Bacterial ecology and evolution across salinity barriers and gradients

Krzysztof T Jurdzinski¹, Maliheh Mehrshad², Luis Fernando Delgado¹, Ziling Deng¹, Meike AC Latz^{1,6}, Anders Torstensson³, Sonia Brugel^{4,5}, Mikael Hedblom³, Markus Lindh ³, Jenny Lycken³, Agneta Andersson^{4,5}, Bengt Karlson³, Stefan Bertilsson², Anders F Andersson¹

1. Department of Gene Technology, KTH Royal Institute of Technology, Science for Life Laboratory, Stockholm, Sweden 2. Depart ment of Aquatic Sciences and Assessment, Swedish University of Agricultural Sciences, Uppsala, Sweden 3. Swedish Meteorological and Hydrological Institute, Oceanographic Services, Västra Frölunda, Sweden 5. Umeå, Sweden 5. Umeå, Sweden 5. Umeå Marine Sciences Centre, Umeå University, SE-905 71, Hörnefors, Sweden 5. 6. University of Copenhagen, Department of Plant and Environmental Sciences, Frederiksberg C, Denmark

Background:

- Well-studied separation of freshwater (F) and marine (M) bacterial communities.
- **Distinct brackish** (B) **bacterial lineages** (Hugerth et al. 2015) with unclear relationship to other aquatic bacteria
- **Bacterial** and **protist community composition shifts along the brackish salinity** gradient. (Herlemann et al. 2011, Hu et al. 2015).

Conclusions:

- Bacterial species are separated between the three aquatic biomes. **Cross-biome transitions** are accompanied by **gain/loss of specific** gene functions and followed by proteome optimization.
- **Protists are ecologically less sensitive to salinity than bacteria**, likely \bullet thanks to the benefits of compartmentalization.

Study 1: Large-scale phylogenomics of aquatic bacteria reveal molecular mechanisms for adaptation to salinity

Workflow

Publicly available metagenome-assembled genomes (MAGs)

Phylogeny reconstruction





Transitions as pairs of monobiomic sister groups (MSGs)





2. Evolutionary dynamics

bioRxiv

THE PREPRINT SERVER FOR BIOLOG

Study 2: Distinct bacterial and protist plankton diversity dynamics uncovered through DNA-based monitoring of the Baltic Sea

Seq.

data

Workflow

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



Sequencing data processing **Remove from** cutadapt further analyses • Remove primers; Denoise, infer amplicon **16S 18S** sequence variants (ASVs), and taxonomically Archeae, chloroplasts, Multicellular annotate using: and mitochondria organisms **16S 18S** 16S for chloroplast and **Diversity metrics estimation** mitochondria removal based on rarefaction **PR**² GTDB silva 🕸 beta diversity **6** alpha diversity Bray-Curtis distances dbOTU richness salinity barrier Additional chimera removal. **5.** Multivariate analyses Cluster ASVs by Principal Coordinate Analysis (PCoA) salinity barrier dbOTU 🖂 sequence and distribution distance-based Redundancy Analysis similarity into dbOTUs. (dbRDA), and variance partitioning,

Results

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

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



Varinace partitioning of changes in bacterial dbOTU richness; protist dbOTU richness.

Proposed explanation



Sodium- or proton-

motive force

ligher alpha-diversity

hiah brackish salinities

Impact of salinity on community composition Bacteria > Protists

Proportion dbOTUs found in both low (<9 PSU) and high (>15 PSU) brackish salinities

Bacteria < Protists

Also many marine protists living

in high brackish salinitie

Potentially other

e.g., contractile vacuol

oregulating organella,



intracellular

ap

Only proton-motive force

7. Proportion barrier-crossing dbOTUs and Bayesian modelling

- Bacterial and protist reads rarefied to the same number per sample
- The same number of stations and observations on the two sides of the
- Account for overall mean abundance and occupancy on preferred side of the
- **Bayesian modeling using JAGS** (Just Another Gibbs Sampler)



dbRDA based varianace partitioning of: a. bacterial community composition; b. protist community composition.





