

Seasonality of Bacterial Phylotypes Affected by Bottom-up and Top-down Control in Piburger See, Austria

Michaela M. Salcher

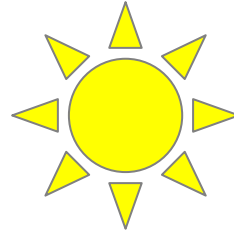


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Switzerland

why seasonality of lakes?



winter stratification



ice cover



0°C

low nutrients
high oxygen

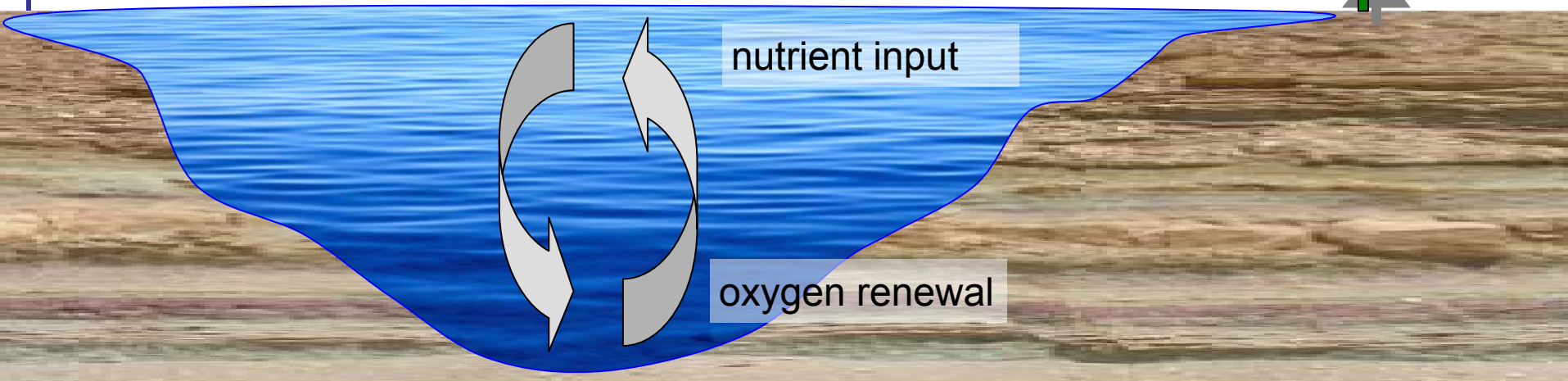
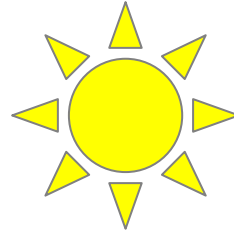
4°C

high nutrients
low oxygen

seasonal changes of a dimictic lake



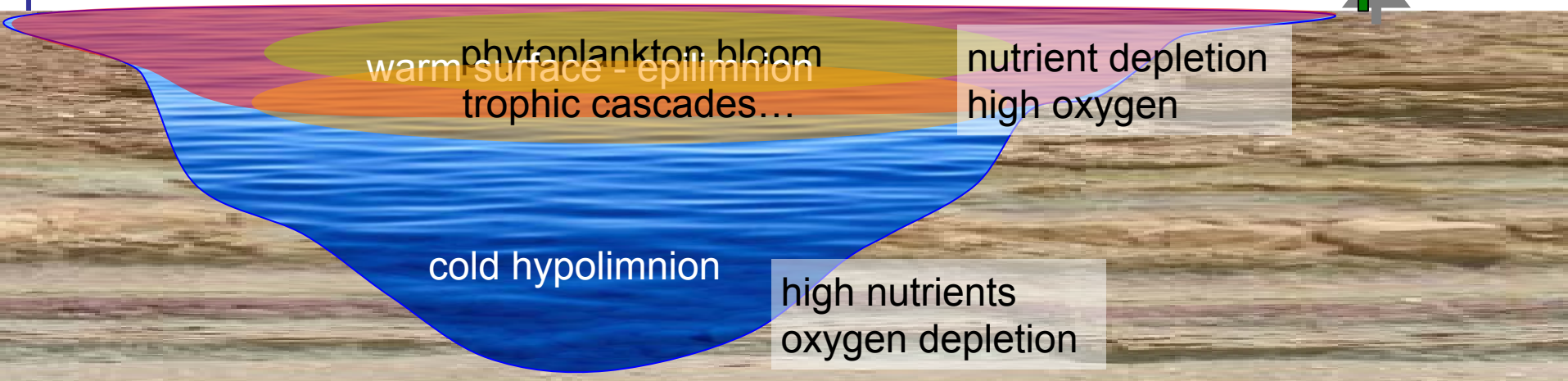
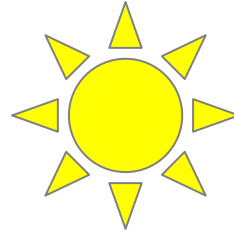
spring mixis



seasonal changes of a dimictic lake



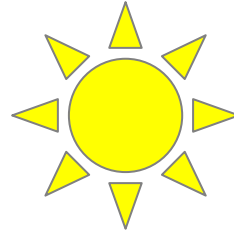
summer stratification



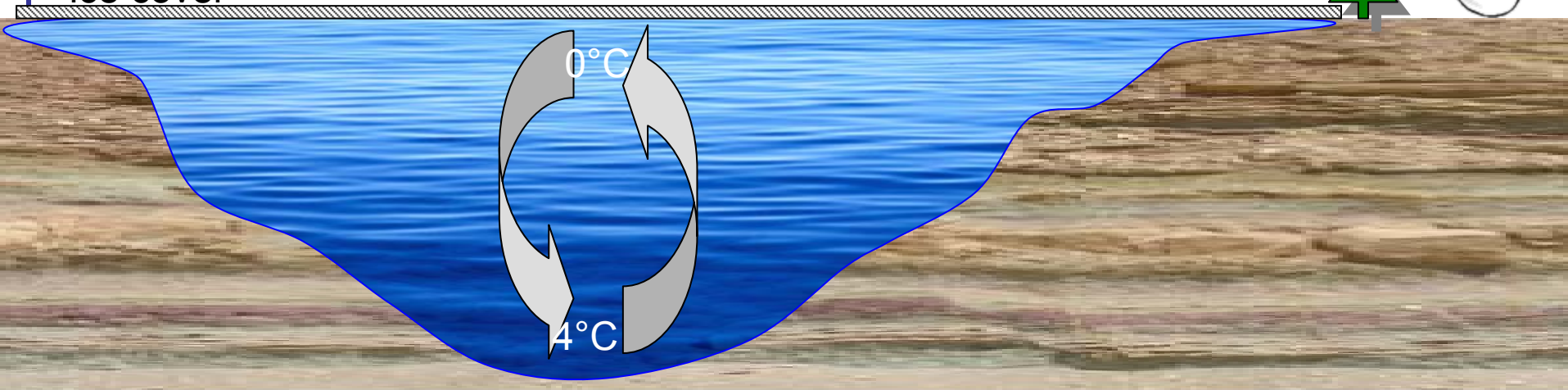
seasonal changes of a dimictic lake



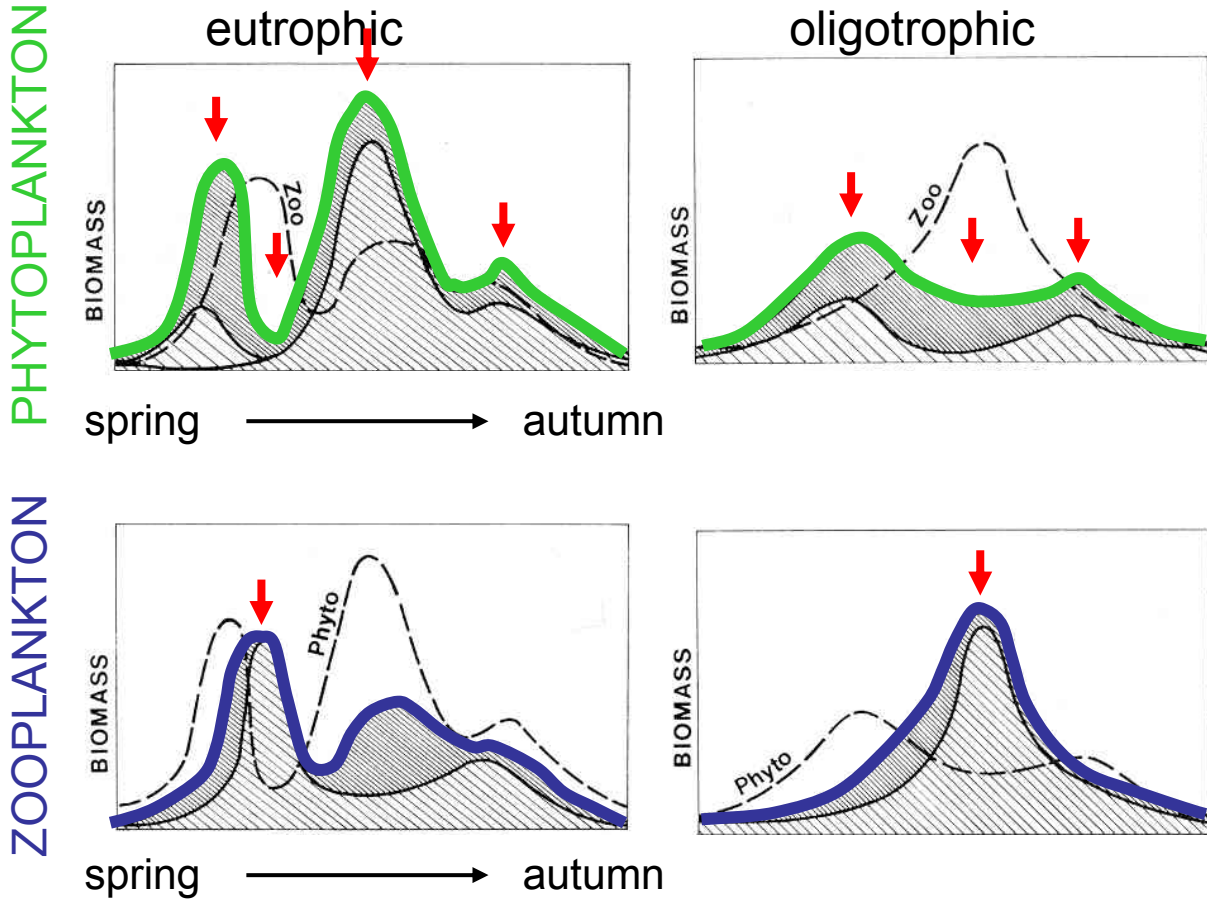
winter stratification
autumnal mixis



ice cover



seasonal changes of the biota



- phytoplankton spring bloom
- small protists, followed by large crustaceans
- clear water phase
- phytoplankton summer bloom
- phytoplankton autumnal bloom

seasonal changes of the biota

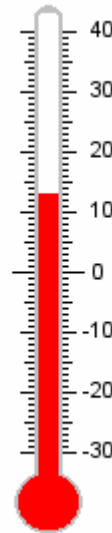


...what about bacteria?

general opinion

driving forces for planktonic bacteria are...

...physico-chemical conditions (temperature, light, oxygen...)



general opinion

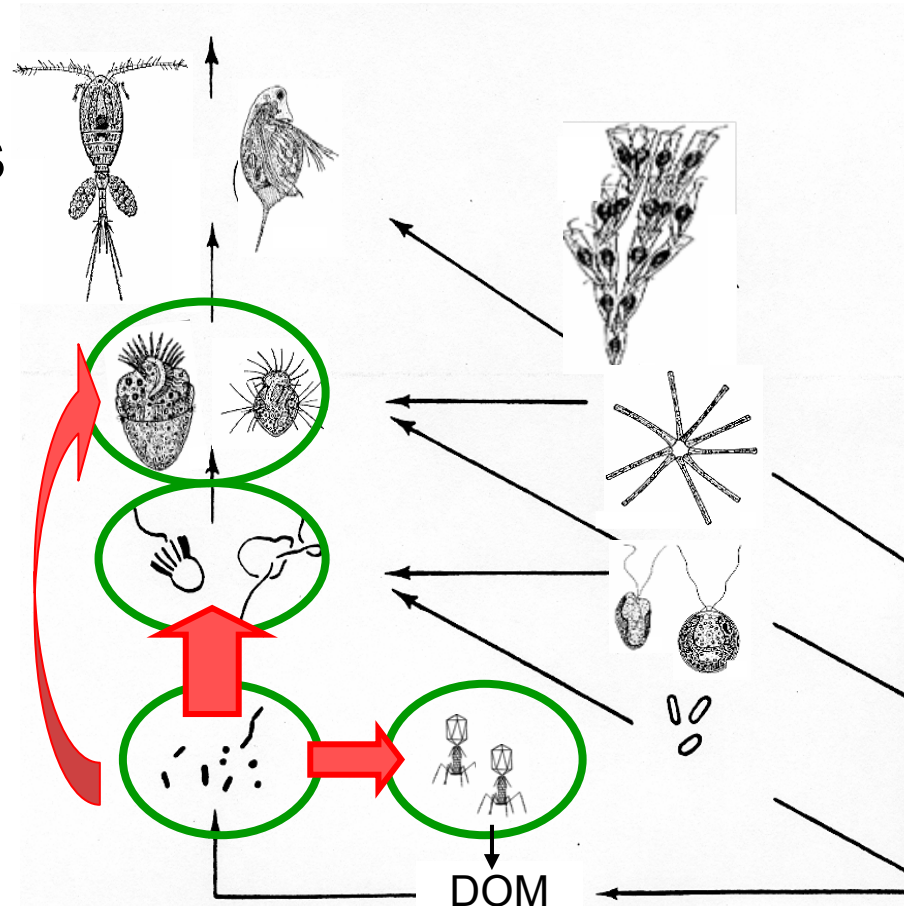


driving forces for planktonic bacteria are...

...grazing by bacterivorous protists (mainly HNF)

...viral lysis

→ **top-down control**

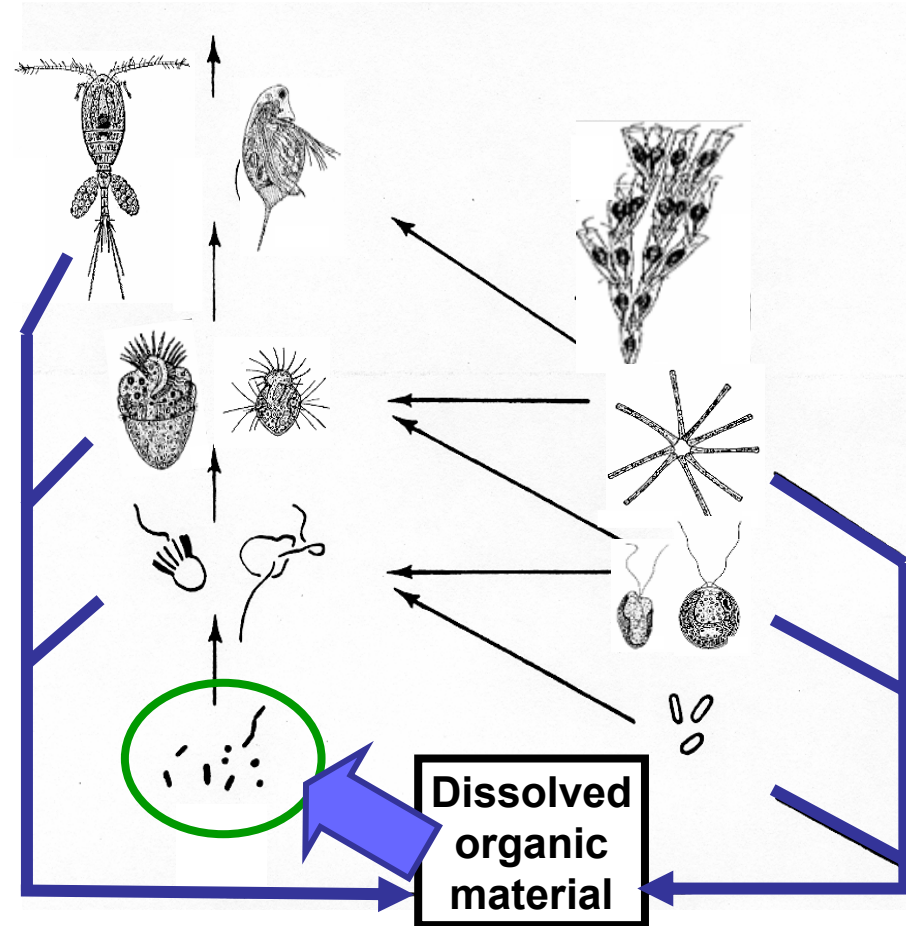


general opinion

driving forces for planktonic bacteria are...

...nutrient availability
(C, P, N)

→ **bottom-up control**



seasonality of bacteria



Control by

WI SB CW SU/FALL WI

TOP-DOWN

HNF

HNF

daphnids

viruses ciliates

mixotrophic algae

BUT:
bacteria are regarded as „black box“
– as one entity!!!

algal autolysis / grazing

daphnids

+C | P+N
+C | P+C | C

CW SU/FALL WI

J J A S O N D

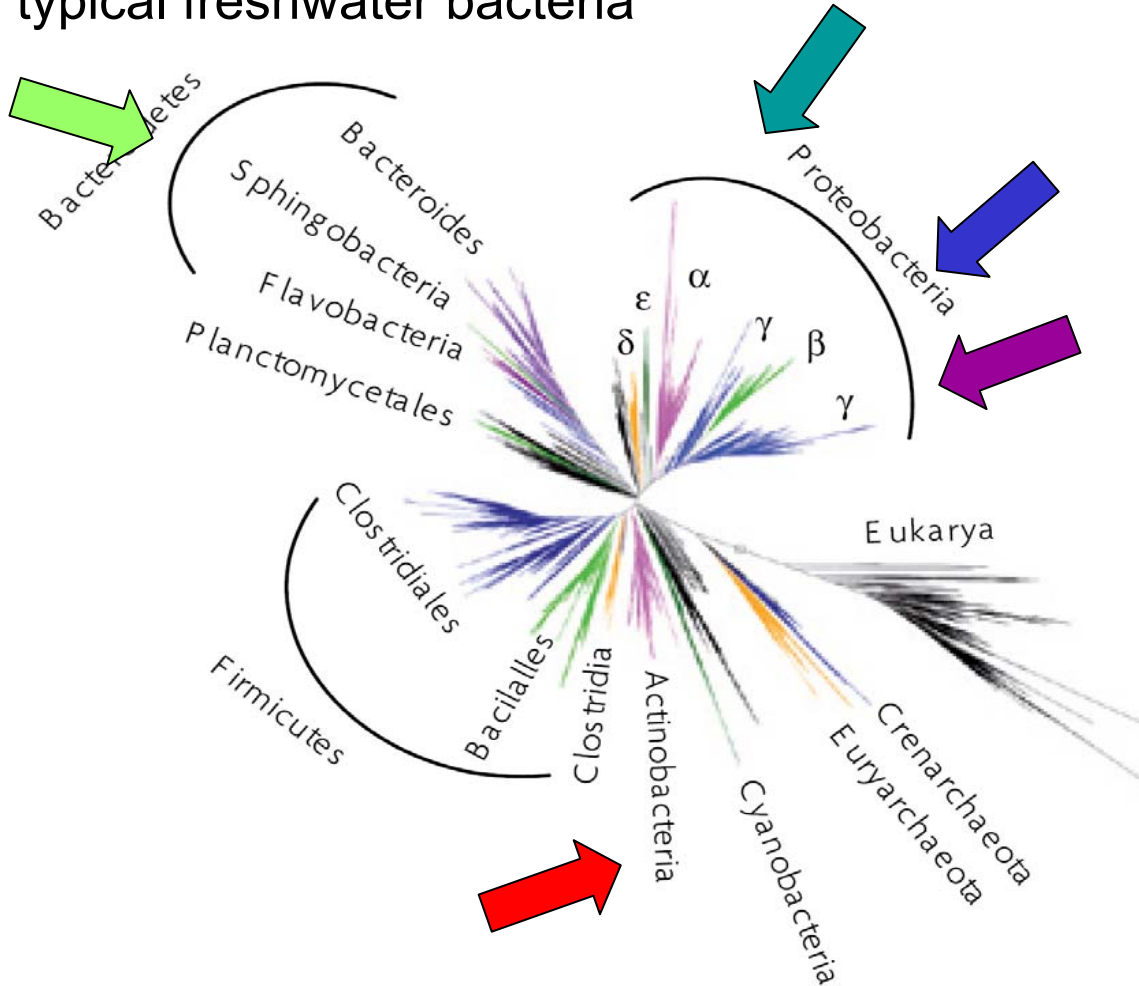


H
lin
ca

open the „black box“ of bacteria



typical freshwater bacteria



Actinobacteria & Betaproteobacteria

→ highly abundant

Cytophaga-Flavobacteria

→ less abundant

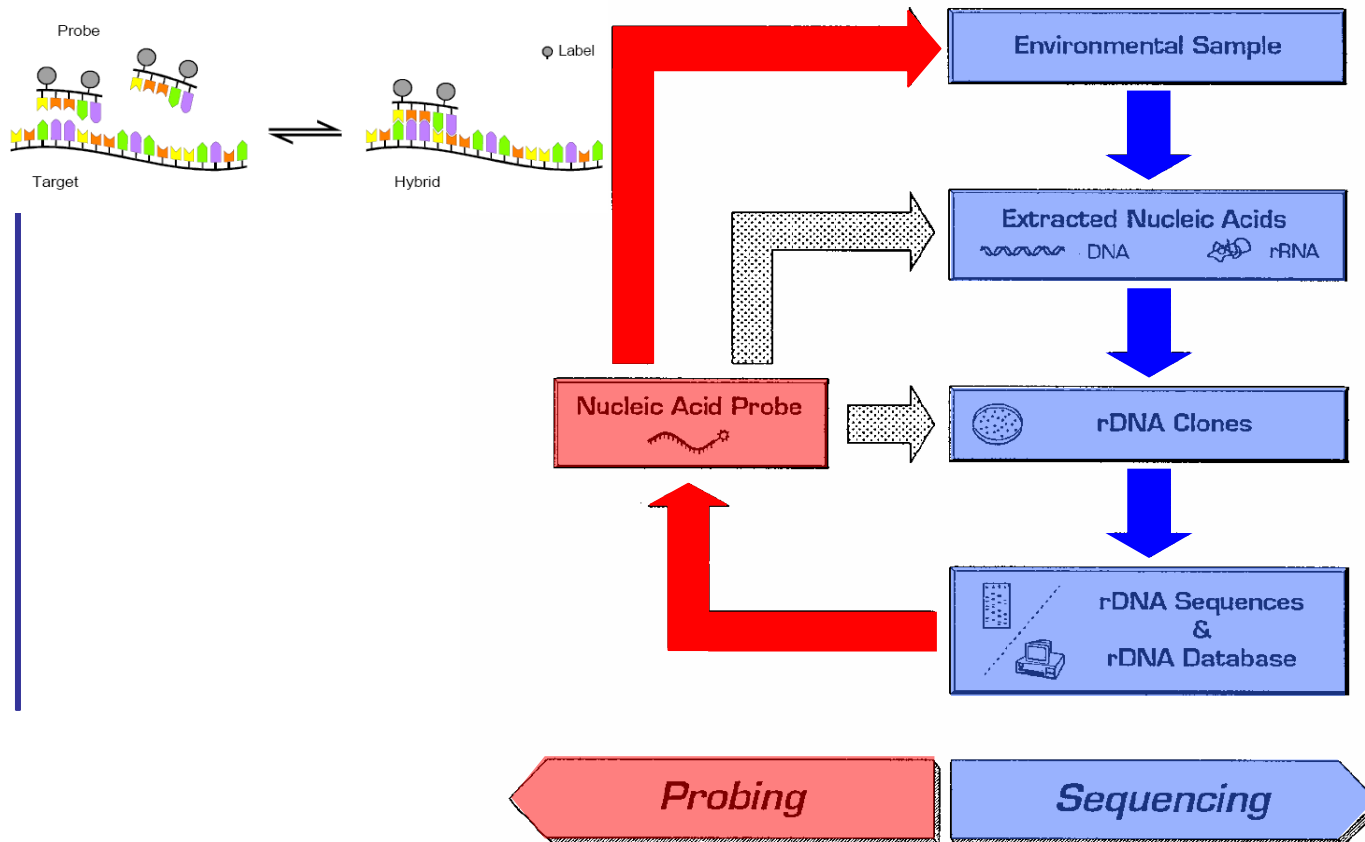
**Alphaproteobacteria
Gammaproteobacteria**

→ „rarely“ abundant

how to study freshwater bacteria?



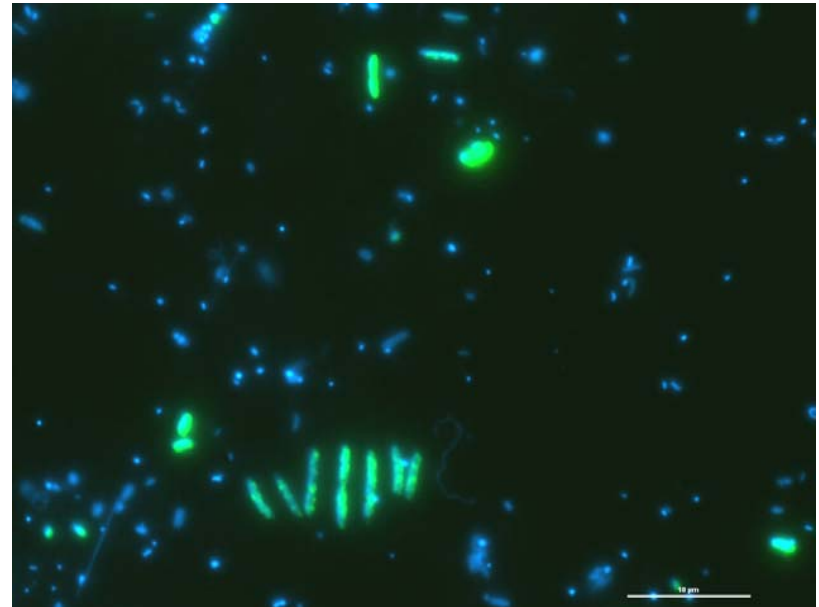
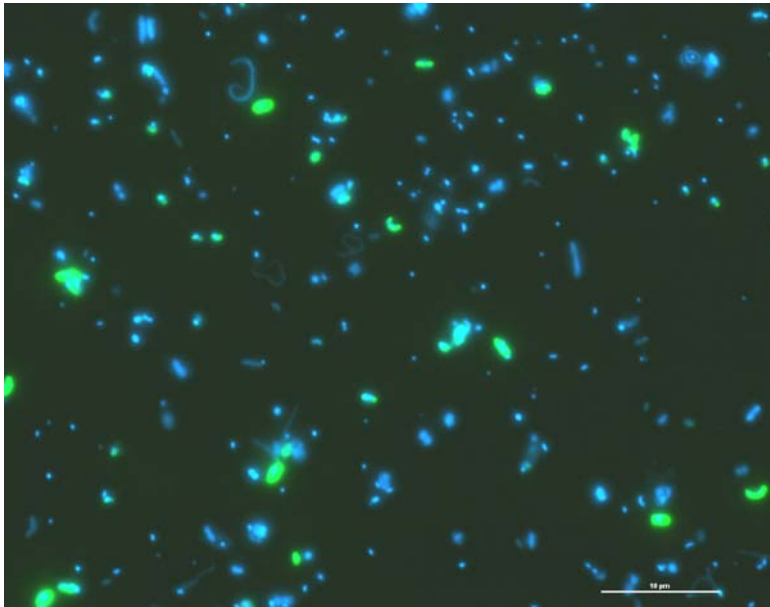
- Cloning and sequencing of 16S rRNA genes
- Fluorescence *in situ* hybridization (FISH)



how to study freshwater bacteria?



- Cloning and sequencing of 16S rRNA genes
- Fluorescence *in situ* hybridization (FISH)
- CARD-FISH: signal amplification → brighter and stable signal
- Biomass evaluation of bacterial phylotypes (image analysis)
- MAR-FISH: incorporation of radiolabeled substrates („activity“) + FISH



...some aims of my PhD thesis



- Seasonality of bacterial phylotypes - cell numbers, biomass, and “activity” (amino acid incorporation) in Piburger See
- Spatial patterns in the distribution of bacterial phylotypes (depth gradient during stratification)
- Identification of the driving forces for the establishment of different bacterial phylotypes

→ lack of knowledge

Tri-phasic approach



SEASONAL MONITORING

Salcher et al. (2008)
Posch et al. (accepted)
Salcher et al. (in prep)

↓ observation of
top-down
↑ & bottom-up
control in nature?

Identification
of the major
**effects of
TOP-DOWN and
BOTTOM-UP CONTROL**
on natural
bacterioplankton

LAB STUDY (chemostat experiment)

Salcher et al. (2005)

FIELD EXPERIMENT

(size fractionation & nutrient enrichment)

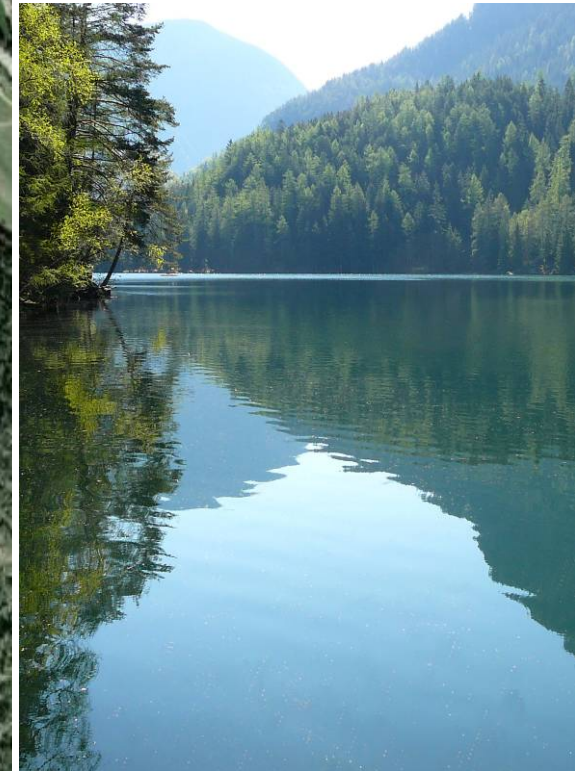
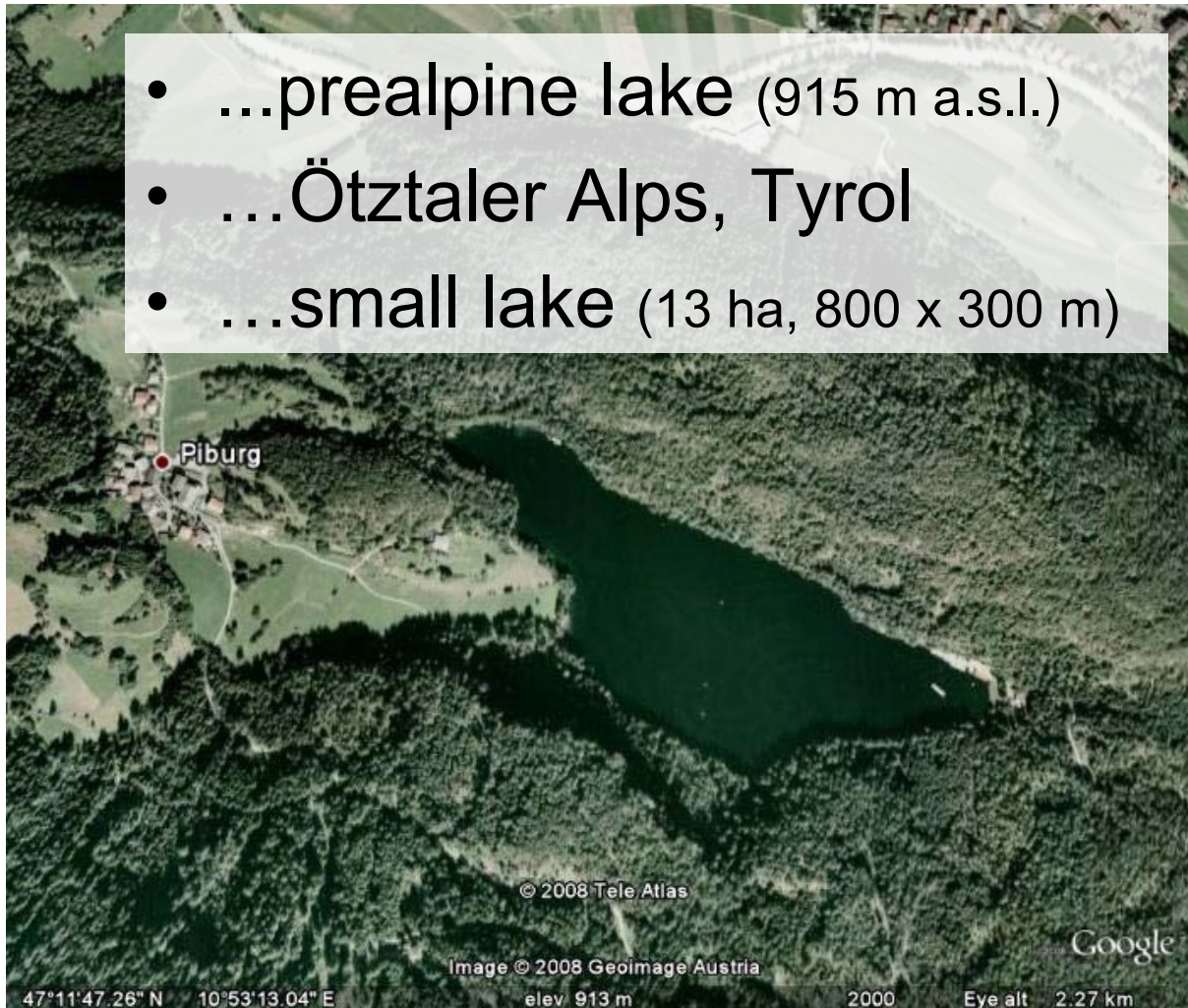
Salcher et al. (2007)
Posch et al. (2007)

Piburger See is...



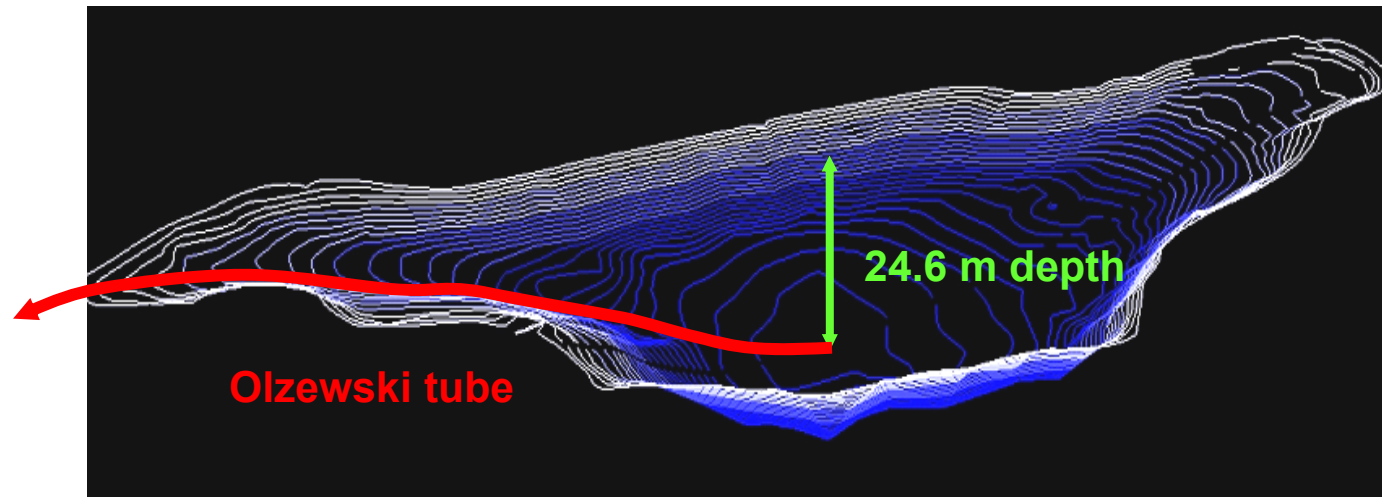
Piburger See is...

- ...prealpine lake (915 m a.s.l.)
- ...Ötztaler Alps, Tyrol
- ...small lake (13 ha, 800 x 300 m)



Piburger See is...

- ... z_m : 24.6 m
- ...dimictic: summer stratification → anoxic hypolimnion
- ...eutrophication in late 1960s
- ...deep water removal (Olszewski tube) in 1970
- ...re-oligotrophication → oligo-mesotrophic



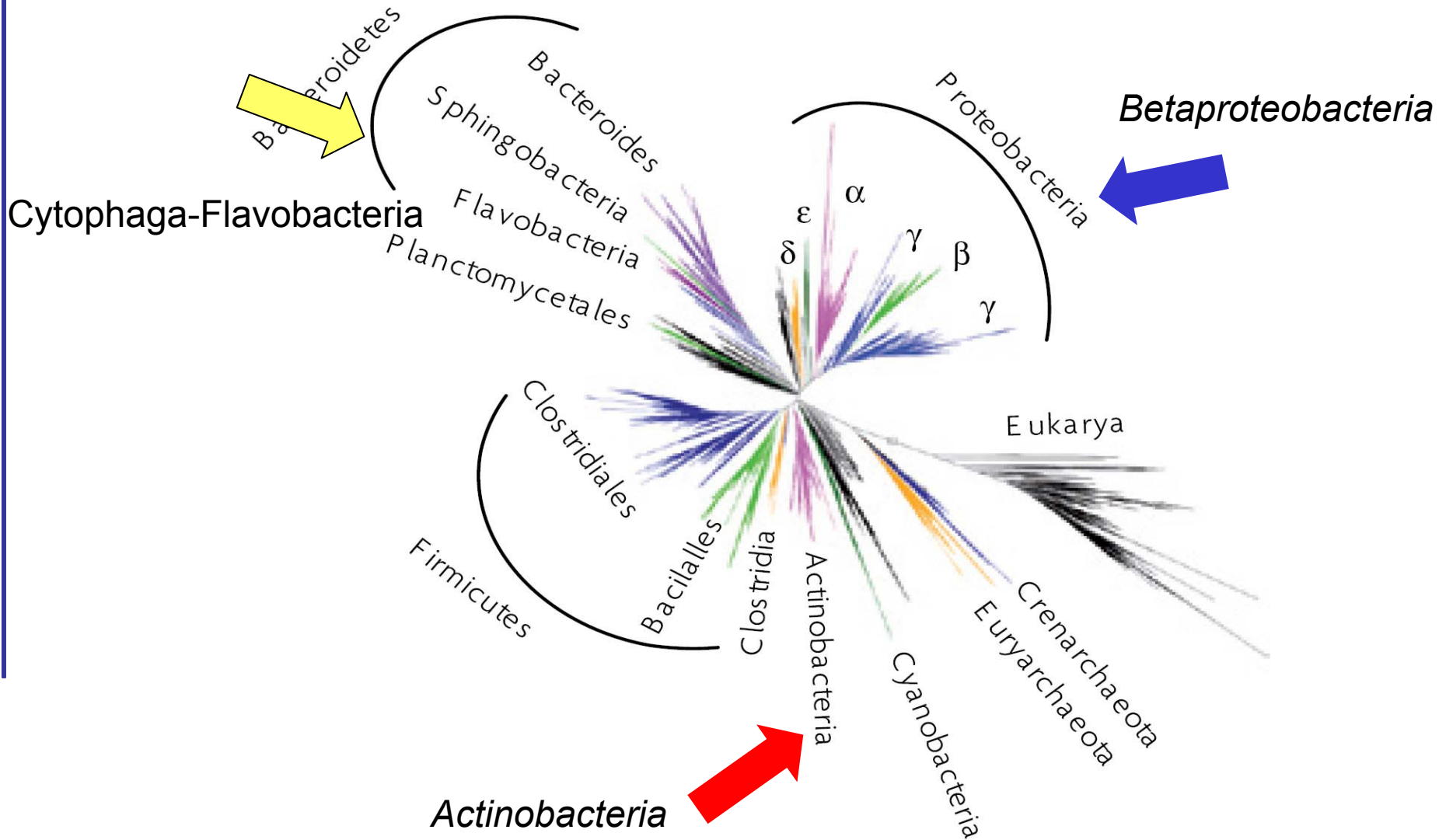


seasonal study

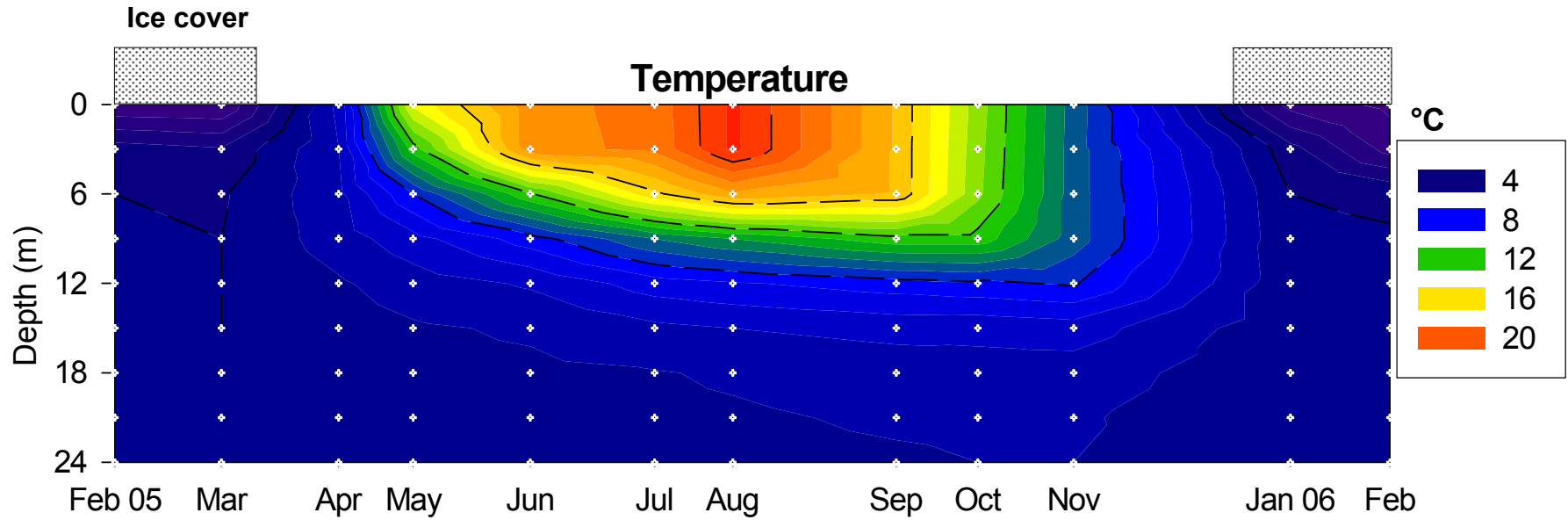
1-year survey (Feb 2005 – Feb 2006)

- physico-chemical monitoring
- algal diversity
- numbers of heterotrophic nanoflagellates
- **Bacterial diversity, abundances, biomass, and activity** (cloning & sequencing of 16S rRNA gene, CARD-FISH, image analysis, MAR-FISH with ^3H -amino acids)

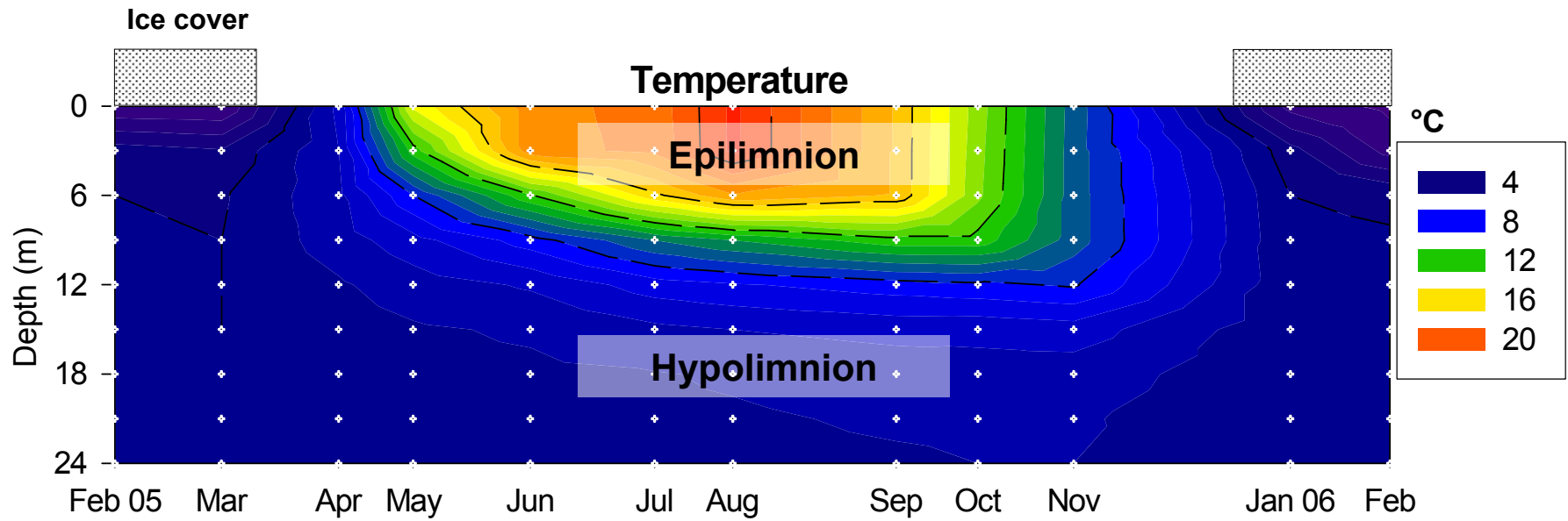
studied phyla / orders



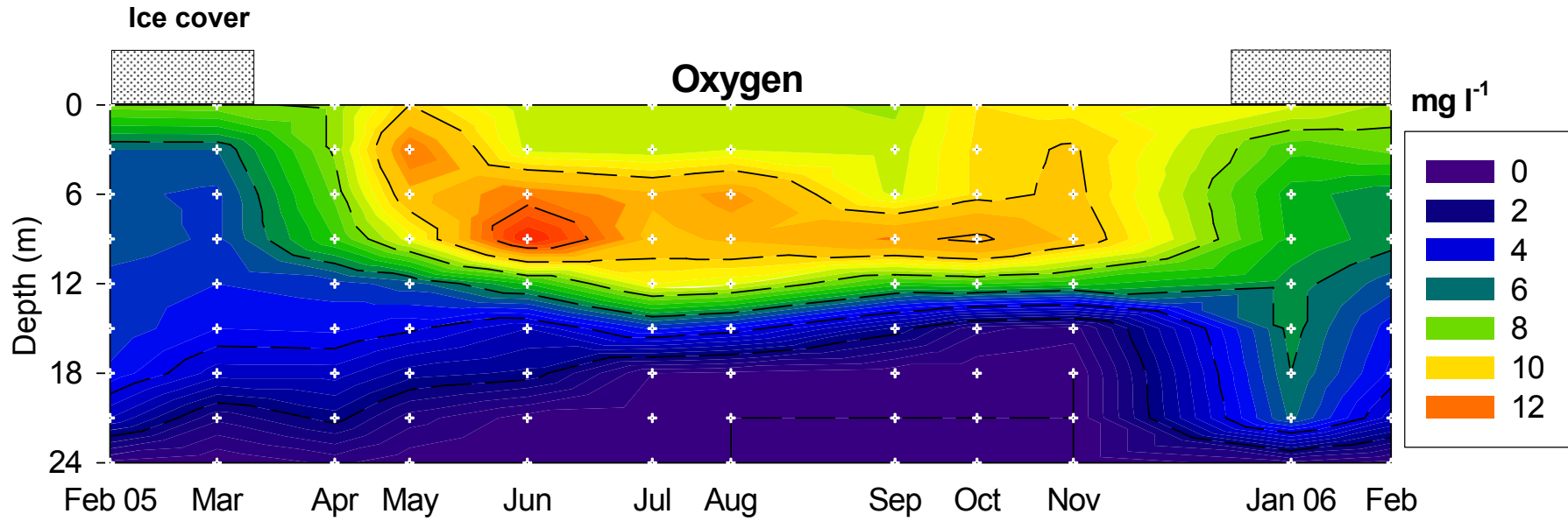
environmental conditions



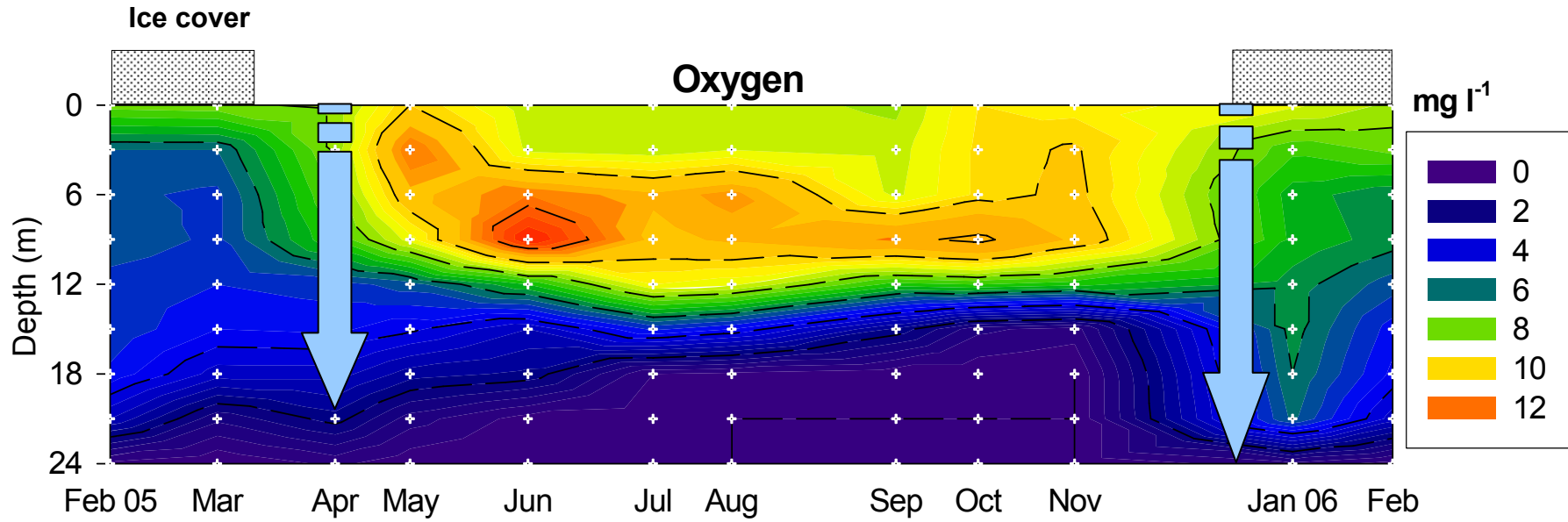
environmental conditions



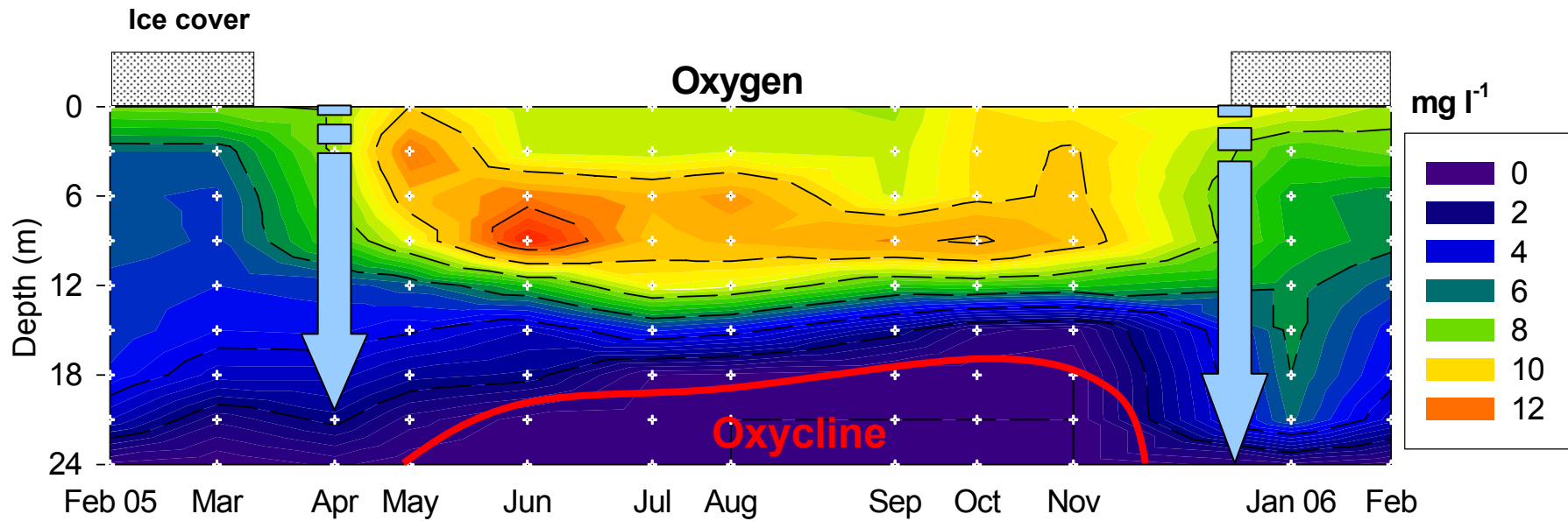
environmental conditions



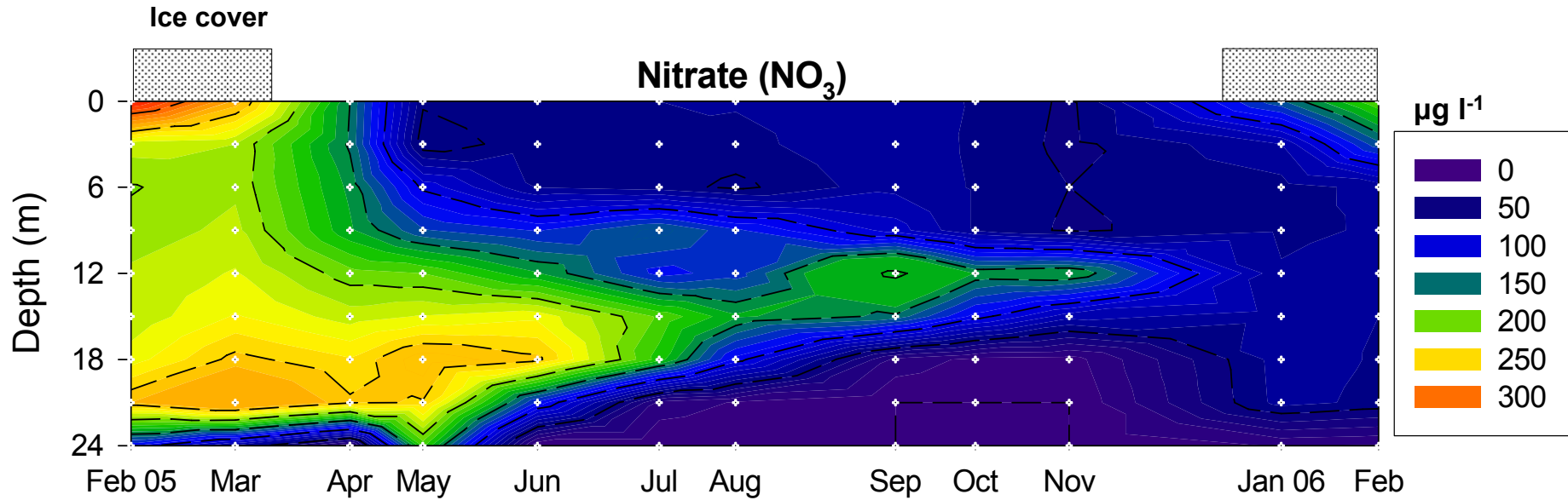
environmental conditions



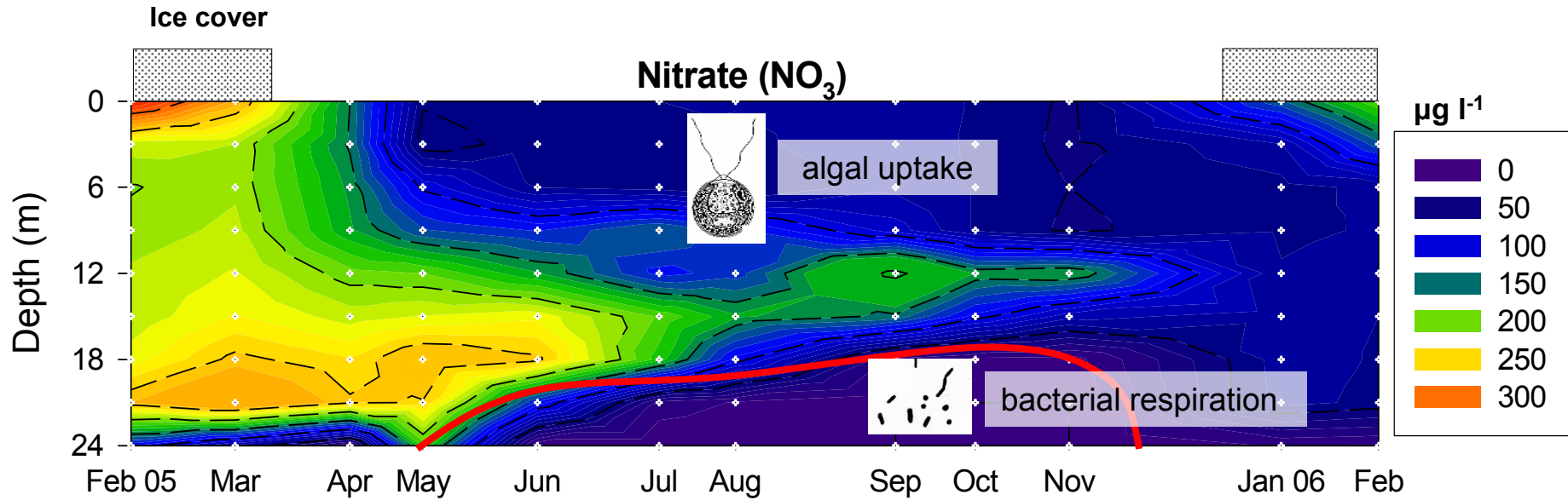
environmental conditions



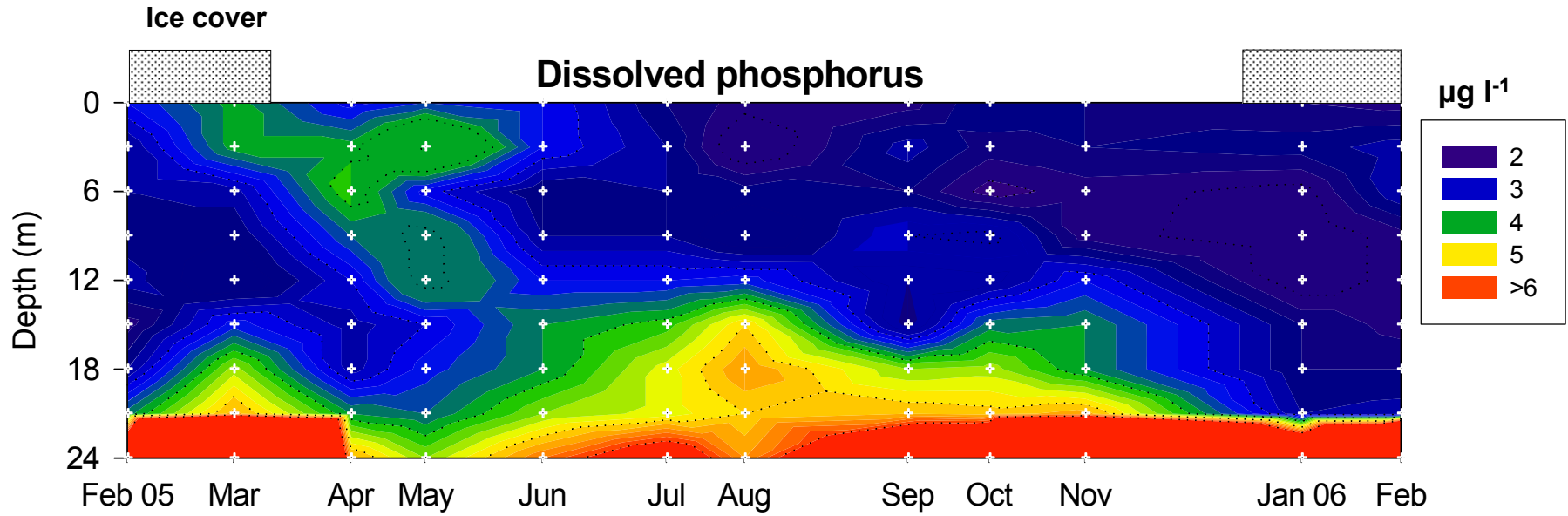
environmental conditions



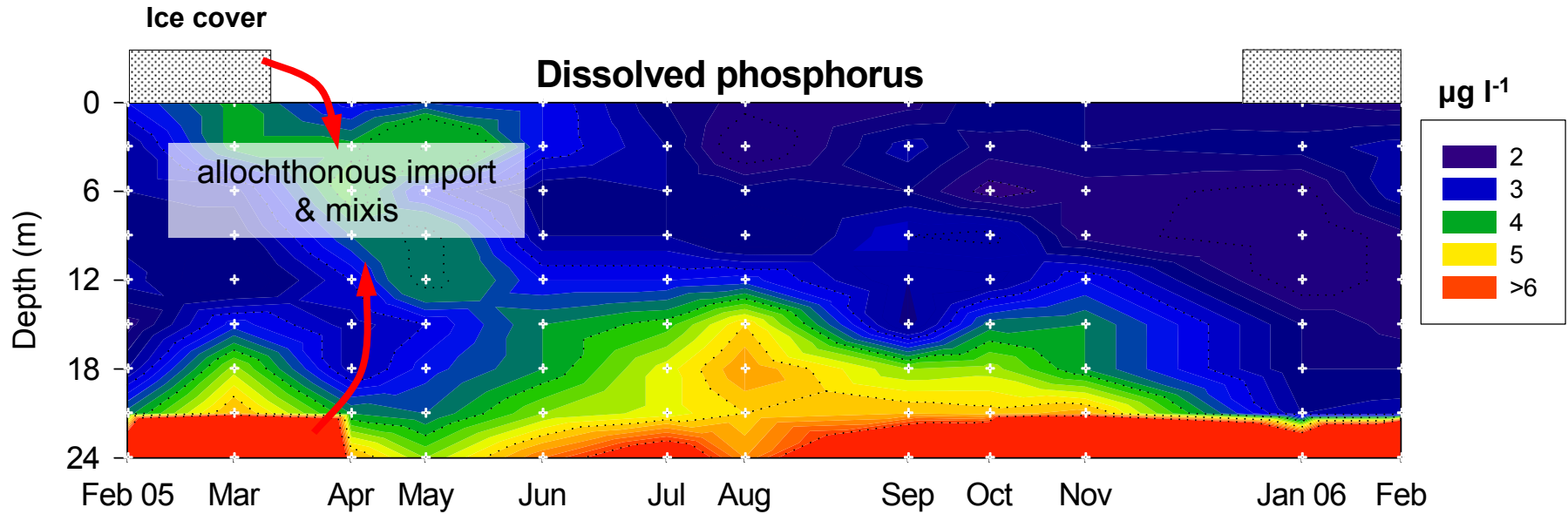
environmental conditions



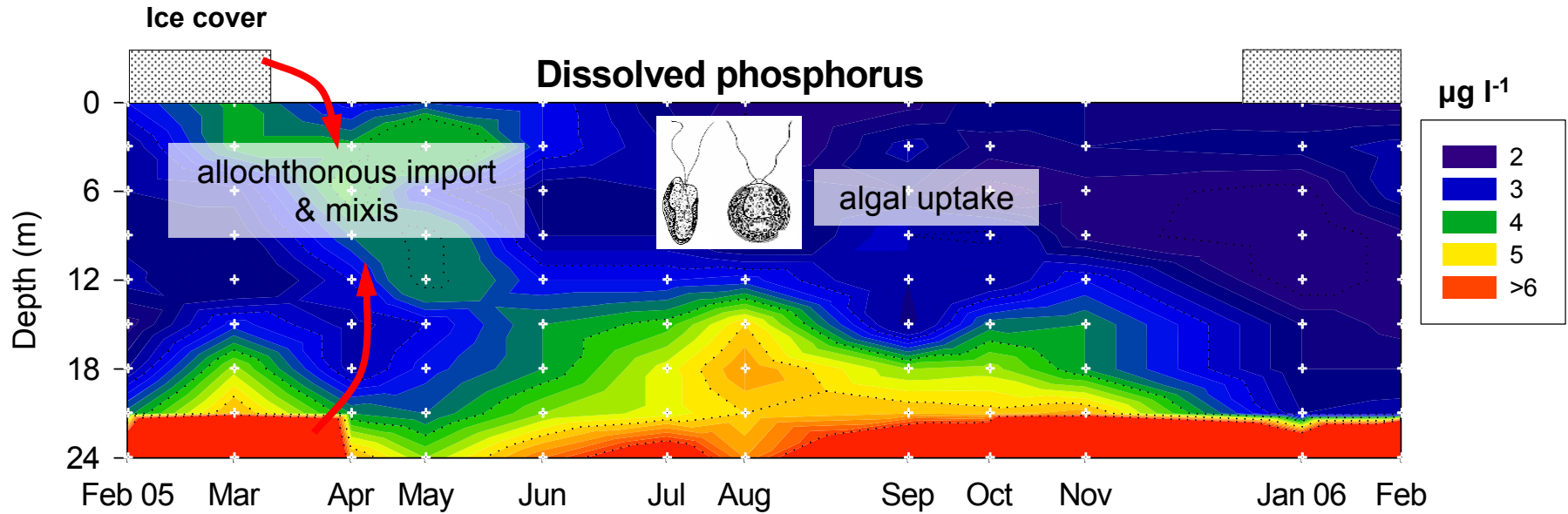
environmental conditions



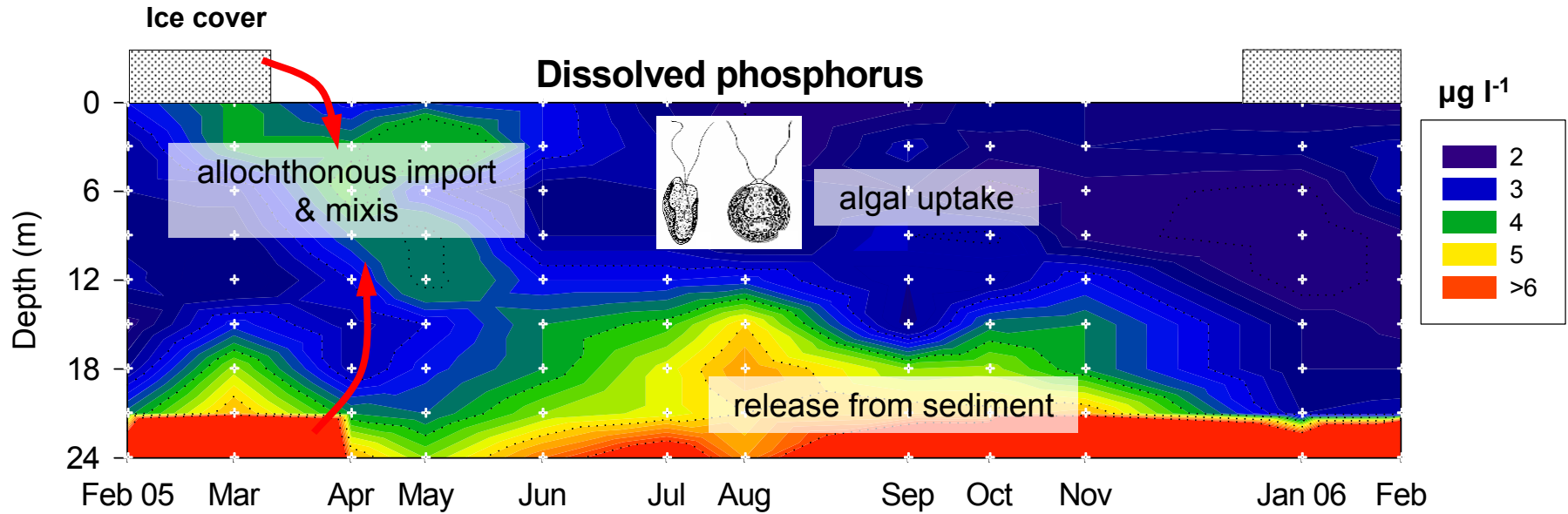
environmental conditions



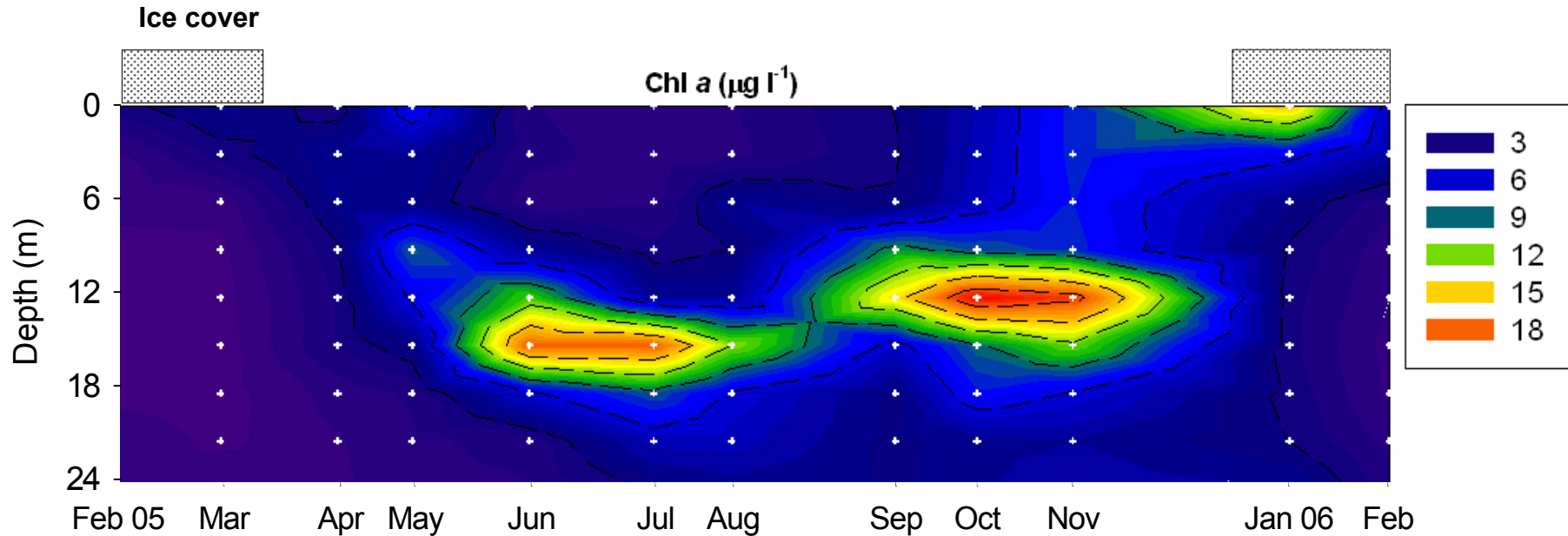
environmental conditions



environmental conditions

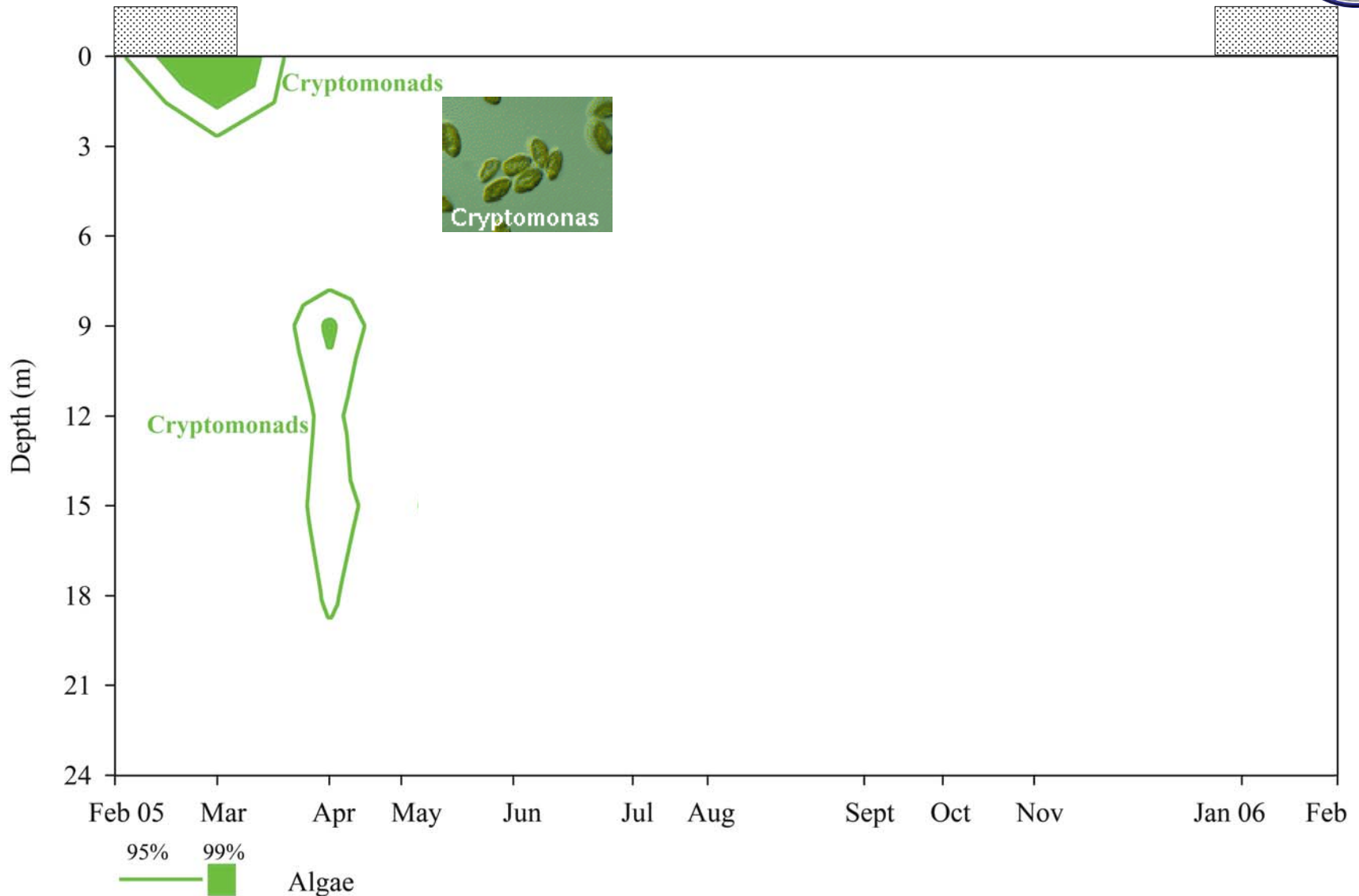


environmental conditions

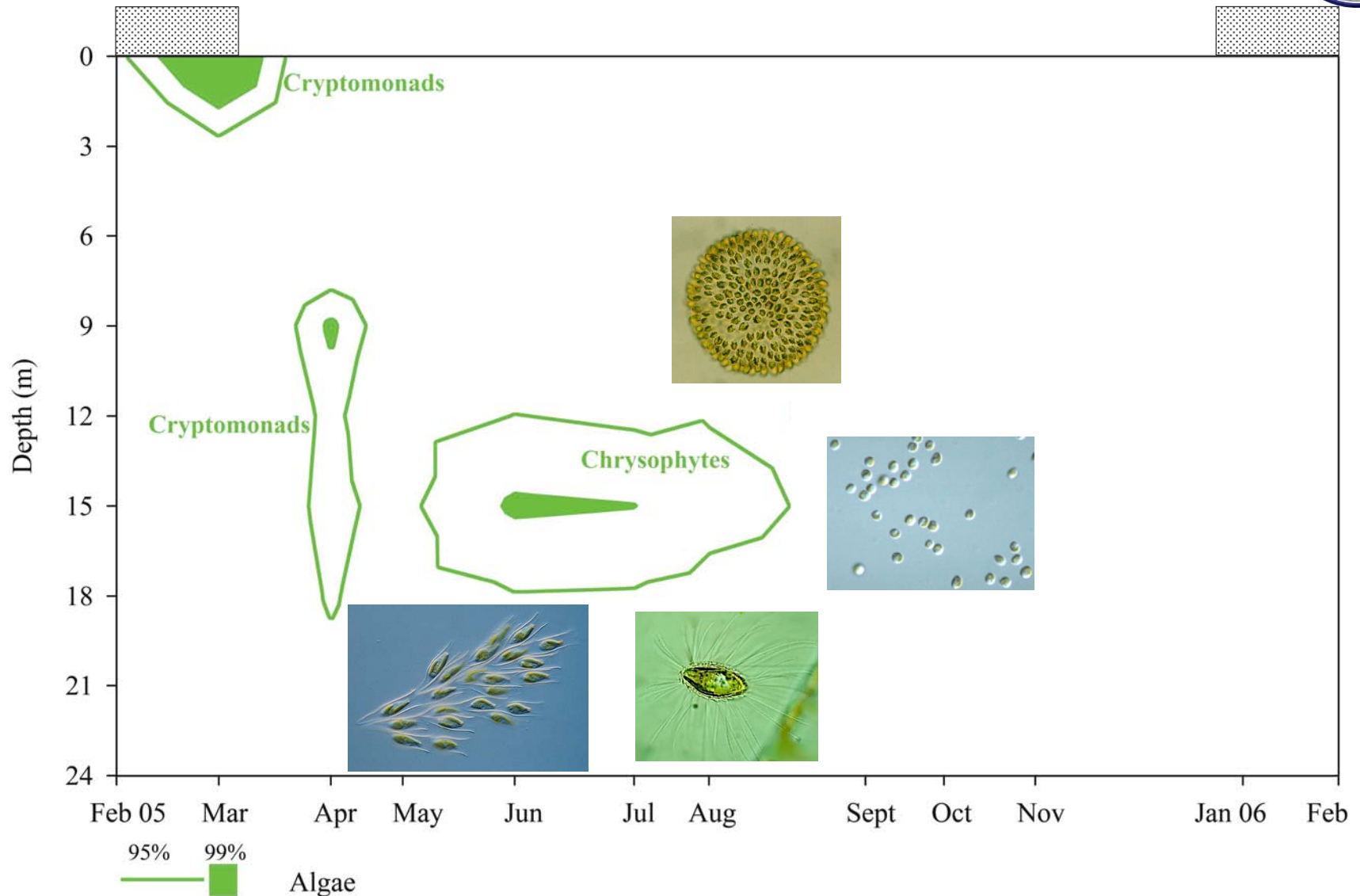


...which algae?

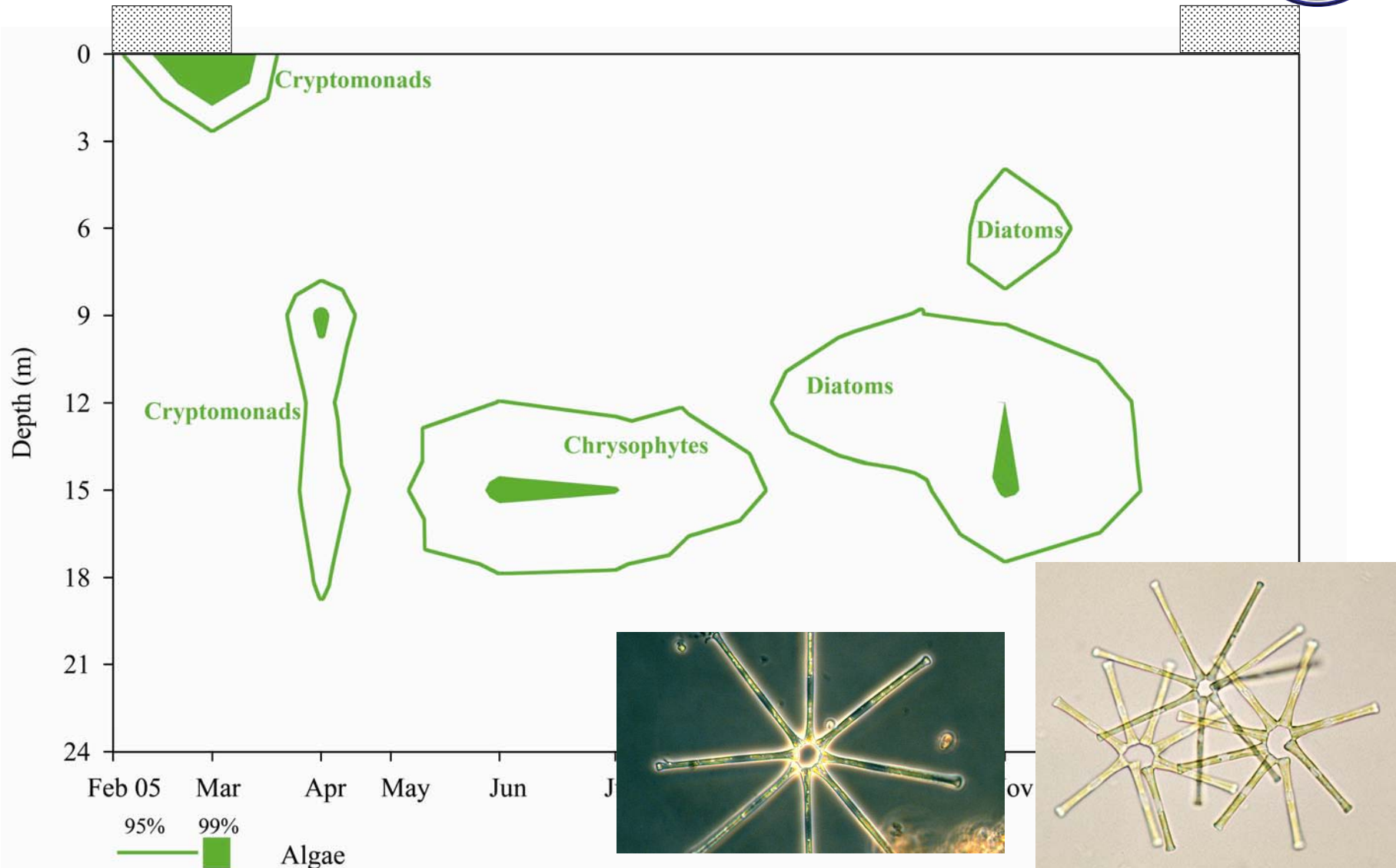
spatio-temporal distribution of algae



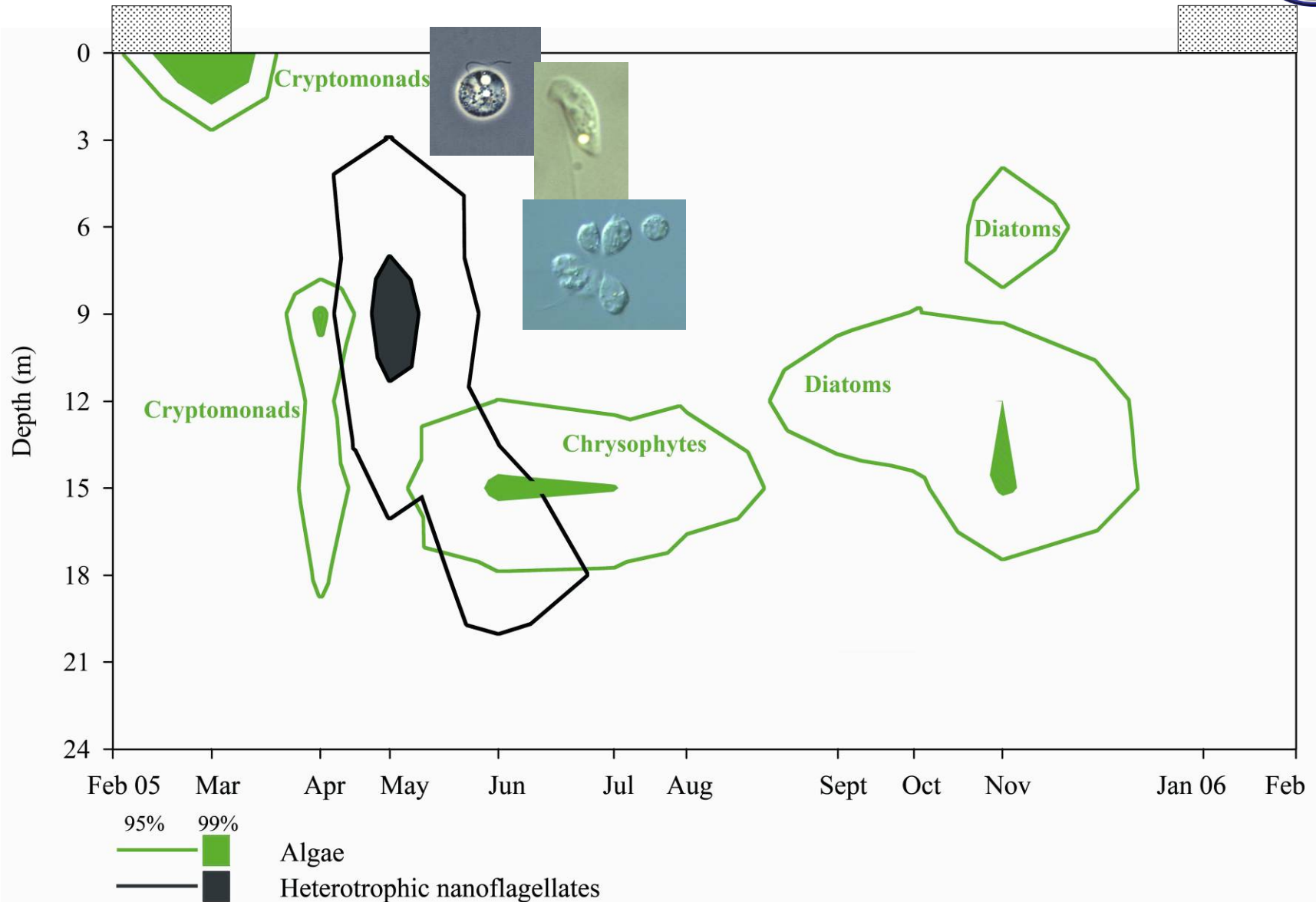
spatio-temporal distribution of algae



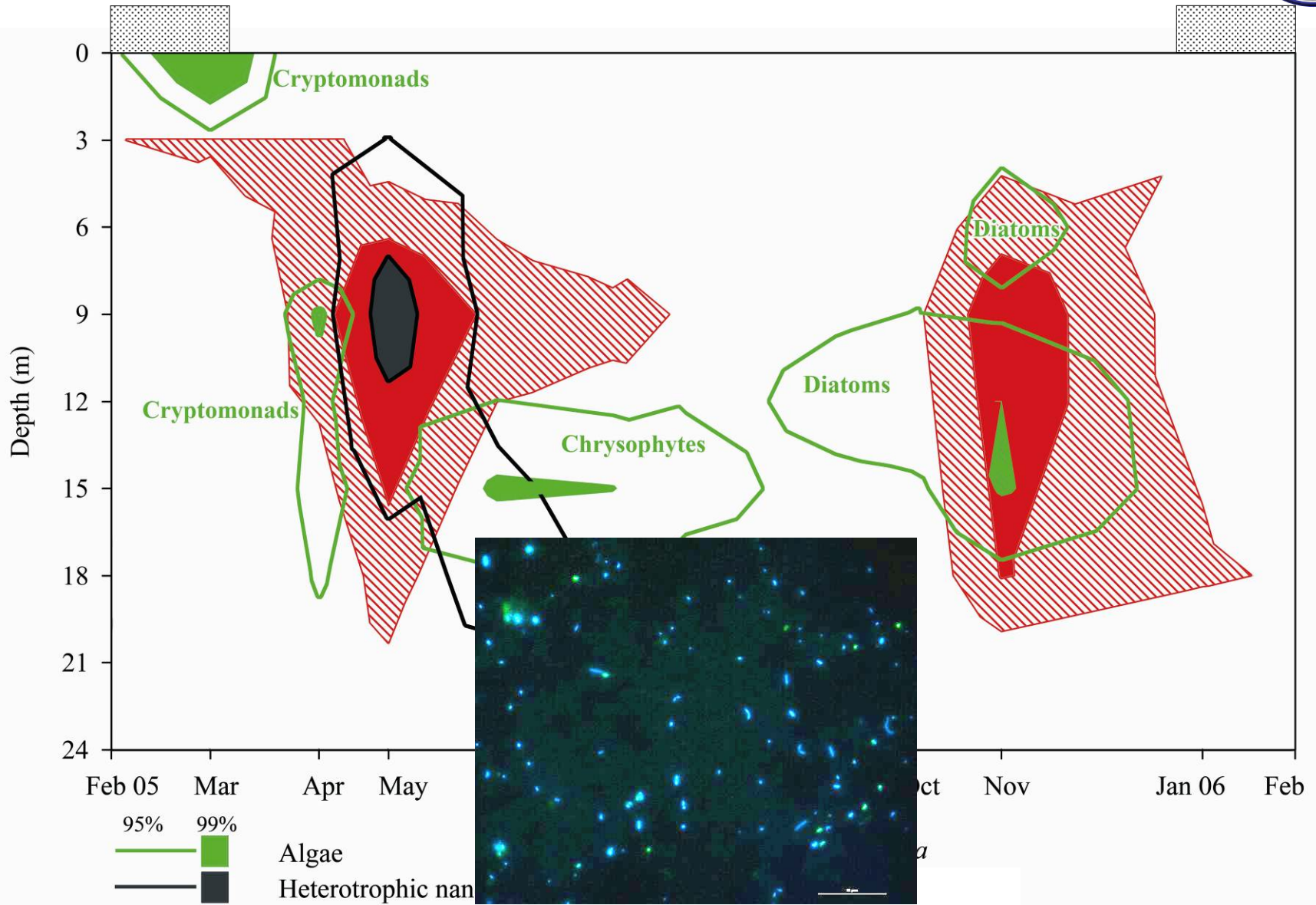
spatio-temporal distribution of algae



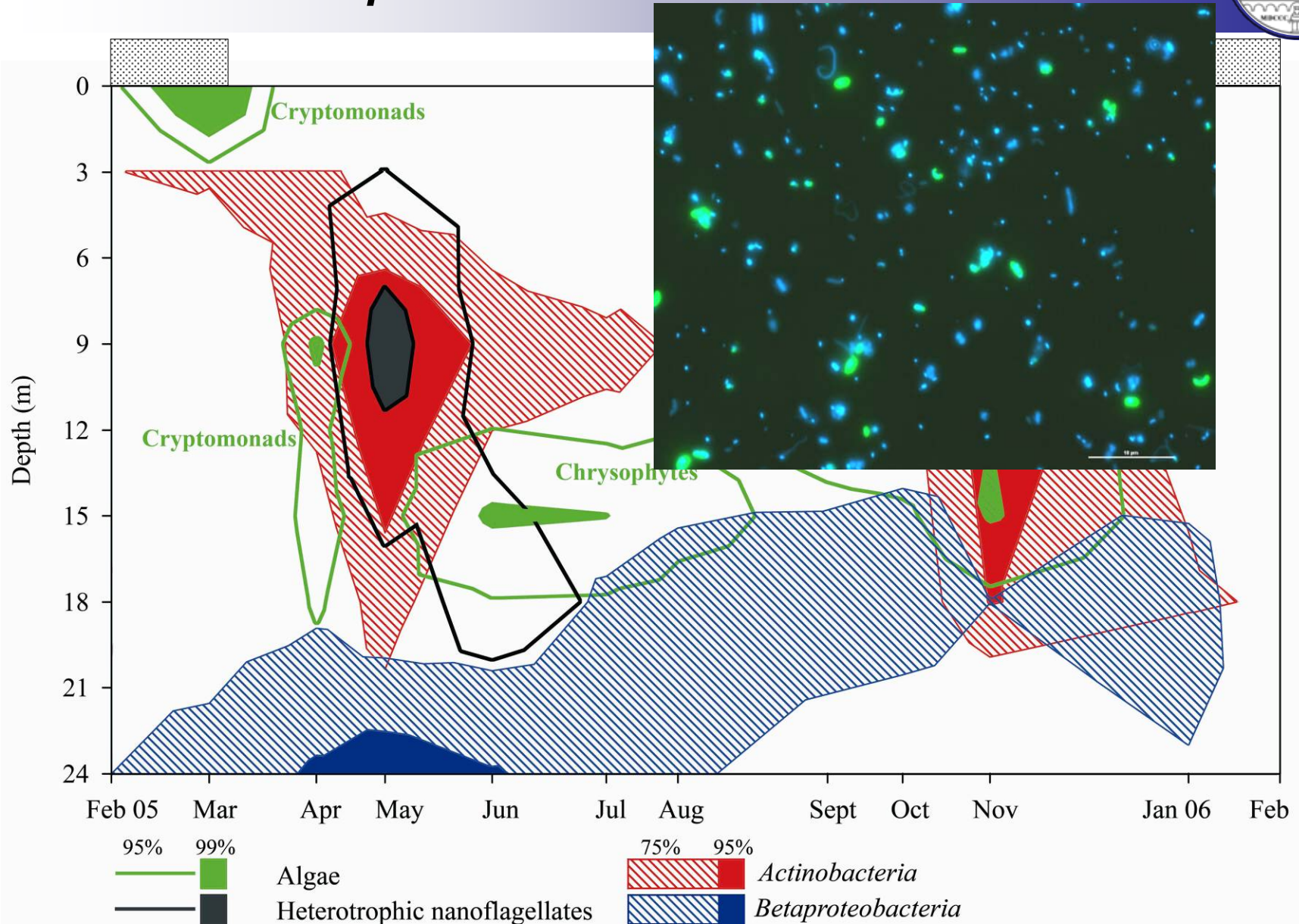
...and heterotrophic flagellates



...Actinobacteria,



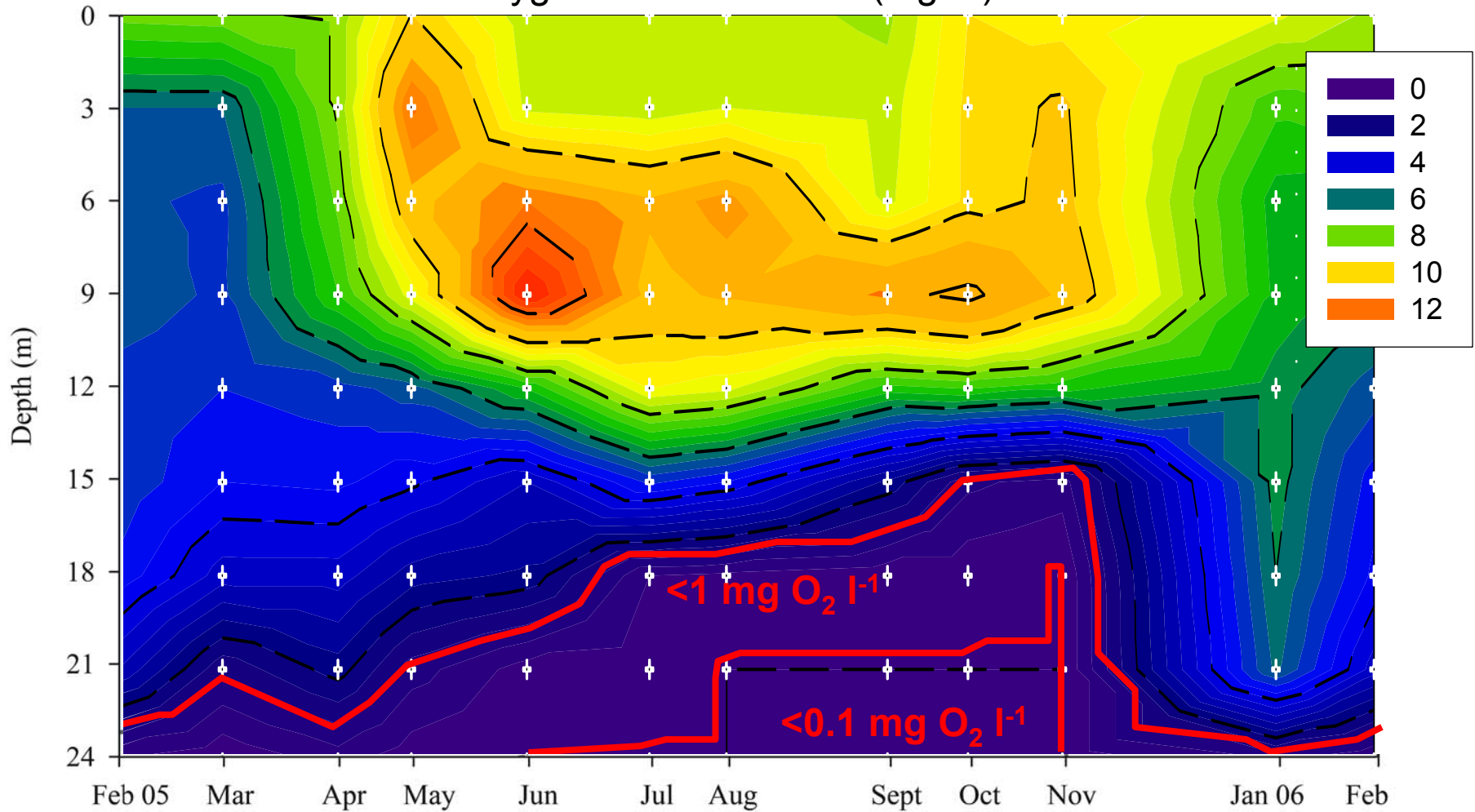
...and *Betaproteobacteria*



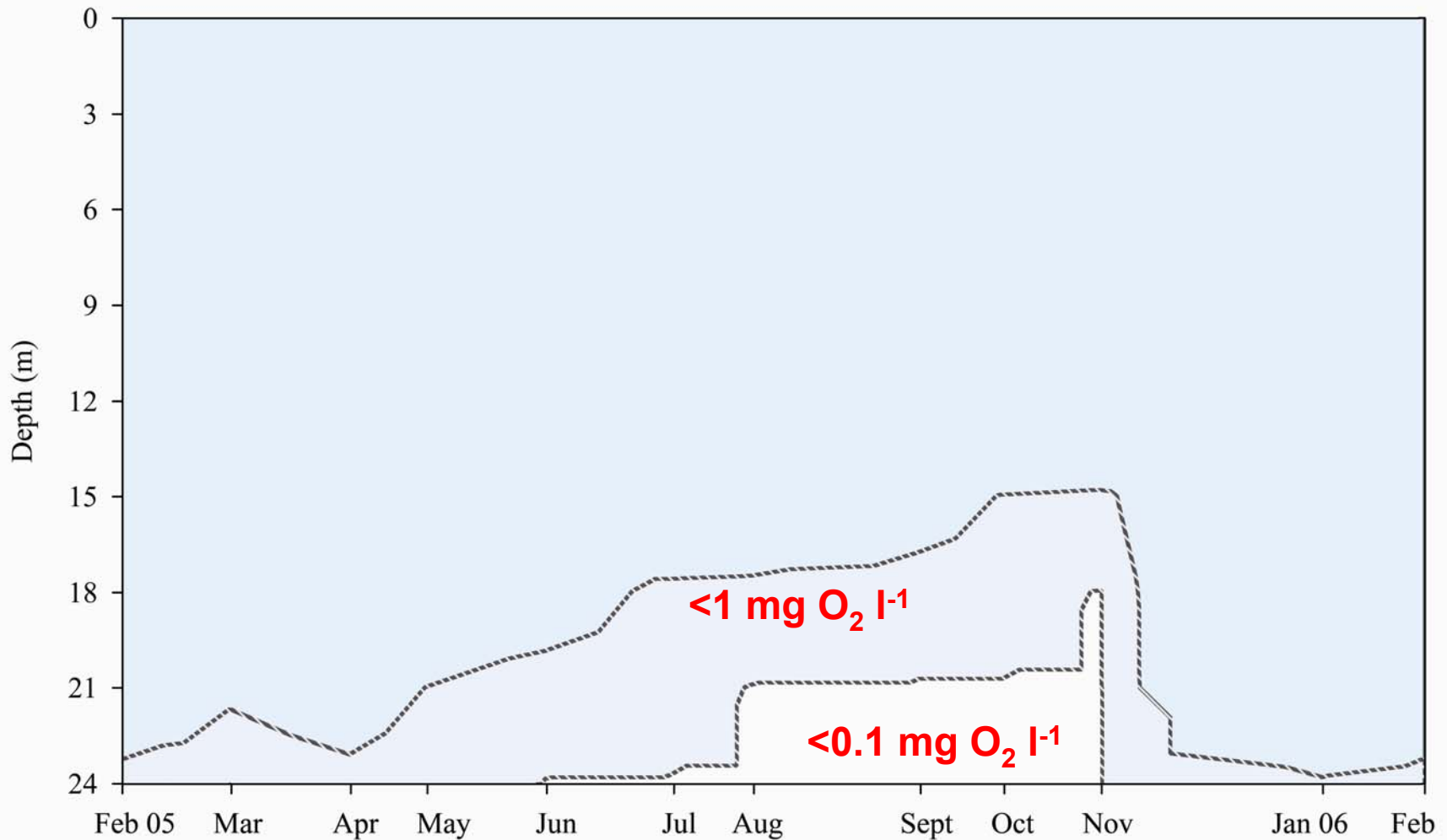
environmental factor - oxygen



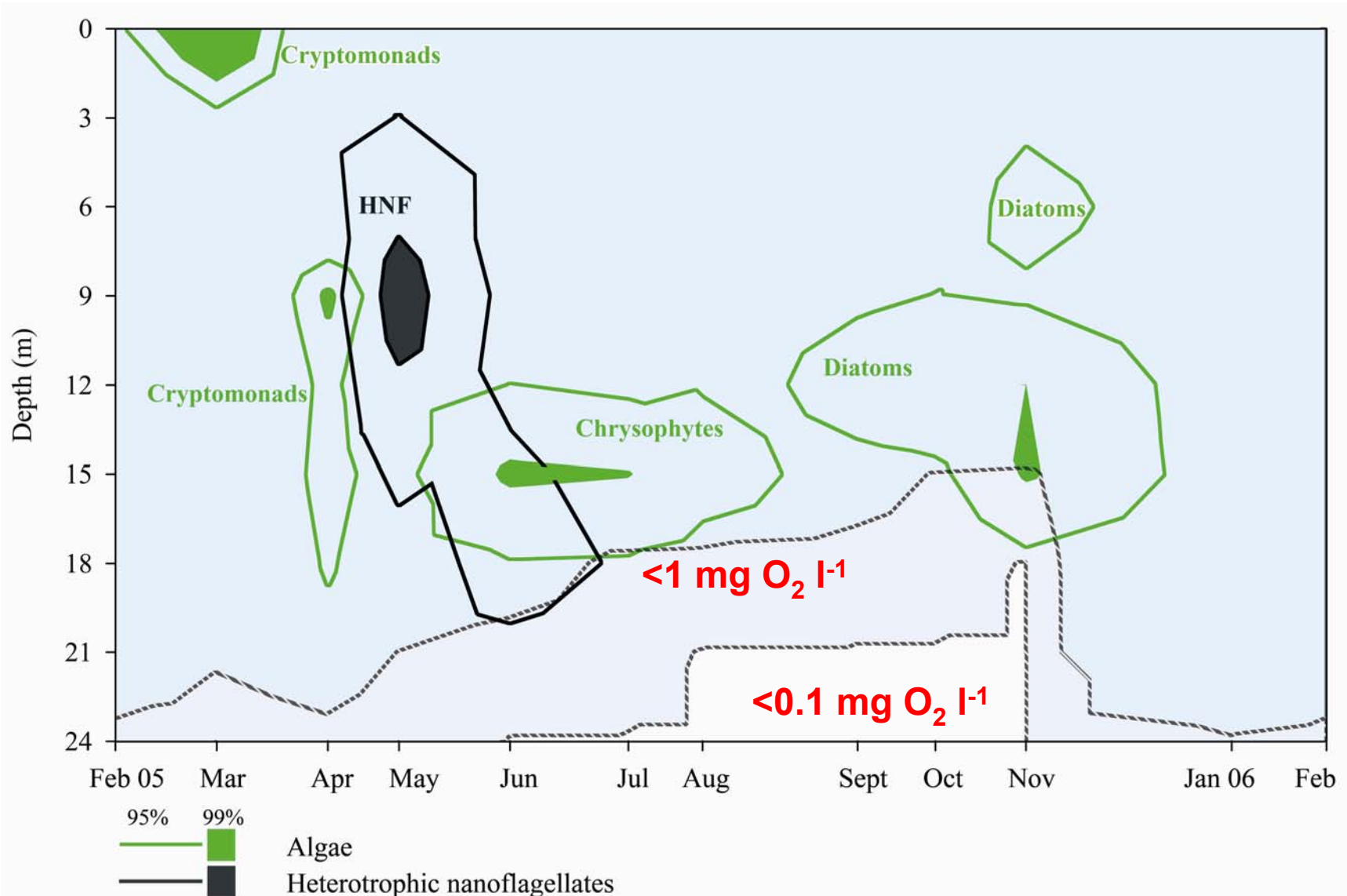
Oxygen concentrations (mg l⁻¹)



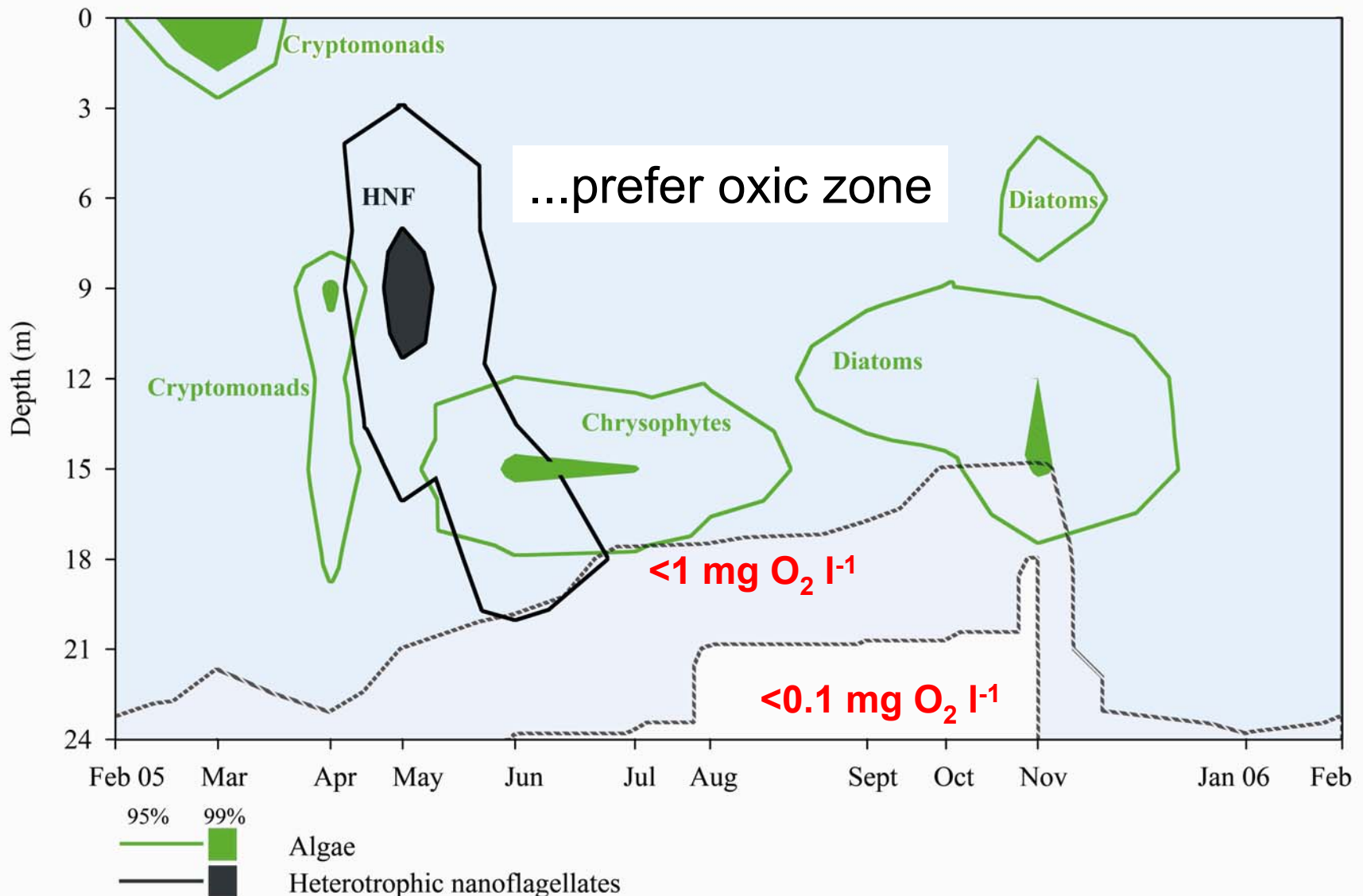
environmental factor - oxygen



spatial distribution of organisms



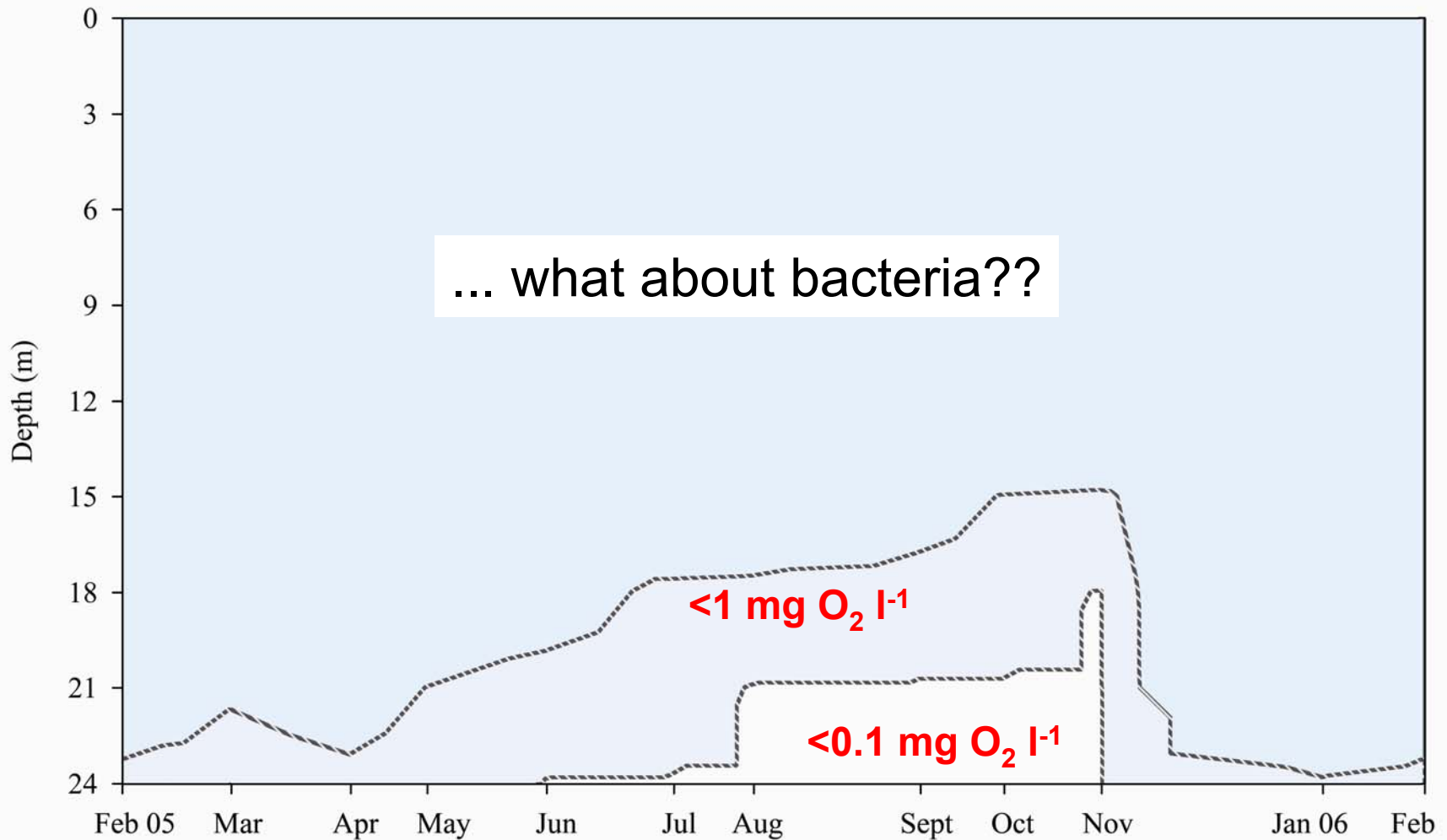
spatial distribution of organisms



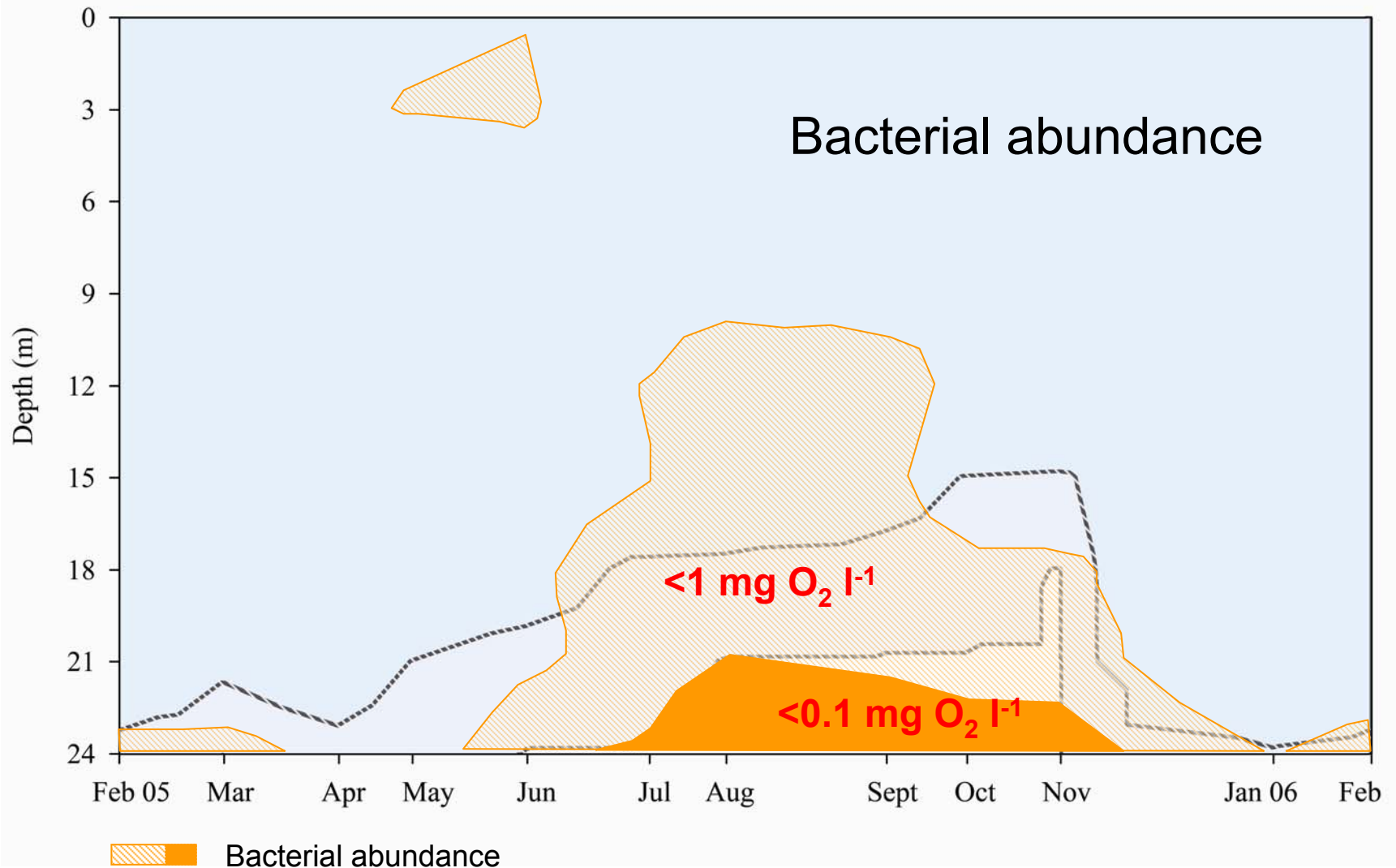
spatial distribution of organisms



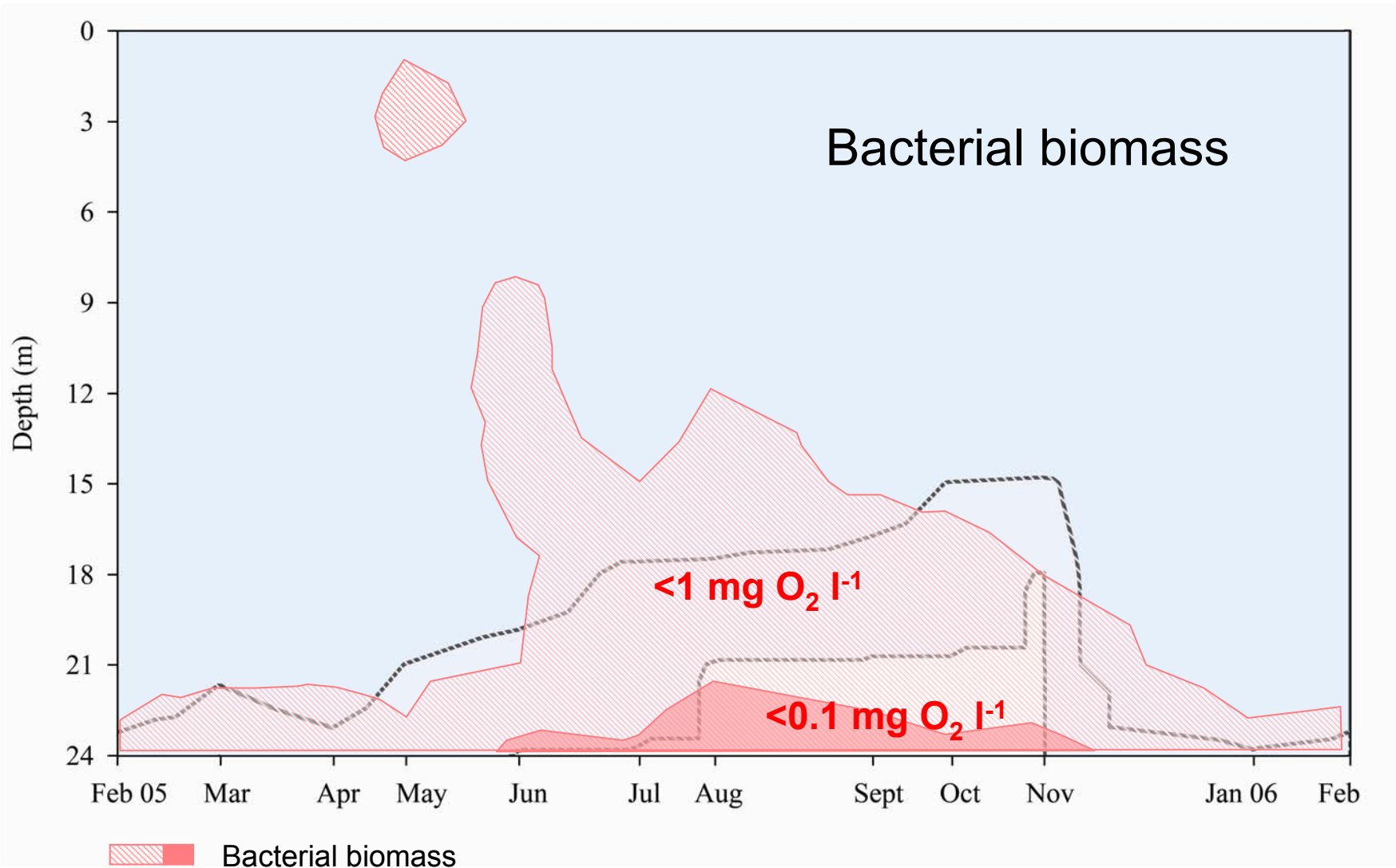
... what about bacteria??



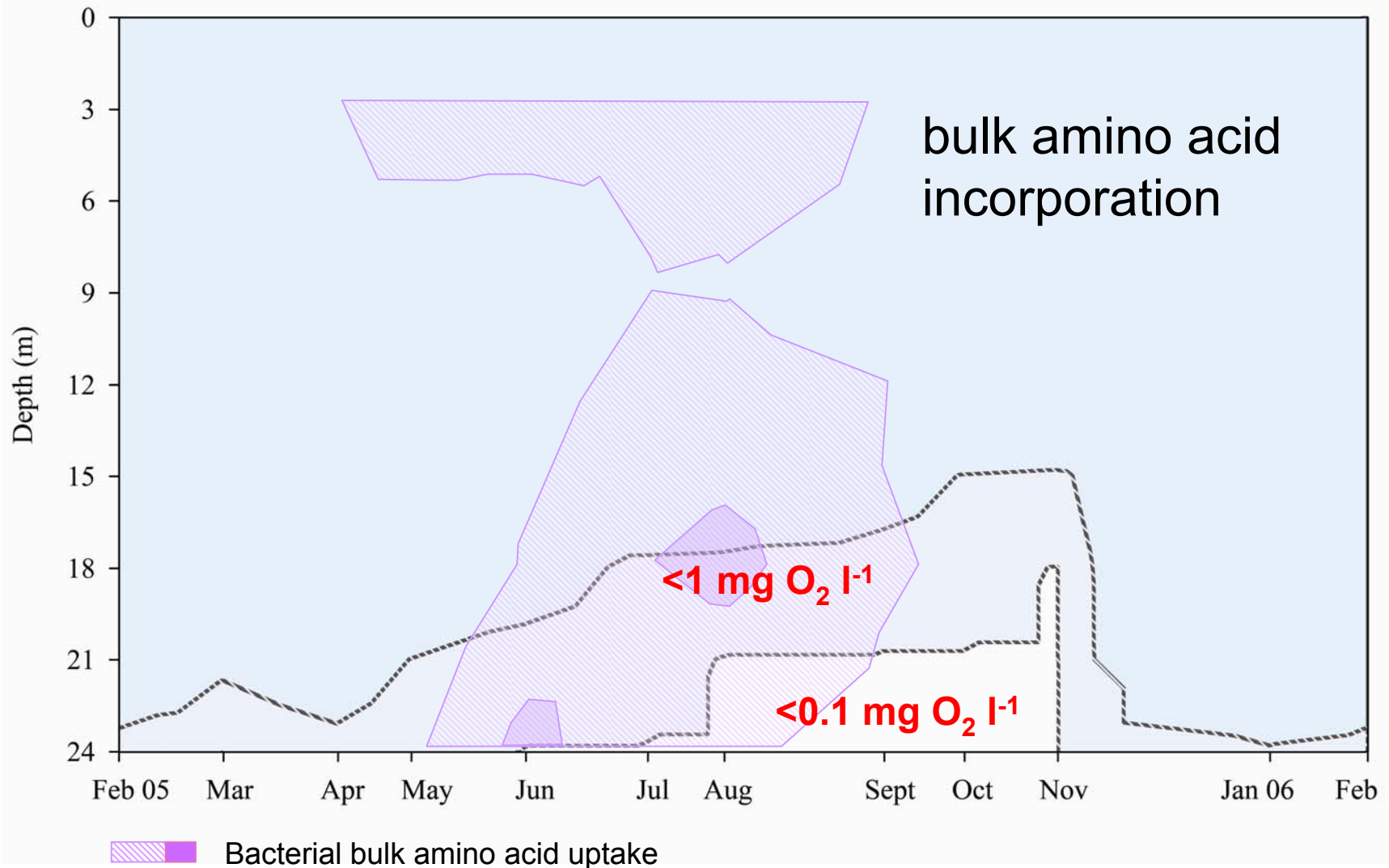
spatial distribution of organisms



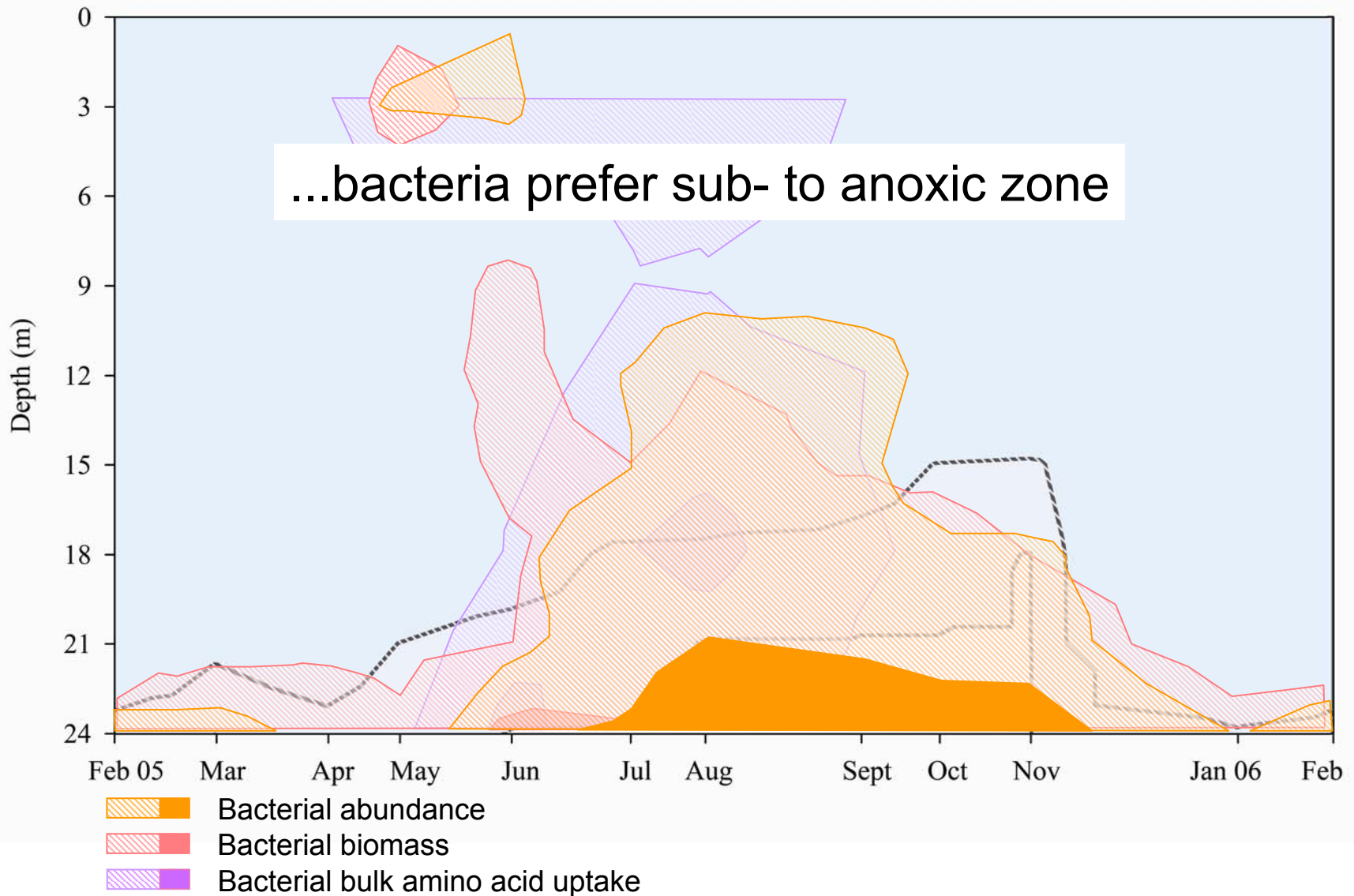
spatial distribution of organisms



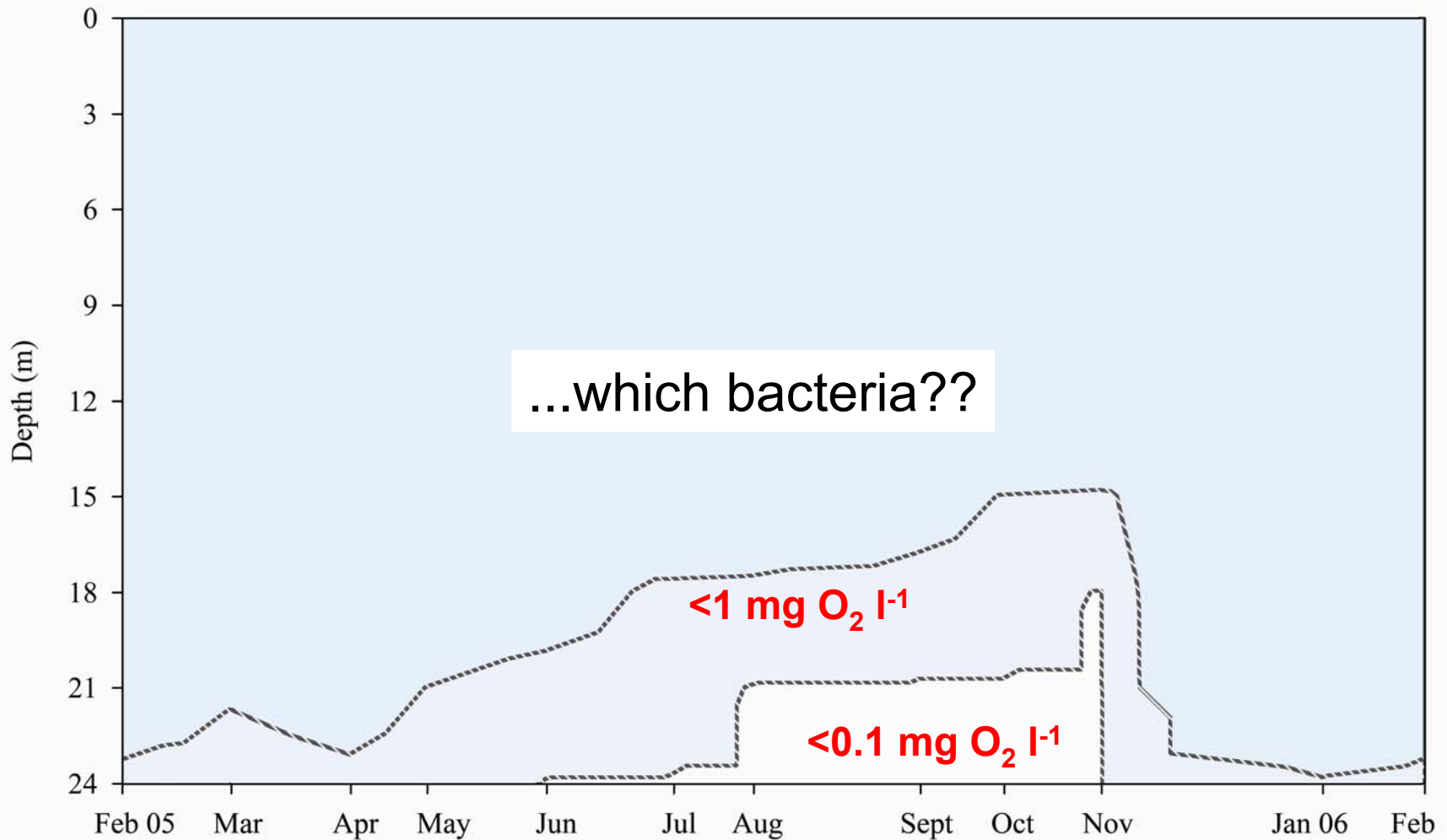
spatial distribution of organisms



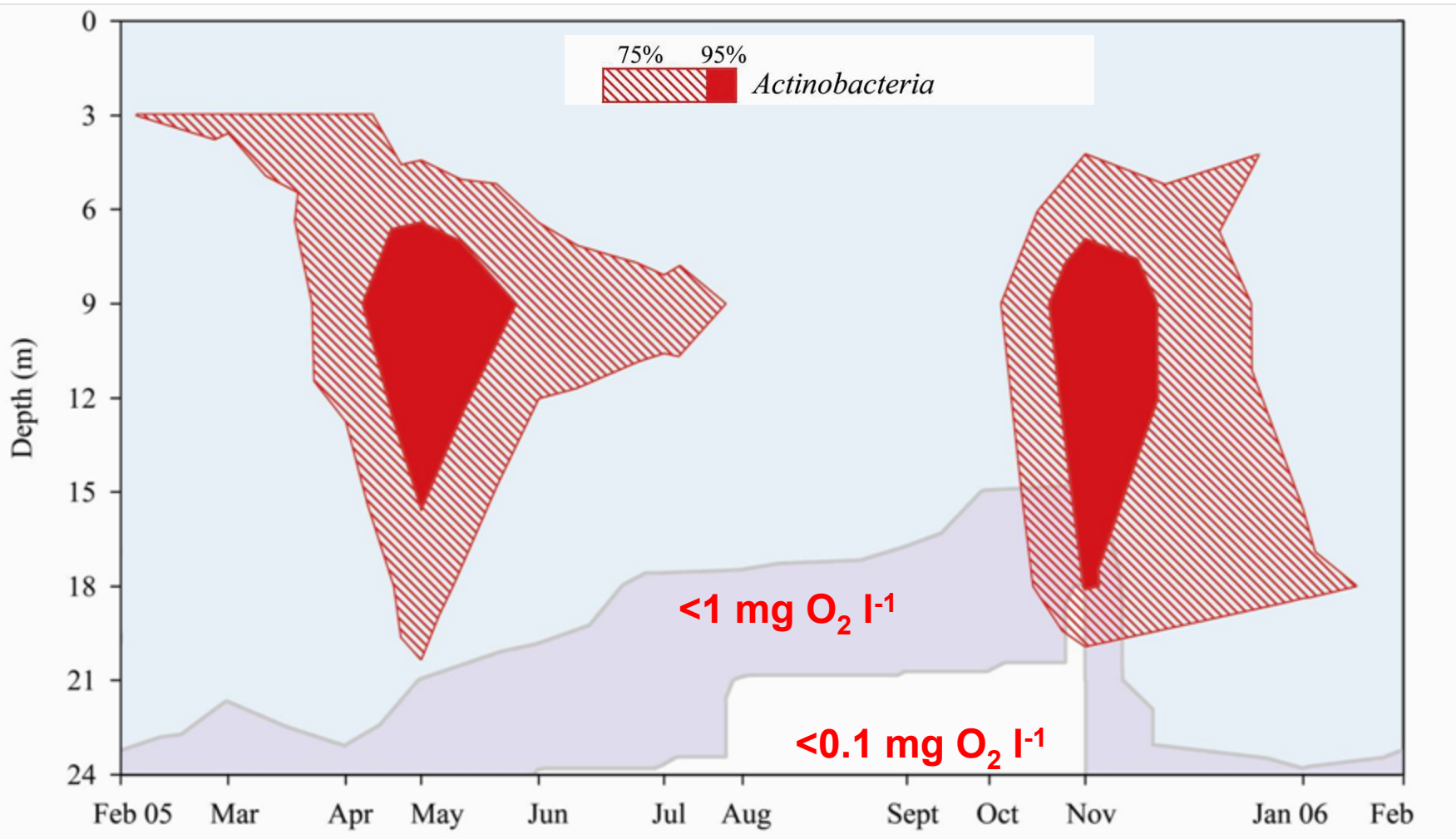
spatial distribution of organisms



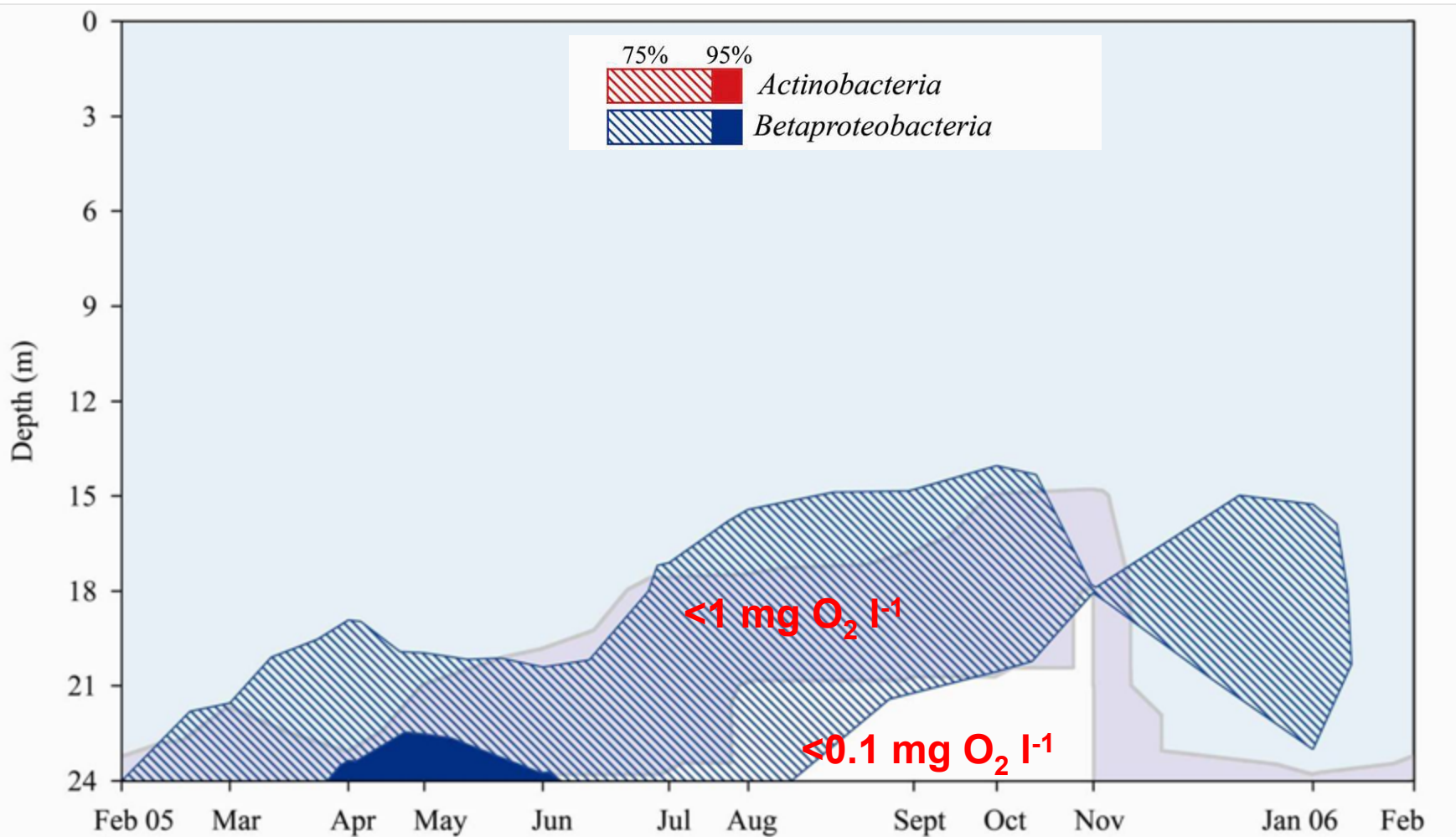
spatial distribution of organisms



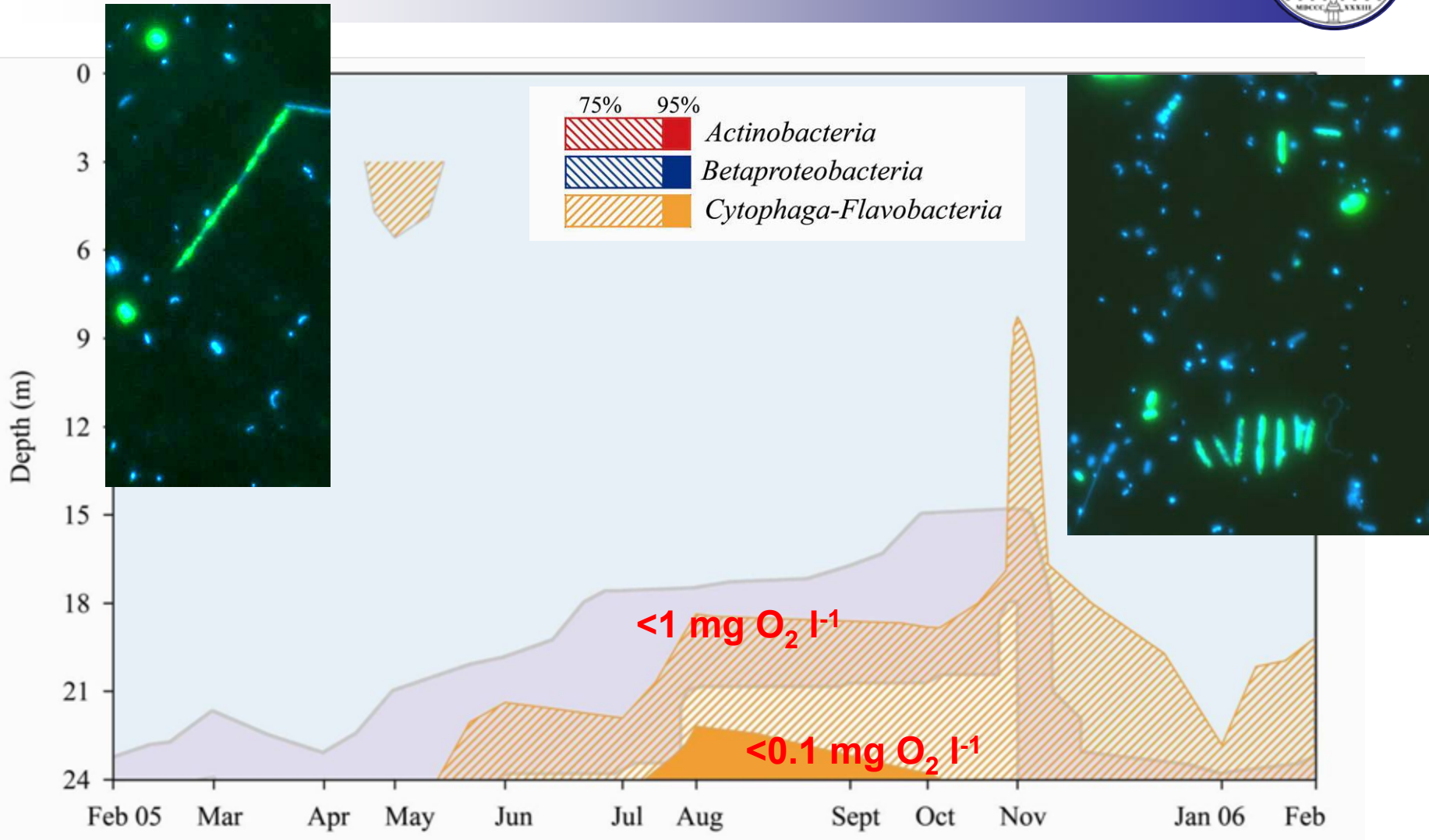
spatial distribution of organisms



spatial distribution of organisms



spatial distribution of organisms



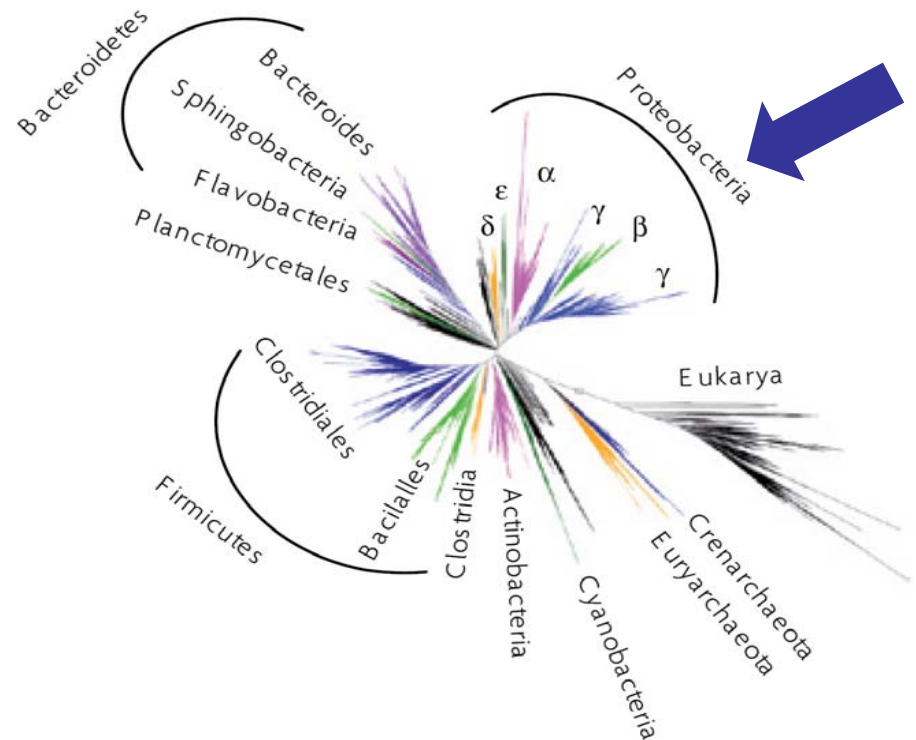
are such lineages homogeneous?

taxonomic resolution of presented data:

- phyla / orders!!
- might harbour distinct populations with very different physiology / habitat preference

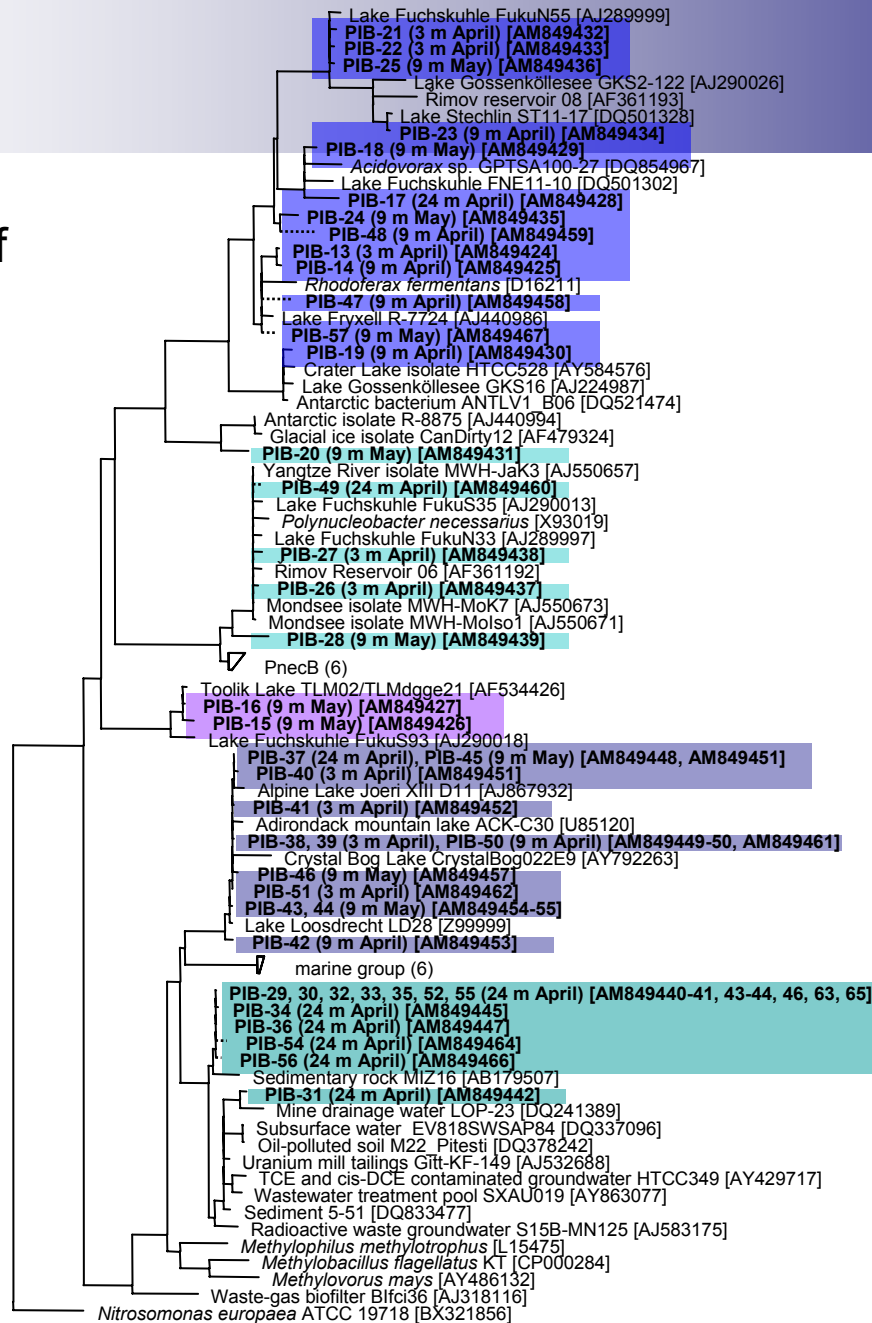
...one example of finer taxonomic resolution:

Betaproteobacteria



phylogeny

4 clone libraries of
16S rRNA gene



beta I

beta II

beta III

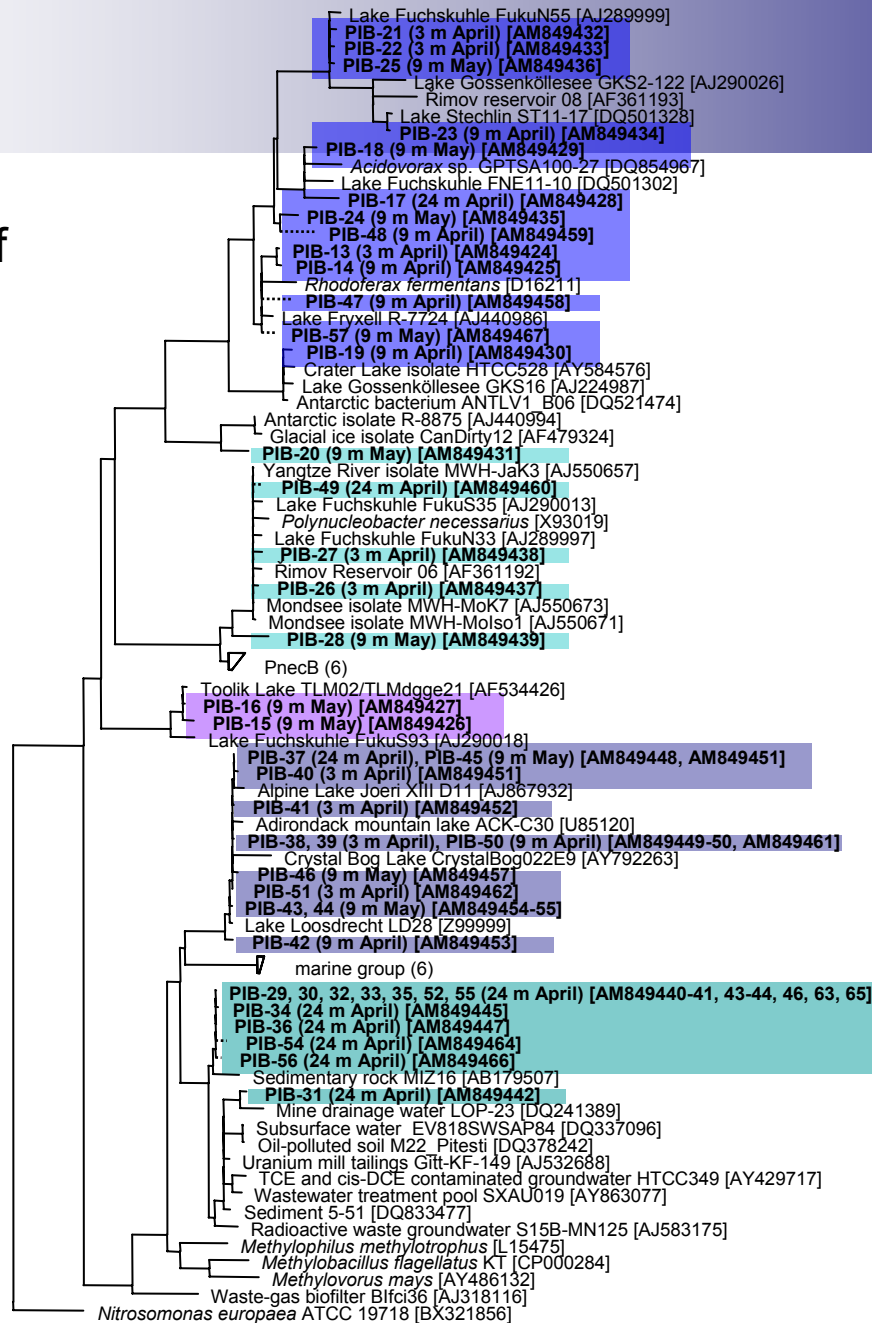
beta IVa

beta IVb

0.10

phylogeny

4 clone libraries of
16S rRNA gene



beta I

beta II

beta III

beta IVa

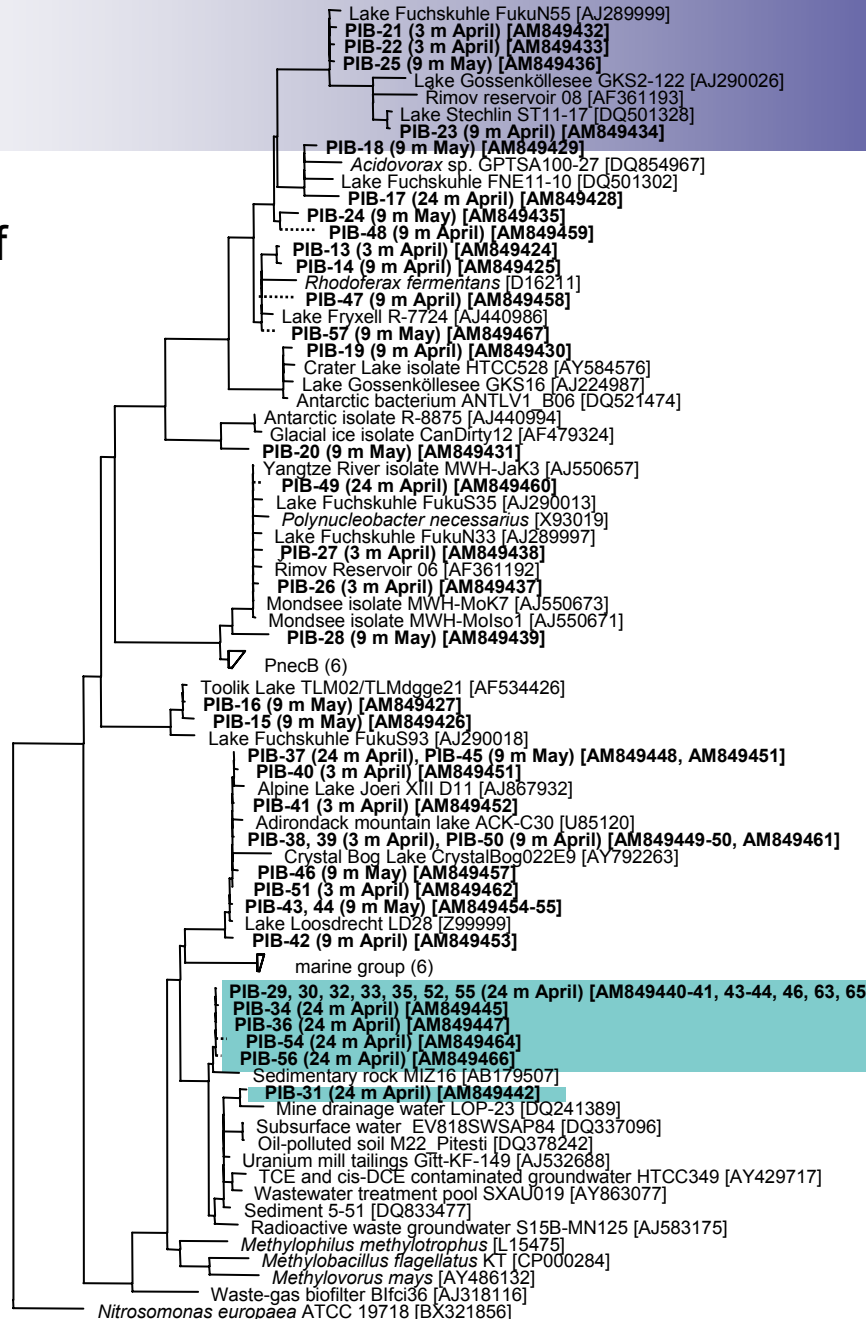
beta IVb

ubiquitous
freshwater
lineages
(Glöckner et
al. 2000)



phylogeny

4 clone libraries of
16S rRNA gene



beta I

beta II

beta III

beta IVa

beta IVb



ubiquitous
freshwater
lineages
(Glöckner et
al. 2000)

„new freshwater“
lineage

...no sequences
from freshwater
...all from anoxic
24 m depth!

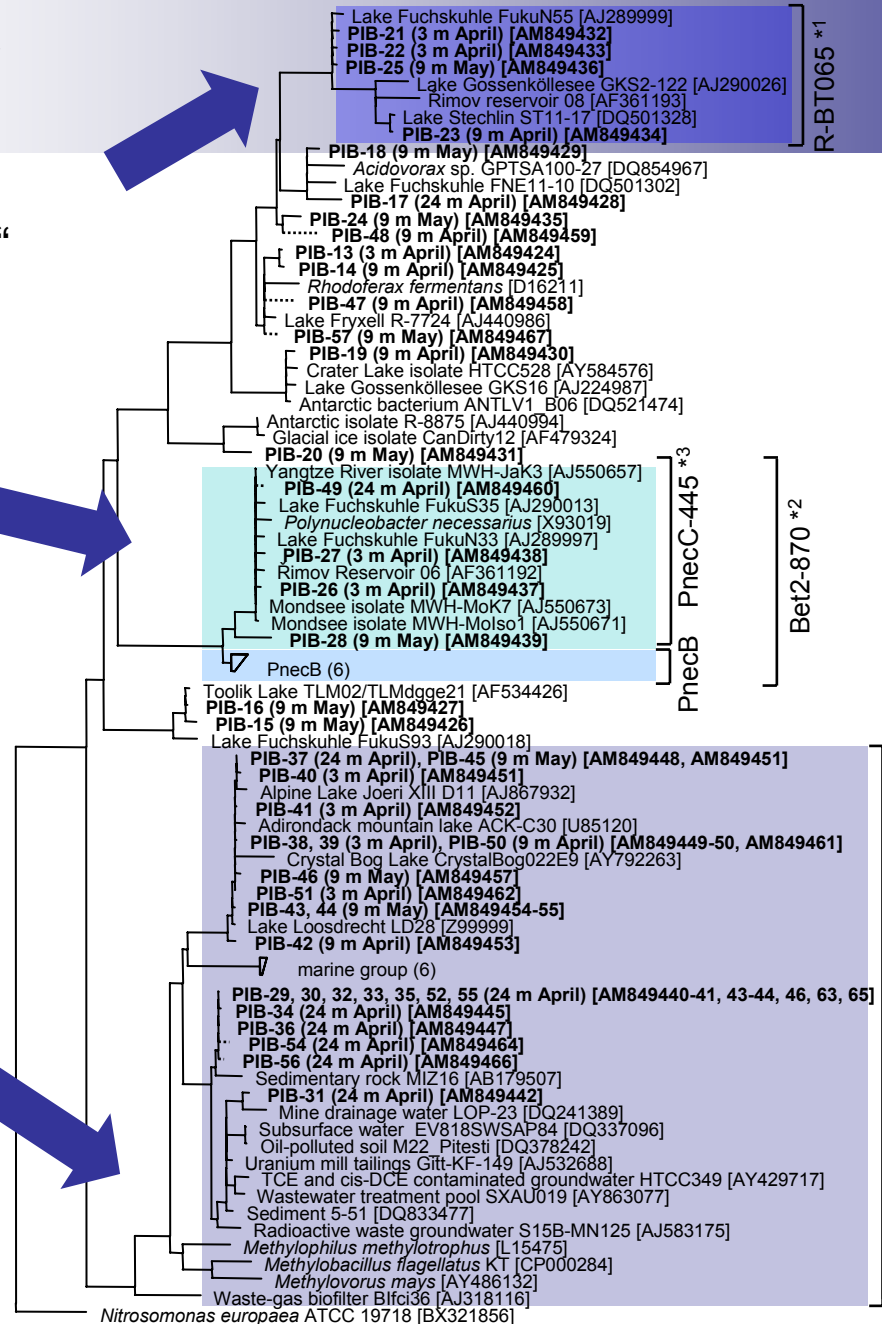
phylogeny



„genus-like“

genus with 2
„species-like“

family



beta I

beta II

beta III

beta IVa

beta IVb

R-BT065 *1

PnecB PnecC-445 *3

Bet2-870 *2

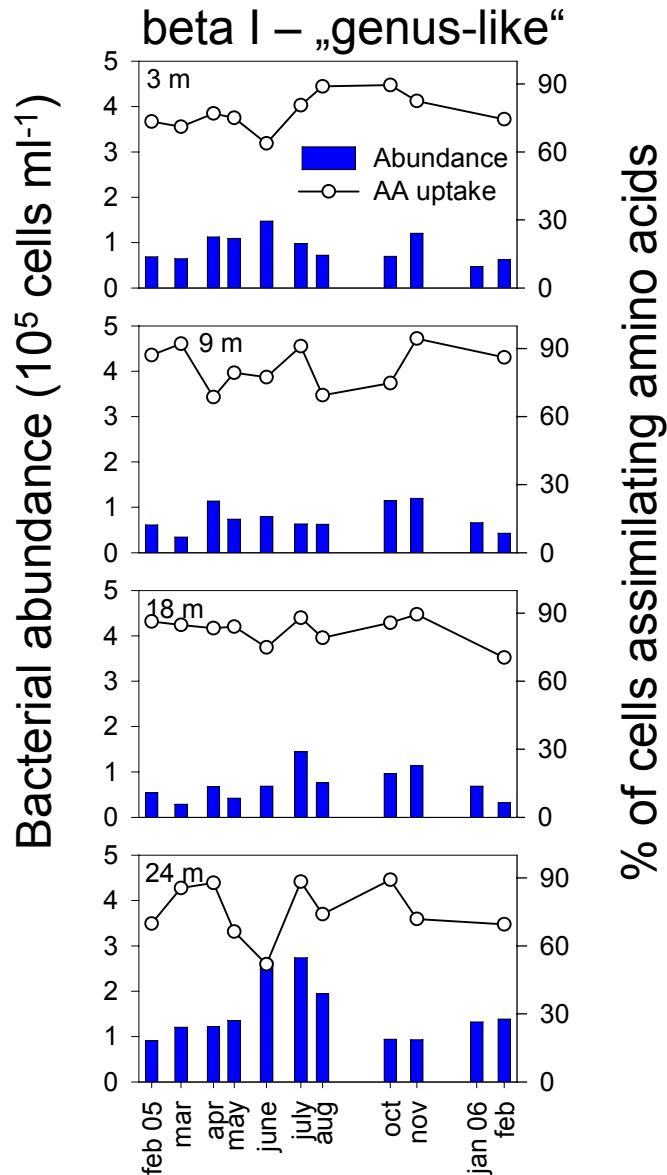
MET1217 *4

0.10

Nitrosomonas europaea ATCC 19718 [BX321856]

*1 Simek et al. 2001; *2 Burkert et al. 2003; *3 Wu & Hahn 2006; *4 Friedrich et al. 2003

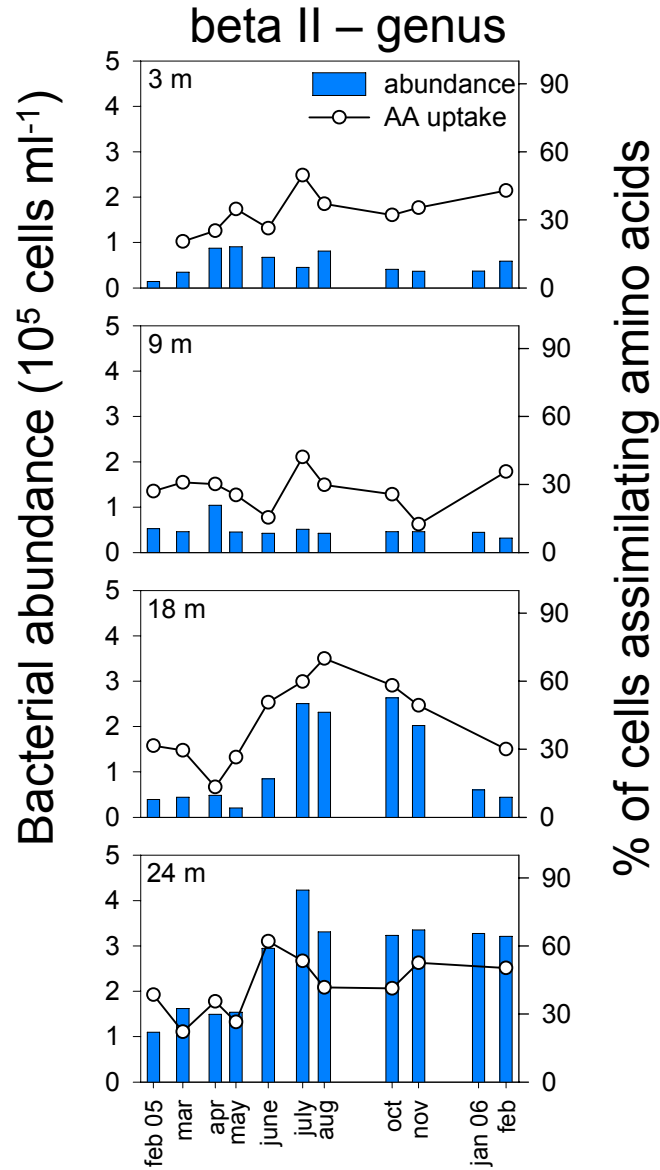
spatio-temporal distribution



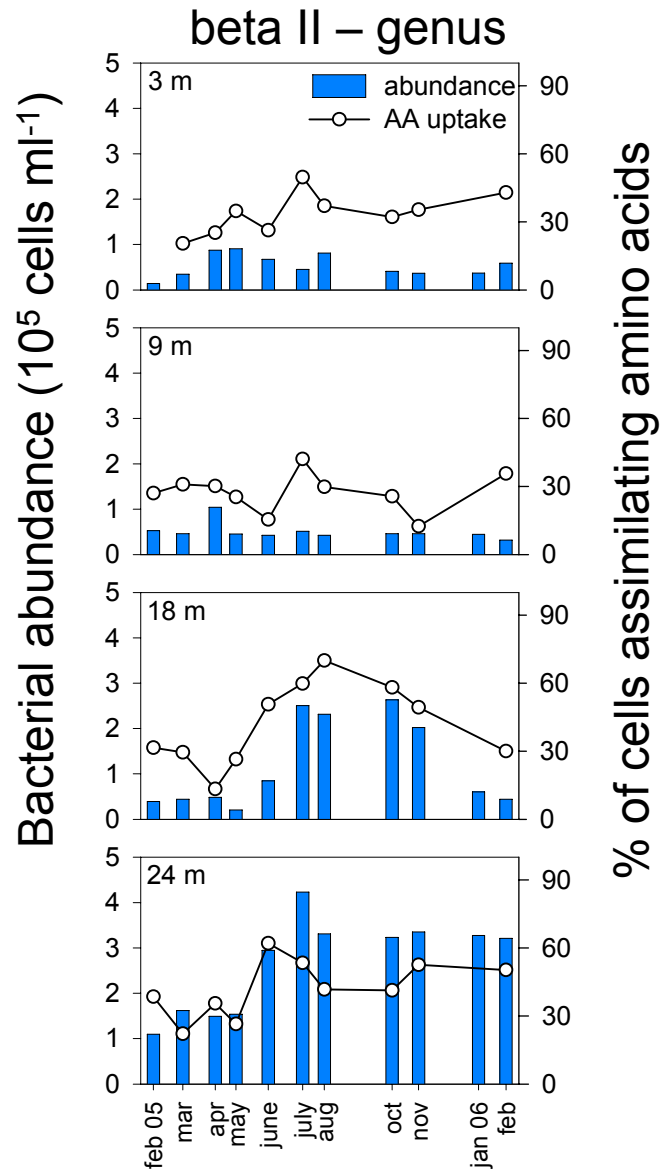
abundant throughout the whole water column

very effective in amino acid uptake (>80% of all beta I)

spatio-temporal distribution



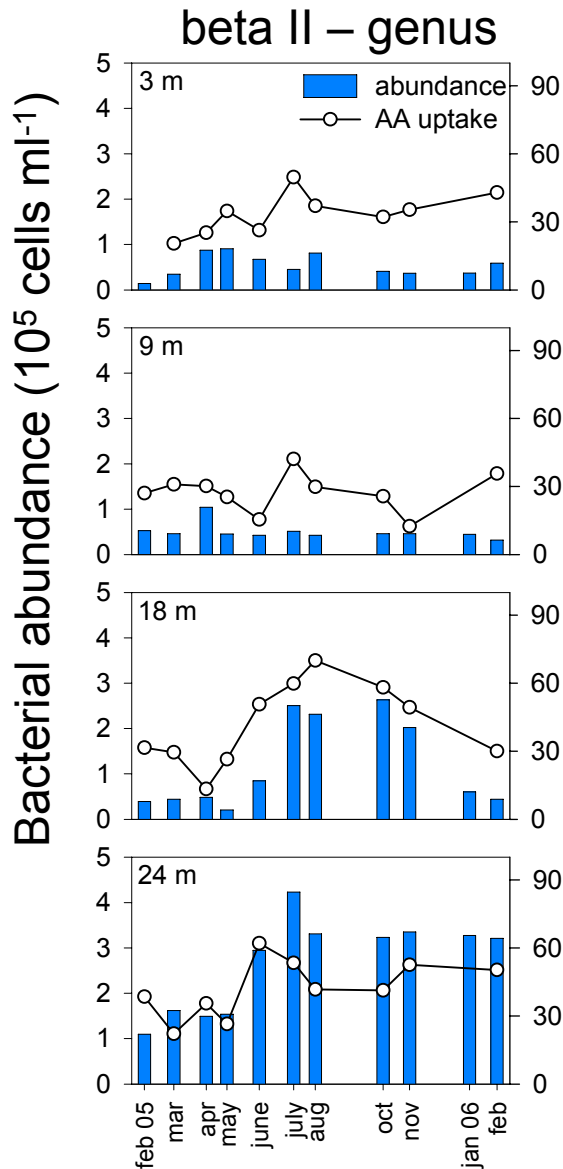
spatio-temporal distribution



pronounced seasonality
in 18 & 24 m depth



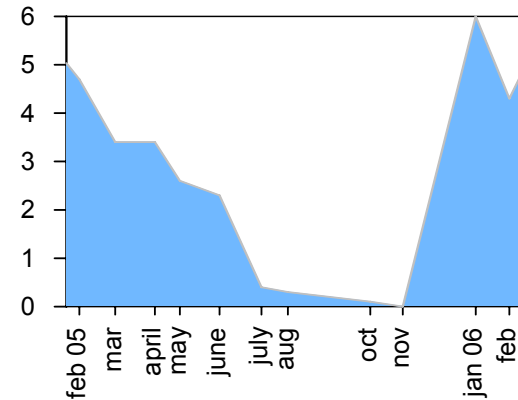
spatio-temporal distribution



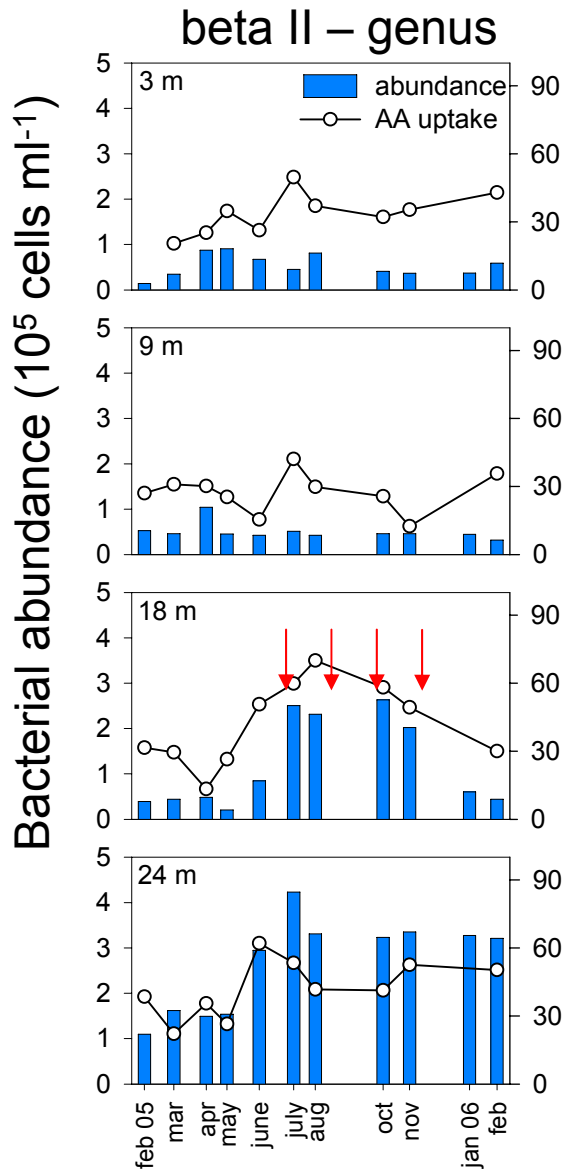
% of cells assimilating amino acids

pronounced seasonality
in 18 & 24 m depth

Oxygen concentration ($mg\ l^{-1}$)



spatio-temporal distribution

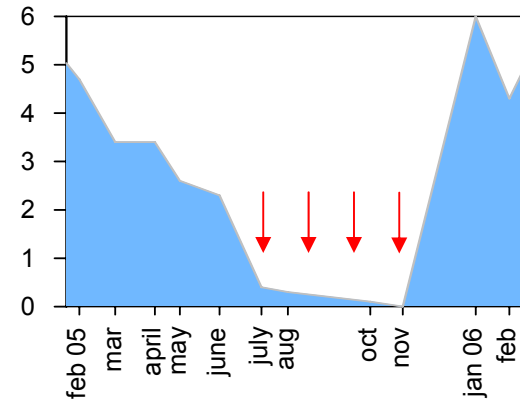


% of cells assimilating amino acids

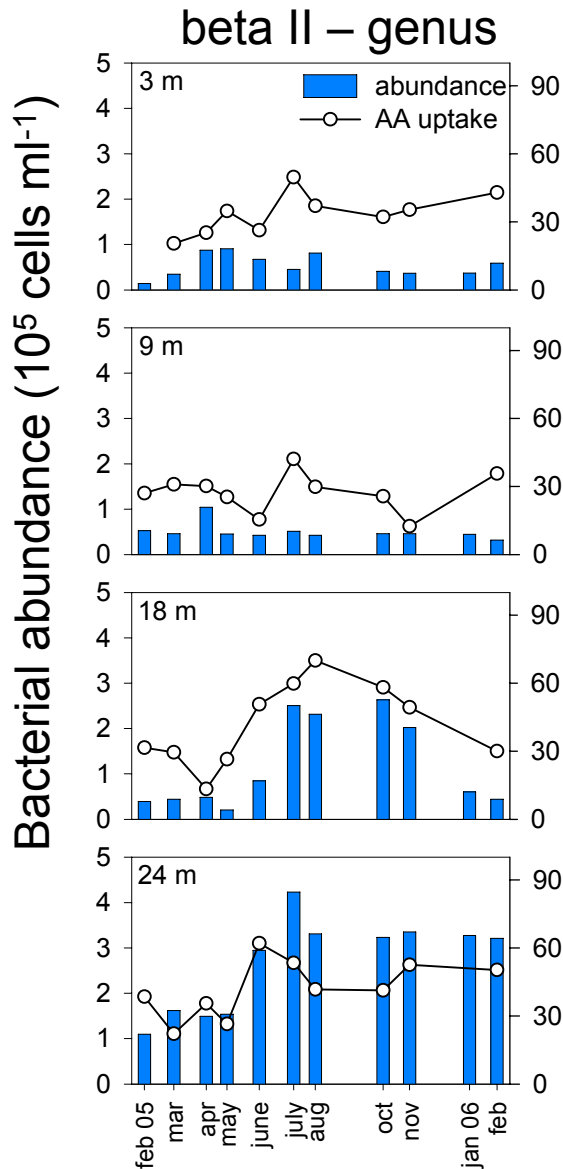
pronounced seasonality
in 18 & 24 m depth

Oxygen concentration ($mg\ l^{-1}$)

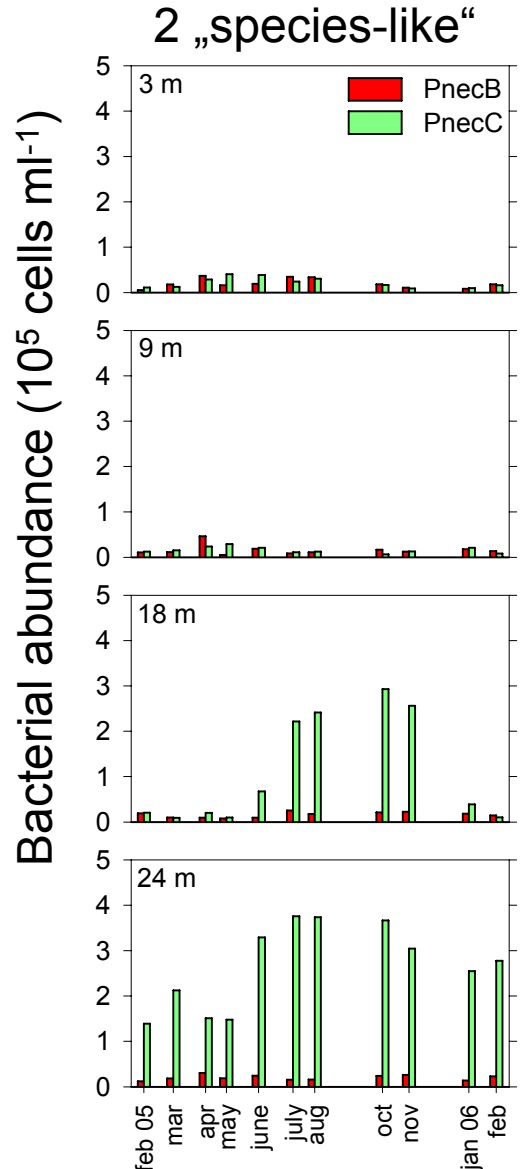
→ oxygen depletion!



spatio-temporal distribution



% of cells assimilating amino acids



most of anaerobic beta II belong to one species!





summary.....

...pronounced seasonality of bacteria

...even more pronounced spatial patterns

...driving forces for the establishment of different bacterial populations...

OXYGEN CONCENTRATION...



...bacteria are most abundant in sub- to anoxic zone

- cell numbers
- biomass
- amino acid incorporation (“activity”)

...mainly *Cytophaga-Flavobacteria* (anoxic)

...& *Betaproteobacteria* (suboxic)

BETAPROTEOBACTERIA



- ...inhomogeneous order which differs in spatio-temporal distribution
- ...some bacteria were abundant in whole water column
- ...others had their maximum in anoxic hypolimnion
- ...even 2 closely related species differed completely
- ...spatio-temporal niche separation triggered mainly by **oxygen concentrations**

acknowledgements

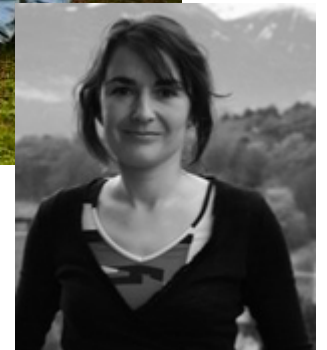


Thomas Posch



Jakob Pernthaler

acknowledgements



acknowledgements



...financial support

FWF

Der Wissenschaftsfonds.



Max-Planck-
Institut für marine
Mikrobiologie

Austrian Science Fund – Project ZFP175540

Max-Planck-Institute for Marine Microbiology



University of Zurich

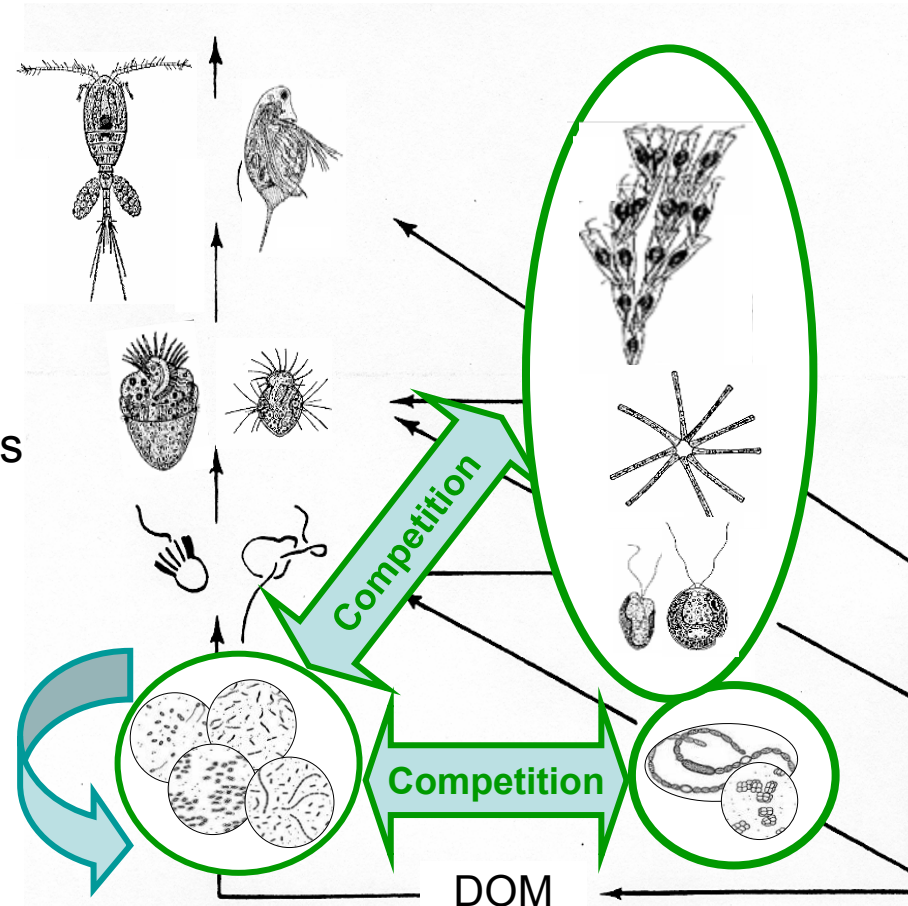
ongoing research

another driving force for planktonic bacteria might be...

...competition for limiting nutrients

- between different bacteria
- between bacteria and algae
- between bacteria and mixotrophic protists

SNF-project:
Competition as driving force for bacterioplankton successions in Lake Zurich (SNF 3100A0-117765)



Fenchel et al. (1988), modified by T. Posch

...thank you for your attention...



The end...

