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Composition and Succession of Eukaryotic Protists During the Iron Fertilization Experiment LOHAFEX in the Southern Ocean

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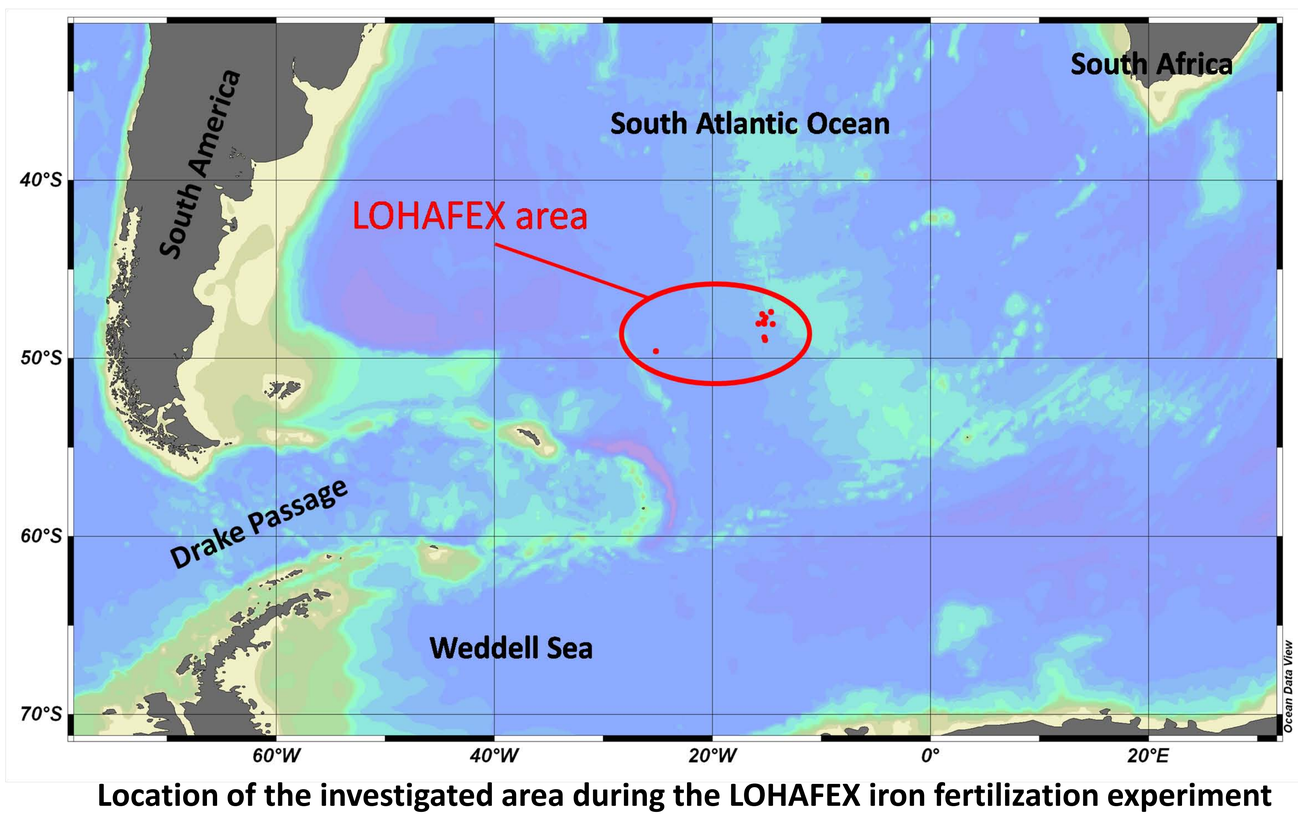
Scientific goal

The objective of this study is to determine the composition and succession of eukaryotic protists, with special emphasis on the picoplankton fraction, during the LOHAFEX iron fertilization experiment.

Introduction

- In the presence of silicic acid ocean iron fertilization experiments have induced diatom blooms that promote carbon sequestration from the atmosphere
- During the RV *Polarstern* cruise ANT XXV/3, the iron fertilization experiment LOHAFEX was carried out from January to March 2009 in an eddy in the Atlantic sector of the Southern Ocean
- At the start of the fertilization the eddy was silicic acid limited
- The pico- and nanoplankton fraction dominated the phytoplankton assemblage during the experiment
- In non-diatom bloom situations the major part of the phytoplankton biomass is often contributed by the picoplankton fraction (0,2 - 2 µm) → more knowledge about that particular fraction is needed



Location of the investigated area during the LOHAFEX iron fertilization experiment

Methods

Due to difficulties in identifying protists in the picoplankton fraction down to the species level with conventional methods (microscopy) we applied molecular approaches:

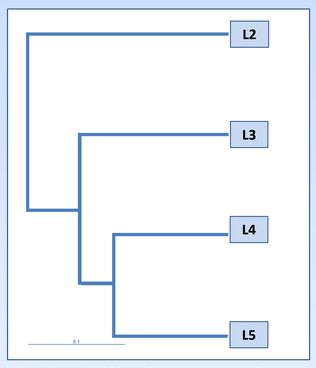
→ Ribosomal fingerprint → Sequencing of 18S rDNA clone libraries → 454-Sequencing

Results (preliminary)

Ribosomal fingerprint

- Diversity is decreasing with time
- The out-group (L4) shows the lowest diversity
- The fertilized sample L5 is more diverse than the out-group (L4)
- L4 and L5 show the most similarity, L2 is most away from the rest

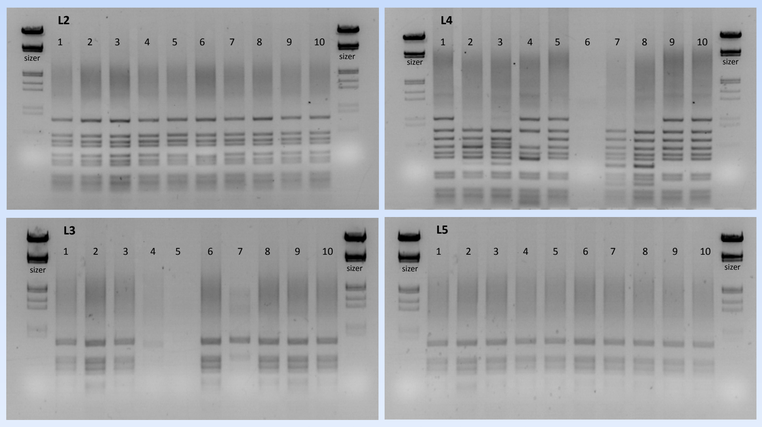
Sample	Days after fertilization	Inside/outside the eddy	Number of Fragments
L2	-1	in	18
L3	+9	in	16
L5	+18	in	14
L4	+16	out	7



UPGMA of ITS fragment analysis

18S clone libraries

- Samples L2, L3 and L5 consist almost of one operational taxonomic unit (OTU)
- Sample L4 consists of more OTU's



RFLP band pattern examples of 10 clones of each sample, digested with HaeIII

Conclusions

- Before the iron fertilization there was a natural bloom situation
→ diversity ribosomal fingerprint → high (L2)
→ diversity clone library → low (L2)
- During iron fertilization the bloom situation continued, but species composition differed (**fertilized succession**)
→ diversity ribosomal fingerprint → high (L3 & L5)
→ diversity clone libraries → low (L3 & L5)
- In the background there was a **natural succession** (out-group shows a non-bloom situation)
→ diversity ribosomal fingerprint → low (L4)
→ diversity clone library → high (L4)

Outlook

- Sequencing of clones from each OTU will give more detailed information about the species composition
- The results of the 454-Sequencing will provide a broader overview of the diversity
→ more information about the effects of iron fertilization on the picoplankton succession and composition
→ comparison of the methods
- Further the outcome will be compared with the results of other methods (e.g. flow cytometry, microscopy)

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