

Salinity structures the microbiome of the green seaweed *Ulva*

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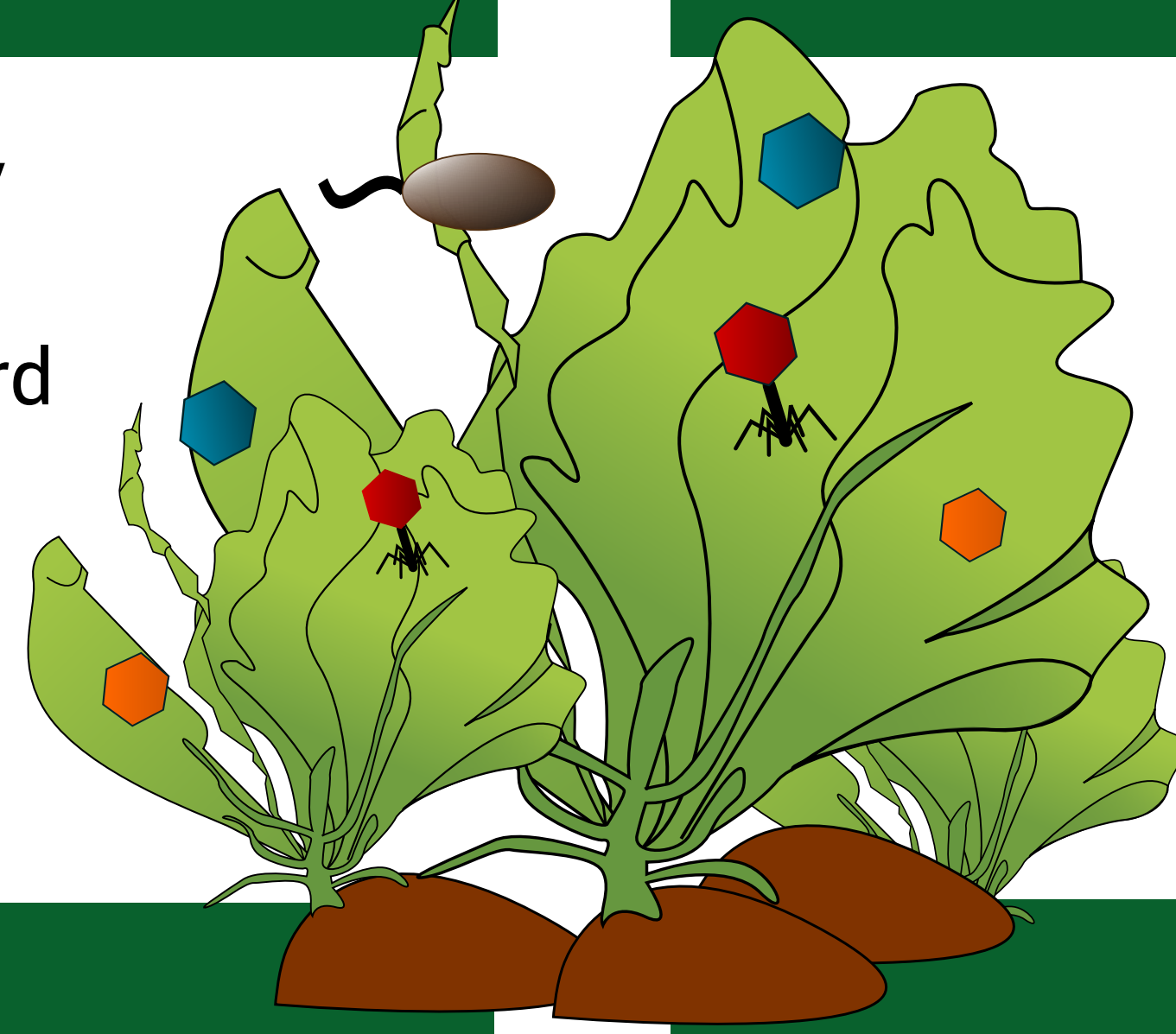
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GREEN SEAWEED *ULVA*

The green seaweed *Ulva* is a model system to study seaweed-bacteria interactions. *Ulva* holobiont dynamics are little understood, especially with regard to environmental drivers. The *Ulva* microbiome was traditionally thought to be largely stochastically defined.



AIM OF THE STUDY

"Characterize the dynamics of *Ulva*-associated bacterial communities across the Atlantic–Baltic Sea salinity gradient"

THE DATASET

- 2000 km of coastline
- 3.5–36 PSU salinity gradient
- 146 sample sites
- 15 *Ulva sensu lato* species
- 481 microbiome samples

METHODS

- 16S rDNA PCR (1600 bp) targeting bacteria
- MinION Mk1B sequencing
- Guppy 5.0.7 basecalling (SUP model)
- 23,955,951 high-quality reads
- Taxonomic identification with Kraken2 + SILVA database

RESULTS

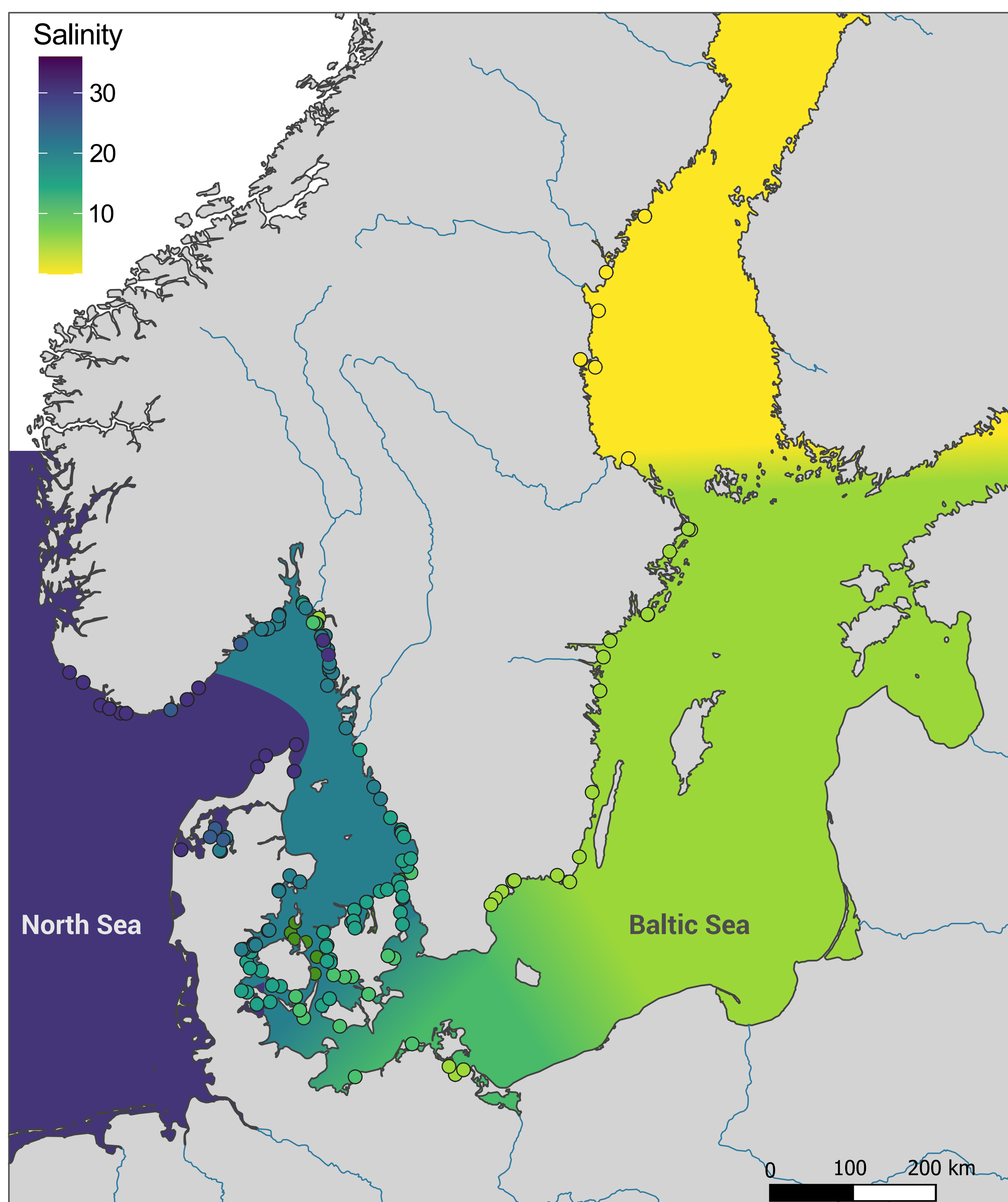
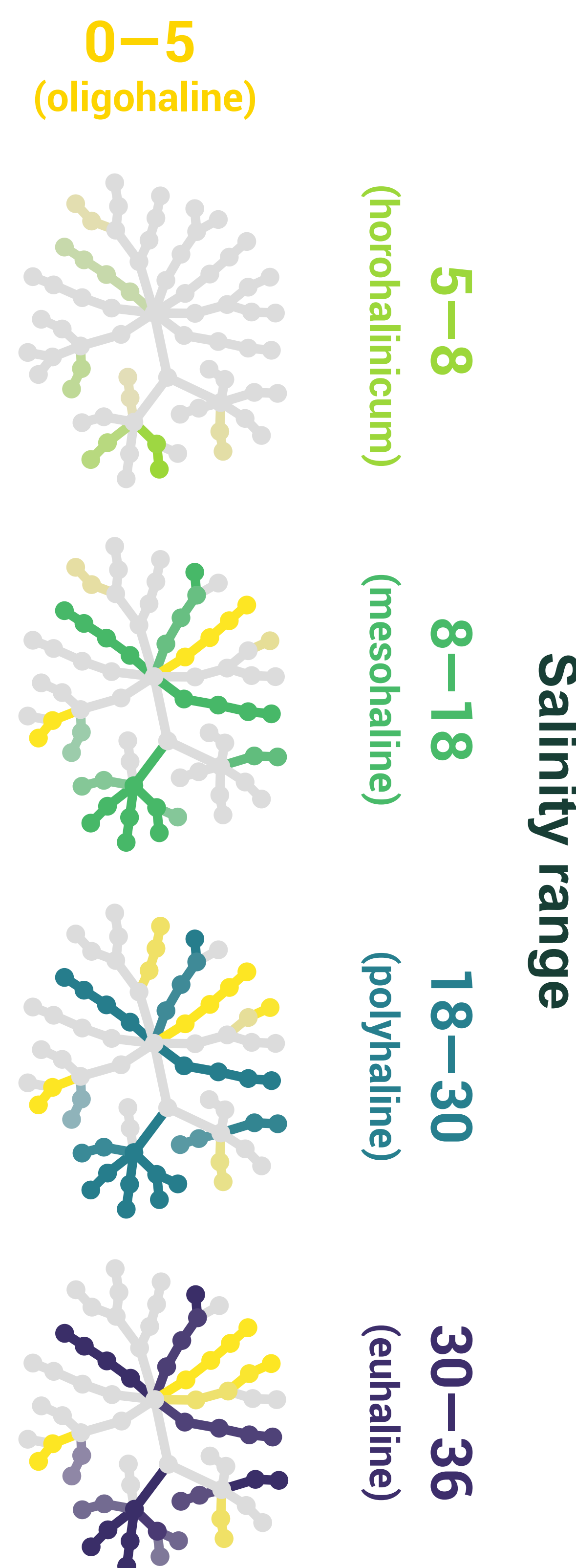


Figure 1. Geographic distribution of all 146 sample sites. Colour corresponds to salinity.



- Microbiome composition differed with: salinity (PERMANOVA, $p < 0.001$, $R^2 = 0.48$) host species (PERMANOVA, $p < 0.0001$, $R^2 = 0.34$)
- Host+salinity explained 34–91% of variation in bacterial abundance
- Typical **low** salinity bacteria: *Cyanobium*, *Lacihabitans*, *Luteolibacter*
- Typical **high** salinity bacteria: *Dokdonia*, *Leucothrix*, *Sulfurovum*

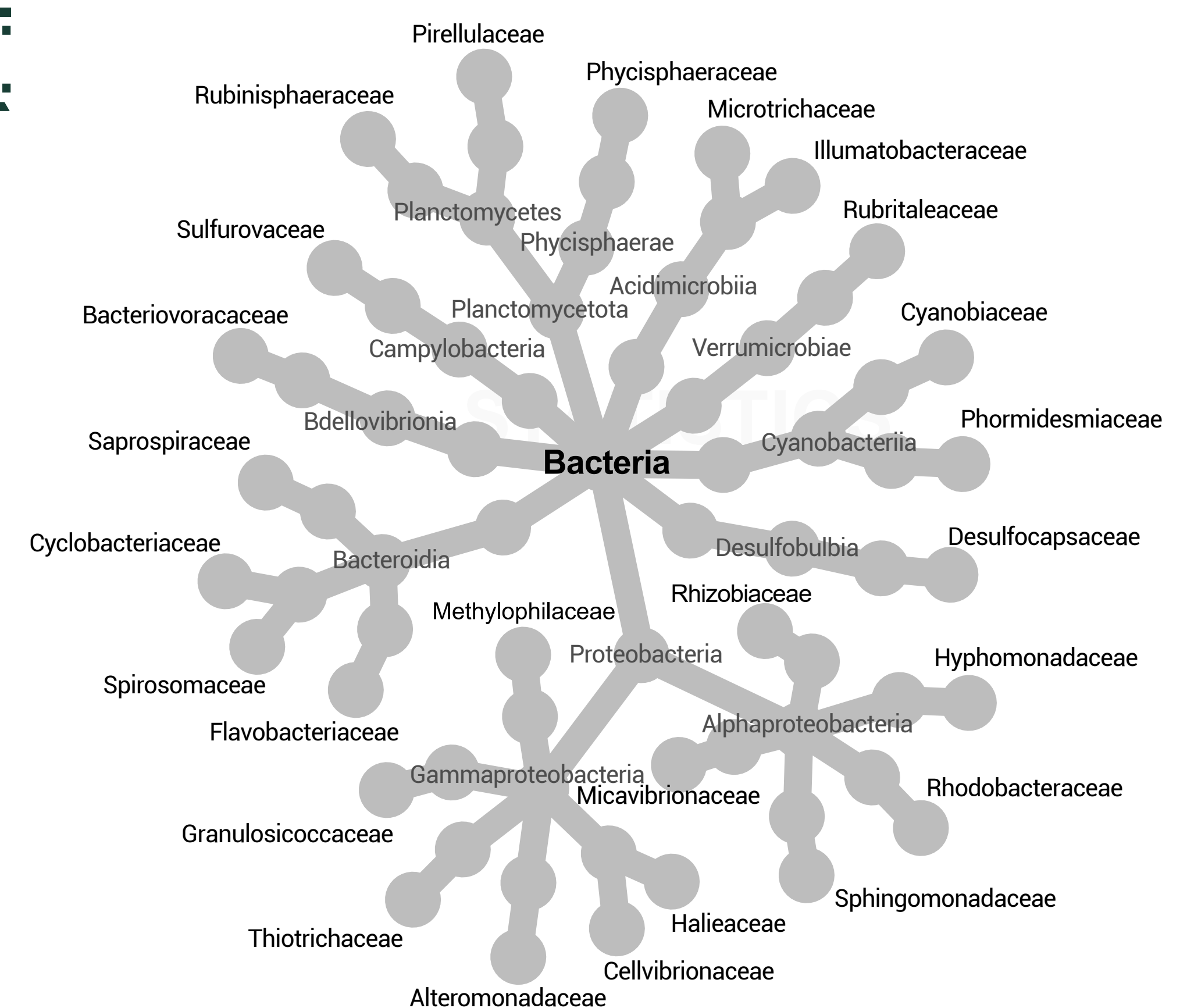


Figure 2. Pairwise comparisons (between the oligohaline versus the four higher salinity regions) of phylogenetic heat trees, depicting 28 bacterial families. Colour corresponds to salinity, and colour intensity to differential abundance (\log_2 fold ratio). Yellow = more abundant in the oligohaline; green-blue-purple = more abundant in higher salinity. The larger, grey tree functions as taxonomic key.

CONCLUSIONS

- *Ulva* microbiome composition is strongly structured by salinity (deterministic mechanism rather than stochastic)
- Largest shift was observed passing the horohalinicum (freshwater-marine transition zone)
- Characteristic bacterial communities may facilitate host's acclimation to low-salinity environment

NEXT STEPS

- Metagenomic profiling
- Sequence full genome of *Ulva* species and selected bacterial partners
- Manipulative laboratory experiments with modified low- and high-salinity bacterial communities



Want to know more? Read the full story in *Molecular Ecology*

SCAN ME