Protists are ecologically less sensitive to salinity than bacteria

Krzysztof T Jurdzinski[1], Meike AC Latz[1,2], Anders Torstensson[3], Sonia Brugel[4,5], Mikael Hedblom[3], Yue O O Hu[1], Markus Lindh[3], Jenny Lycken[3], Agneta Andersson[4,5], Bengt Karlson[3], **Anders F Andersson**[1]

1. Department of Gene Technology, KTH Royal Institute of Technology, Science for Life Laboratory, Stockholm, Sweden 2. University of Copenhagen, Department of Plant and Environmental Sciences, Frederiksberg C, Denmark
3. Swedish Meteorological and Hydrological Institute, Oceanographic Services, Västra Frölunda, Sweden
4. Umeå University, Department of Ecology and Environmental Sciences, Umeå, Sweden 5. Umeå Marine Sciences Centre, Umeå University, SE-905 71, Hörnefors, Sweden

Background:

- Well-studied **separation of freshwater** and **marine bacterial communities**.
- **Distinct brackish bacterial species** (Hugerth et al. 2015) with unique adaptations (Jurdzinski, Mehrshad et al., 2023).
- Bacterial and protist **community composition shift along the brackish salinity gradient** (Herlemann et al. 2011, Hu et al. 2015).

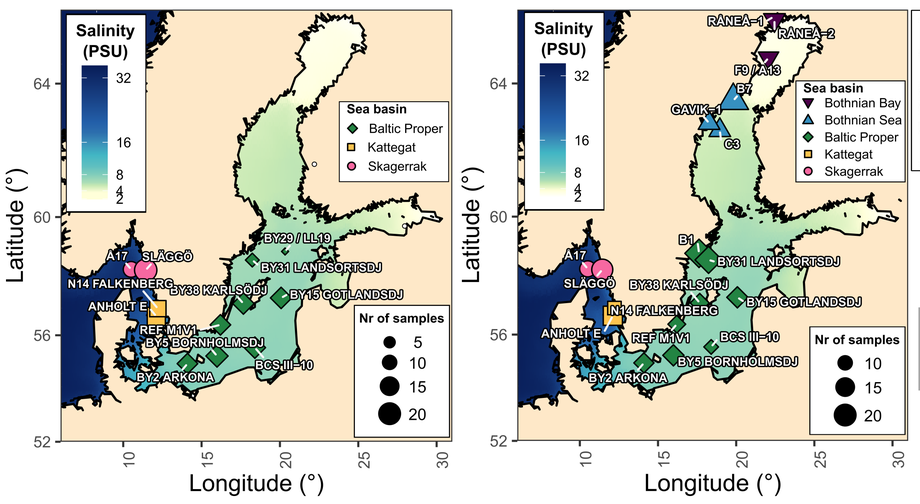
Conclusions:

- **Salinity** has a **dominant** impact on **bacterial but not protist** brackish **community composition.**
- **Bacterial alpha diversity increases with inorganic nitrogen.**
- **Compartmentalization** likely decreases the impacts of altered salinity and pH on eukaryotic cells.

Material and methods

16S and 18S metabarcoding combined with Swedish marine monitoring program

2016-2017 (new) | 2019-2020 available at: scientific data



Seq. data

Sequencing data processing

- **Denoise, infer amplicon sequence variants (ASVs)**, and **taxonomically annotate** using:

Implemented using

Reference databases:

18S: PR2 | 16S: GTDB

Remove chloroplasts and mitochondria

- Additional **chimera removal** UCHIME
- **Cluster ASVs by sequence and distribution similarity** into **dbOTUs**. dbOTU3

dbOTUs should represent **species or higher taxonomic levels** (no intraspecies variation; usually genera)

Full study: **Distinct bacterial and protist plankton diversity dynamics uncovered through DNA-based monitoring of the Baltic Sea**

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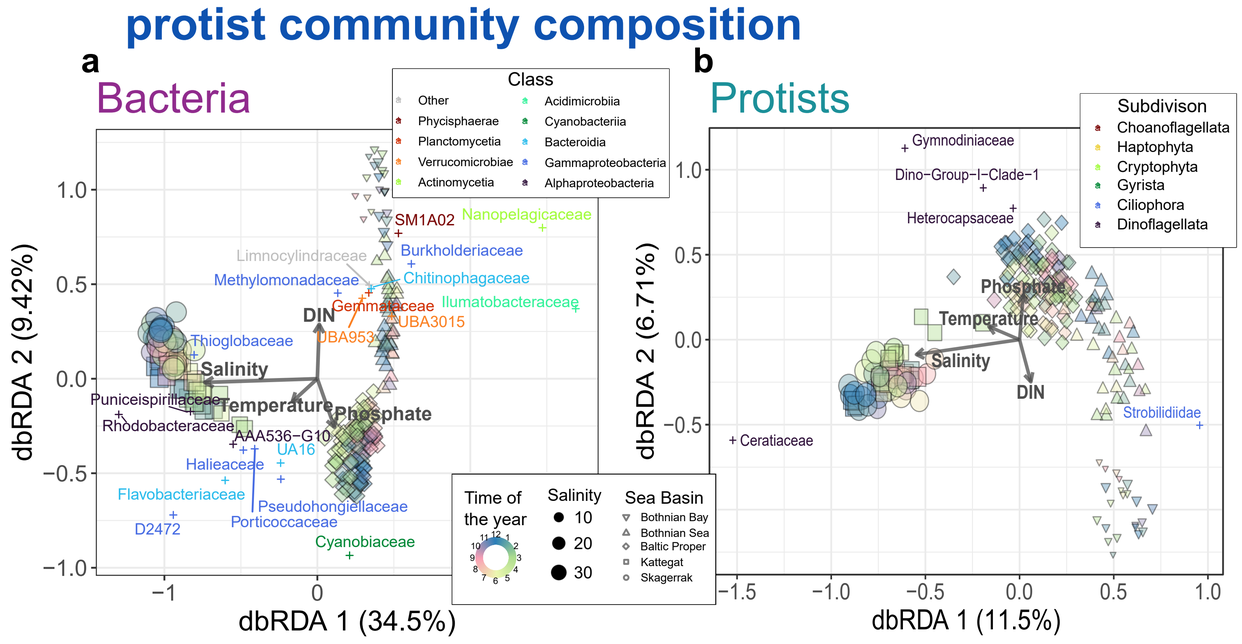
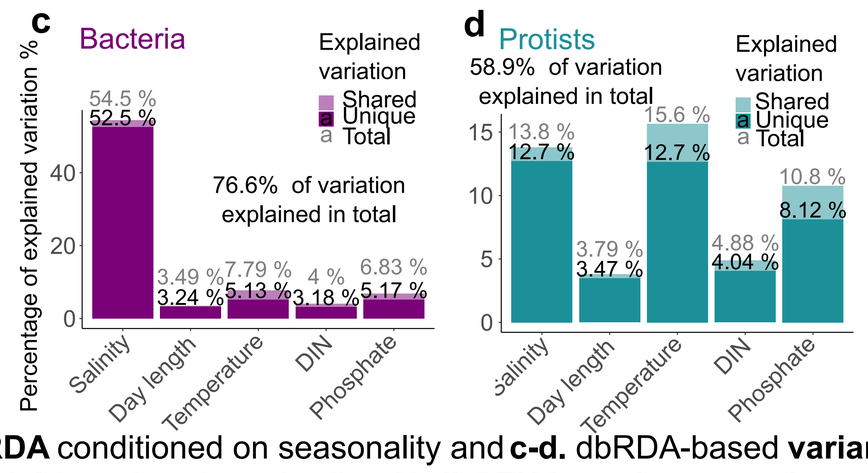
Results

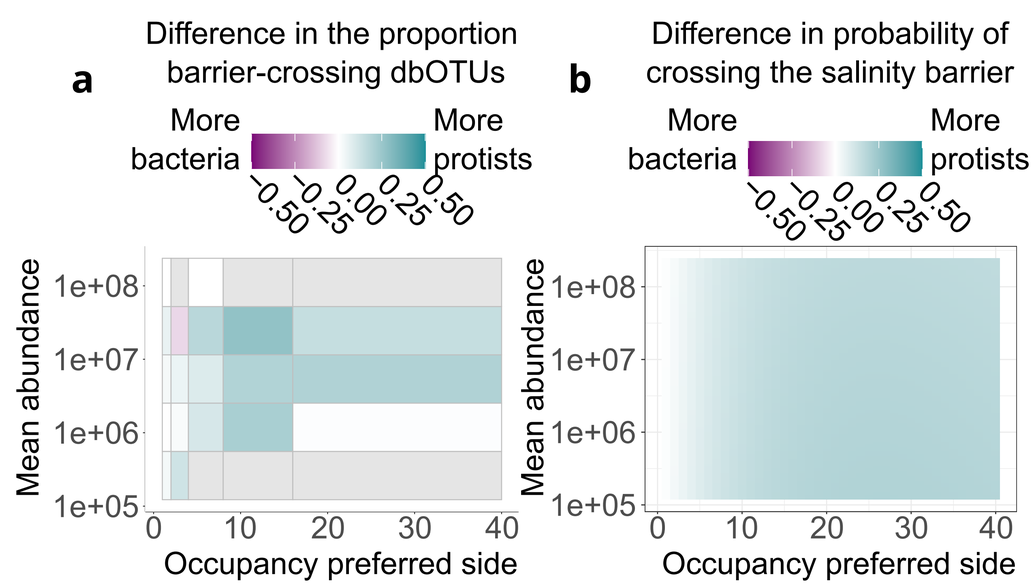
1. Higher impact of salinity on bacterial than protist community composition





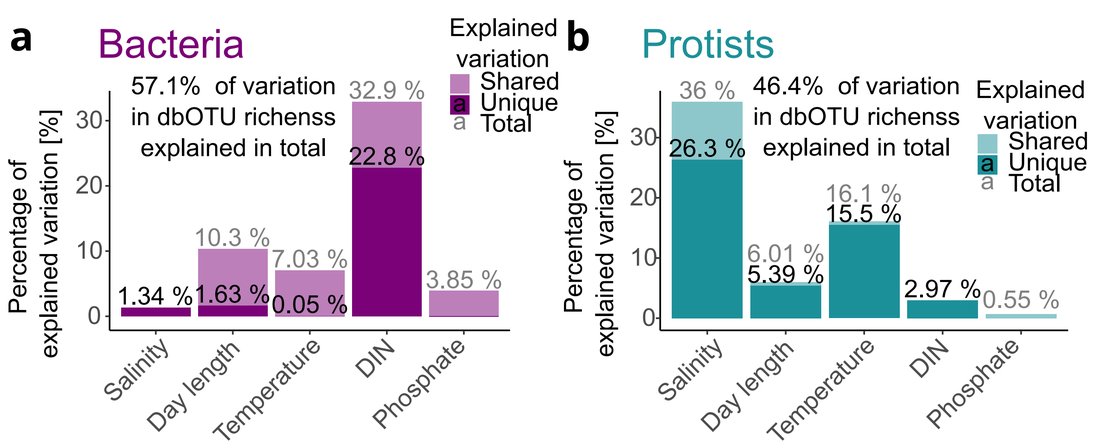
a-b. dbRDA conditioned on seasonality and **c-d.** dbRDA-based **variance partitioning** of **bacterial (a., c.)** and **protist (b., d.) dbOTU-based community composition**

2. Protists inhabit both low (<9 PSU) and high (>15 PSU) brackish salinities more often than bacteria



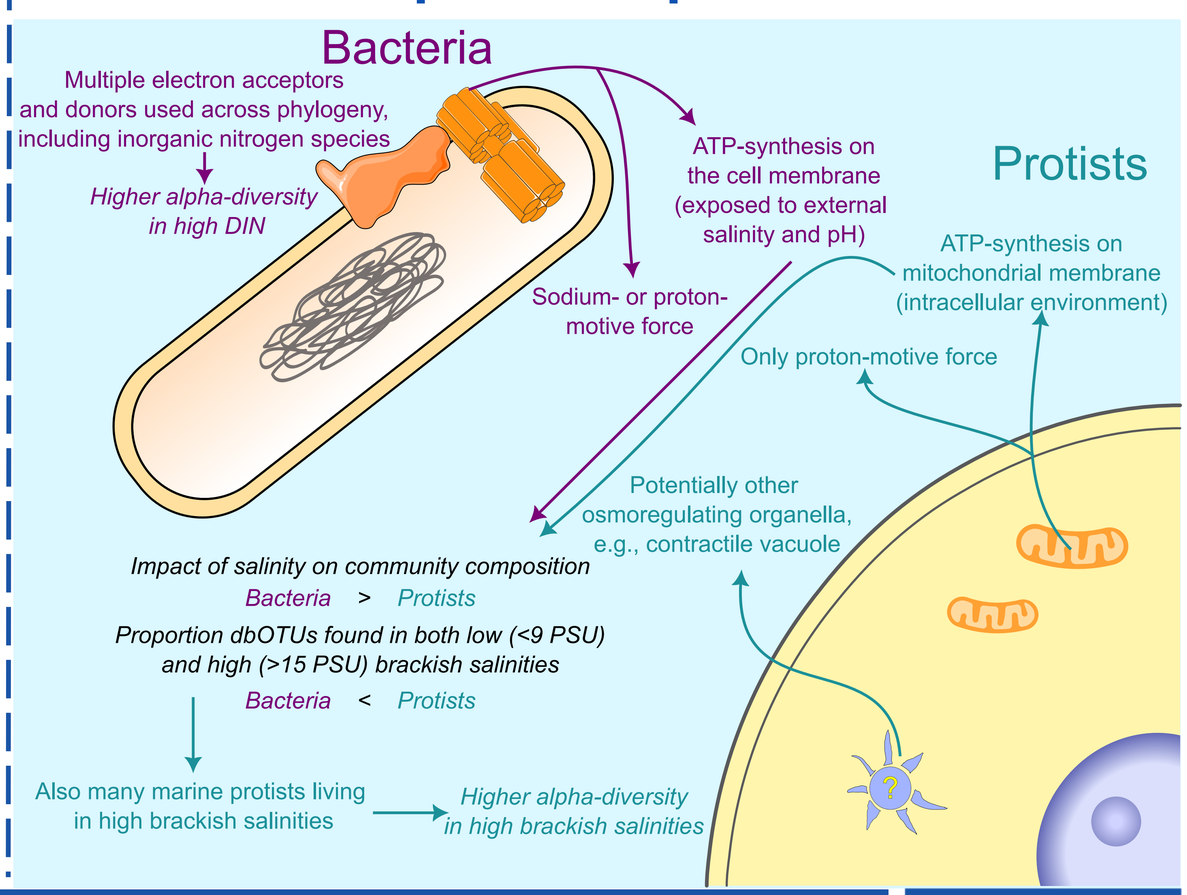
Difference in **proportion of barrier-crossing dbOTUs** (**a.**) and **probability a dbOTU is found in both low and high brackish salinities**(**b.**; based on **Bayesian modeling**). Both are given as a function of mean abundance (when present) and maximum abundance at the preferred side of the salinity barrier.

3. Bacterial alpha diversity correlates with inorganic nitrogen, protists are more diverse in near-marine salinities



Variance partitioning of changes in **bacterial (a.)** and **protist (b.) dbOTU richness.**

Proposed explanation



Krzysztof T. Jurdzinski
PhD student • KTH Royal Institute of Technology • SciLifeLab Stockholm
Email: krzysztof.judzins@scilifelab.se
@ktjurdzinski @K_T_Jurdzinski

Personal website **KTJ microbes** ktjmicrobes.com

Environmental genomics

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