Salinity drives the structure of bryozoan and entoproct assemblages in recreational marinas of North Portuguese coast

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INTRODUCTION & AIM

- The growing demand for leisure boating have increased the number of recreational marinas. Marinas, impact original soft bottom ecosystems by adding hard structures that can be colonized by fouling animals such as bivalves, sponges, ascidians… But also, some other small and poorly studied groups, like **Bryozoa and Entoprocta**.
- Marinas are key points for the introduction and secondary spread of **non-indigenous species** (NIS). Several studies are focused on NIS records in marinas, but little is known about native fouling communities associated with floating pontoons or which factors shape these NIS/native assemblages.
- **Aim:** The present study aims to explore the **Effect of salinity on the structure of bryozoan and entoproct assemblages in recreational marinas of the North Portuguese Coast**.

MATERIAL AND METHODS

- **Study area:** This study was done in May 2023 at 6 marinas of North Portugal: 3 marine and 3 brackish marinas (Figure 1).
- **Sampling procedure:** At each marina, 3 sites were haphazardly selected and fouling community of 4 random 10×10 cm grids per site was scrapped. Collected animals were washed through a 0.5 mm mesh sieve and fixed in a 4% formaldehyde solution. Bryozoans and entoprocts were sorted and identified to the lowest level possible.
- **Data analysis:** PERMANOVA analysis was conducted to test for differences on the assemblage structure of bryozoans and entoprocts according to the following design: Habitat, a fixed factor with 2 levels (Marine and Brackish); Marina, a random factor nested in Salinity with 3 levels (3 marine and 3 brackish marinas); and Site a random factor with 3 levels and 4 replicates per site nested in Marina and Salinity. Multivariate patterns were illustrated by non-metric multidimensional scaling (nMDS) ordination of replicates for site. SIMPER routine was used to determine the species responsible for differences.

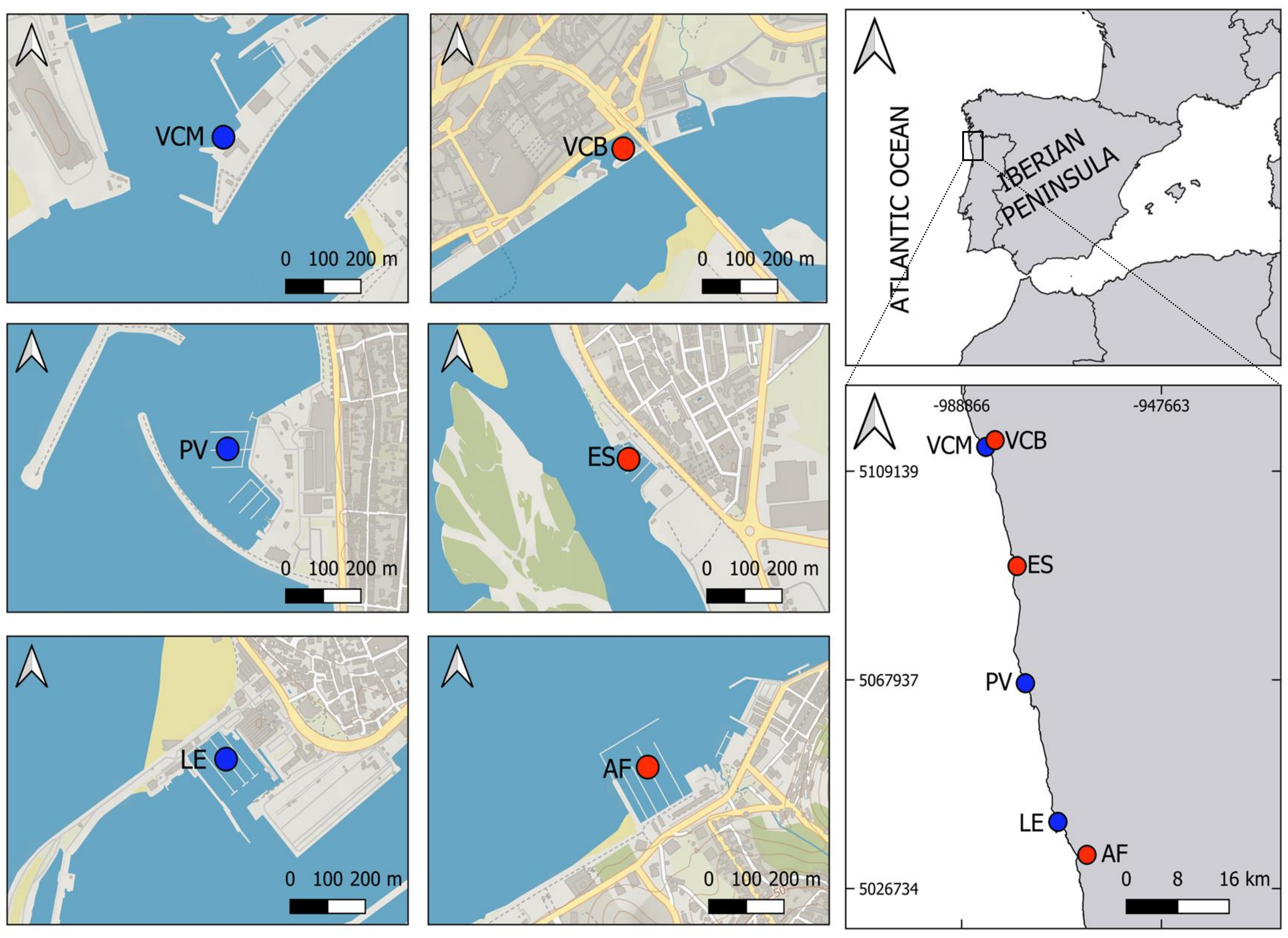

Figure 1. Location of the studied marine (blue) and brackish (red) marinas along the North Portuguese coast.

RESULTS

- A total of 5594 colonies belonging to 24 species were found: 19 Bryozoa and 5 Entoprocta. Bryozoans dominated marine habitats in terms of abundance (97.5%) and species richness (~77.3%). Entoprocts were the most abundant group in brackish marinas (81.2%) (Figure 2).
- Results showed that the assemblage structure of bryozoans and entoprocts was significantly different between marine and brackish marinas ($p<0.05$). Moreover, the documented multivariate pattern was also observed as a clear separation between habitats in the nMDS ordination (Figure 3).
- SIMPER analysis identified 8 species as the most responsible for differences among habitats (Table 1). 3 species individually contributed more than 20%: the byozoans *Amathia gracillima* (Hincks, 1877) and *Watersipora subatra* (Ortmann, 1890) and the entoproct *Barentsia benedeni* (Foettinger, 1887).
- Among these, *B. benedeni*, dominant in brackish marinas, is considered a native species. On the other hand, *A. gracillima* is a cryptogenic species, while *W. subatra* is regarded as a NIS. Thus, marine habitats were dominated by cryptogenic and NIS bryozoans.

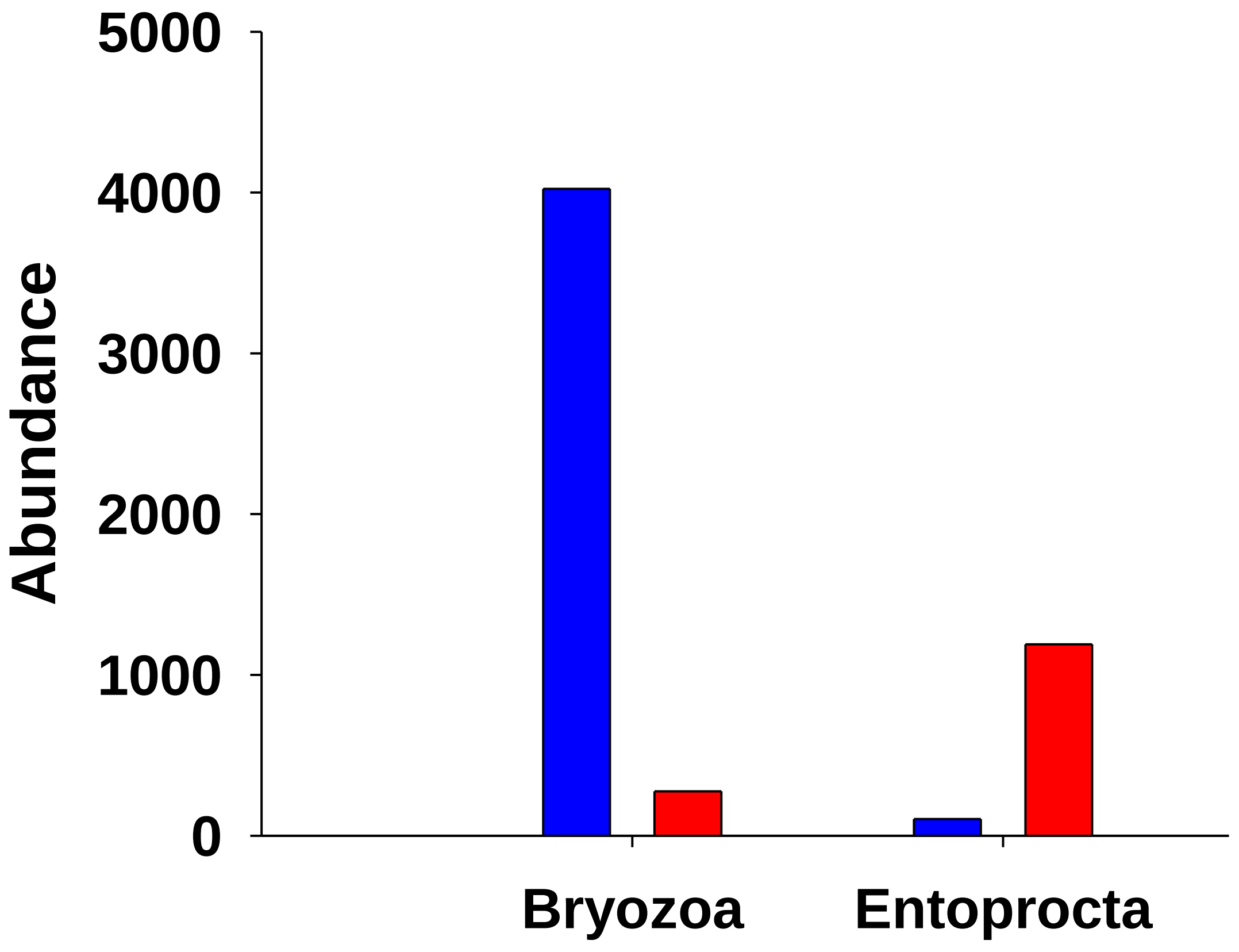

Figure 2. Abundance of bryozoans and entoprocts in marine (blue) and brackish (red) marinas.

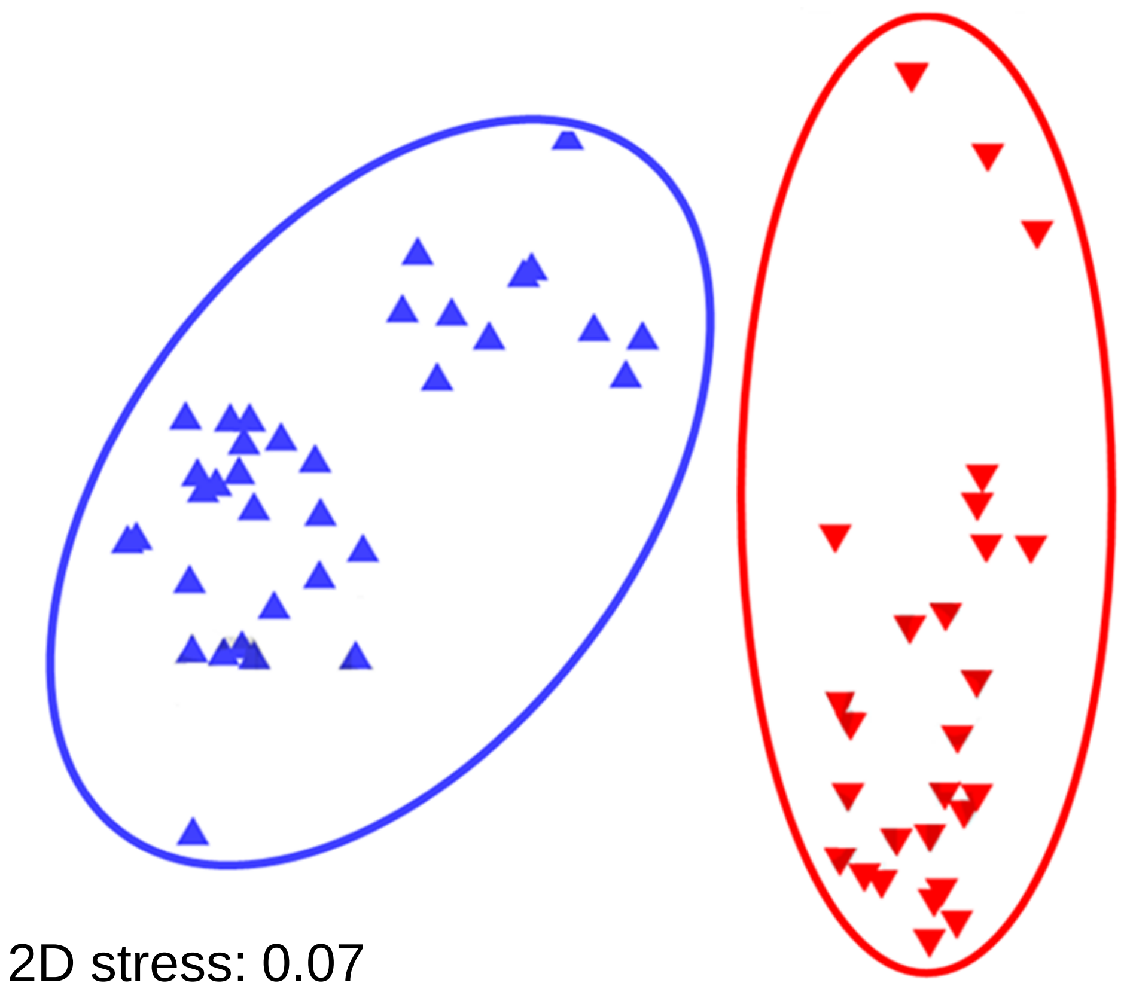

Figure 3. nMDS plots of centroids per site from marine (blue) and brackish (red) marinas.

Table 1. Contribution (δi) of individual taxa and cumulative percentage (δi%) of bryozoan and entoproct assemblages associated with floating pontoons of marine and brackish marinas to the average Bray - Curtis dissimilarity. SD = standard deviation.

Taxon	Average abundance		δi	δi%	δi/SD (δi)
	Coastal	Estuarine			
Amathia gracillima	29.00	0.00	25.43	25.95	1.38
Barentsia benedeni	0.47	33.08	22.75	23.21	0.90
Watersipora subatra	37.92	0.03	21.86	22.30	1.36
Tricellaria inopinata	18.81	0.00	7.21	7.35	0.72
Amathia imbricata	1.72	5.33	5.02	5.13	0.65
Cryptosula pallasiana	7.22	0.00	2.63	2.68	0.61
Amathia gracilis	2.83	0.83	2.33	2.38	0.85
Barentsia gracilis	0.86	0.00	2.11	2.15	0.42

CONCLUSIONS

- Results of this study pointed out **that salinity is an important driver of fouling assemblages**.
- Since dominant species in marine areas were cryptogenic or NIS, our data should be used to develop NIS monitoring programs.

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