

Marine protist diversity and community structure at the West Antarctic Peninsula

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Introduction

The **Western Antarctic Peninsula** is climatically extremely variable and belongs to the **fastest warming regions on earth**.⁴

Recent **changes in the phytoplankton community composition** from large diatoms to small flagellated cryptophytes have been **associated with regional climate change** and are potentially inducing further **shifts in the dominance of major grazers** in this region, i.e. Antarctic krill (*Euphausia superba*) and salps (*Salpa thompsoni*).^{5,6}

In order to enhance our understanding of these changes, compiling a comprehensive dataset **characterizing the regional plankton community structure and potential environmental drivers** is crucial.

OBJECTIVE:

How is the plankton community at the West Antarctic Peninsula structured and which environmental parameters are driving respective spatial differences?

Methods

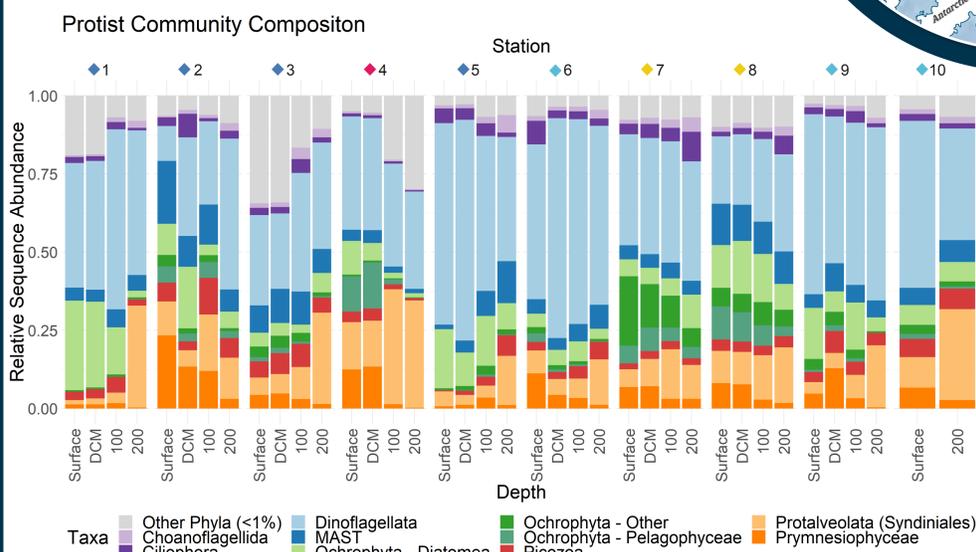
Samples were taken with a **CTD at ten different stations** and **four different depths** during the RV Polarstern cruise PS112 in late **summer/autumn** (March - May 2018) to the South Shetland Islands and the **Antarctic Peninsula**.

We used **Illumina sequencing**, targeting the **18S rDNA V4 region**, to investigate the protist community. The bioinformatic processing of the sequences was performed with a **custom-made pipeline** (Q-zip).⁷ **Silva.v132** served as main reference for taxonomic annotations.

Metazoan OTUs were removed from the dataset and the number of **reads were scaled to the smallest library size** to account for uneven sequencing depths.

Community Composition

Quality control and filtering resulted in a diverse range of more than **four million protist sequences** and roughly **13 thousand** operational taxonomic units (OTUs).

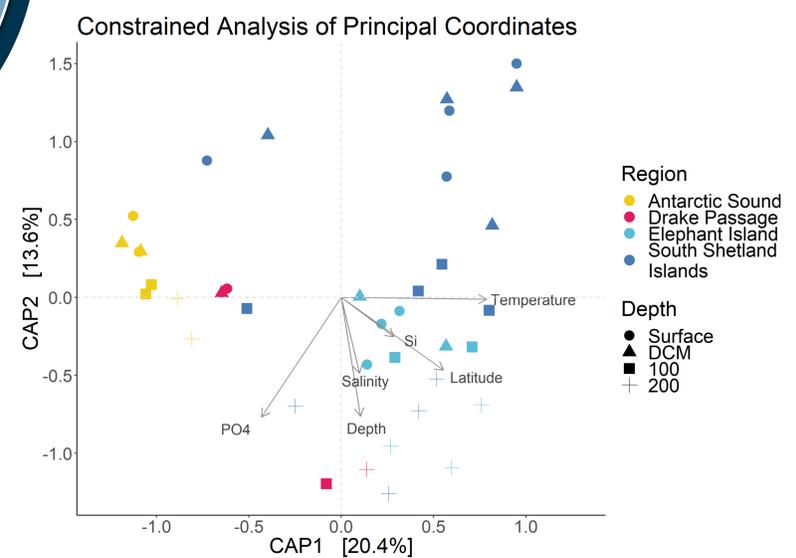


Most sequence reads belonged to **dinoflagellates (42%)**, followed by the **parasitic group of Syndiniales (12%)** and **diatoms (9%)**. Among **different stations and depths** the **relative abundances** of taxonomic groups often **varied** considerably.

28% of the **dinoflagellate** sequences were annotated as *Gyrodinium*, an often heterotrophic genus. More than **half of the diatoms** were identified as *Thalassiosira* (56%).

Compositional Dissimilarity

Constrained Analysis of Principal Coordinates (CAP) based on Bray-Curtis distances displaying the variation between protist assemblages, constrained by relevant abiotic parameters and dissolved nutrient concentrations.



Temperature was the **main factor** contributing to the **first axis (CAP1)** and separated the **Antarctic Sound (AS)** samples from other regions.

The dissimilarities along the **second axis (CAP2)** were **mainly correlated to depth** and led to a **gradual clustering** of **South Shetland Island (SSI)**, **Elephant Island (EI)** and **200m samples**.

The **large dissimilarities** among **SSI** samples also coincided with a gradient in dissolved inorganic **phosphate (PO4)** concentrations.

Drake Passage samples displayed a clear separation of **deep and shallow** depths.

Dissolved **silica (Si)** and **salinity** also **contributed significantly** to the dissimilarity of samples but **with lower correlation** to the ordination axes.

Conclusions

We observed a **highly diverse** assemblage of protists at the WAP. Community structure showed distinct **differences among regions and depths**, which were mainly **determined by temperature, depth, dissolved phosphate and latitude**.

Outlook

This study is part of the project **POpulation Shift and Ecosystem Response - Krill vs. Salps (POSER)**. The presented results will be complemented by **further analyses**, including microscopy, 16S sequencing, pigment analysis and flow cytometry. Furthermore, they will serve as basis for the analysis of **experiments** conducted on board that aimed at estimating the possible consequences of a shift from the currently still predominant krill population to an increasing occurrence of salps.

Scan for further information:

