Phytoplankton functional diversity

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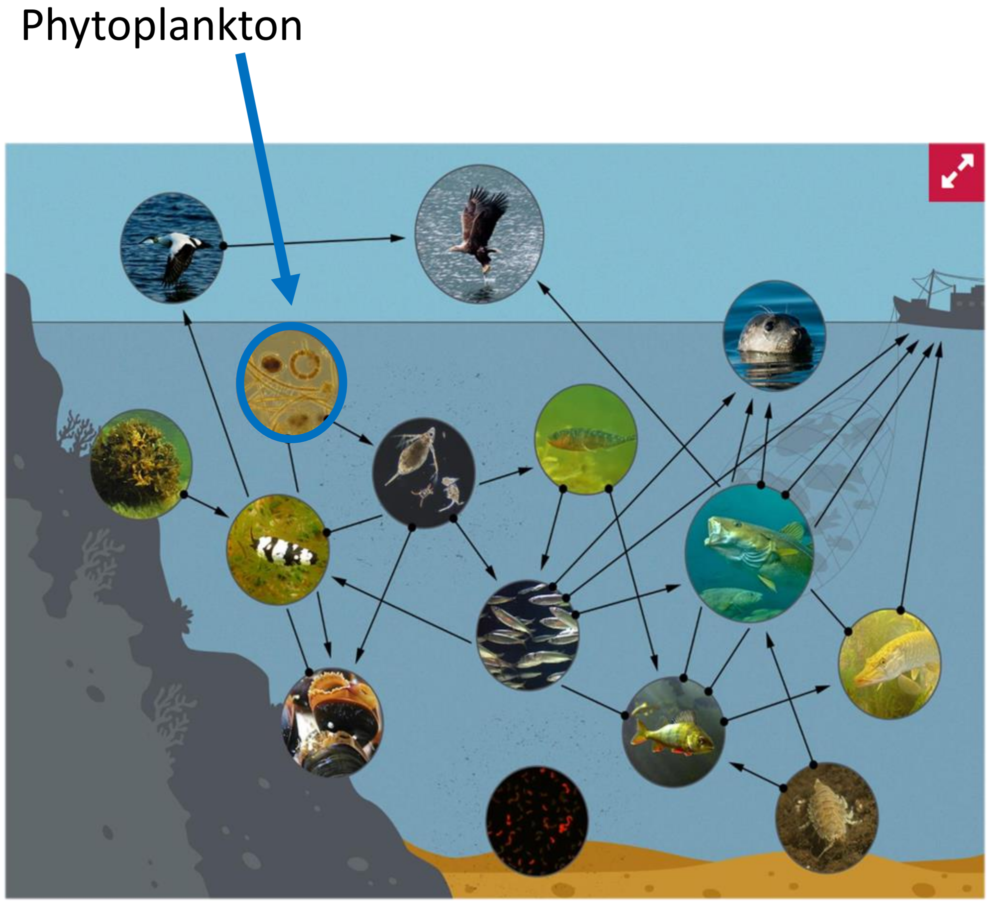
Phytoplankton form the basis of pelagic food webs



Marine food web.
Figure modified from the original figure in Itämeri.fi web page:
https://itameri.fi/fi-FI/Opi_ja_tutki/Ekologia/Ravintoverkko
Photos: H. Arponen, H. Kaartokallio, J. Lappalainen, S. Lehtinen, R. Lumiaro, Metsähallitus, E. Nikunen, J.-T. Roininen, A. Saura, S. Tasala.

Primary production

- phytoplankton produces ca. ½ of the **oxygen** of Earth
- phytoplankton produces ca. ½ of the **net primary production** of Earth
- ca. 60-70% of phytoplankton production is **consumed** daily by small zooplanktonic grazers

Phytoplankton taxonomical and functional composition

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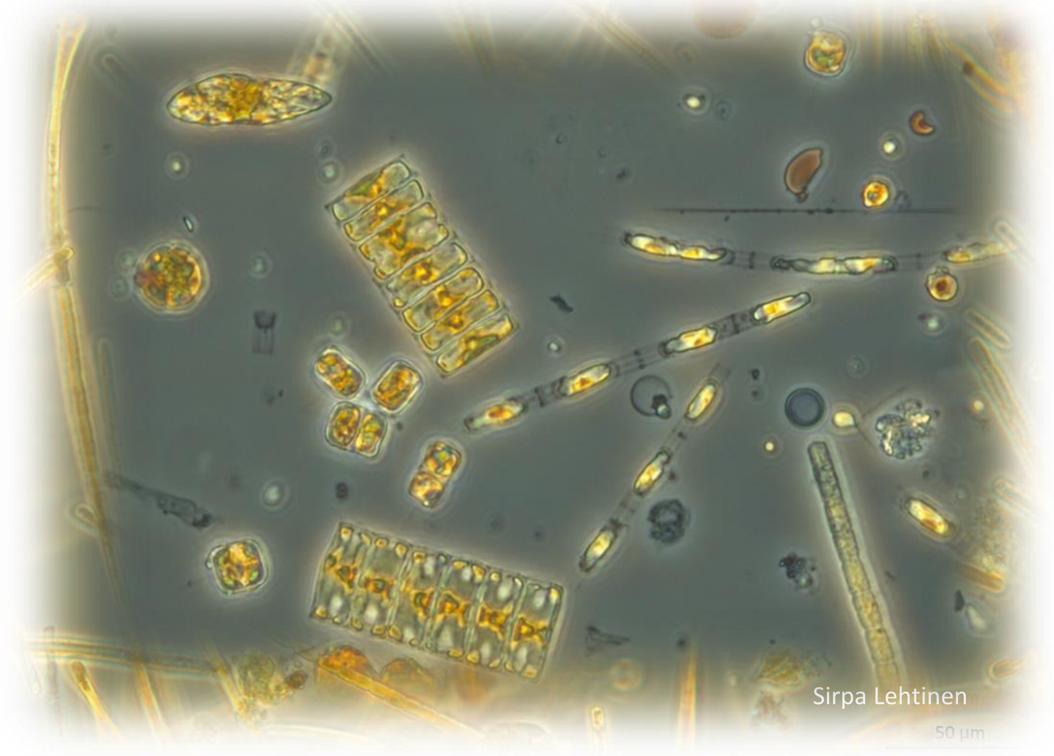
Phytoplankton consists of a **large number of species** with different functional traits and characteristics

- For example, in the Baltic Sea alone, ca. 2000 phytoplankton species are currently known
- **Species composition varies** spatially along environmental variables such as salinity and nutrients, and temporally due to seasonal succession
- **Functional traits** = measurable properties of organisms that influence an organism’s performance or fitness (for example, size, growth rate, pigment composition)
- **Functional characteristics** include also information on e.g. organism’s harmfulness or quality as food for the higher trophic levels
- **Trait-based approach** offers the possibility to draw conclusions beyond a single ecosystem, since the **results are not restricted to local taxonomic composition**
  - most traits are present in all phytoplankton communities in various environments, even though the species identities for carrying those traits vary

Various methods have their own roles in research and monitoring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- **Chlorophyll-a: “How much is there?”**
- **Taxonomic approach: “Who are there?”**
- **Trait-based approach: “What are they doing there?”**

For the higher food web levels, it is not the same if there is a same amount of phytoplankton with good food quality characteristics or with low food quality characteristics (or even harmful characteristics)


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Assigning functional traits for species

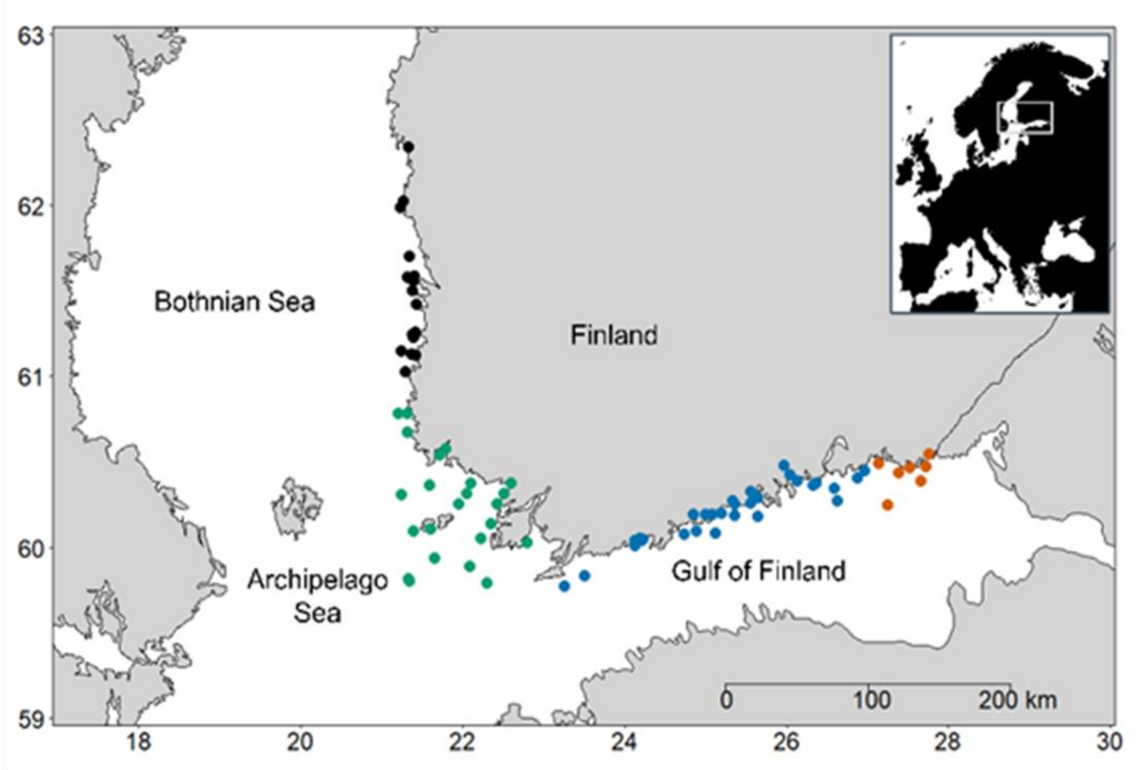
Functional traits are usually assigned for species based on **organism's potential** of carrying a certain trait or characteristics

- Traits are assigned based on existing **scientific literature** and **observations** during sample analysis
- **Experimental** laboratory work is continuously conducted to achieve new information on functional traits
- Some trait data tables for various local species list already exist, and they are developed continuously

Which **set of functional traits** are considered, depends on

- **available trait information** for the species in question
- the research **question** of a study
- the **aim** of the monitoring program

Case study:
Phytoplankton morpho-functional trait variability along coastal environmental gradients



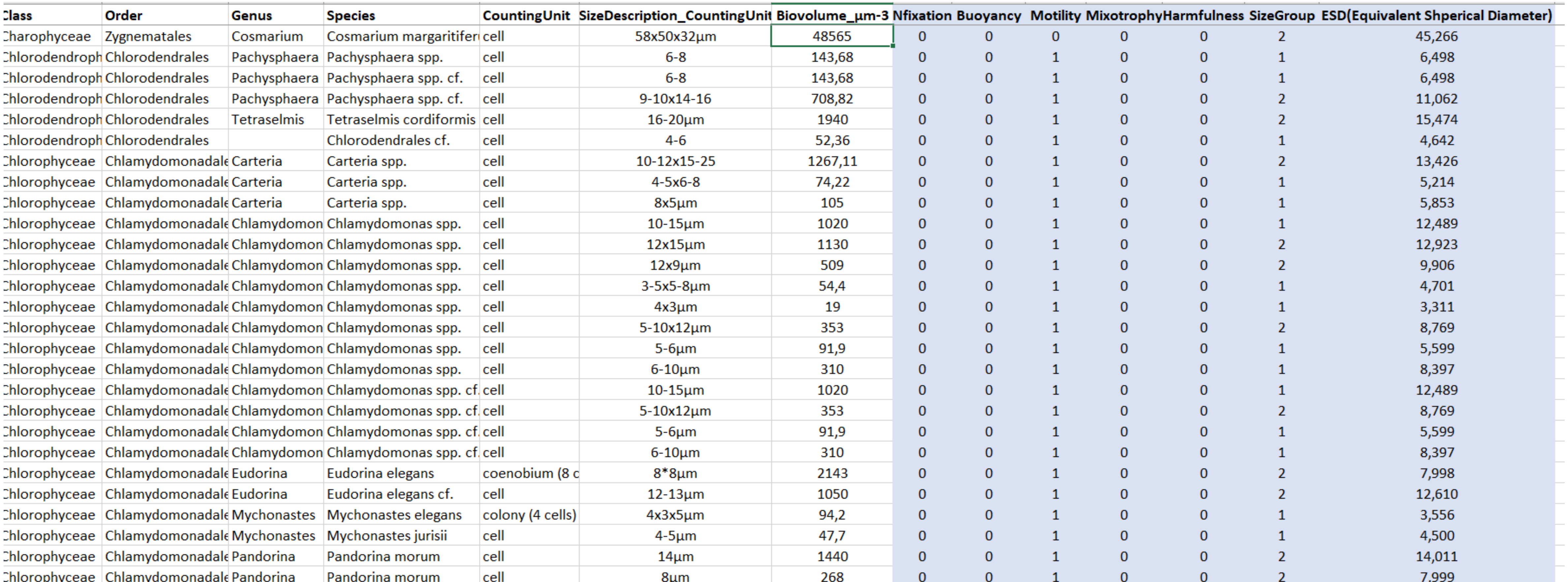
Map showing the location of the coastal sampling stations in the northern Baltic Sea. Black: Bothnian Sea (BS; 17 stations, 110 samples); green: Archipelago Sea (AS; 24 stations, 201 samples); blue: western Gulf of Finland (wGF; 31 stations, 460 samples); red: eastern Gulf of Finland (eGF; 8 stations, 141 samples).

- **Baltic Sea** is a large, semi-enclosed brackish water (2-25 psu) basin in the northern Europe
- The pelagic food web of the Baltic Sea is affected by e.g. anthropogenic **eutrophication** and global **climate change**

- Study area consisted of **four locations** in the Finnish coast, where salinity varies between ca. 2-6 psu
- **>900 phytoplankton samples** from **summer period** from **11 years**
- **Environmental data** included temperature, salinity, stratification, water transparency, total phosphorus, and nutrient loading source type (river, point, sediment, offshore)

From phytoplankton taxonomic information to functional information: creating a functional trait data table

- Trait data table: 753 taxa, 2160 unique counting units (a counting unit may be e.g. a cell or a filament of certain length etc.)
- Trait values express the **potential** for a certain trait
- **Traits in this study** were selected based on their relevance in connection to the environmental variables and pressures: **nitrogen fixing, buoyancy, motility, mixotrophy, harmfulness, size**



Class	Order	Genus	Species	CountingUnit	SizeDescription_CountingUnit	Biovolume_µm-3	Nfixation	Buoyancy	Motility	Mixotrophy	Harmfulness	SizeGroup	ESD(Equivalent Shperical Diameter)
Charophyceae	Zygnematales	Cosmarium	Cosmarium margaritifer	cell	58x50x32µm	48565	0	0	0	0	0	2	45,266
Chlorodendroph	Chlorodendrales	Pachysphaera	Pachysphaera spp.	cell	6-8	143,68	0	0	1	0	0	1	6,498
Chlorodendroph	Chlorodendrales	Pachysphaera	Pachysphaera spp. cf.	cell	6-8	143,68	0	0	1	0	0	1	6,498
Chlorodendroph	Chlorodendrales	Pachysphaera	Pachysphaera spp. cf.	cell	9-10x14-16	708,82	0	0	1	0	0	2	11,062
Chlorodendroph	Chlorodendrales	Tetraselmis	Tetraselmis cordiformis	cell	16-20µm	1940	0	0	1	0	0	2	15,474
Chlorodendroph	Chlorodendrales		Chlorodendrales cf.	cell	4-6	52,36	0	0	1	0	0	1	4,642
Chlorophyceae	Chlamydomonadale	Carteria	Carteria spp.	cell	10-12x15-25	1267,11	0	0	1	0	0	2	13,426
Chlorophyceae	Chlamydomonadale	Carteria	Carteria spp.	cell	4-5x6-8	74,22	0	0	1	0	0	1	5,214
Chlorophyceae	Chlamydomonadale	Carteria	Carteria spp.	cell	8x5µm	105	0	0	1	0	0	1	5,853
Chlorophyceae	Chlamydomonadale	Chlamydomon	Chlamydomonas spp.	cell	10-15µm	1020	0	0	1	0	0	1	12,489
Chlorophyceae	Chlamydomonadale	Chlamydomon	Chlamydomonas spp.	cell	12x15µm	1130	0	0	1	0	0	2	12,923
Chlorophyceae	Chlamydomonadale	Chlamydomon	Chlamydomonas spp.	cell	12x9µm	509	0	0	1	0	0	2	9,906
Chlorophyceae	Chlamydomonadale	Chlamydomon	Chlamydomonas spp.	cell	3-5x5-8µm	54,4	0	0	1	0	0	1	4,701
Chlorophyceae	Chlamydomonadale	Chlamydomon	Chlamydomonas spp.	cell	4x3µm	19	0	0	1	0	0	1	3,311
Chlorophyceae	Chlamydomonadale	Chlamydomon	Chlamydomonas spp.	cell	5-10x12µm	353	0	0	1	0	0	2	8,769
Chlorophyceae	Chlamydomonadale	Chlamydomon	Chlamydomonas spp.	cell	5-6µm	91,9	0	0	1	0	0	1	5,599
Chlorophyceae	Chlamydomonadale	Chlamydomon	Chlamydomonas spp.	cell	6-10µm	310	0	0	1	0	0	1	8,397
Chlorophyceae	Chlamydomonadale	Chlamydomon	Chlamydomonas spp. cf.	cell	10-15µm	1020	0	0	1	0	0	1	12,489
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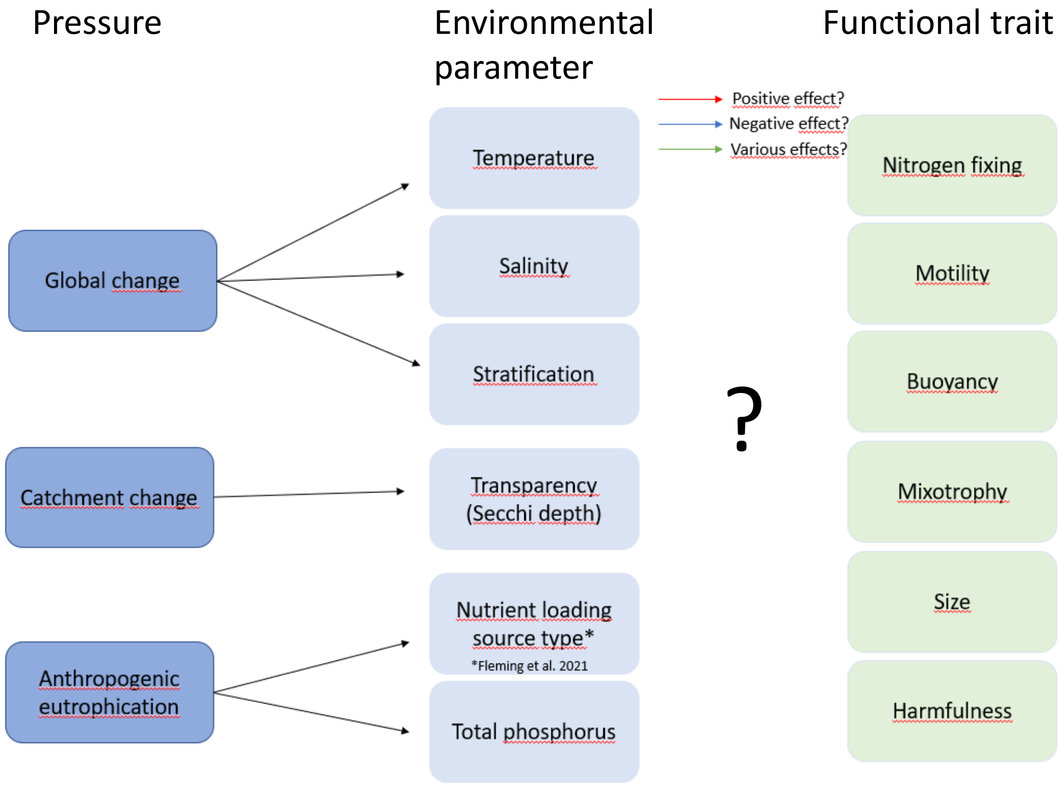
Chlorophyceae	Chlamydomonadale	Chlamydomon	Chlamydomonas spp. cf.	cell	6-10µm	310	0	0	1	0	0	1	8,397
Chlorophyceae	Chlamydomonadale	Eudorina	Eudorina elegans	coenobium (8 c	8*8µm	2143	0	0	1	0	0	2	7,998
Chlorophyceae	Chlamydomonadale	Eudorina	Eudorina elegans cf.	cell	12-13µm	1050	0	0	1	0	0	2	12,610
Chlorophyceae	Chlamydomonadale	Mychonastes	Mychonastes elegans	colony (4 cells)	4x3x5µm	94,2	0	0	1	0	0	1	3,556
Chlorophyceae	Chlamydomonadale	Mychonastes	Mychonastes jurisii	cell	4-5µm	47,7	0	0	1	0	0	1	4,500
Chlorophyceae	Chlamydomonadale	Pandorina	Pandorina morum	cell	14µm	1440	0	0	1	0	0	2	14,011
Chlorophyceae	Chlamydomonadale	Pandorina	Pandorina morum	cell	8µm	268	0	0	1	0	0	2	7,999

Aim



Pressure

Environmental parameter

Functional trait

Positive effect?
Negative effect?
Various effects?

Global change
Catchment change
Anthropogenic eutrophication

Temperature
Salinity
Stratification
Transparency (Secchi depth)
Nutrient loading source type*
*Fleming et al. 2021
Total phosphorus

?

Nitrogen fixing
Motility
Buoyancy
Mixotrophy
Size
Harmfulness

Examine how certain phytoplankton functional traits are linked to

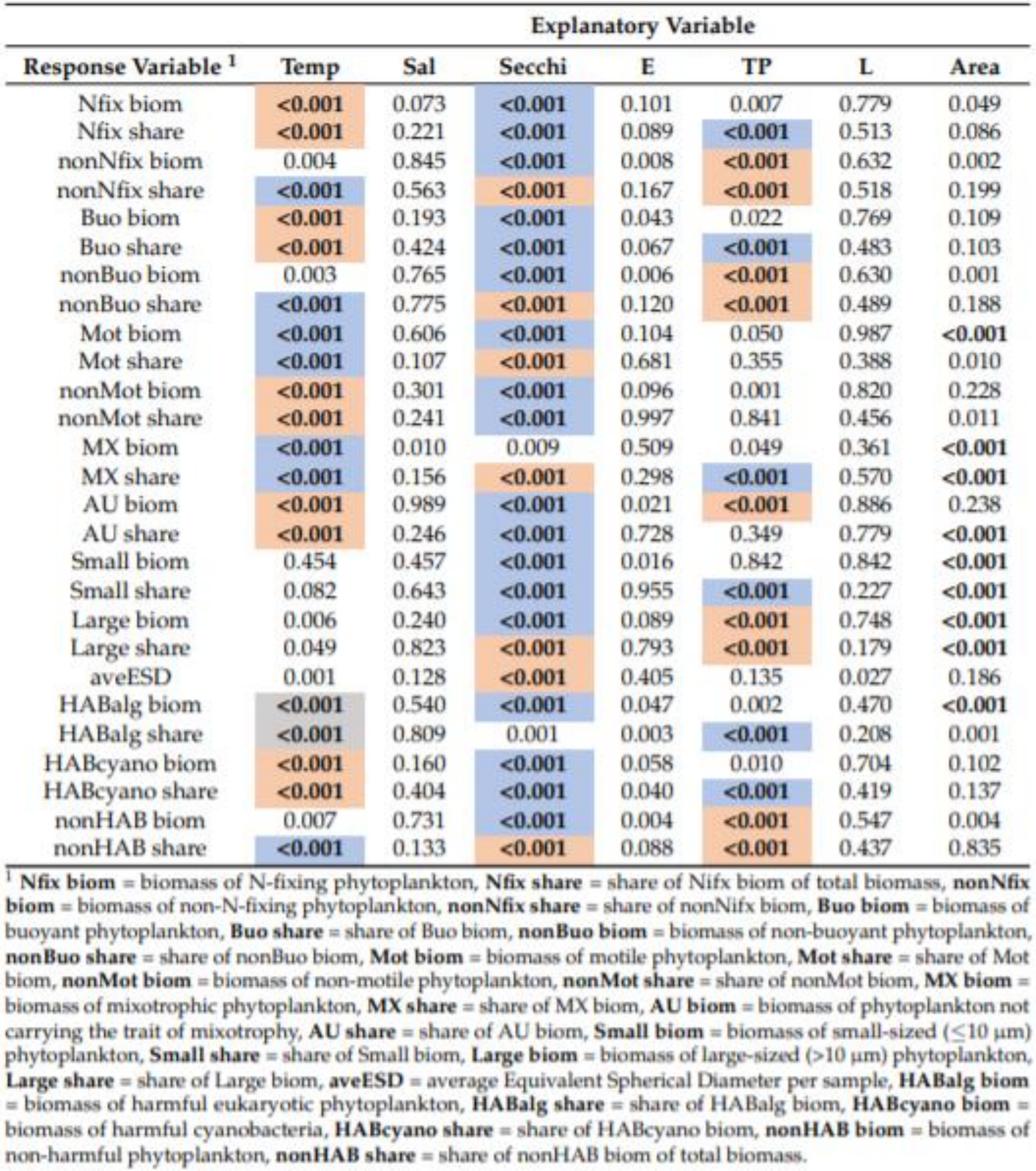
1) **changes in physical features due to global change** (temperature, salinity, stratification)

2) **water quality features due to catchment change** (water transparency measured as Secchi depth)

3) **nutrient availability due to nutrient loading** (total phosphorus, nutrient loading source type (*river, point, sediment, offshore))

Results: Effects of environmental variables on functional traits

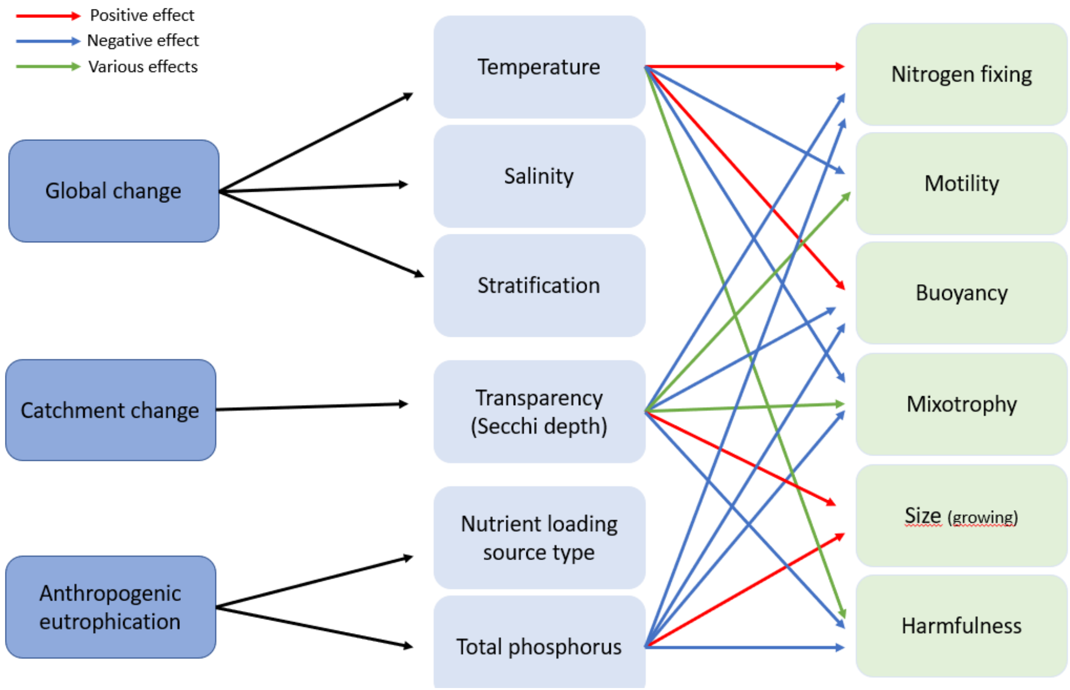
- *p*-values of the generalized additive mixed models (GAMM)
- Response variables:
  - **biomass of cells having/ lacking the potential for a certain trait**
  - **share of total biomass of cells having/ lacking the potential for a certain trait**
- Explanatory variables (fixed variables):
  - temperature (Temp)
  - surface salinity (Sal)
  - water transparency measured as Secchi depth (Secchi)
  - stratification index (E)
  - total phosphorus concentration (TP)
  - loading source type (L)
  - sea area (Area)
- Random factor:
  - hierarchical data structure (sea area > water body > sampling station).
- Orange/pink: significant linear positive effect
- Blue: significant negative linear effect
- Grey: significant non-linear (unimodal) effect



	Explanatory Variable						
Response Variable [1]	**Temp**	**Sal**	**Secchi**	**E**	**TP**	**L**	**Area**
Nfix biom	**<0.001**	0.073	**<0.001**	0.101	0.007	0.779	0.049
Nfix share	**<0.001**	0.221	**<0.001**	0.089	**<0.001**	0.513	0.086
nonNfix biom	0.004	0.845	**<0.001**	0.008	**<0.001**	0.632	0.002
nonNfix share	**<0.001**	0.563	**<0.001**	0.167	**<0.001**	0.518	0.199
Buo biom	**<0.001**	0.193	**<0.001**	0.043	0.022	0.769	0.109
Buo share	**<0.001**	0.424	**<0.001**	0.067	**<0.001**	0.483	0.103
nonBuo biom	0.003	0.765	**<0.001**	0.006	**<0.001**	0.630	0.001
nonBuo share	**<0.001**	0.775	**<0.001**	0.120	**<0.001**	0.489	0.188
Mot biom	**<0.001**	0.606	**<0.001**	0.104	0.050	0.987	**<0.001**
Mot share	**<0.001**	0.107	**<0.001**	0.681	0.355	0.388	0.010
nonMot biom	**<0.001**	0.301	**<0.001**	0.096	0.001	0.820	0.228
nonMot share	**<0.001**	0.241	**<0.001**	0.997	0.841	0.456	0.011
MX biom	**<0.001**	0.010	0.009	0.509	0.049	0.361	**<0.001**
MX share	**<0.001**	0.156	**<0.001**	0.298	**<0.001**	0.570	**<0.001**
AU biom	**<0.001**	0.989	**<0.001**	0.021	**<0.001**	0.886	0.238
AU share	**<0.001**	0.246	**<0.001**	0.728	0.349	0.779	**<0.001**
Small biom	0.454	0.457	**<0.001**	0.016	0.842	0.842	**<0.001**
Small share	0.082	0.643	**<0.001**	0.955	**<0.001**	0.227	**<0.001**
Large biom	0.006	0.240	**<0.001**	0.089	**<0.001**	0.748	**<0.001**
Large share	0.049	0.823	**<0.001**	0.793	**<0.001**	0.179	**<0.001**
aveESD	0.001	0.128	**<0.001**	0.405	0.135	0.027	0.186
HABalg biom	**<0.001**	0.540	**<0.001**	0.047	0.002	0.470	**<0.001**
HABalg share	**<0.001**	0.809	0.001	0.003	**<0.001**	0.208	0.001
HABcyano biom	**<0.001**	0.160	**<0.001**	0.058	0.010	0.704	0.102
HABcyano share	**<0.001**	0.404	**<0.001**	0.040	**<0.001**	0.419	0.137
nonHAB biom	0.007	0.731	**<0.001**	0.004	**<0.001**	0.547	0.004
nonHAB share	**<0.001**	0.133	**<0.001**	0.088	**<0.001**	0.437	0.835

[1] **Nfix biom** = biomass of N-fixing phytoplankton, **Nfix share** = share of Nifx biom of total biomass, **nonNfix biom** = biomass of non-N-fixing phytoplankton, **nonNfix share** = share of nonNifx biom, **Buo biom** = biomass of buoyant phytoplankton, **Buo share** = share of Buo biom, **nonBuo biom** = biomass of non-buoyant phytoplankton, **nonBuo share** = share of nonBuo biom, **Mot biom** = biomass of motile phytoplankton, **Mot share** = share of Mot biom, **nonMot biom** = biomass of non-motile phytoplankton, **nonMot share** = share of nonMot biom, **MX biom** = biomass of mixotrophic phytoplankton, **MX share** = share of MX biom, **AU biom** = biomass of phytoplankton not carrying the trait of mixotrophy, **AU share** = share of AU biom, **Small biom** = biomass of small-sized ($\leq$10 µm) phytoplankton, **Small share** = share of Small biom, **Large biom** = biomass of large-sized (>10 µm) phytoplankton, **Large share** = share of Large biom, **aveESD** = average Equivalent Spherical Diameter per sample, **HABalg biom** = biomass of harmful eukaryotic phytoplankton, **HABalg share** = share of HABalg biom, **HABcyano biom** = biomass of harmful cyanobacteria, **HABcyano share** = share of HABcyano biom, **nonHAB biom** = biomass of non-harmful phytoplankton, **nonHAB share** = share of nonHAB biom of total biomass.

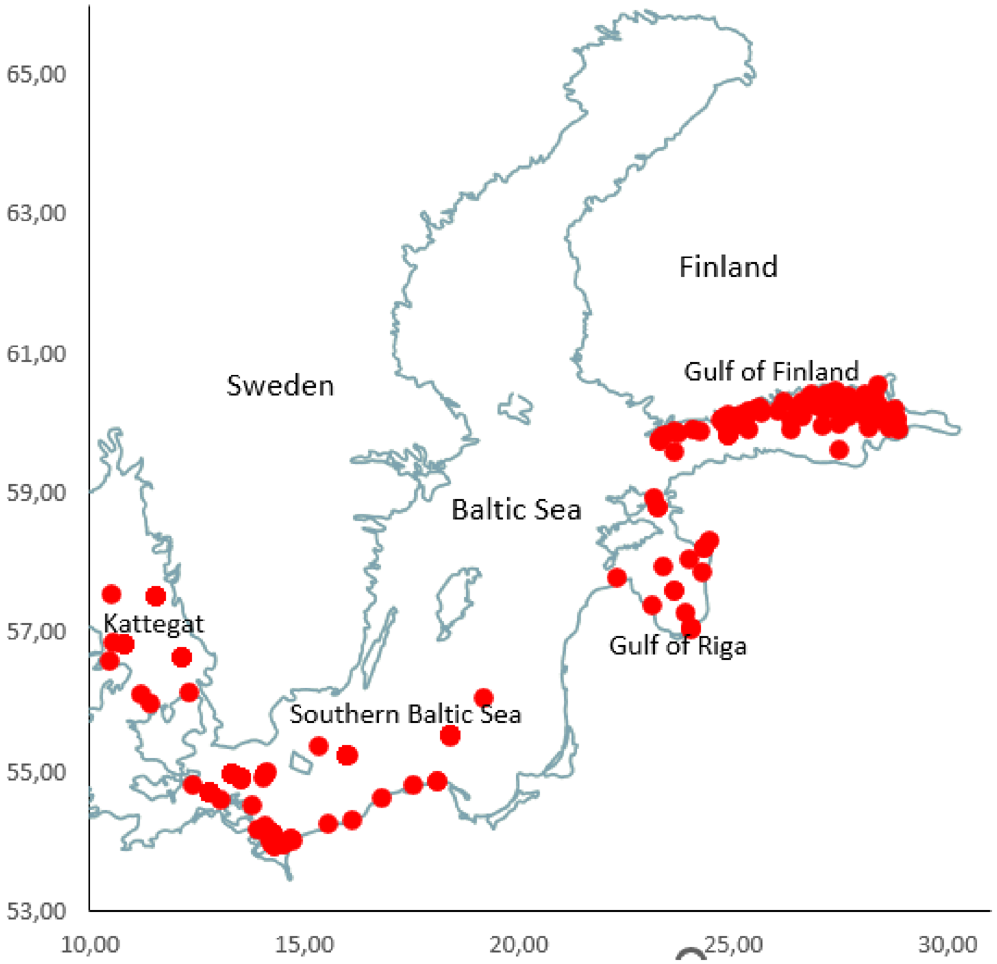
Conclusions



1) Changes in physical features due to **global change**
   - **temperature affected most of the studied traits** (negatively/positively)
   - salinity and stratification did not have clear effects on traits
2) Water quality features due to **catchment change**
   - only **larger size** was positively correlated with **water transparency**
   - e.g. **harmfulness** was negatively correlated with water transparency
3) Nutrient availability due to **nutrient loading**
   - only **larger size** was positively correlated with total phosphorus
   - the nutrient loading source type did not relate to any of the studied traits

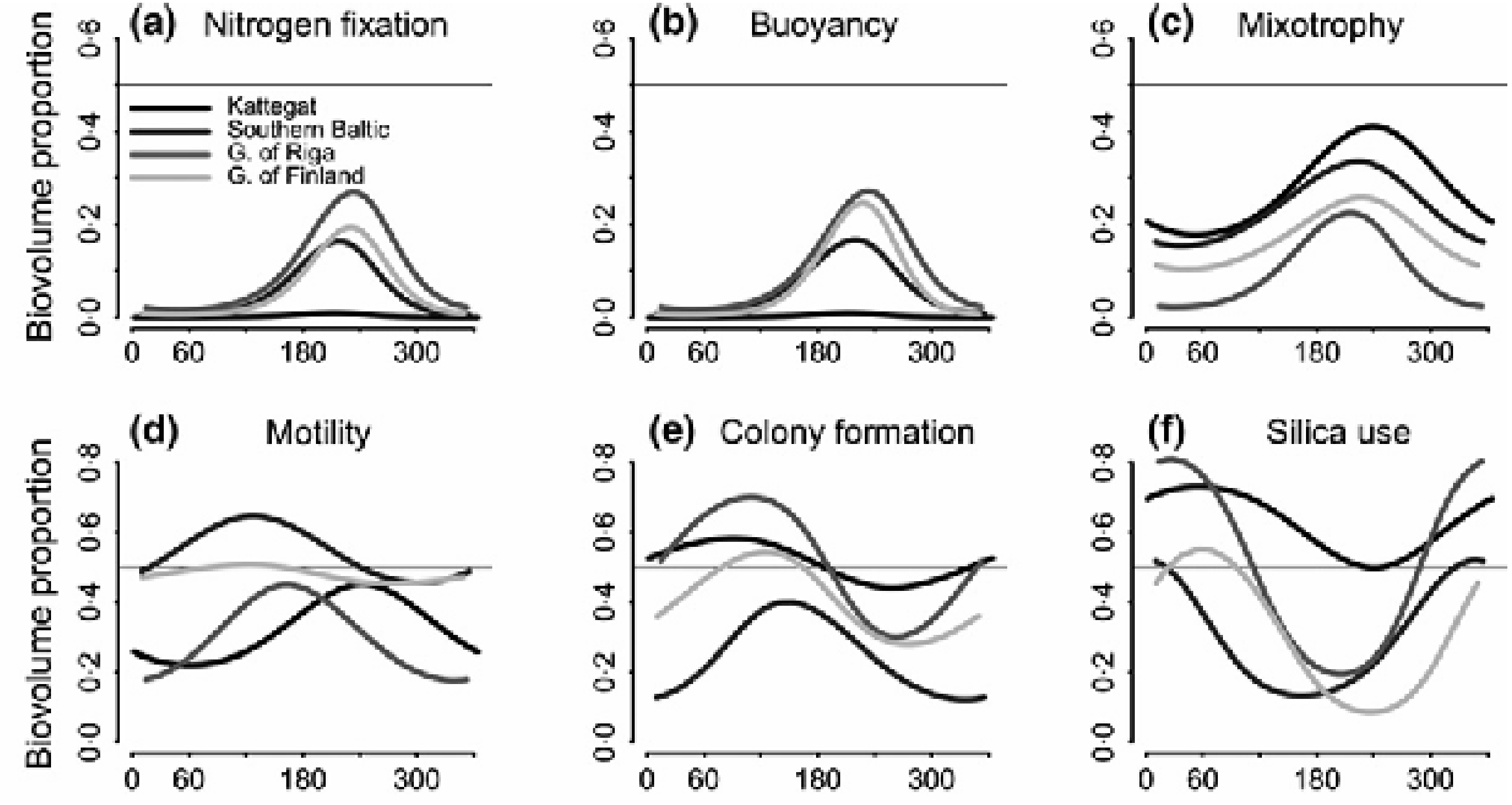
Read the full article:
Lehtinen S, Suikkanen S, Hällfors H, Tuimala J, Kuosa H (2021) Phytoplankton morpho-functional trait variability along coastal environmental gradients. Microorganisms 9, 2477.
https://doi.org/10.3390/microorganisms9122477

Another case study:
Community assembly and drivers of phytoplankton functional structure



- Salinity in the study area varies between 2-25 psu
- **>5000 phytoplankton samples** from **spring to late summer** from **16 years**
- **Functional traits:**
  - nitrogen fixation
  - buoyancy
  - silica use
  - motility
  - forming chains or colonies
  - mixotrophy
  - size
  - pigments (combines the presence of chl-c, chl-b, and phycobilins)

Seasonal patterns of individual functional traits



Y-axis: biovolume proportion of a certain trait of the total phytoplankton biovolume

X-axis: day of the year

Seasonal and regional patterns of the community-weighted mean values of certain **individual traits**.
Figure from Klais et al. (2016)

Read the full article:
Klais R, Norros V, Lehtinen S, Tamminen T, Olli K (2016) Community assembly and drivers of phytoplankton functional structure. Functional Ecology. doi:10.1111/1365-2435.12784

Collaboration using Faroese data

- Phytoplankton and environmental data collected ca. every ten days by Fiskaaling during one whole year from the **Kaldbak fjord**
- **Assigning suitable trait values** for phytoplankton species
- Running **statistical analyses** on (1) seasonal functional trait variability and (2) relations between the phytoplankton traits and environmental variables
- **In the future**, the aim would be to develop a method to use phytoplankton functional composition and diversity for forecasting future effects on the higher levels of the food web (e.g. cultured and wild fish)

Thank you!

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