

Eukaryotic Picoplankton Composition and Succession during the Iron Fertilization Experiment LOHAFEX in the Southern Ocean

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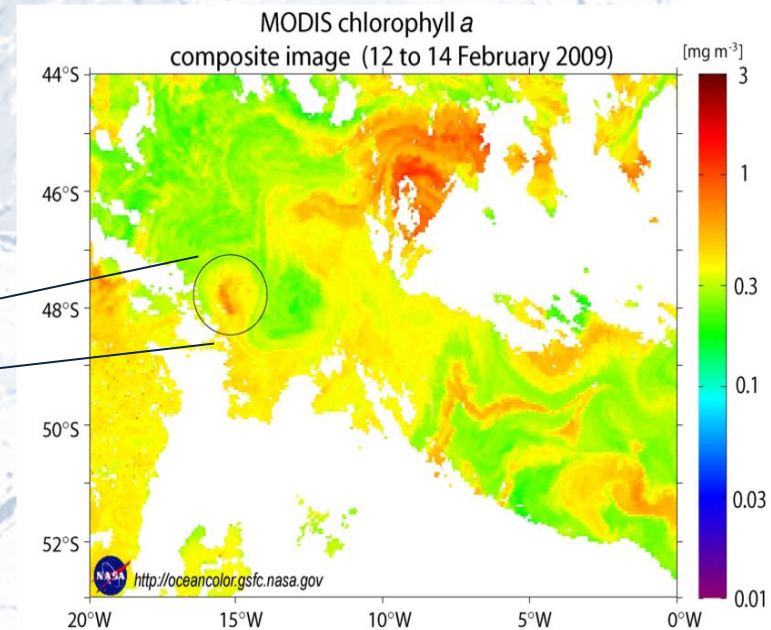
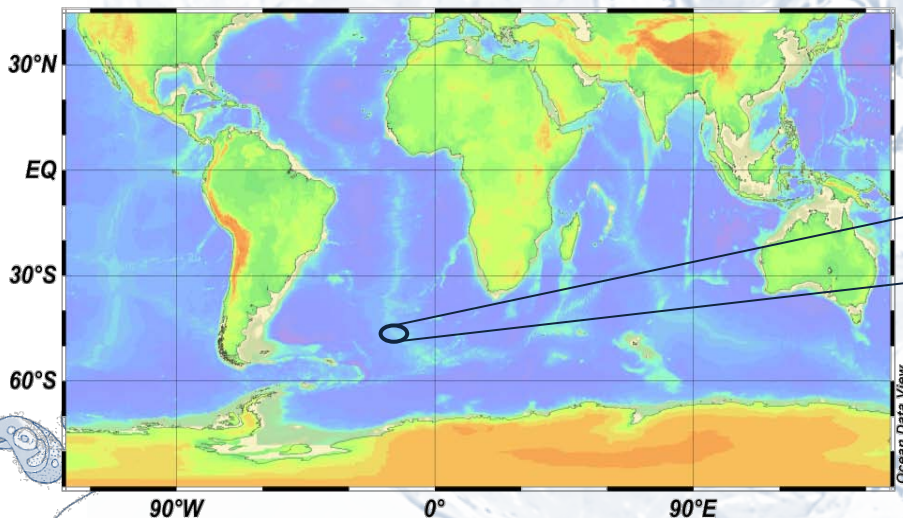
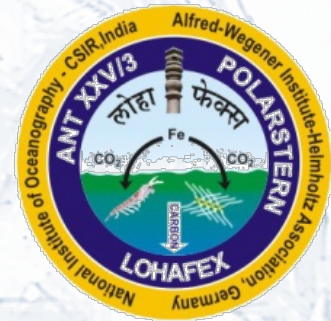
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LOHAFEX

- **RV *Polarstern* cruise ANT XXV/3 (austral summer 2009)**
- **joint Indo-German experiment**
- **Atlantic sector of the Antarctic Circumpolar Current (ACC)**

LOHA = iron (Hindi)
FEX = fertilization experiment



LOHAFEX

overall intention of the experiment:

→ investigate the fate of iron fertilized bloom biomass

general outcome:

- **experiment was carried out in a silicic acid depleted mesoscale eddy:**
 - prevented diatoms from accumulating biomass**
 - domination of nano- and picoplankton (<10 μm)**
- **fertilization had little effect on vertical flux**
 - heavy grazing of large copepod population**



Objectives

- influence of iron fertilization on eukaryotic pico- and nanoplankton (<6 μm)
- composition and succession during the experiment



microscopy:
cell counts

molecular approach:
454-pyrosequencing



Sampling

microscopy

days after fertilization	location
0	(in patch)
2	in patch
4	out patch
5	in patch
10	in patch
14	in patch
16	out patch
23	in patch
25	in patch
30	out patch
33	in patch
35	out patch
37	in patch
38	out patch

454-pyrosequencing

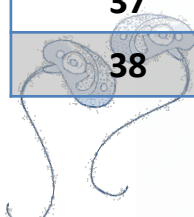
days after fertilization	sample name	location	iron [nmol/l]
0	L2	(in patch)	0.19
10	L3	in patch	0.24*
16	L4	out patch	0.19
18	L5	in patch	1.10

* not measured in the center of the patch

microscopy: CTD 0-80 m

454-pyrosequencing: CTD 20 m

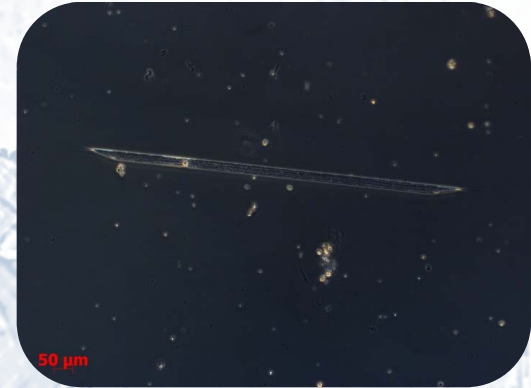
eddy



Methods

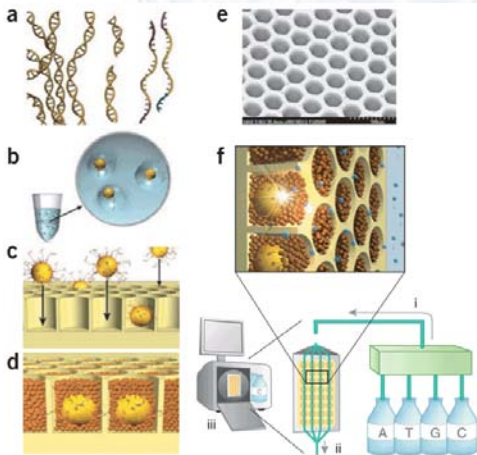
microscopy:

- cells were identified and counted in transects using an inverted light microscope
- biovolume and biomass was determined



molecular approach (454-pyrosequencing):

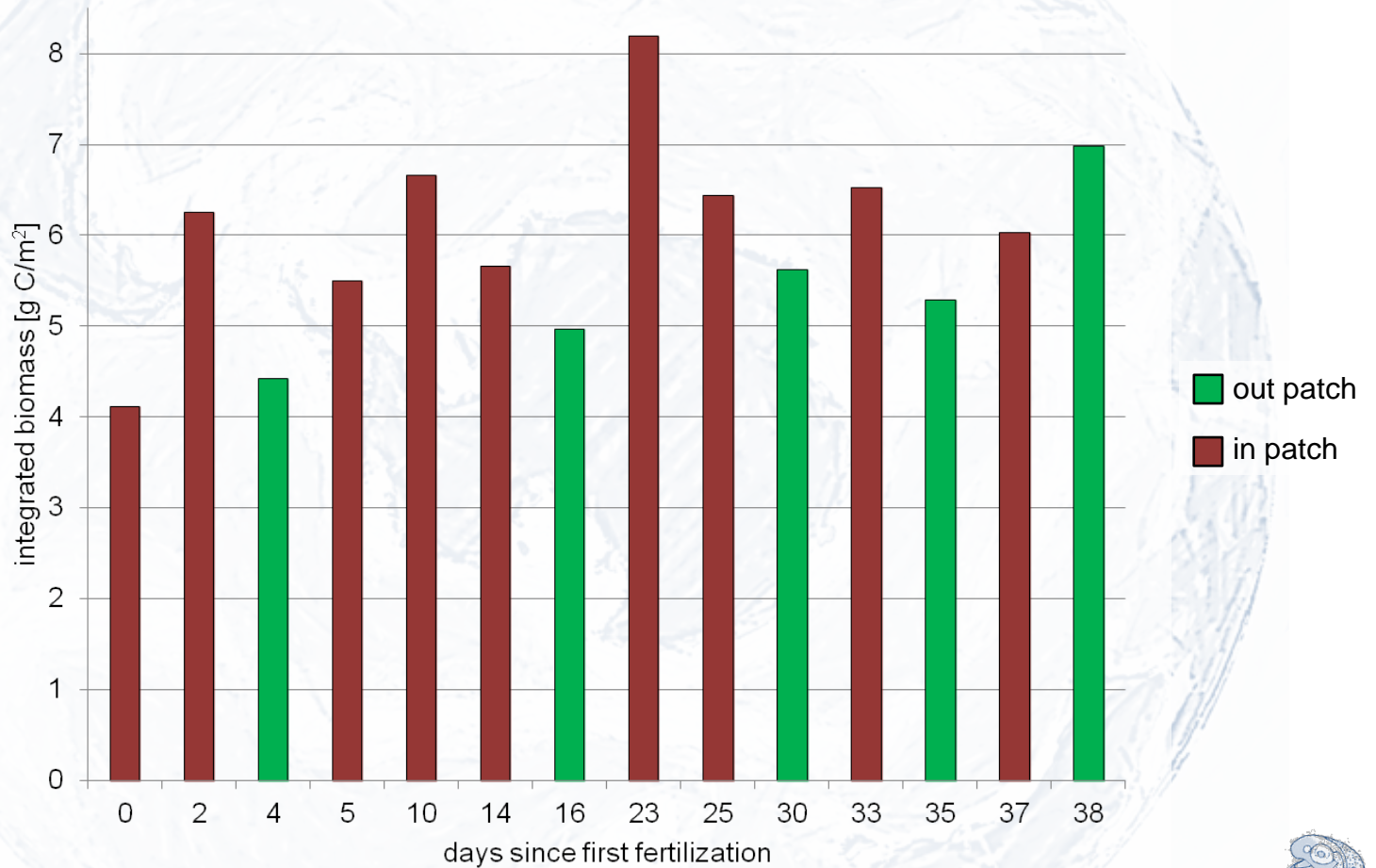
- amplification of highly variable V4-region of 18S rRNA gene (app. 670 bp)
- quality check, chimera check and assembling of reads (97% identity)
- placement in a reference tree (Phyloassigner)



454-pyrosequencing process
(Rothberg and Leamon 2008)



Results

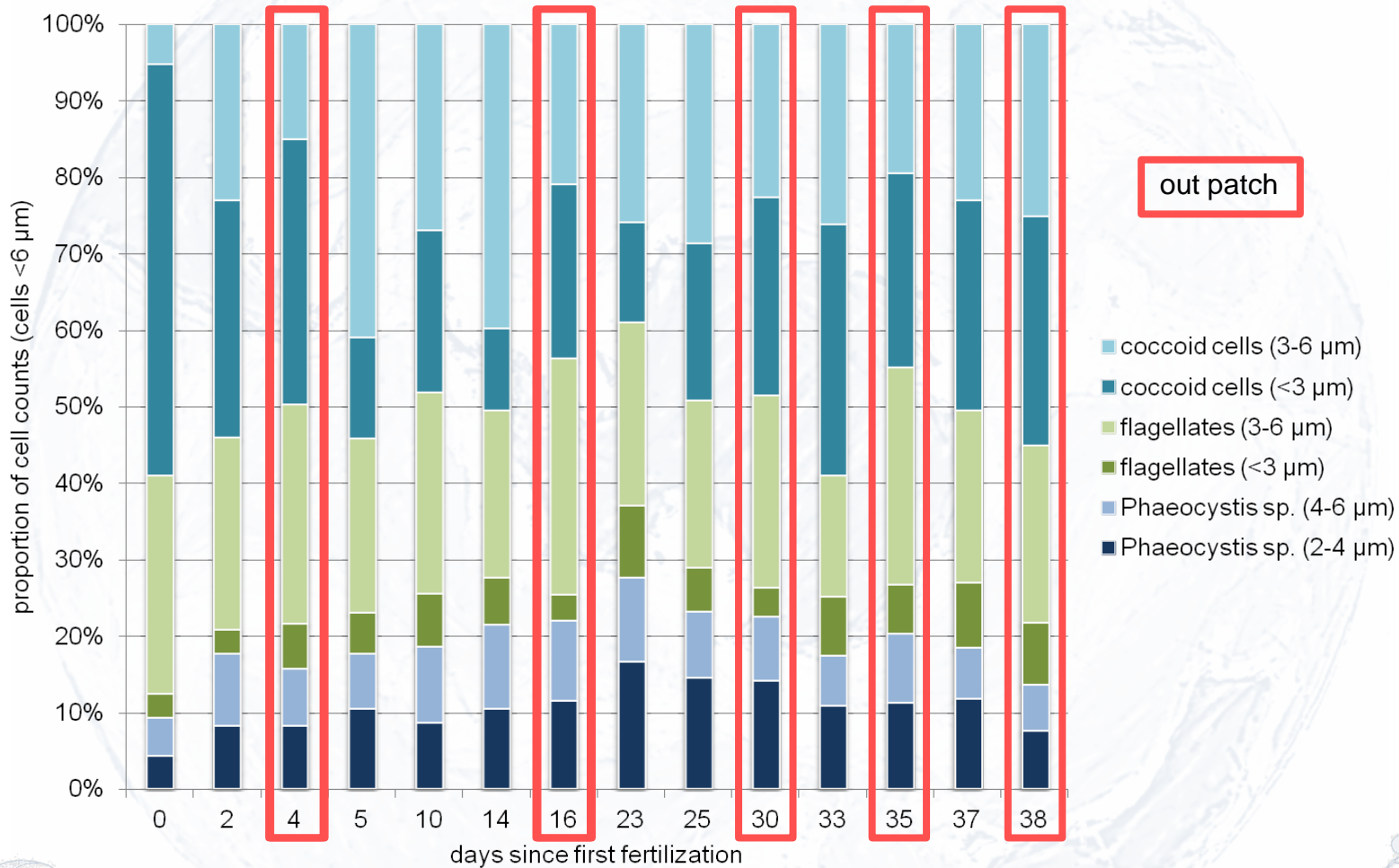


integrated biomass
(0-80 m, all cells)



Microscopy

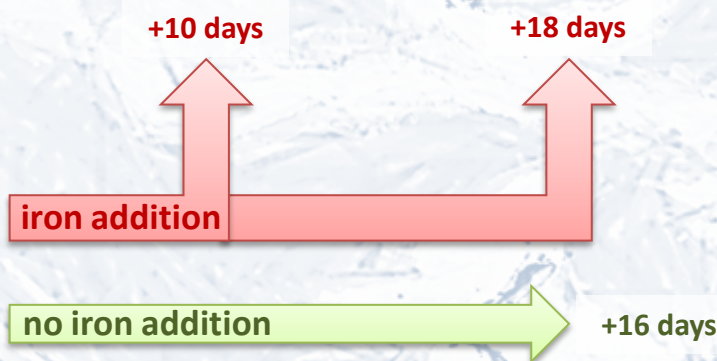
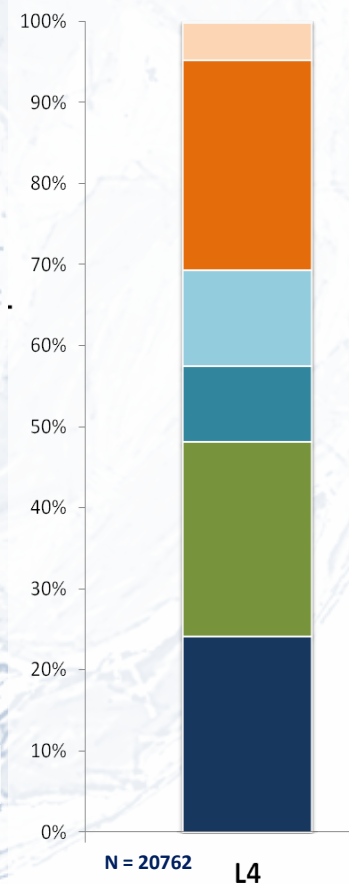
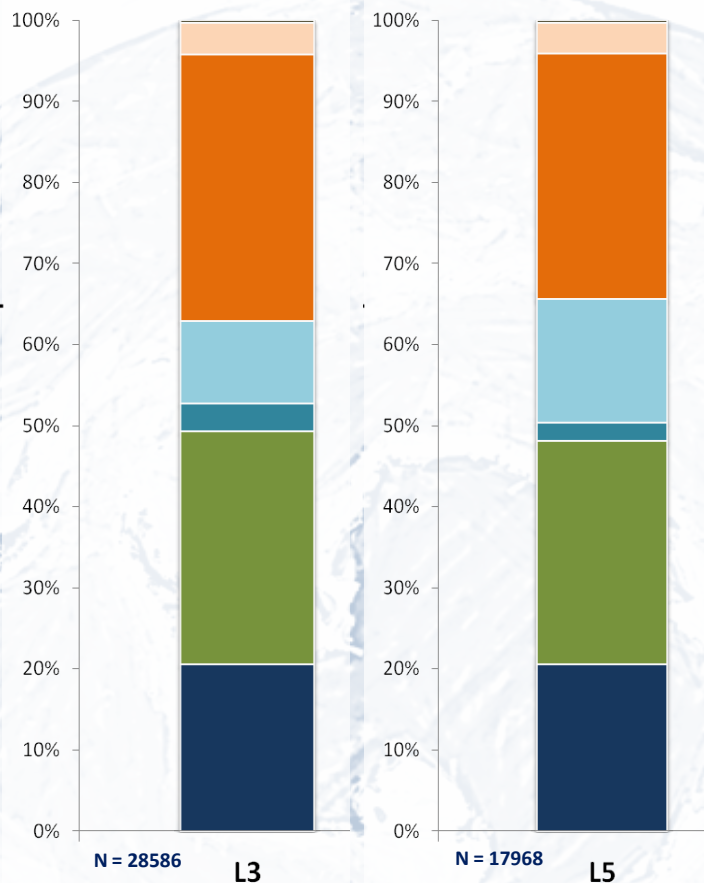
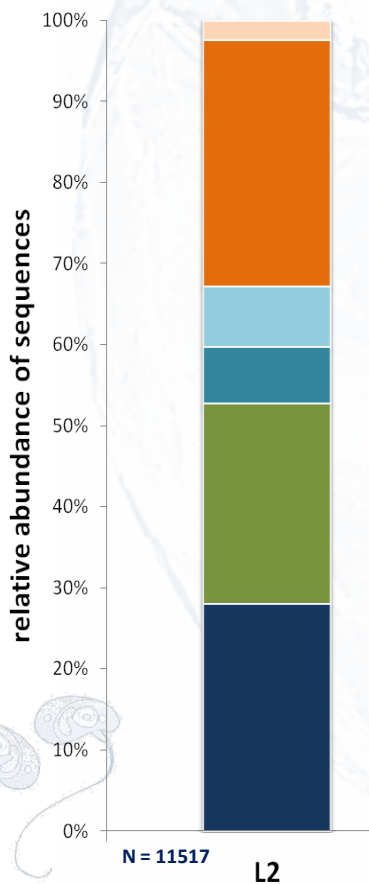
Results



integrated cell counts
(0-80 m, cells <6 μm)

Results

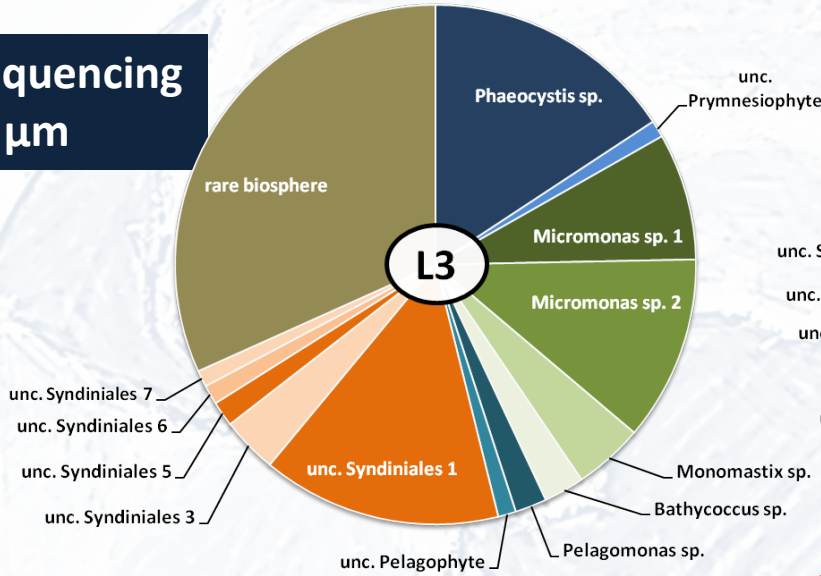
454-pyrosequencing
0.2-5 μm



Results

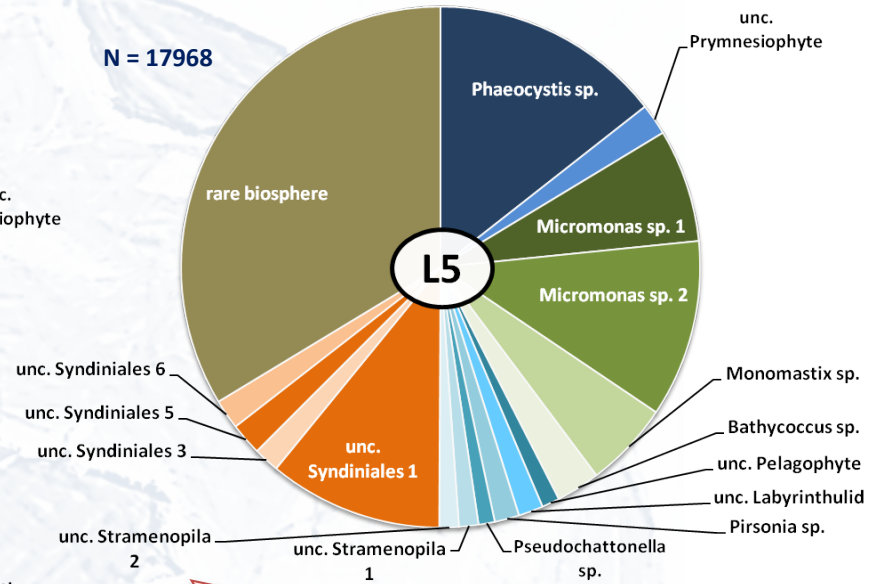
454-pyrosequencing
0.2-5 μm

N = 28586



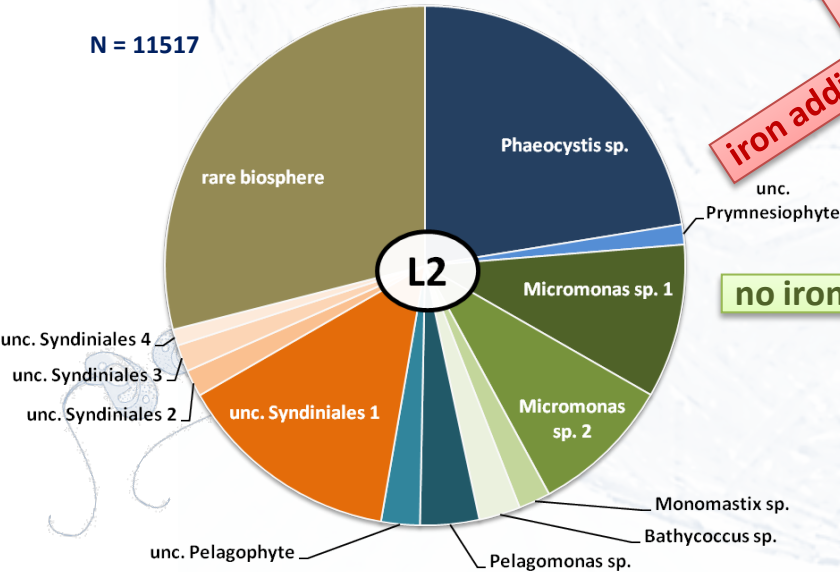
+10 days

N = 17968



+18 days

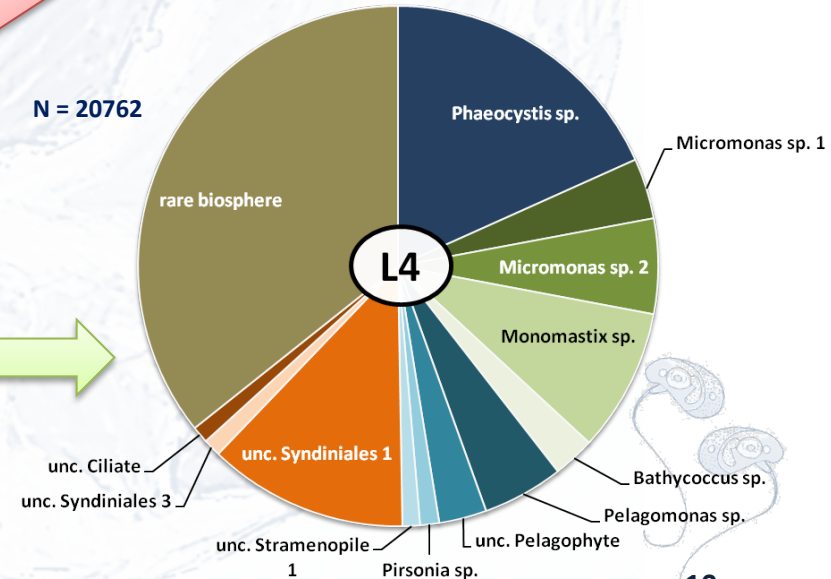
N = 11517



no iron addition

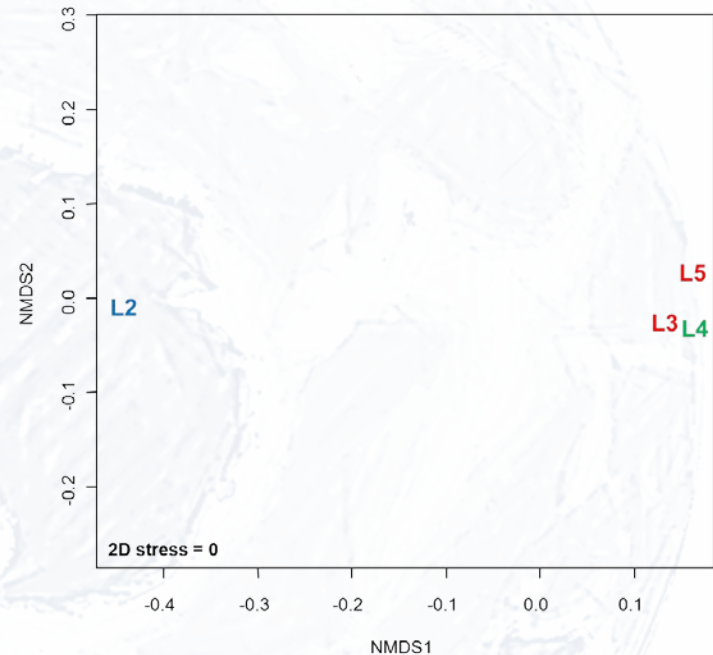
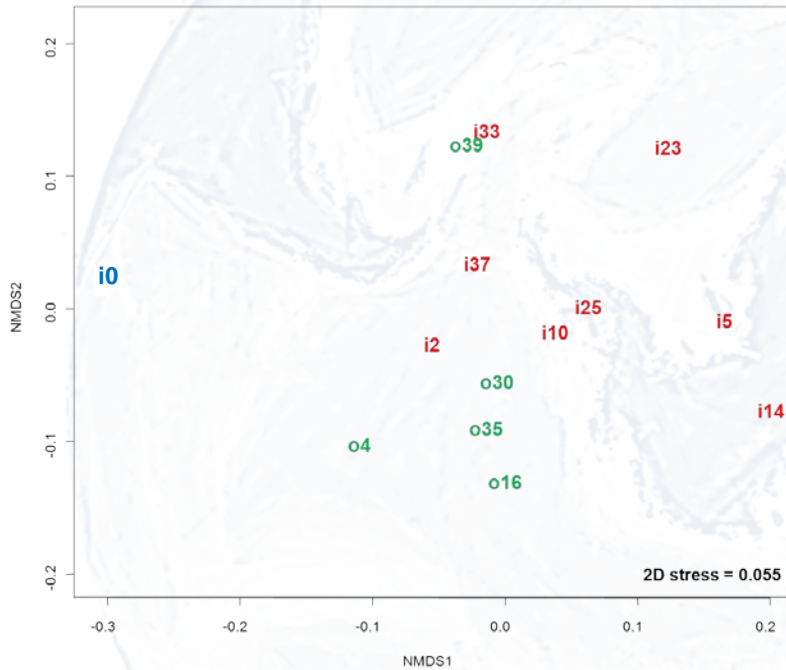
+16 days

N = 20762



10

Results



**MDS plot (Bray Curtis)
integrated cell counts
(0-80 m, cells <6 μm)**

**MDS plot (Jaccard)
454-pyrosequencing
(0.2-5 μm)**



Conclusions

- iron fertilization slightly enhanced biomass production during the first three weeks
- but composition of eukaryotic <math><6\ \mu\text{m}</math> fraction did not change significantly (no winner or loser)
- rather natural/temporal succession than iron induced succession
- <math><6\ \mu\text{m}</math> assemblage was dominated by *Phaeocystis* sp., prasinophytes (*Micromonas* sp., *Monomastix* sp.) and small dinoflagellates (Syndiniales)





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**Thank you for
your attention!**

Questions?

