Invasive seaweed shapes its microbiome

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Introduction

- **Seaweeds, as ecosystem engineers, together with their epiphytic biofilms (microbiomes), play a crucial role in the aquatic environments as a holobiont. However, how different seaweeds may dictate their microbiome remains unclear, with some seaweeds having been reported to recruit protective bacteria and deter pathogenic ones via surface metabolites (Saha and Weinberger 2019).**

- **We studied marine biofilm formation on articial substrate adjacent to three seaweed species including one invasive (*Gracilairia vermiculophylla*) and two native species, (*Fucus serratus*, *Fucus vesiculosus)* and compared it with mature epiphytic biofilm from the same seaweeds.**

Methods

- **Experiment was conducted during Nov-Dec.**
- **Samples were collected after 7 and 14 days of exposure.**
- **The 16S-V4 amplicons were sequenced via 600 Illumina MiSeq at Max Planck Institute.**

- **Amplicon sequence variants (ASVs) were generated via DADA2. Taxonomy assigned via SILVA 138.1 database and PhytoREF database (for chloroplast classification).**

Results

- **Among top 1000 ASVs, Proteobacteria was the most abundant, followed by Bacteroidetes.**

- **The lowest abundance of chloroplast (from cyanobacteria and microalgae) was observed with the invasive Seaweed *G. vermiculophylla* (Fig. 1A), revealing its potential to deter photosynthetic microorganisms.**

- **Bacteroidetes, on the other hand, was highest with the invasive seaweed (Fig. 1A).**

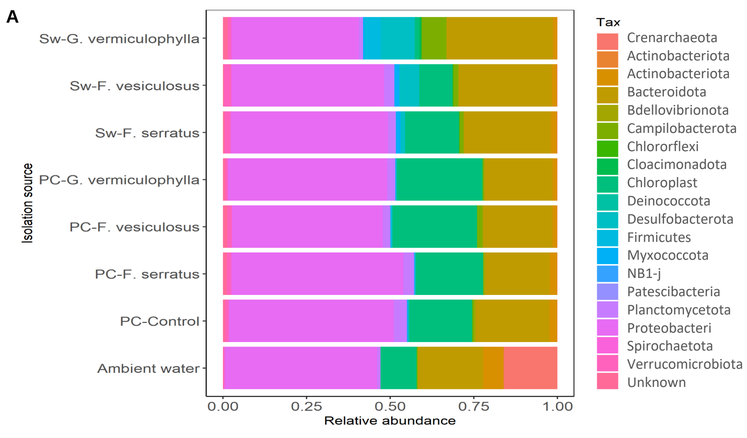


Figure 1. Barplots show the proportional composition of prokaryotes (A) and microalgae (B) phyla associated with Samples organized by their isolation source.

Purpose

To find out whether the potential of seaweed holobionts to modify their microbiome is linked with their success and population expansion

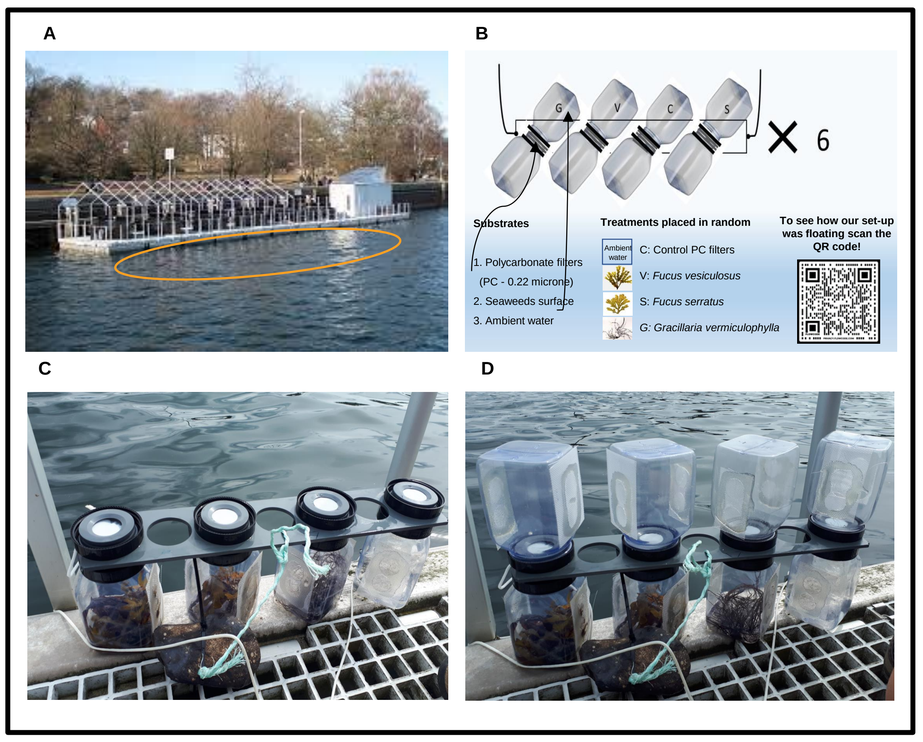


Figure 2. Location and design of experimental set-up (A,B), Examples of the attached, transparent kautex bottles with polycarbonate filters in the middle for the settlement of seaweed's neighboring biofilm (C, D).

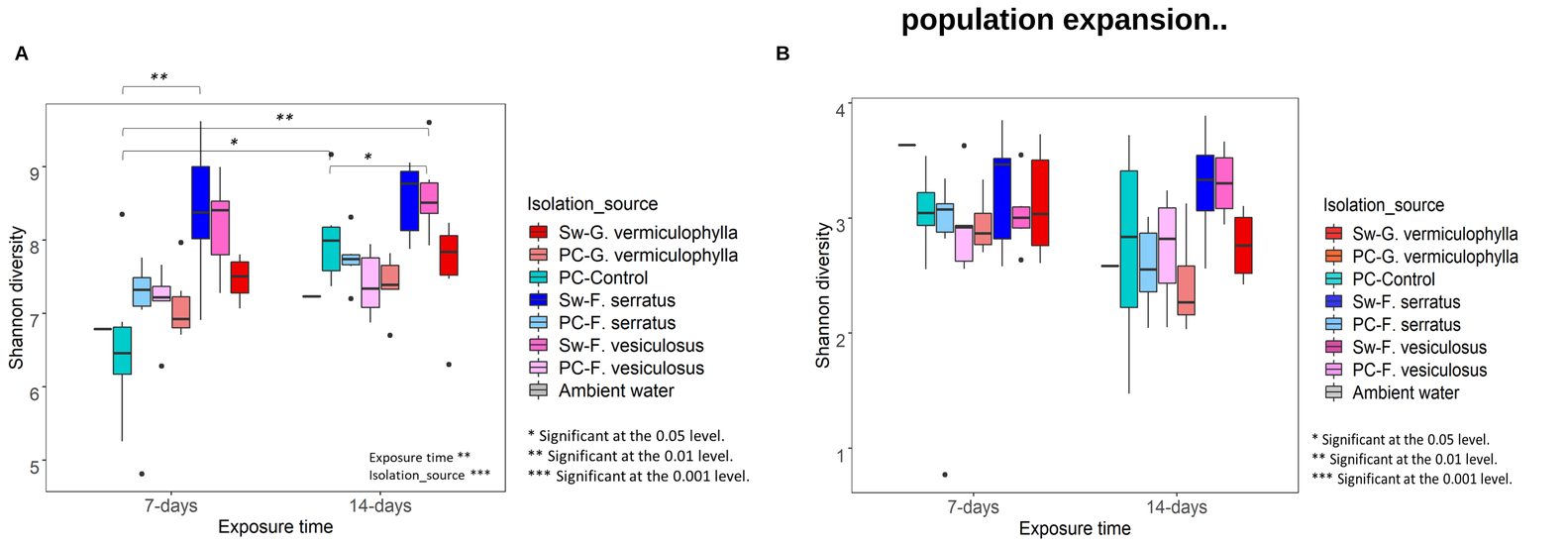


Figure 3. Prokaryotes (A) and microalgae (B) alpha diversity values for all samples, organized by exposure time and sample type.

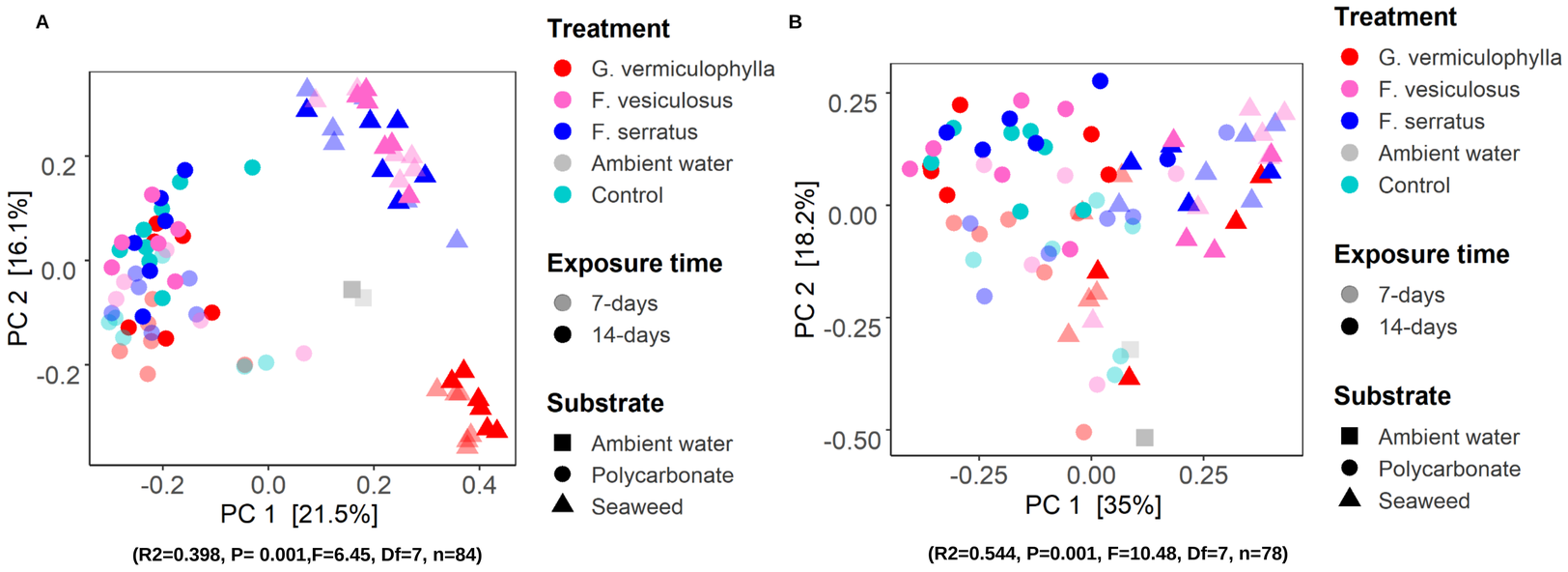
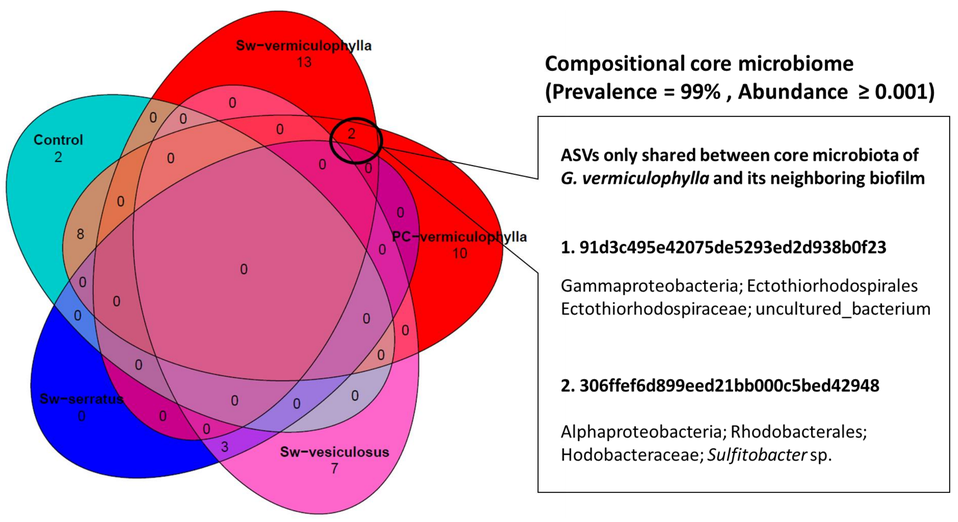


Figure 4. Principal coordinates analysis (PCoA) of prokaryotic (A) and microalgae (B) epiphytic biofilms, neighboring biofilm, and ambient water samples.



Compositional core microbiome
(Prevalence = 99% , Abundance ≥ 0.001)

ASVs only shared between core microbiota of *G. vermiculophylla* and its neighboring biofilm

1. 91d3c495e42075de5293ed2d938b0f23

Gammaproteobacteria; Ectothiorhodospirales Ectothiorhodospiraceae; uncultured_bacterium

2. 306ffef6d899eed21bb000c5bed42948

Alphaproteobacteria; Rhodobacterales; Hodobacteraceae; *Sulfitobacter* sp.

Figure 5. Venn diagram of the number of ASVs belonging to core microbiome of seaweeds biofilm (Sw-...), control polycarbonate filter (Control) and neighboring biofilm of G. vermiculophylla (PC- vermiculophylla).

Conclusions

Despite no significant differences between neighboring biofilms of three seaweeds at the community level, *G. vermiculophylla* had the highest potential to either attract or deter microbes in the environment. This potential of the given invasive seaweed may be associated with its success and population expansion..

Acknowledgements

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References

Saha, M., & Weinberger, F. (2019). https://doi.org/10.1111/1365-2745.13193

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