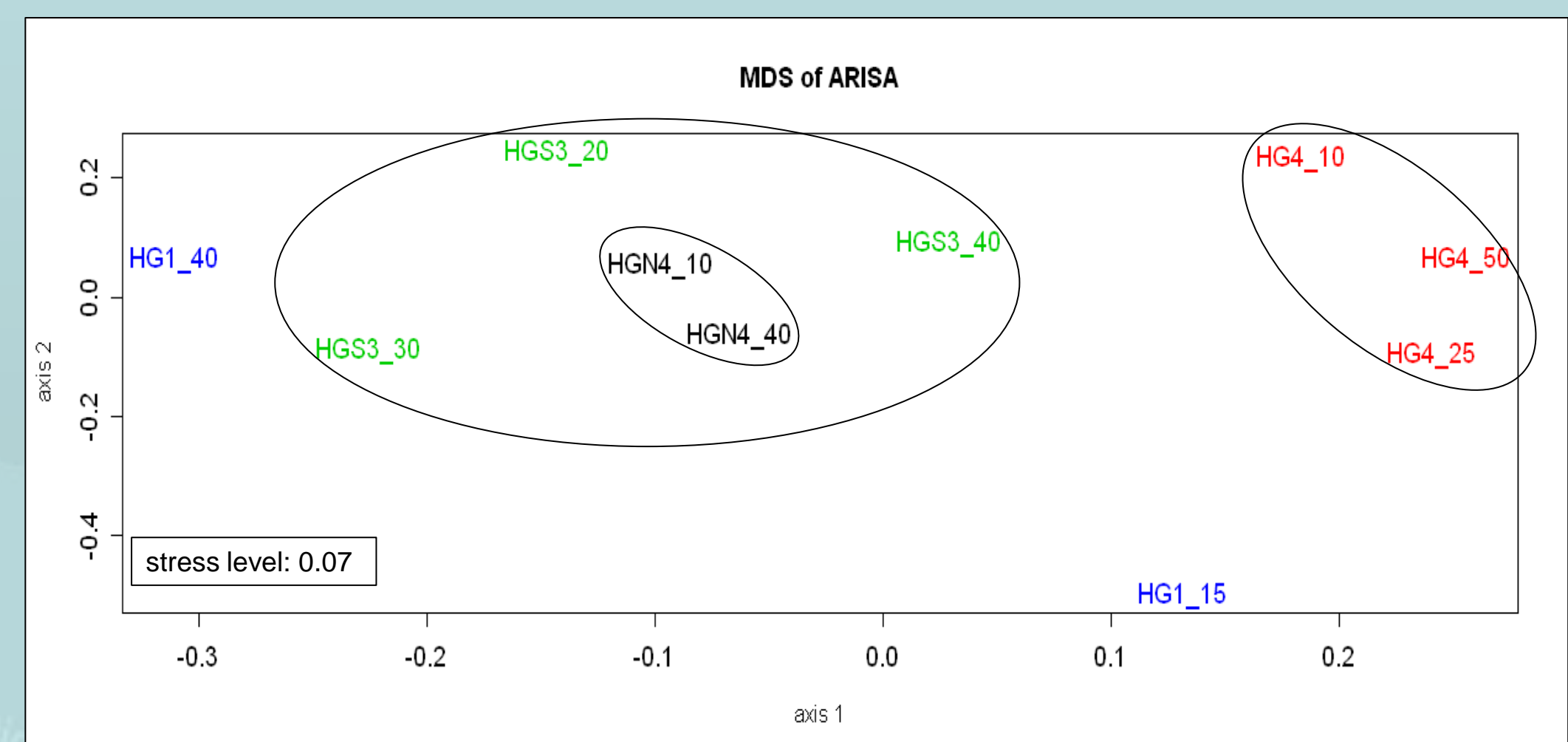
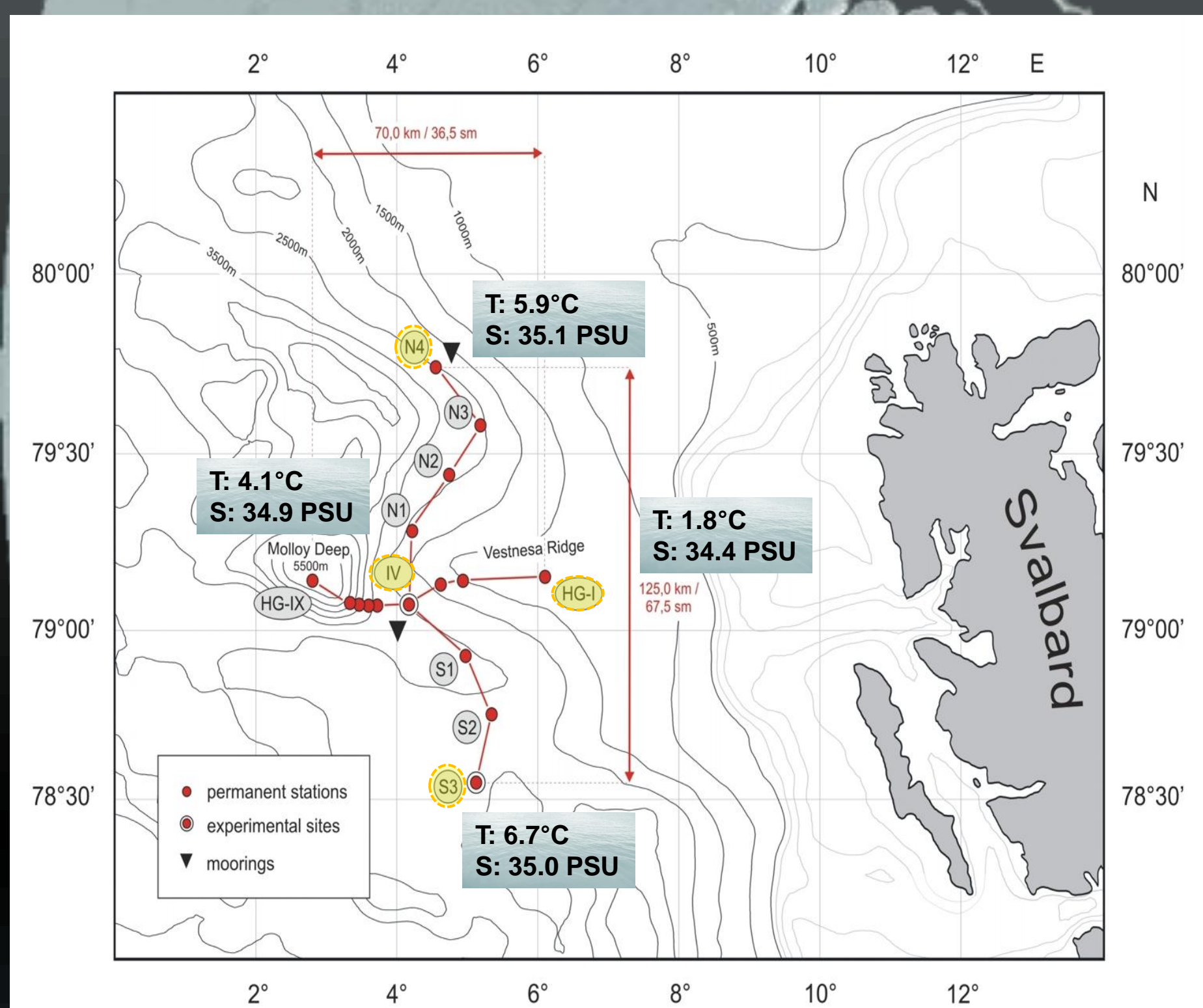


Fig.1: MDS plot of the ARISA analysis of the 0.2 – 3.0 µm size fraction (“Hausgarten”, Fram Strait)

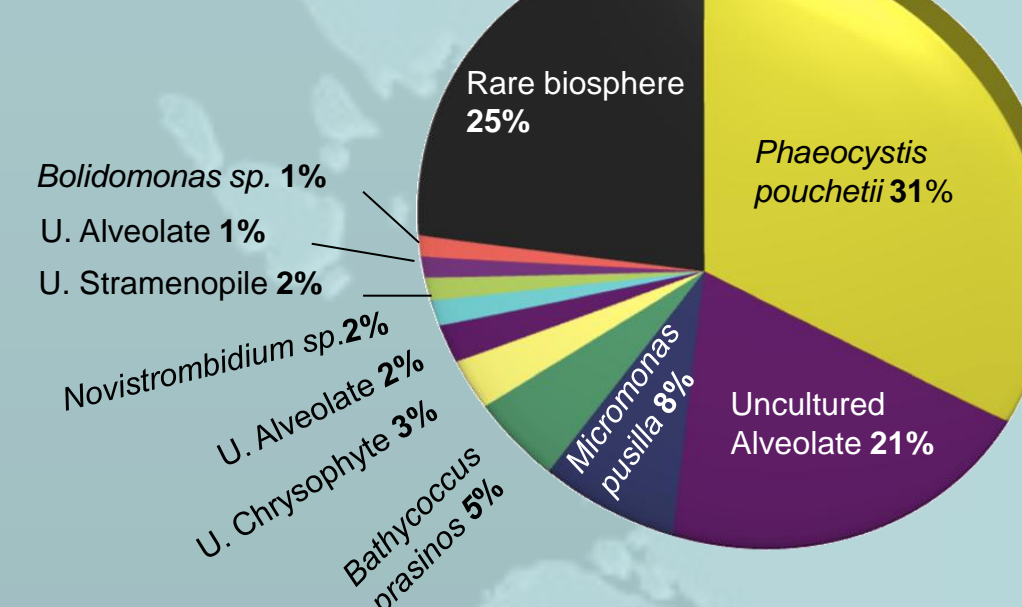
ARISA

- clustering of the northern (HGN4) and southern (HGS3) stations
- HG1 shows a heterogeneous community structure over depth

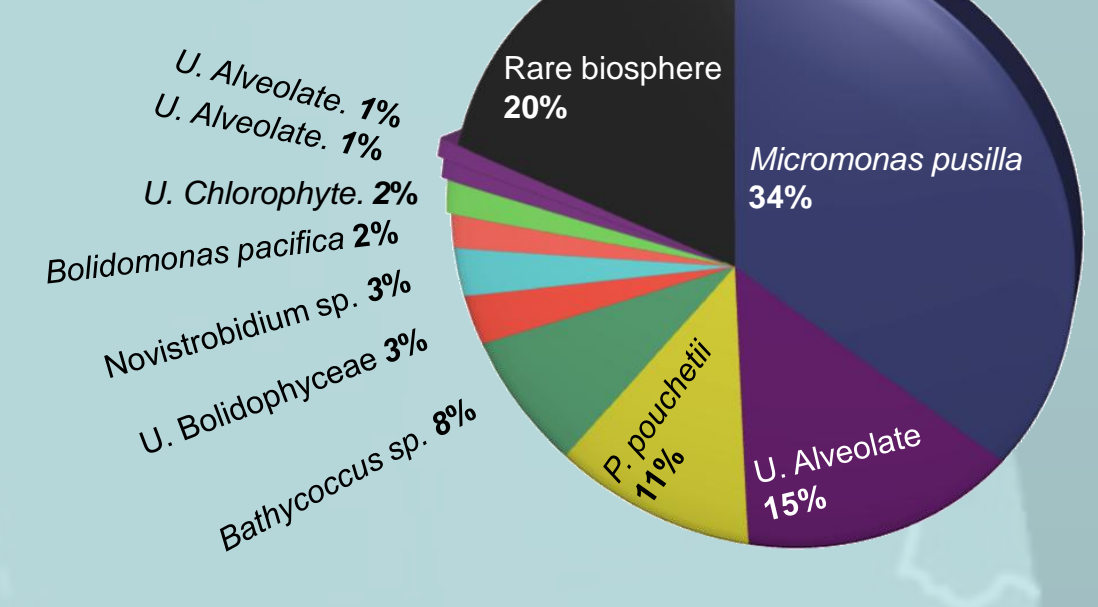


„AWI-Hausgarten“: The investigation area between 2 - 6°E and 78 - 80°N is located within the frontal zone which is separating the warm and cold water masses originating from the West Spitzbergen Current and East Greenland Current, respectively. Based on the heterogeneous hydrographic condition differences in the picoplankton community according to the water masses is likely.

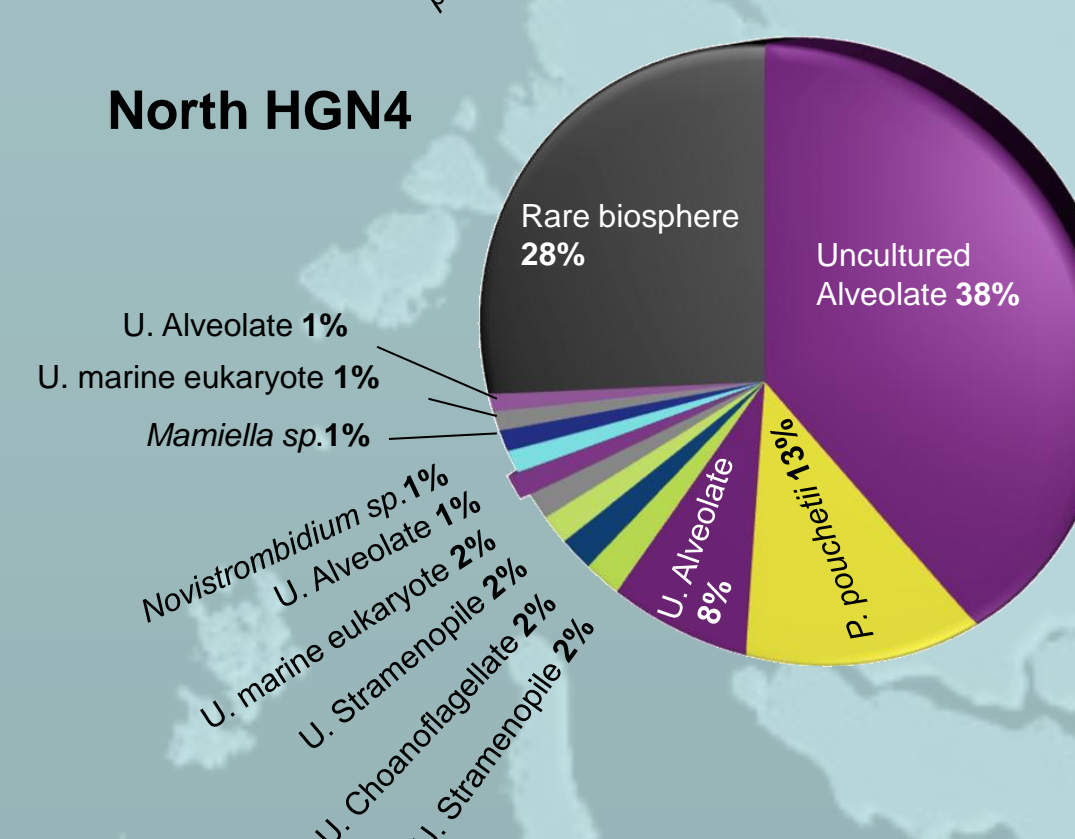
West HG4



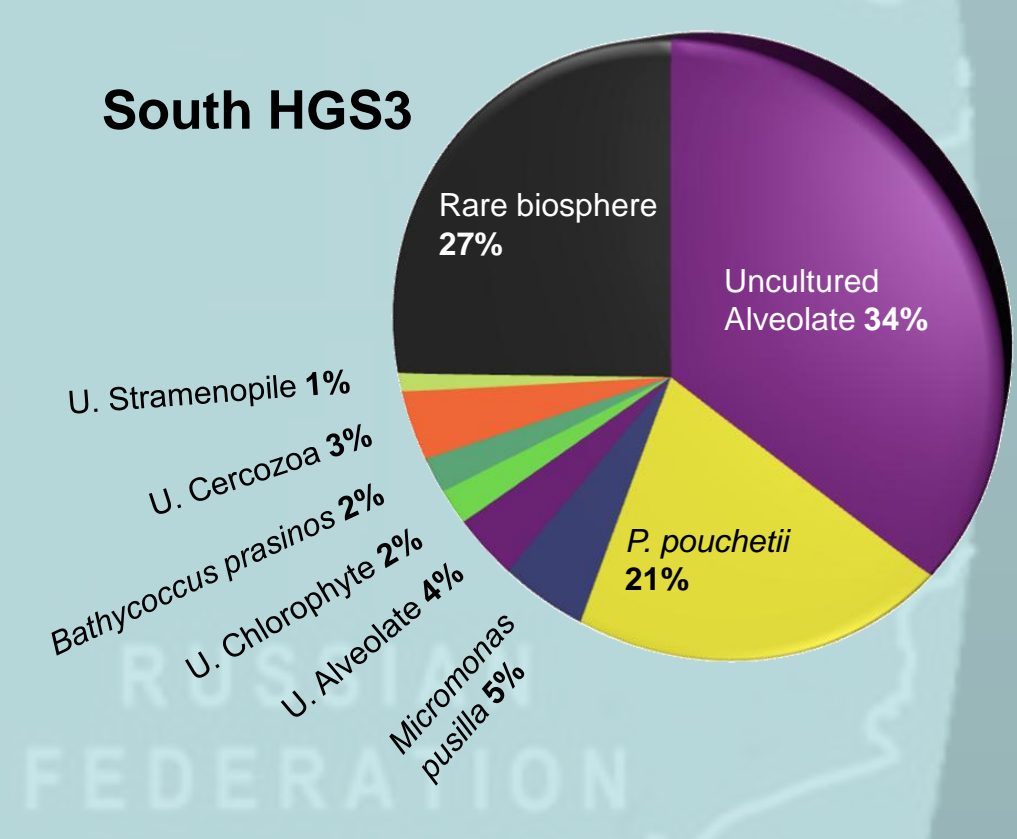
East HG1



North HGN4



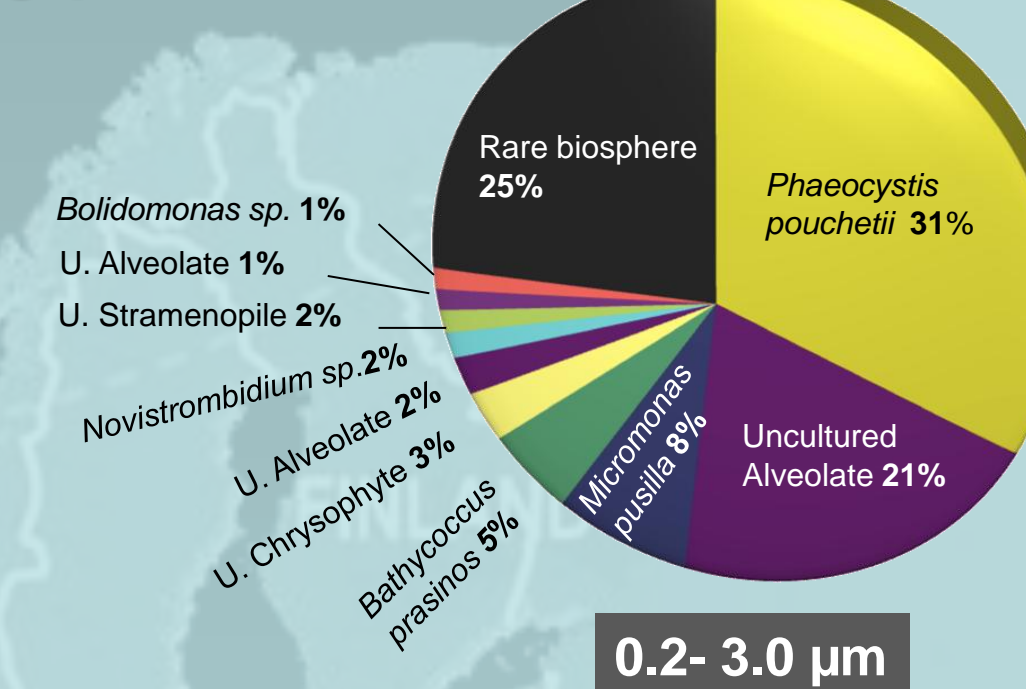
South HGS3



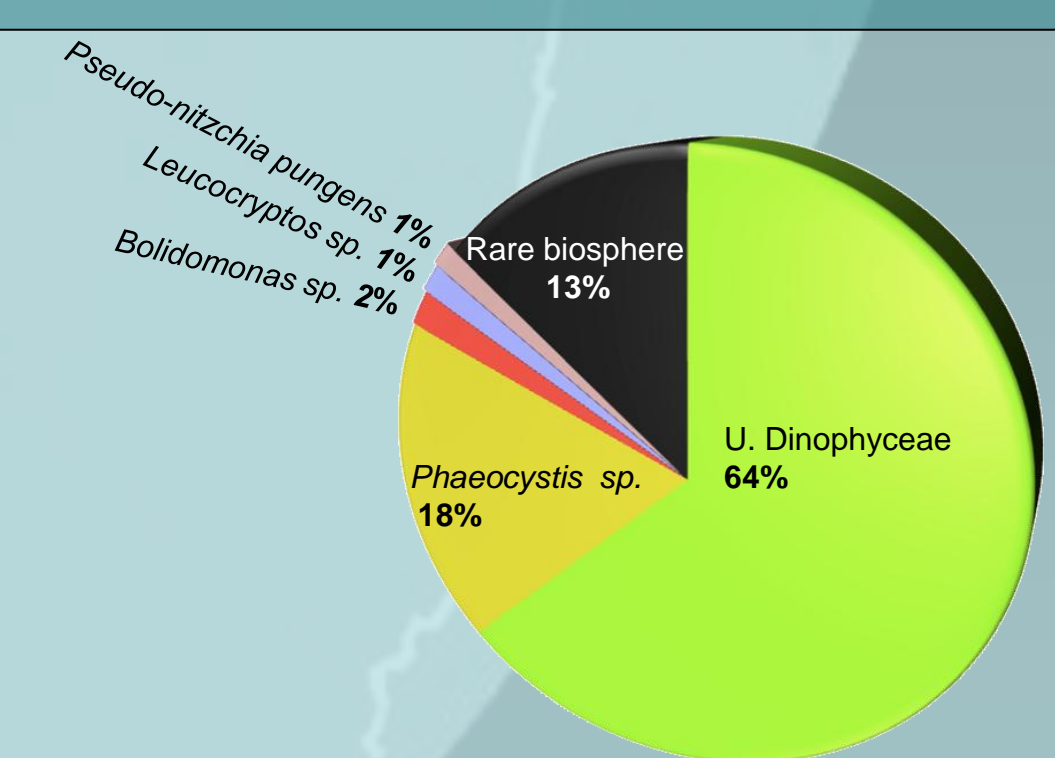
Pyrosequencing

- northern and southern station display a similar diversity
- western and eastern station display a distinct diversity and differ in most abundant taxa

HG4



0.2- 3.0 µm



3.0- 10 µm

- The small size fraction (0.2- 3.0 µm) shows a higher diversity within the abundant and rare biosphere
- *Phaeocystis* remains abundant at both size fractions

Objective

The study aims to assess the genetic diversity of picoplankton (0.2- 3.0 µm) in relation to local environmental parameters. In this process factors that possibly influence the composition and distribution of picoplankton taxa will be verified.

Conclusion & Outlook

The ARISA approach is well established for bacteria. Represented data confirm the applicability of this tool to investigate the genetic community structure even for picoeukaryotes. First results of the pyrosequencing approve the outcome of the ARISA approach. The comparison of the four stations reveals a higher similarity of the northern and southern stations. This observation could be explained by the inflow of the West Spitzbergen current which crosses both stations and thus results in related abiotic conditions. Overall *Phaeocystis pouchetii*, *Micromonas pusilla* and an uncultured Alveolate dominate most of the composition. These data indicate the presence of few, very abundant taxa besides many different but not abundant taxa. The abundance of *Micromonas pusilla* at HG1 could indicate a possible impact of the Kongsfjord and needs to be approved by further sampling. Comparing the two size fractions (0.2- 3.0 µm and 3.0- 10µm) picoplankton reveals a higher diversity. Further the relatively high percentage of *Phaeocystis* within the pico- and nanoplankton point to high relevance of this genus in this area.

- Additional expeditions to the “AWI-Hausgarten” have already been and will be taken place to clarify first results and to deliver further insights in the annual variability of picoplankton diversity and distribution.