Protist diversity in the Southern Ocean revealed by molecular tools

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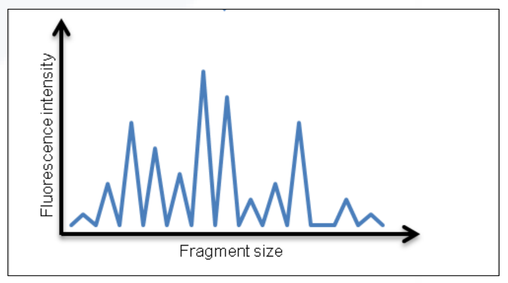
Research questions

- Are different large-scale water masses characterized by distinct protist community assemblages?
- Are there regional protist community patterns within a single large-scale water mass?
- How can molecular tools help to reveal protist community patterns?

Methods

ARISA (automated ribosomal intergenic spacer analysis)

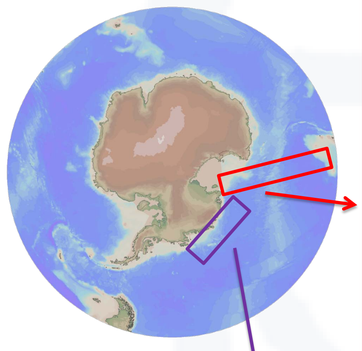
- Amplification of intergenic spacer region (between 18S and 28S rRNA gene)
- Determination of fragment lengths → presence/absence matrix of different fragment lengths
- Comparison of fragment length structure (~community structure) of several samples



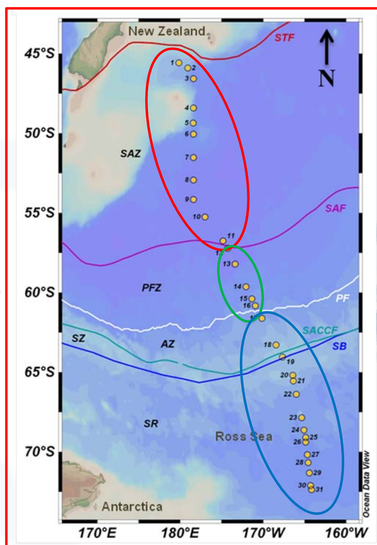
454-pyrosequencing

- Amplification of the hypervariable V4 region of the 18S rRNA gene (~670 bp) → sequencing on a Roche FLX system
- Raw sequence reads processing:
  - Removing of low quality reads (too short, too long, more than one uncertain base, chimeric sequences)
  - Clustering of remaining reads into operational taxonomic units at the 97% similarity level (Lasergene 10)
  - Formation of consensus sequences → remove of singletons → alignment of consensus sequences (HMMER)
  - Placement (pplacer) into a reference tree (1,200 high quality sequences of SILVA SSU Ref 108)

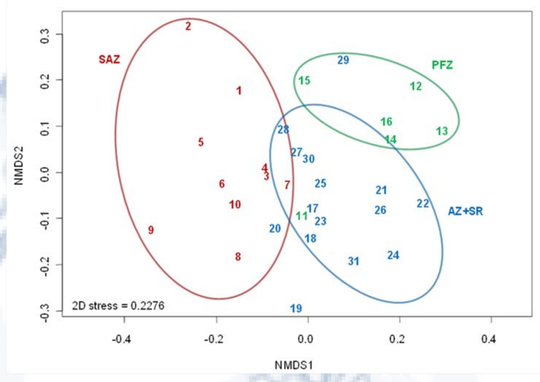
Results



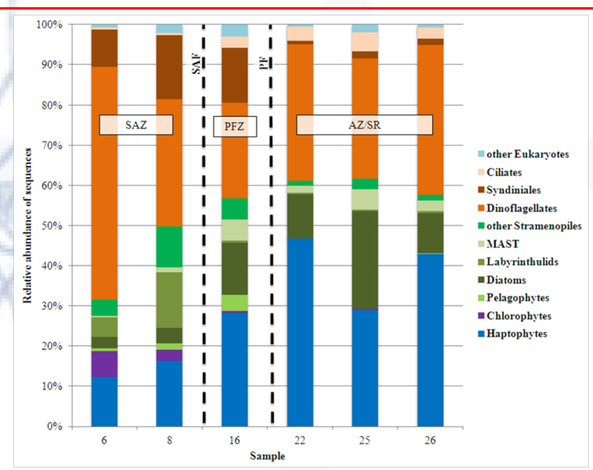
STF = Subtropical Front
SAF = Subantarctic Front
PF = Polar Front
SAZ = Subantarctic Zone
PFZ = Polar Frontal Zone
AZ = Antarctic Zone
SR = Subpolar Region



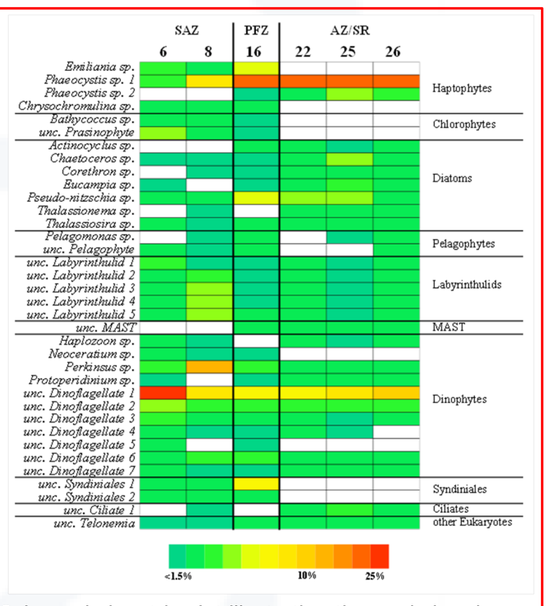
Study area, oceanic fronts and regions, and sample stations



MDS plot based on the Jaccard distances calculated based on ARISA outcome

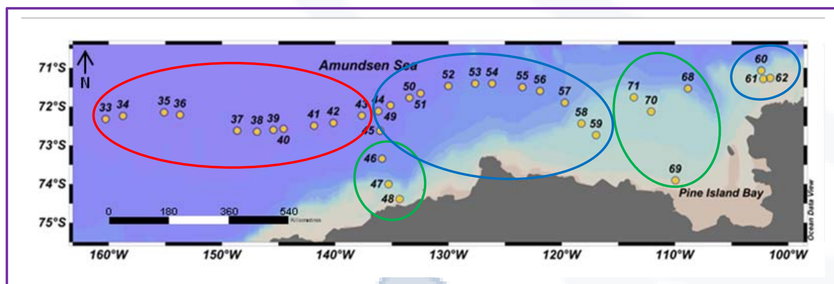


Relative abundance of sequence reads (gained via 454-pyrosequencing) assigned to major taxonomic groups

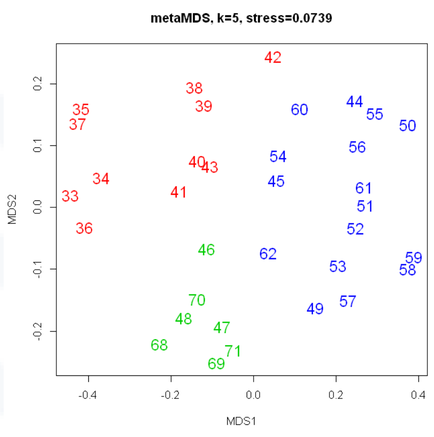


Color-coded matrix plot illustrating the read abundance and affiliation of the 36 most abundant phylotypes

- Three groups separated by the SAF and PF
- In the north, smaller species and dinoflagellates dominated
- Diatom abundance increased southwards
- Haptophytes dominated south of PF



Study area (Amundsen Sea) and sample stations



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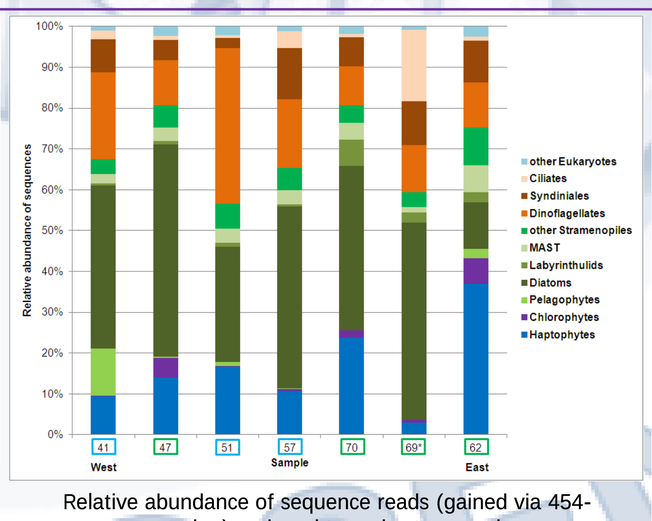
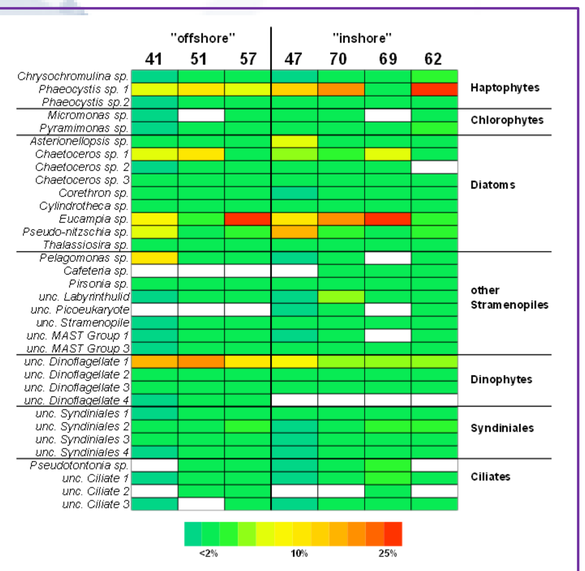


Relative abundance of sequence reads (gained via 454-pyrosequencing) assigned to major taxonomic groups
offshore inshore



Color-coded matrix plot illustrating the read abundance and affiliation of the 34 most abundant phylotypes

- Two overall groups (offshore and inshore)
- Diatoms were the dominating taxonomic group
- *Eucampia* sp. and *Pseudo-nitzschia* sp. dominated inshore and *Chaetoceros* sp. offshore
- At the most eastern station, *Phaeocystis* sp. dominated
- Under the ice, ciliates showed their highest and haptophytes their lowest abundance

Conclusions

- Each water mass harbored characteristic protist assemblages. Most prominent separator was the Polar Front.
- Within a single water mass, protist assemblages differed according to geographical and environmental conditions. (offshore and inshore).
- ARISA and 454-pyrosequencing constitute powerful tools to investigate protist distribution and composition patterns.

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