
PICES-2025
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Innovative Approaches and Applications to Foster Resilience in North Pacific Ecosystems
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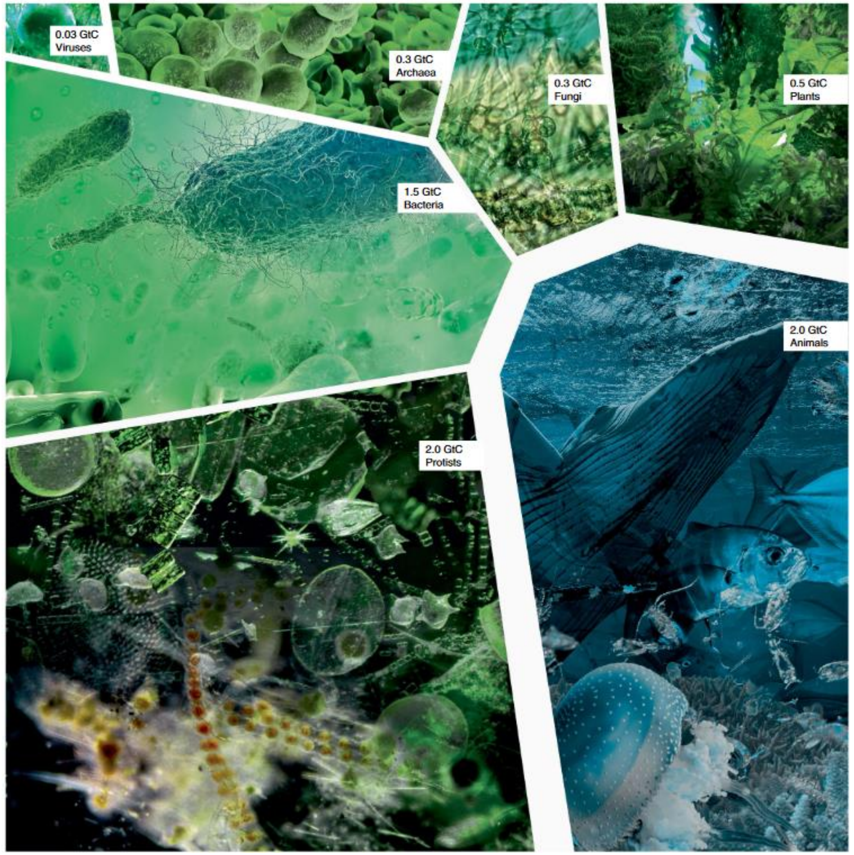
Shifts in phytoplankton and bacterioplankton communities induced by simulated freshwater intrusion near ice shelves in the Pacific sector of the Southern Ocean

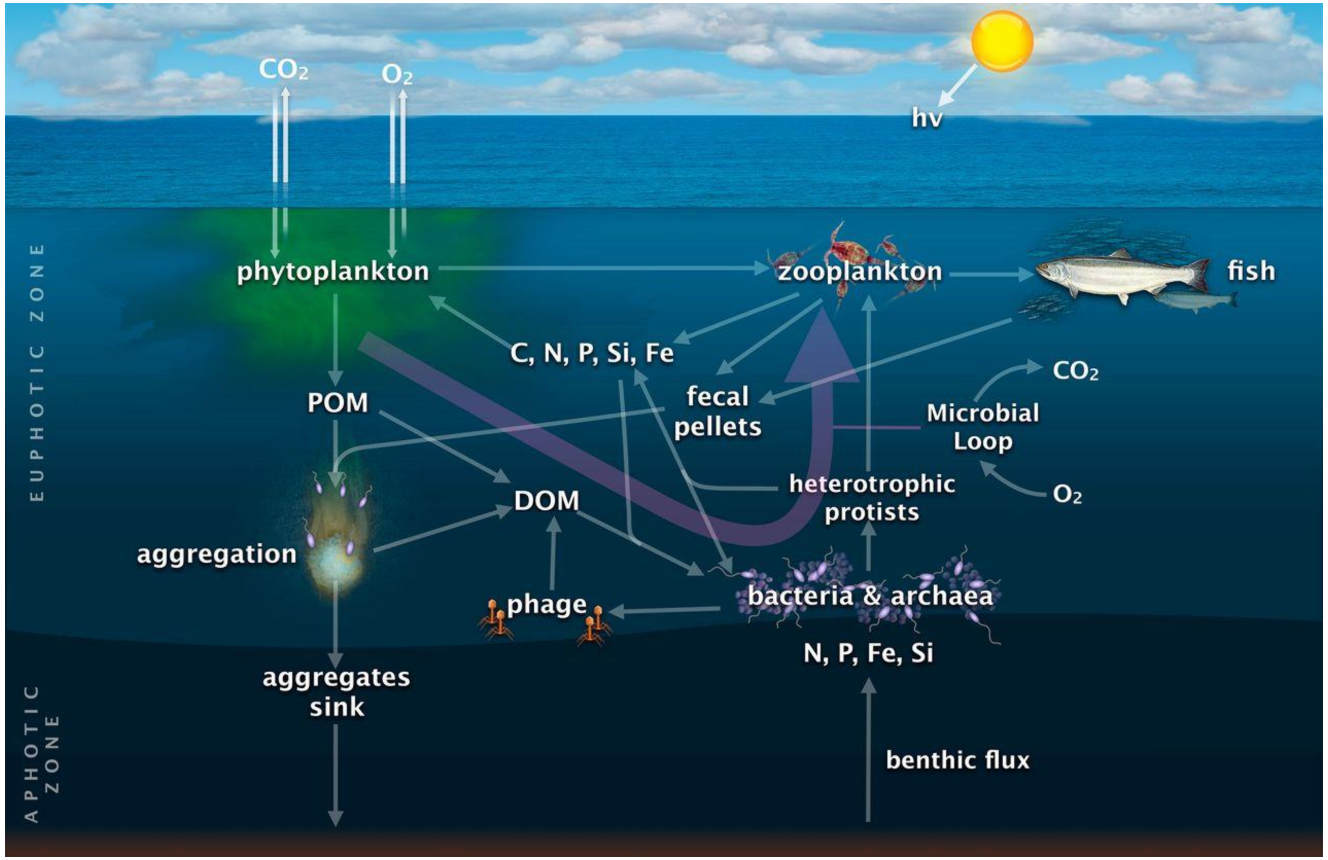
Jaeho Choi

Ph. D. student
Seoul National University
Korea Polar Research Institute

Marine microbial community in ocean environment



Abreu *et al.* (2022)

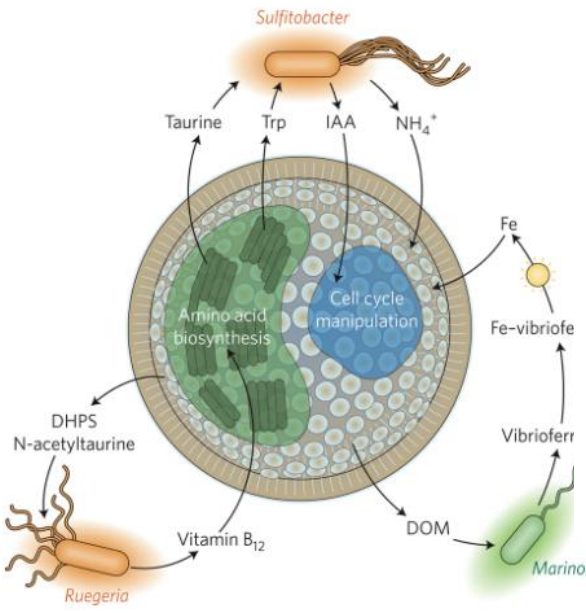


Worden *et al.* (2015)

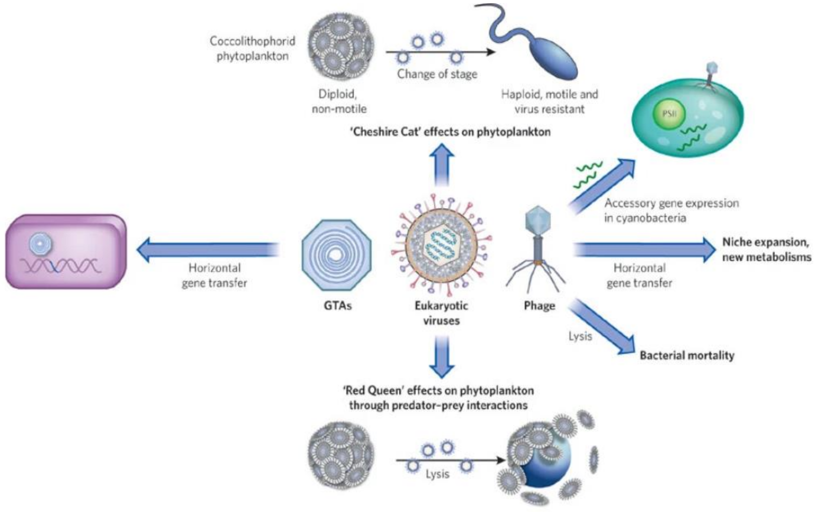
- Marine microbial community constitute 70% of the living biomass in the global ocean and they play pivotal roles in ocean ecosystem food webs and global biogeochemical cycles.

Marine microbial community interactions

Microbial interaction

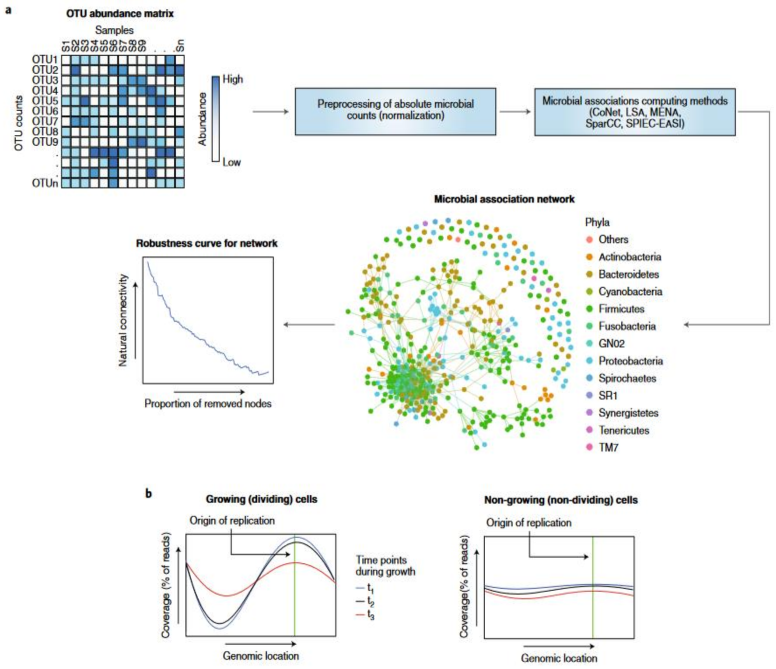


Seymour *et al.* (2017)



Rohwer *et al.* (2009)

High throughput sequencing

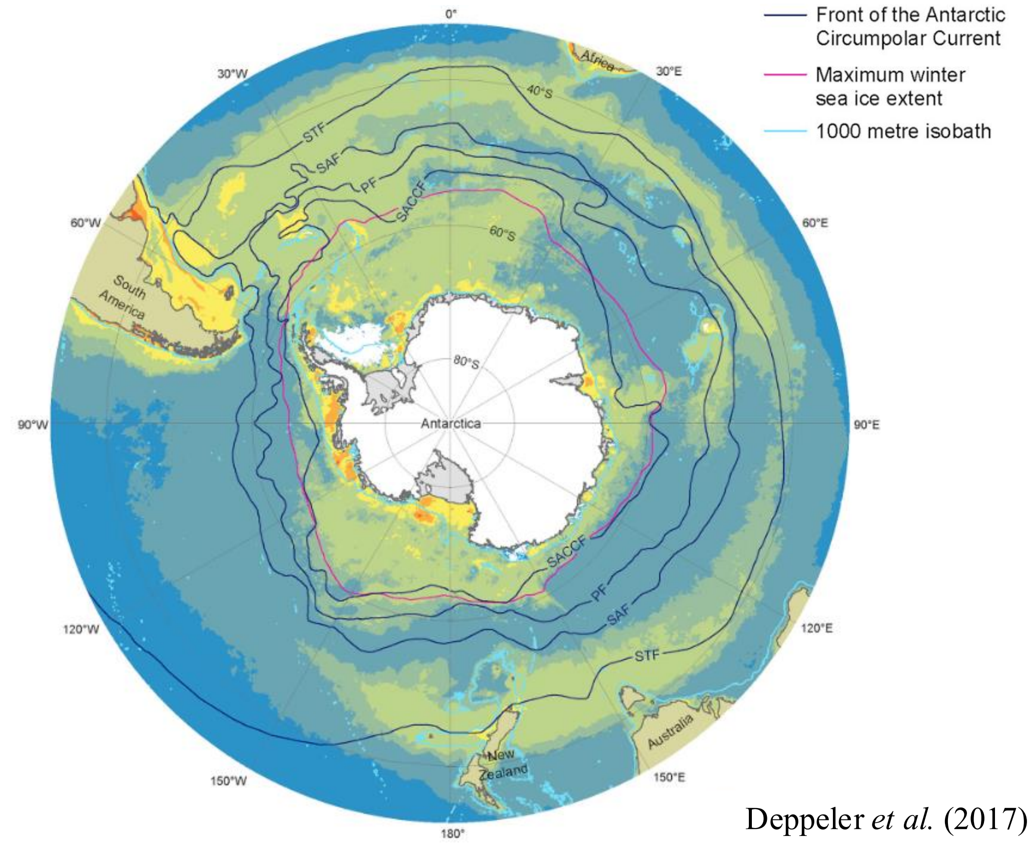


Kumar *et al.* (2019)

- Structuring marine microbial community composition are selection by biotic interaction.
- eDNA sequencing able to address the large complexity of microbial interactions.

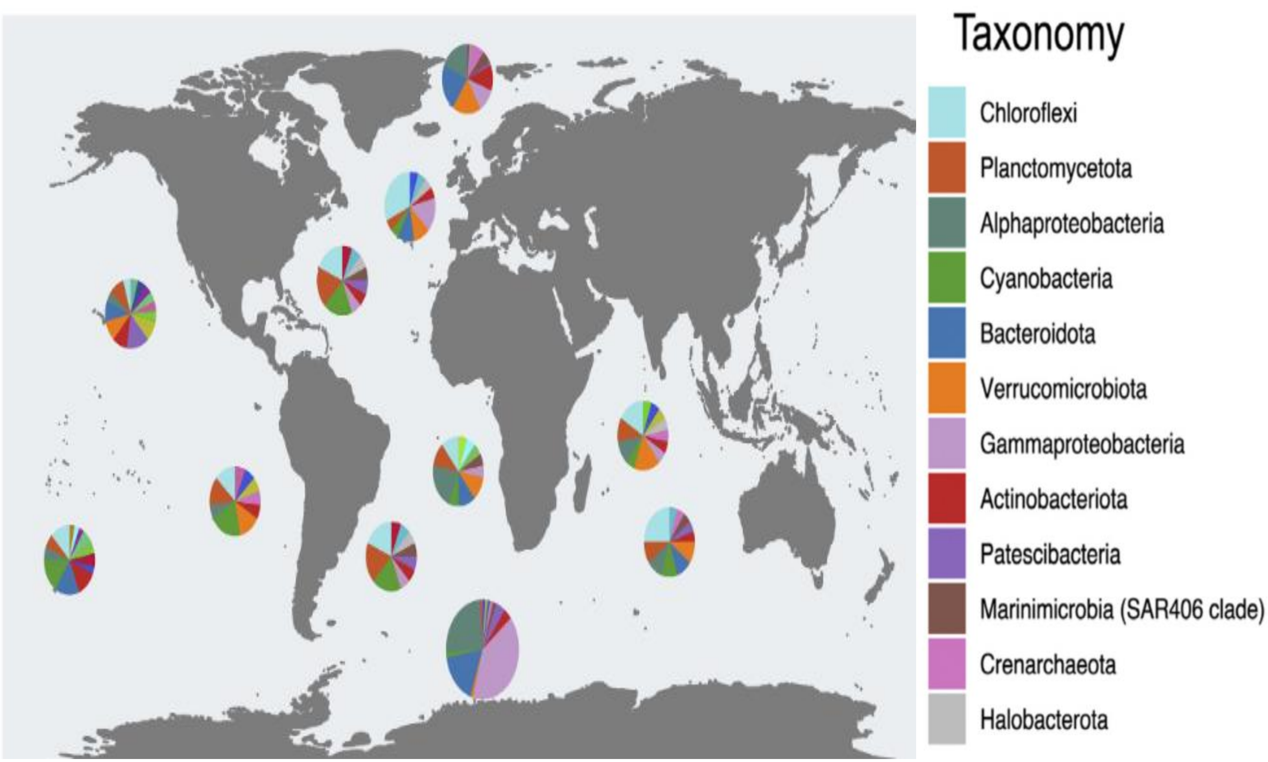
Southern Ocean

Southern Ocean environment



Deppeler *et al.* (2017)

Unique microbial community structure

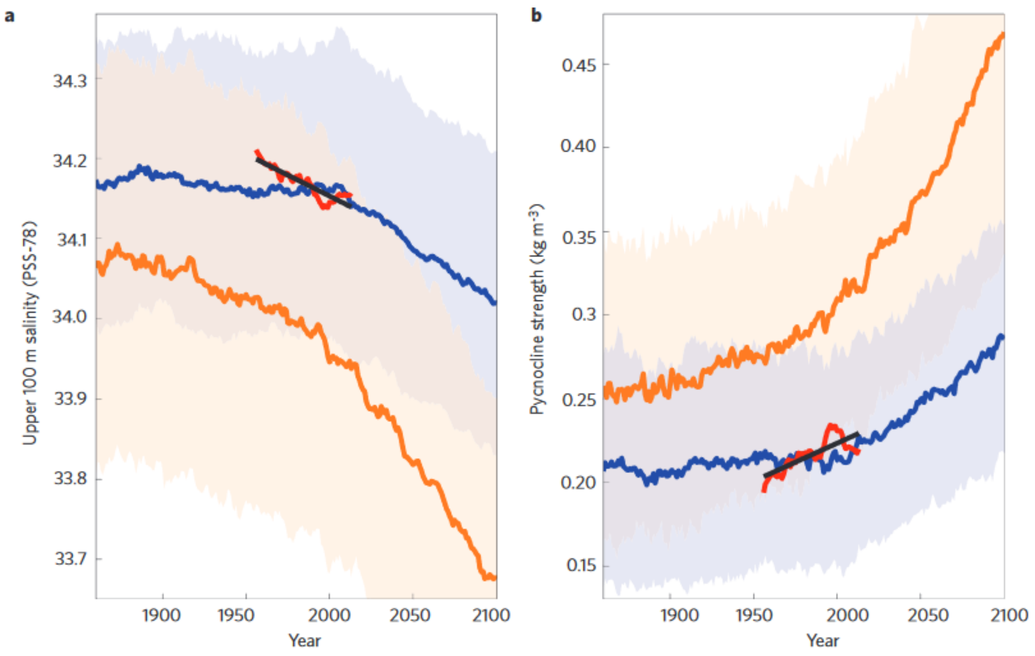


Castillo *et al.* (2022)

- The Southern Ocean accounts for approximately 25% of the oceanic uptake of atmospheric CO_2 despite only representing 20% of the total ocean surface area (Castillo *et al.* 2022).

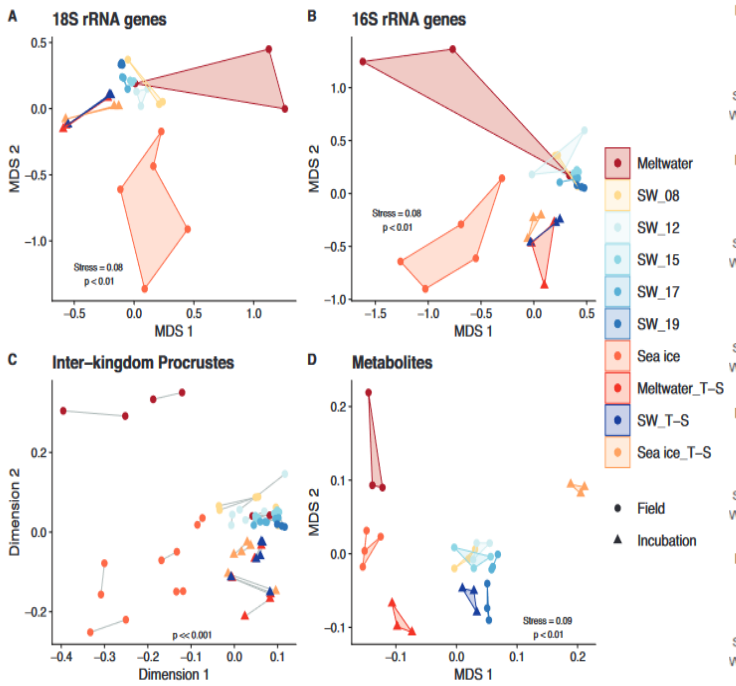
Southern Ocean freshening

Freshening in Southern Ocean

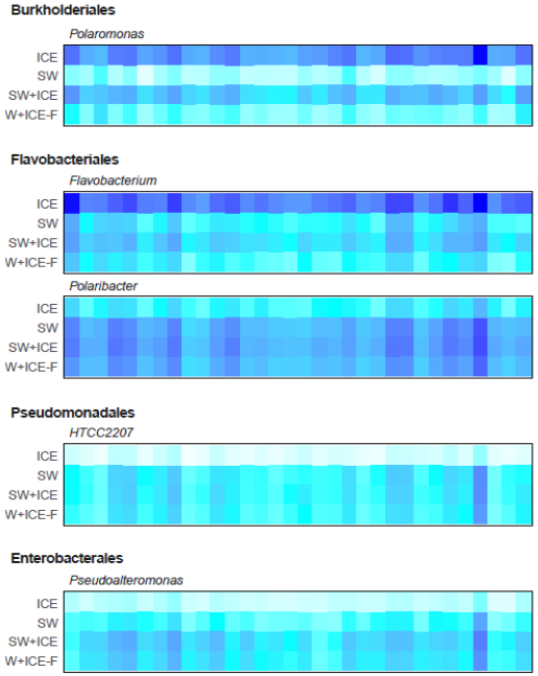


Lavergne *et al.* (2014)

Freshening microcosm experiment



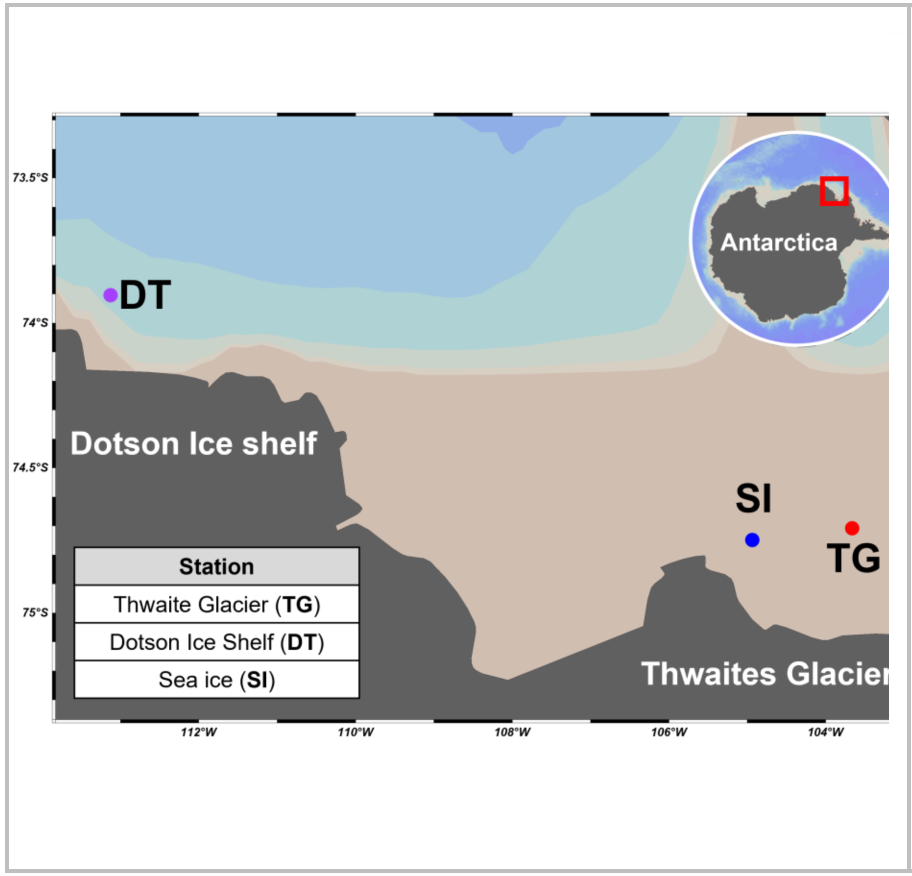
Dawson *et al.* (2023)



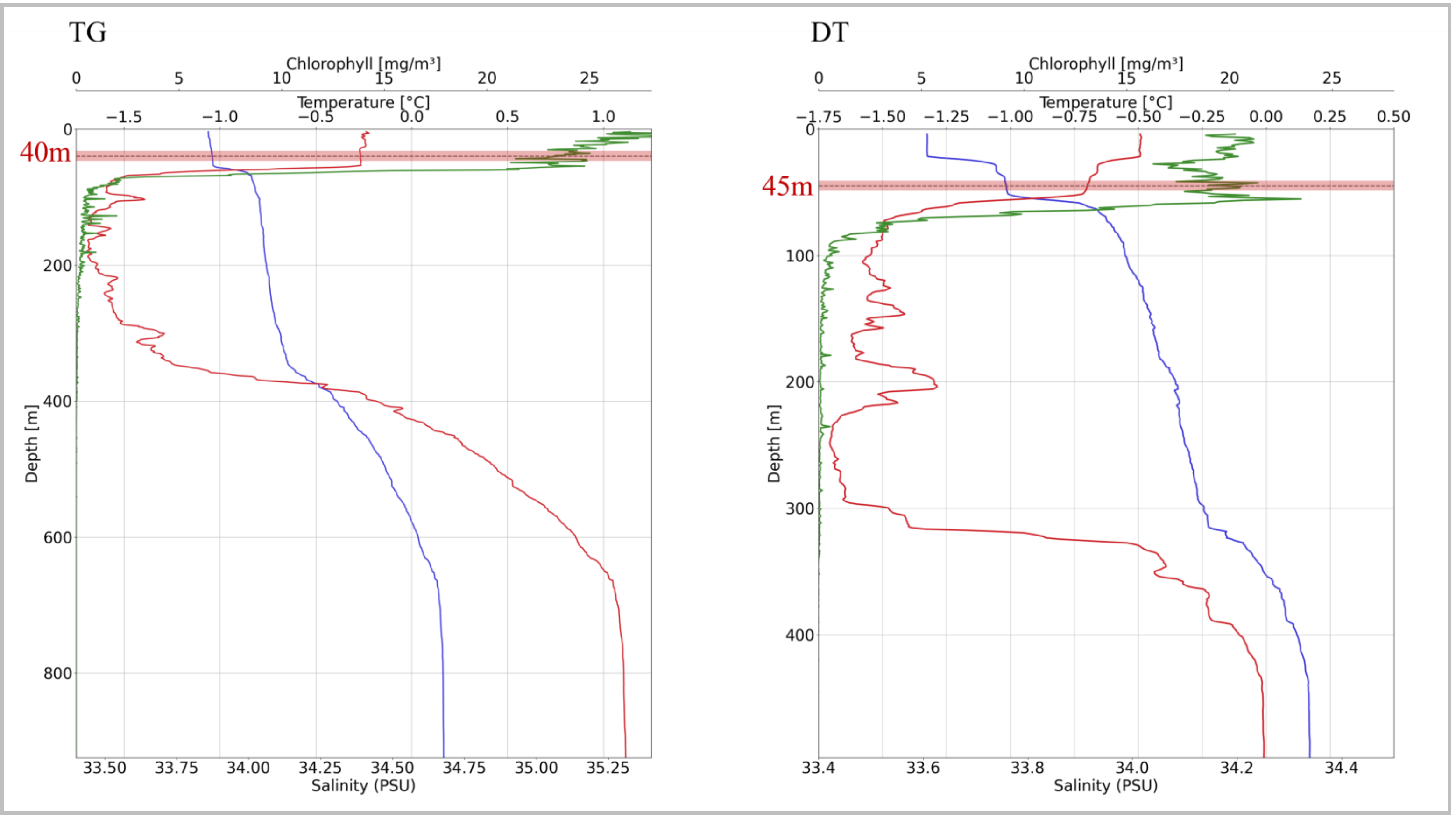
Alcamán-Arias *et al.* (2021)

- Climate change-driven surface freshening in the Southern Ocean is expected to intensify salinity stratification, impacting microbial community structure, interactions, and functions.

Materials and methods – sampling

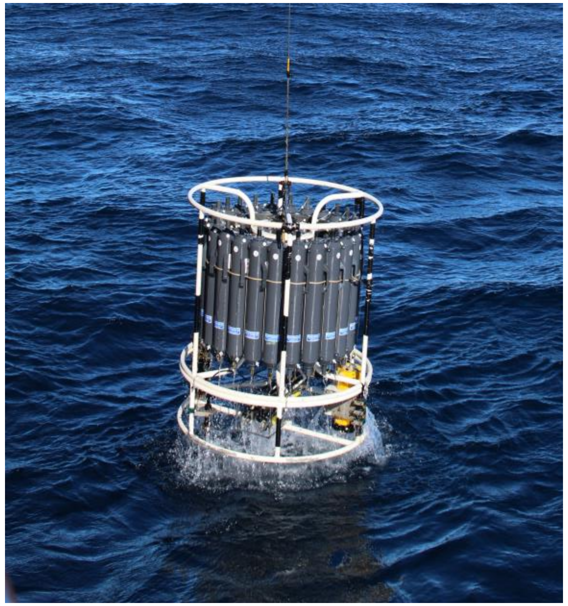


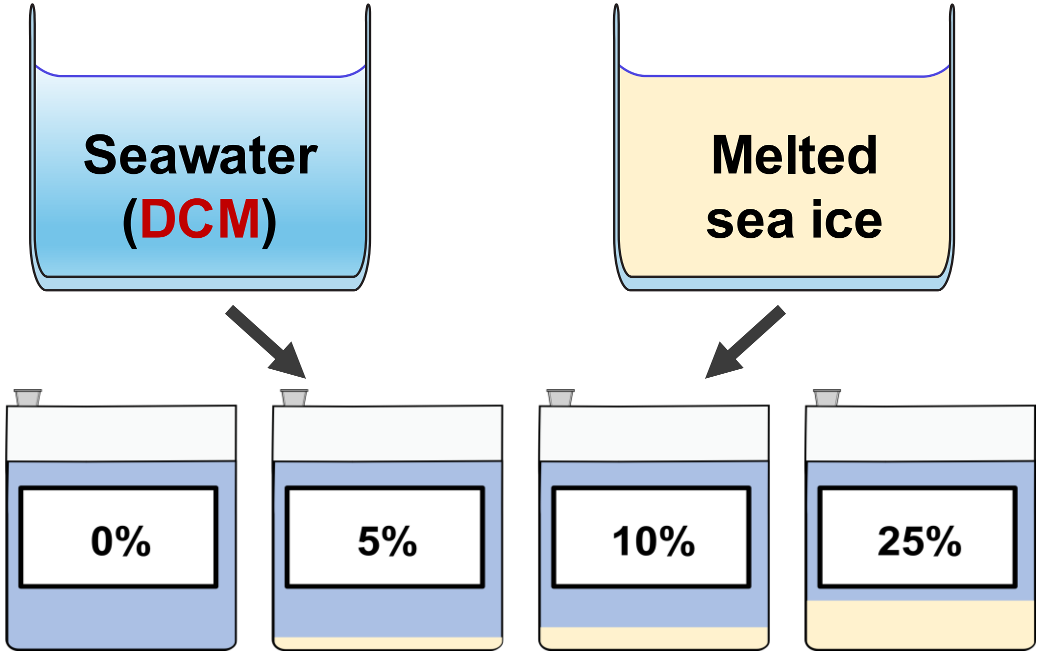
Station
Thwaite Glacier (**TG**)
Dotson Ice Shelf (**DT**)
Sea ice (**SI**)



- CTD with Niskin bottle were used for seawater sample during January 7th – 31st, 2024.
- Deep chlorophyll maximum (DCM) layer was sampled for microcosm experiment.

Materials and methods – experimental procedure





Sampled depth
TG DCM: 40 m
DT DCM: 45 m

Incubation temperature (°C)
TG samples : -1
DT samples : 1

Subsampling
Day 2 (T2)
Day 7 (T7)

Salinity (PSU)
TG DCM: 33.8
DT DCM: 34.0
Sea ice : 3.3

- Niskin bottle were used for seawater sample at DCM layer during 2023-2024 Antarctic expedition.
- Dilution microcosm experiment were conducted in *in situ* temperature with light (40 μmol m^{-2} s^{-1}).

Materials and methods – experimental procedure

Analysis

20 µm filtration

- **Microphytoplankton** (>20 µm)
- **Particle-attached (PA)** prokaryotes

3 µm filtration

- **Nanophytoplankton** (3 − 20 µm)
- **Particle-attached (PA)** prokaryotes

0.2 µm filtration

- **Picophytoplankton** (0.2 − 3 µm)
- **Free-living (FL)** prokaryotes

Bacterial abundance

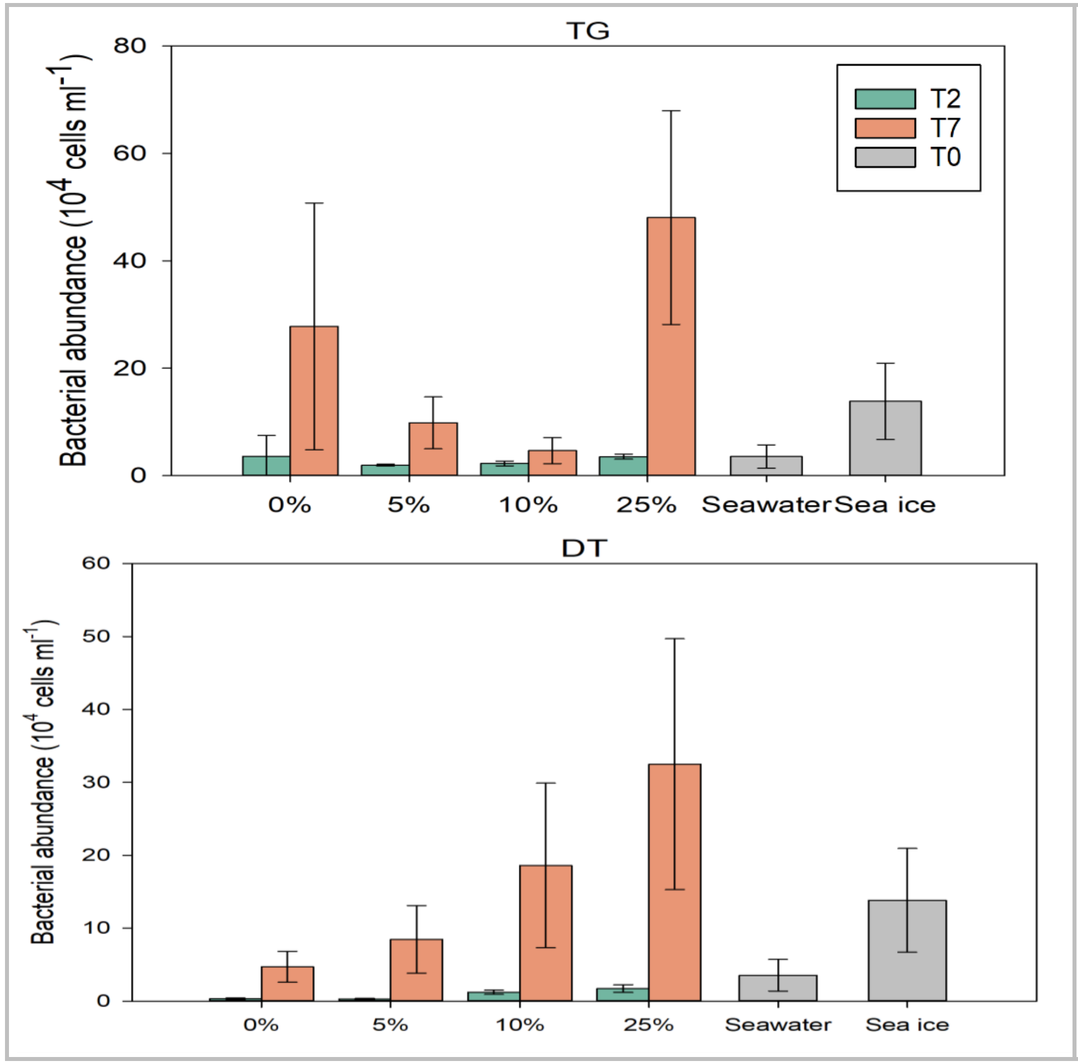
Metabolic activity

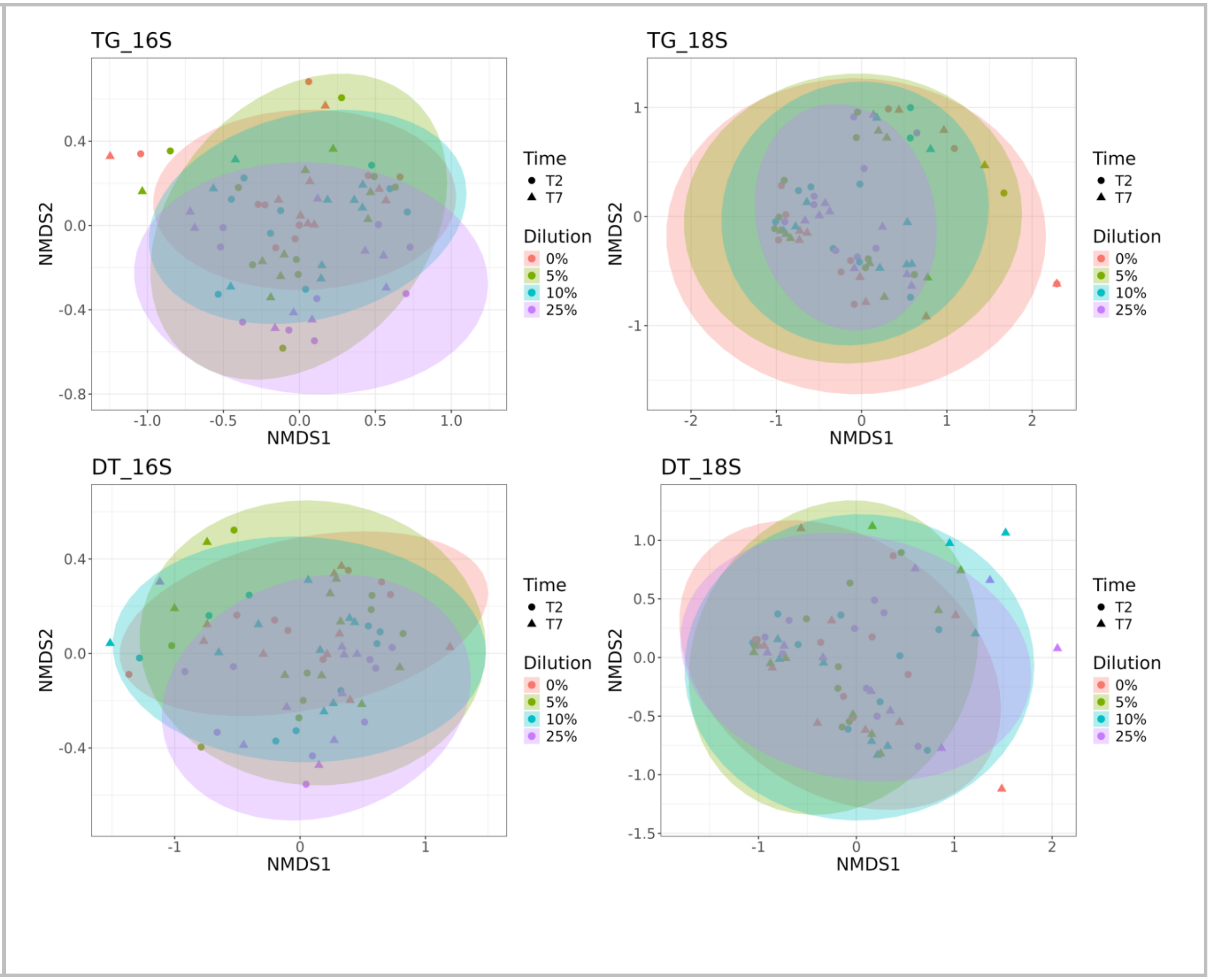
Filtration	**0.5 L** of each subsample (triplicate)
DNA extraction & PCR	**16S/18S** rRNA gene (**515Y/926R** primer set) Parada *et al.* (2019)
Sequencing (NGS)	Illumina MiSeq platform PE300
Sequence processing	FastQC, Trimmomatic, Cutadapt, Qiime2, R
Bacterial abundance	Flow cytometry (SYBR green)
Community activity	RT-qPCR, qPCR (16S, 18S rRNA/rDNA ratio)

Data analysis

- Community **diversity**
- Bacterial **abundance**
- **Taxonomic** analysis
- **Co-occurrence** network analysis (FlashWeave)
- rDNA, rRNA ratio analysis

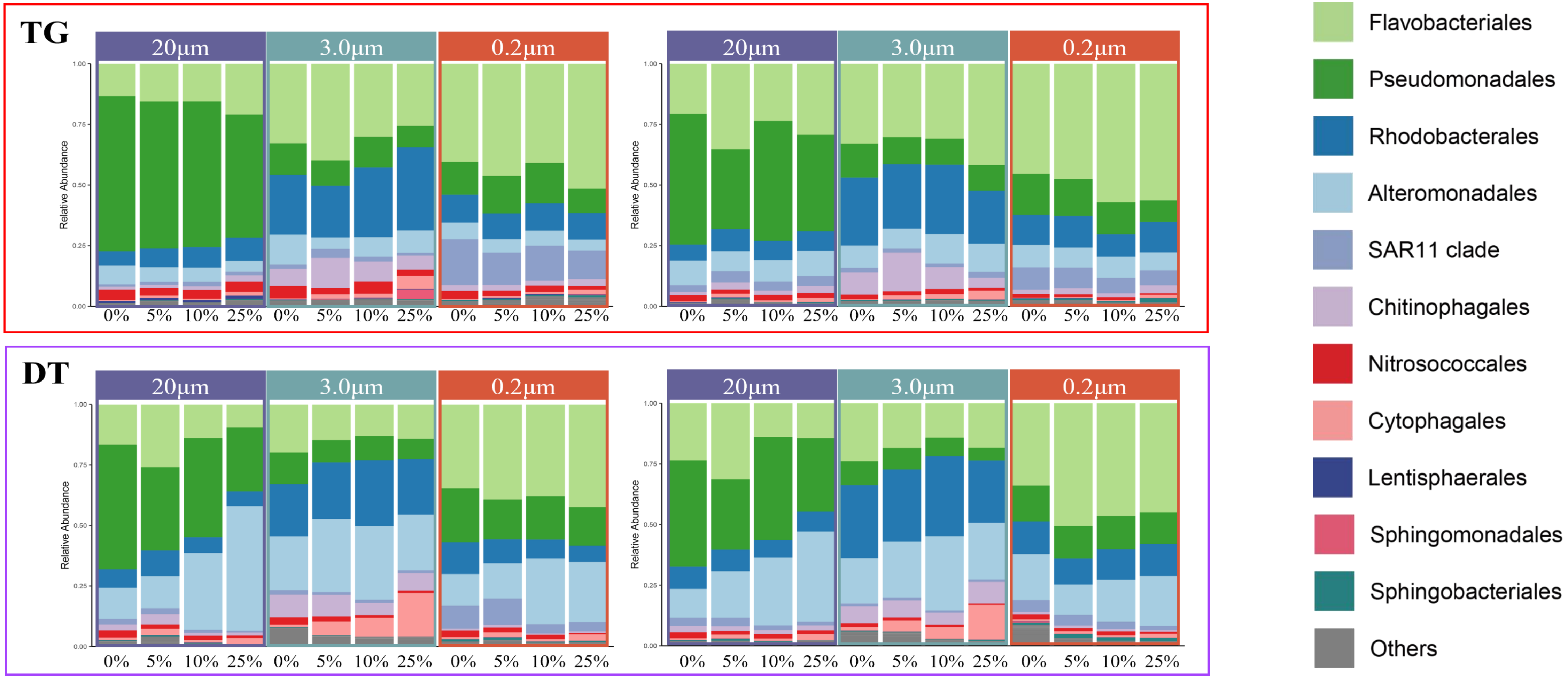
Diversity of microbial community





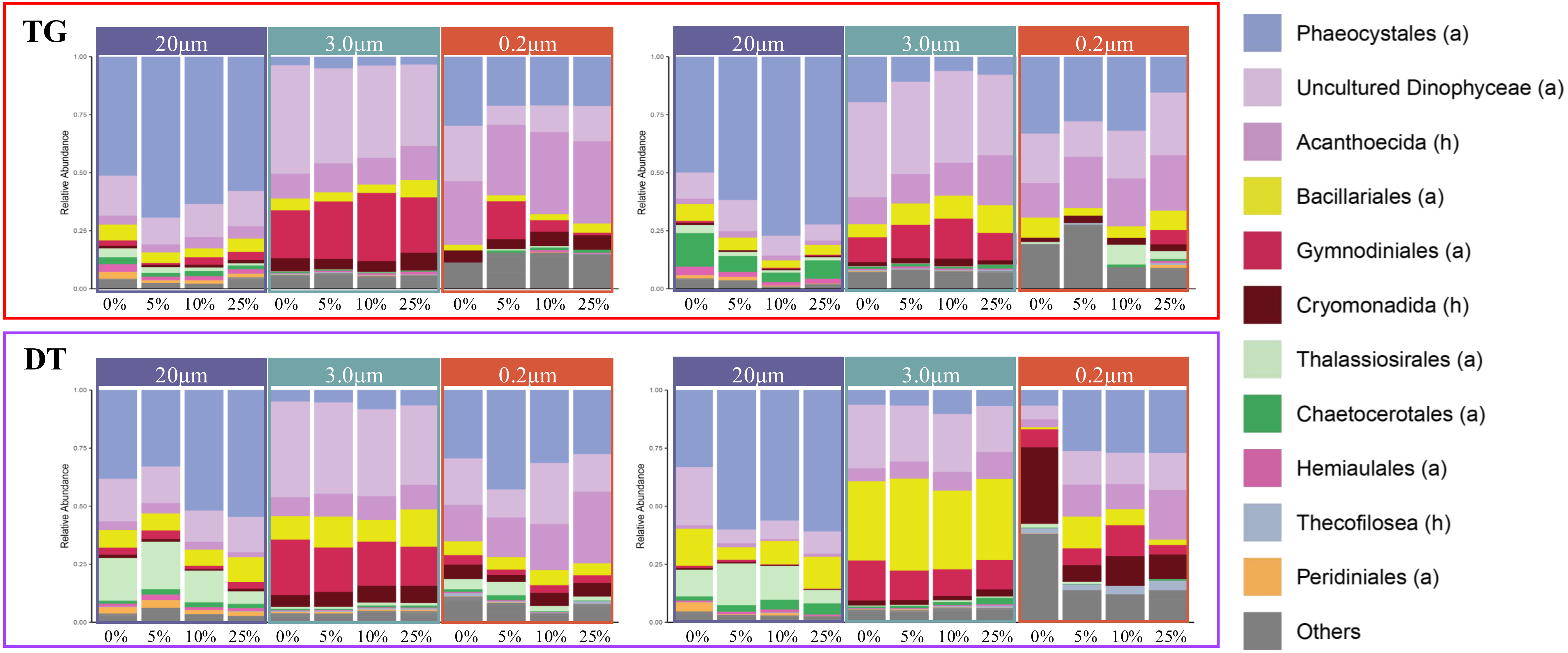
- Both prokaryotic, eukaryotic community **is a stronger influence** by the **dilution level** on the overall composition than the time interval measured.

Community after incubation



- Flavobacteriales significantly increased as the dilution increased for TG.
- In DT region, Alteromonadales and Cytophagales increased as the dilution increases.

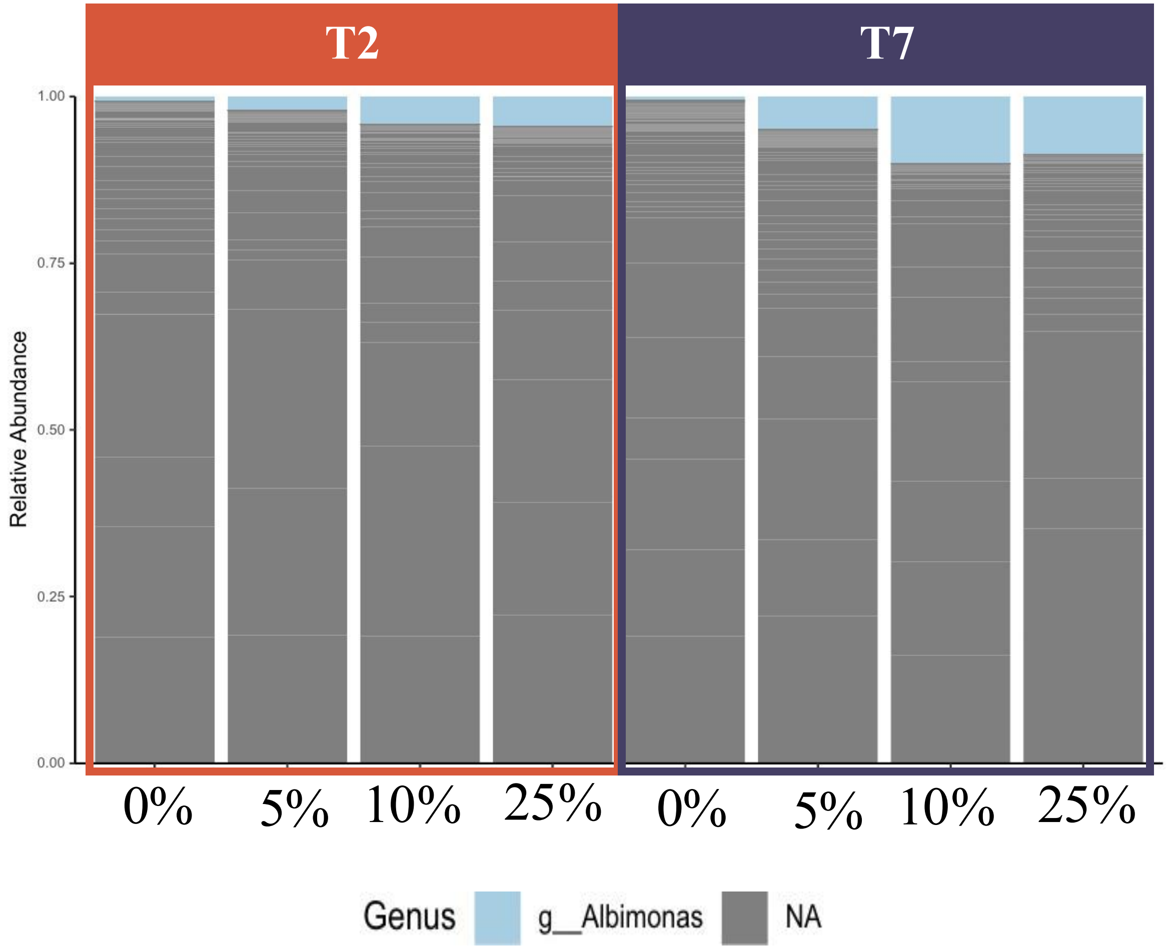
Community after incubation



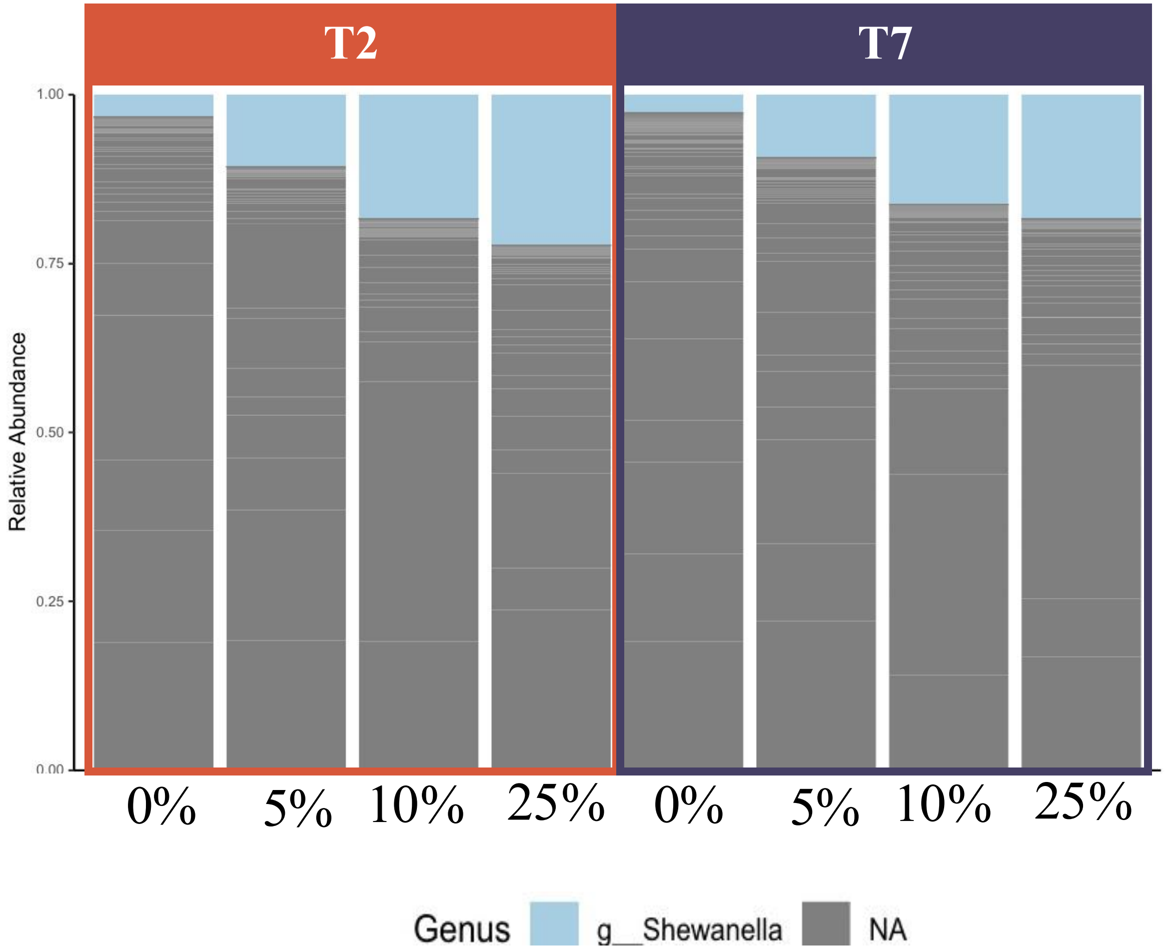
- Phaeocystales, Bacillariales, Gymnodiniales increase as the dilution increased in TG.
- Phaeocystales increased while Thalassiosirales decreased with higher dilution in DT.

Community after incubation

TG

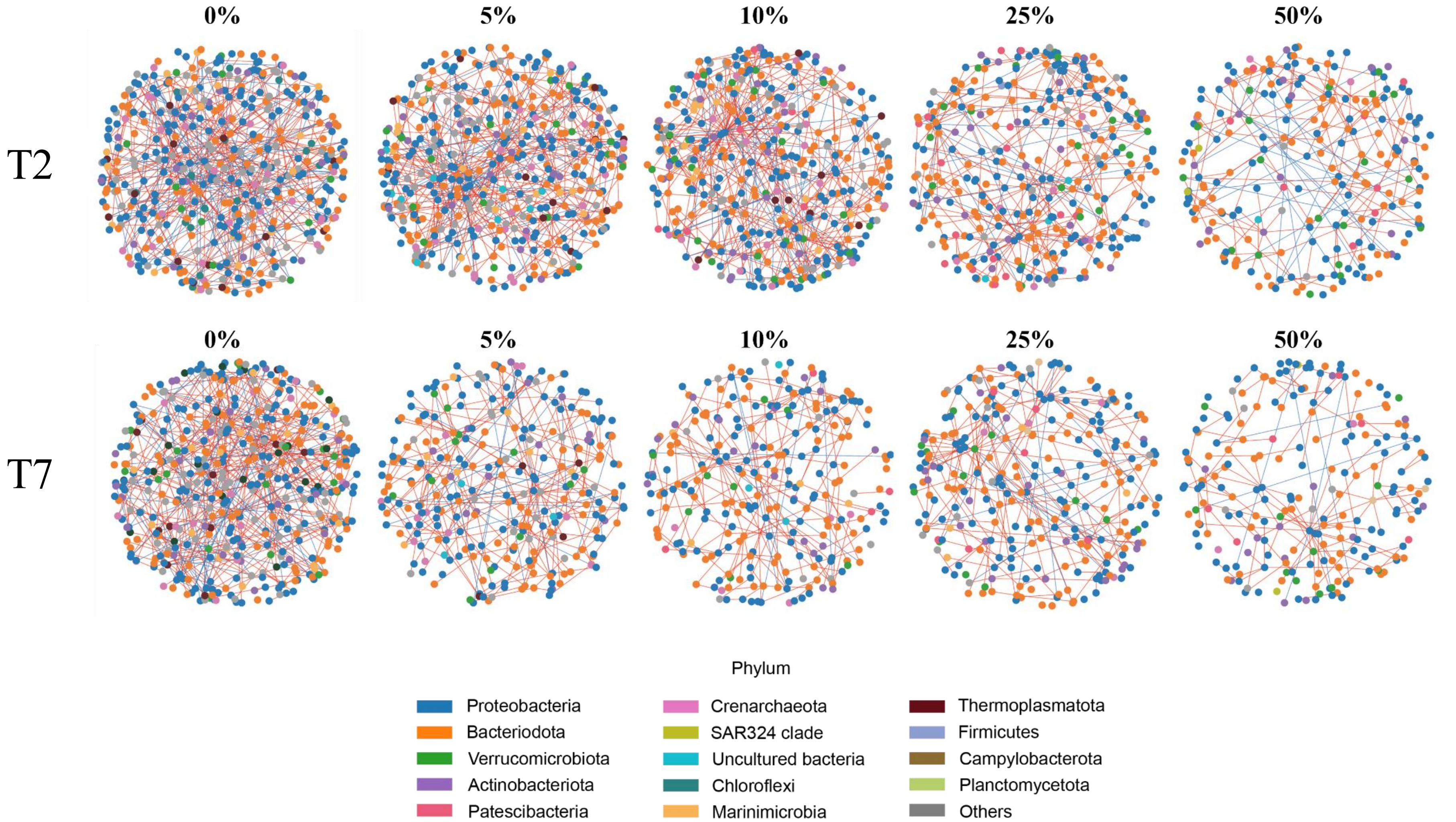


DT



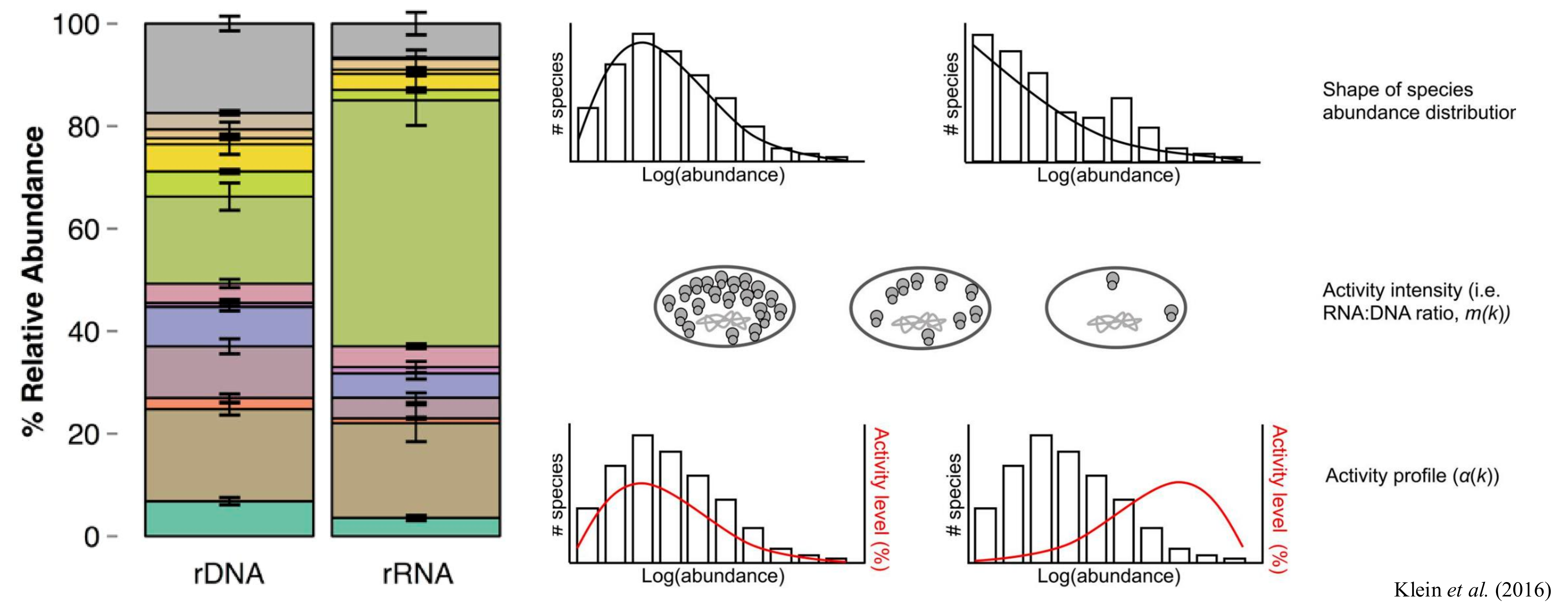
- The abundance of *Albimonas* sp. and *Shewanella* sp. exhibited an increased with the freshening.
- May serve as biological sentinels for monitoring the freshening in Southern Ocean.

Co-occurrence network



- Co-occurrence network analysis showed that increased dilution weakened prokaryotic community interactions by reducing connection at higher meltwater concentrations.

Metabolic activity of microbial community



Klein *et al.* (2016)

- rRNA/rDNA ratio indicates greater metabolic activity, is an effective method for assessing microbial responses to environmental changes and will be used to evaluate phytoplankton and prokaryote activity

Conclusion

•eDNA sequencing of 16S, and 18S rDNA sequencing confirmed that microbial communities are sensitive to meltwater intrusion simulation at Southern Ocean.

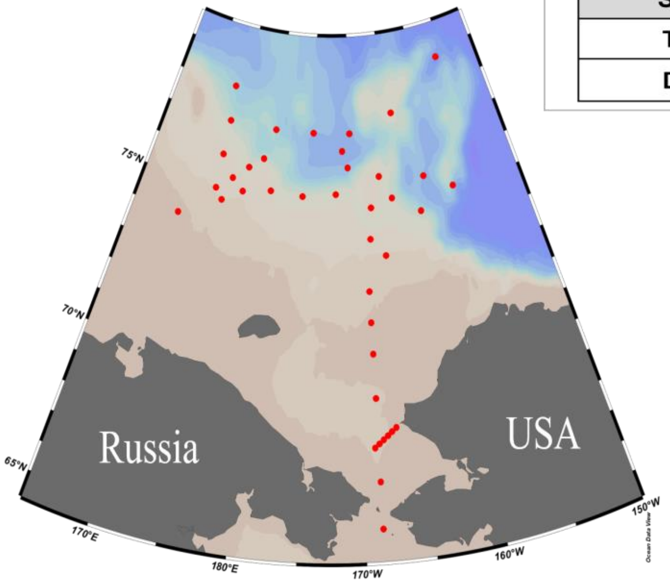
•Observed distinct, site-specific changes in community composition, demonstrating significant spatial variability in how marine ecosystems will respond to freshening.

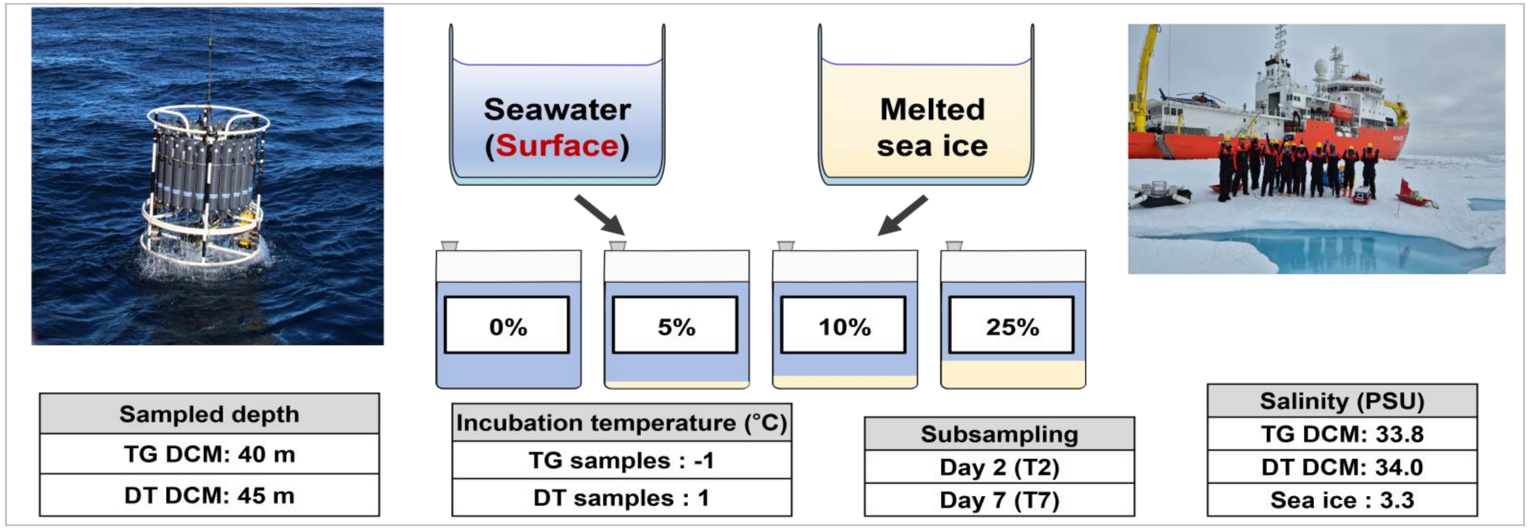
•Some genera may potentially serve as biological sentinels for monitoring the freshening of the Southern Ocean.

•Increased freshening significantly destabilized microbial networks, directly impacting community interactions and potentially compromising critical ecosystem functions in the Southern Ocean.

Future study

K-AWARE
KOREA - ARCTIC OCEAN WARMING & RESPONSE OF ECOSYSTEM





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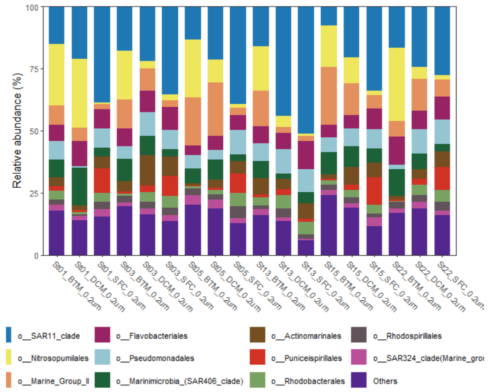
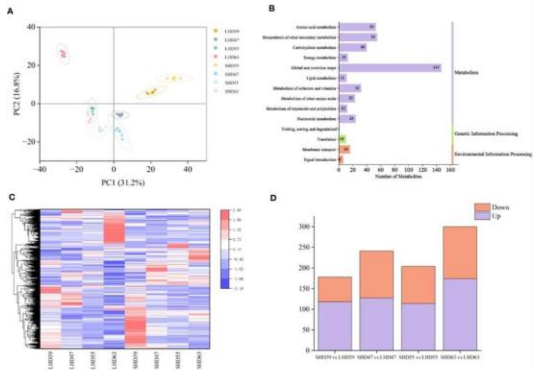
Metagenomics



Metabolomics



- Microbial interactions on both metagenomics and metabolomics to reveal the community and the metabolite changes in the Bering strait.

Thank you