

A Molecular Assessment of the Diversity and Biogeographical Distribution of Eukaryotic Protists in the Arctic Ocean

Estelle Kiliás¹, Eduard Bauerfeind¹, Eva-Maria Nöthig¹, Christian Wolf¹, Katja Metfies¹

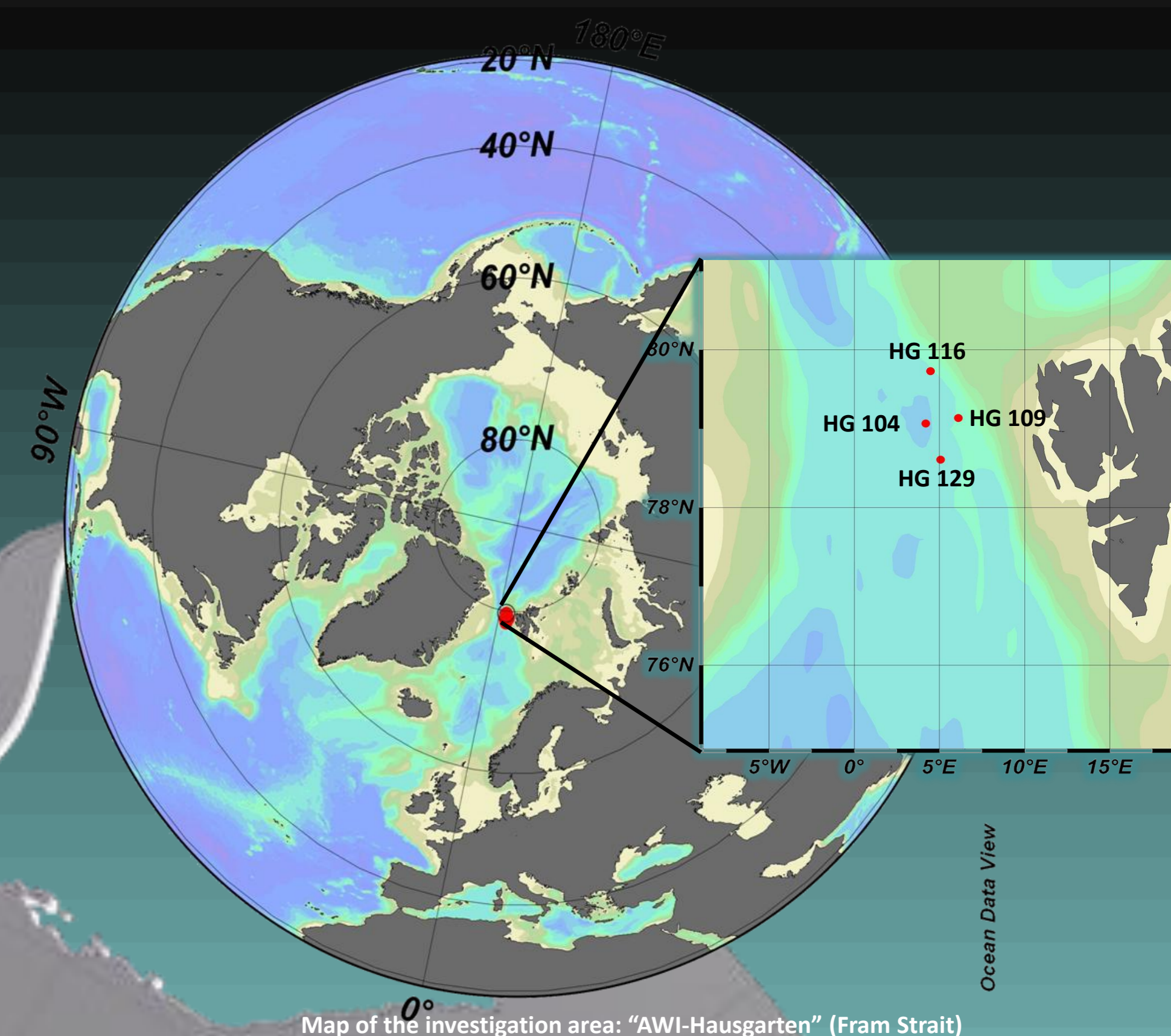
¹Alfred-Wegener-Institute for Polar and Marine Science, Am Handelshafen 12, 27570 Bremerhaven, Germany

Objective

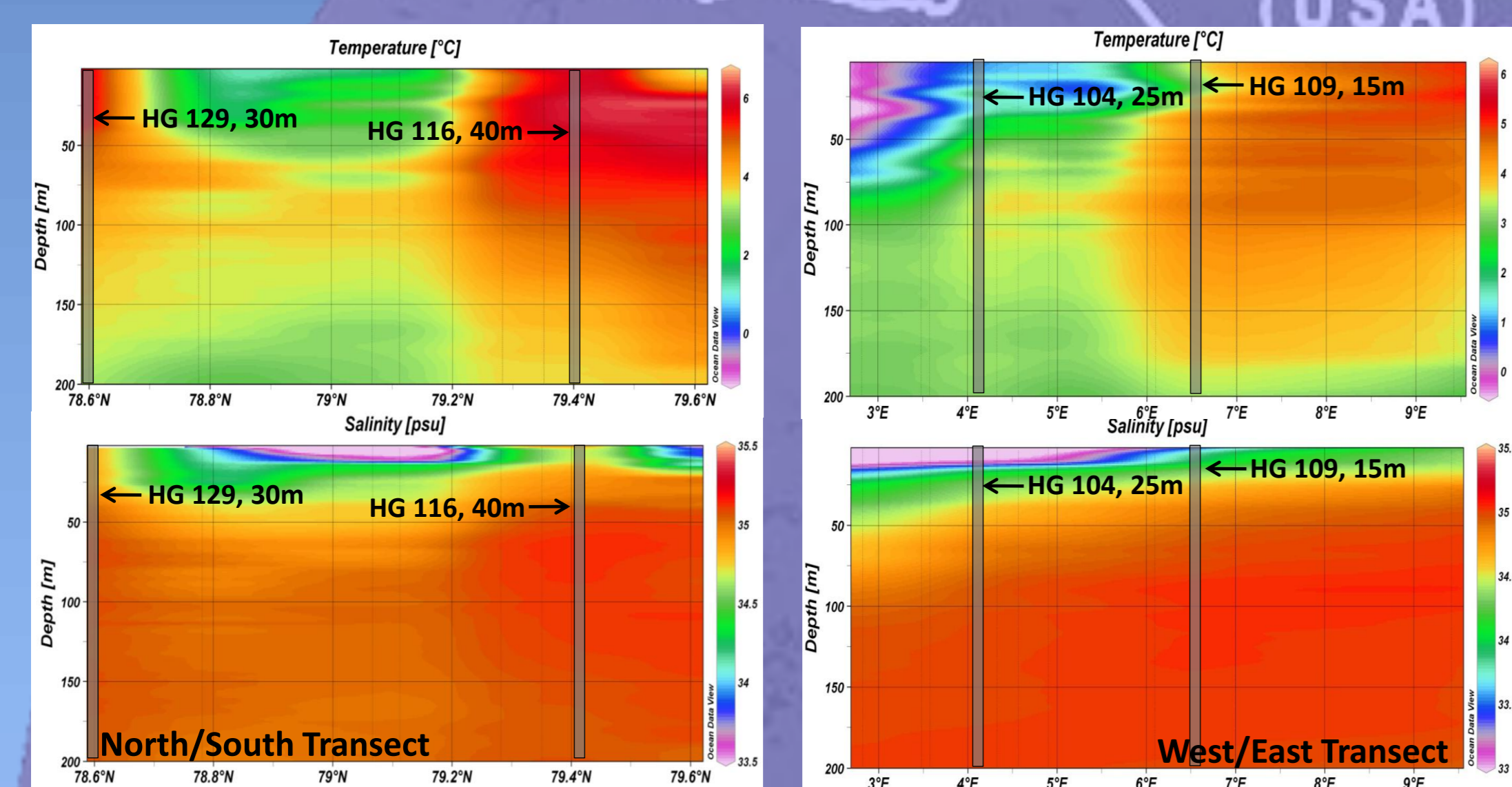
The aim of this study is the assessment of the diversity and distribution of eukaryotic protists in the Arctic Ocean, with special emphasis on the picoplankton fraction. In order to elucidate the impact of changing conditions on the picoplankton community in the Arctic Ocean the results will be compared with regard to abiotic factors.

Introduction

It is expected that the progressing environmental change, reflected by increasing air temperatures and radiation, or a decreasing sea ice cover will strongly impact Arctic marine ecosystems. This requires an evaluation of the impact on local phytoplankton communities, who are transforming CO₂ in biomass and display therefore a major part of primary producers. Important premises of such an evaluation are comprehensive information on the present phytoplankton diversity, distribution and variability. Recent investigations indicate that rising temperatures in the marine environment promote a shift in the phytoplankton community towards small cells (e.g. picoplankton). Considering the increasing importance of picoplankton in marine ecosystems, we are currently assessing the picoplankton community in samples taken in 2009 in the "AWI-Hausgarten" (Fram Strait) during the RV Polarstern expedition ARK XXIV/2 by the application of 18S rDNA clone libraries, 454-sequencing and ribosomal fingerprints.



Results

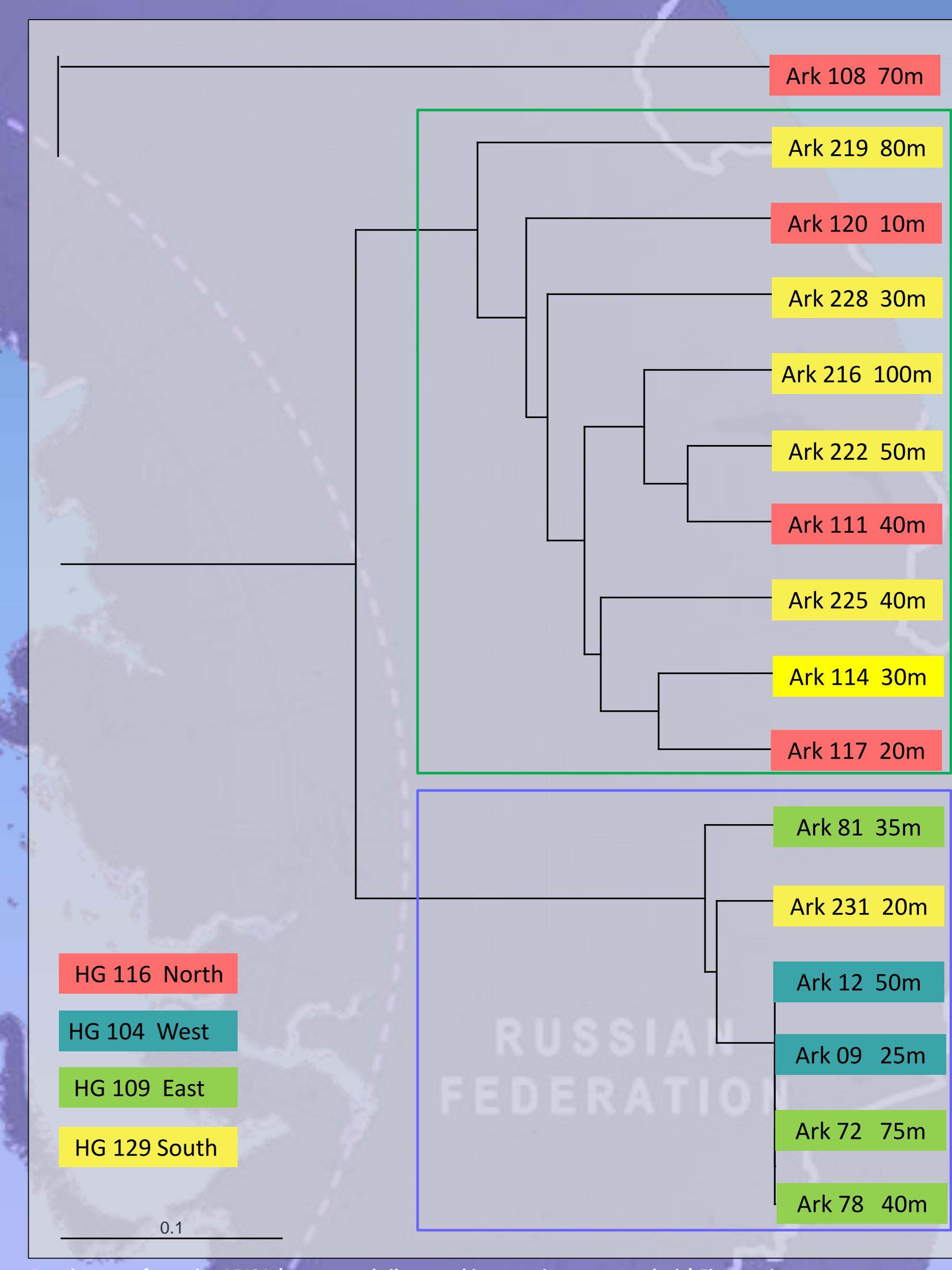
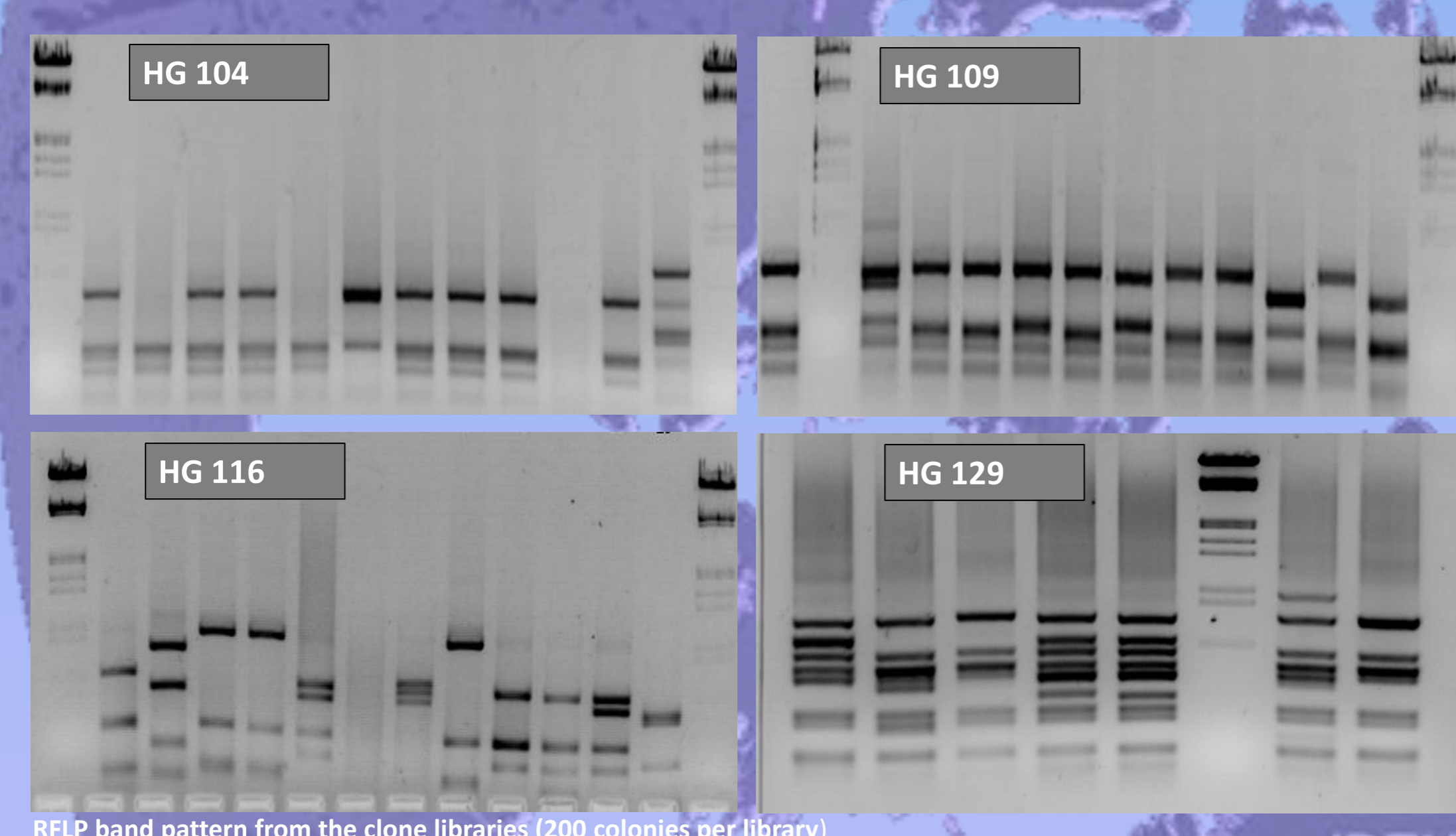


Clone library

- northern & southern stations show a variety of operational taxonomic units (OTUs) while the western and eastern stations are less variable & dominated by one pattern

ARISA Fingerprint

- A dendrogram reveals two major branches
- One major branch is constituted by taxa from the HG 116 & HG 129 stations and the second branch is constituted by HG 104 & HG 109 stations
- conspicuous resemblance in the composition of the deeper water layer taxa from HG 129 & the upper layer from HG 116
- same similarity between deeper water layer taxa of station HG 109 & upper of HG 104



Conclusion & Outlook

The dendrogram indicates two main branches. One containing the stations HG 129 and HG 116 and the other comprising HG 104 and HG 109. This observation points to a higher similarity of the northern/southern stations and accordingly the eastern/western stations. By taking the depth into account the upper layer of station HG 116 resemble the deeper water layer of HG 129. Similarly it can be observed for the second branch that the upper layer of HG 104 is similar to HG 109. This observation could be explained by a phytoplankton bloom situation versus post bloom situation. At station HG 109 and HG 129 the bloom is already descended to deeper layers. This is in agreement with the local ice coverage which could only be found in slight dimensions at station HG 104 and HG 116. The results from the clone libraries support these assumption. Here the northern (HG 116)/ southern (HG 129) stations display a high similar degree of diversity. In contrast, the western (HG 104)/ eastern (HG 109) stations demonstrate a roughly uniform diversity.

- To attain a better insight in the spatial distribution of picoeukaryote diversity in the "Hausgarten" further environmental samples from ArkXXIV/2 (2009) will be analyzed
- Additionally a third method (454-sequencing) of the 18S rDNA V4-Region will provide a high resolution picture of the picoeukaryote community structure & OTUs that differ in pattern will be sequenced to get a more precise approach of the diversity
- Future expeditions will take additional samples consisting the four "Hausgarten" stations to assess annual variability (2010-2012)