

Co-occurrence and diversity patterns of benthonic and planktonic communities in a shallow marine ecosystem.

Raquel Ríos-Castro^{a#}, Cecilia Costas^{b#}, Alberto Pallavicini^{c,d}, Luigi Vezzulli^e, Beatriz Novoa^a, Eva Teira^b, Antonio Figueras^a

Introduction

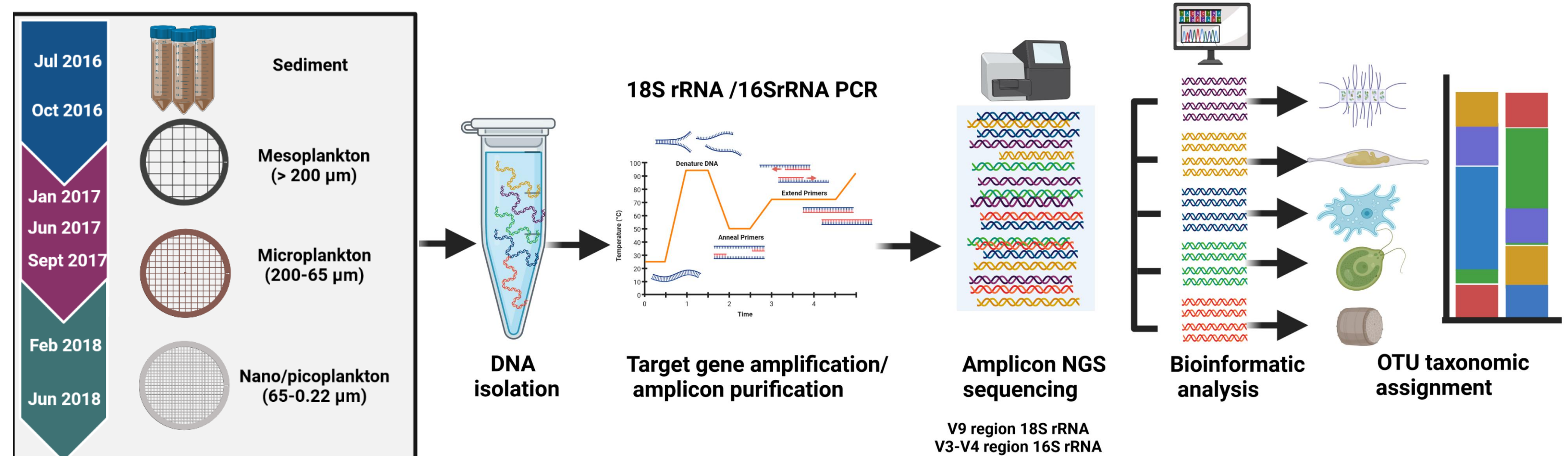
Shallow marine zones include some of the most dynamic marine habitats, where organisms respond quickly to human influences in the terrestrial ecosystem and interact within and between contrasting environments (e.g., sediment, water) by contributing to community structure, activity and resistance to environmental changes. The study of the taxonomic diversity of small **eukaryotic and prokaryotic organisms** in marine ecosystems has been growing since the application of high-throughput sequencing tools, circumventing the difficulties of isolating and culturing, and thus, improving our knowledge on their ecological role in the environment. However, few studies have simultaneously analysed the diversity of microbial communities in shallow waters and sediments.

DNA metabarcoding was used to explore the diversity and taxonomic composition of eukaryotes and prokaryotes in sediments and plankton in a shallow area within Ría de Vigo to depict possible associations among the most frequent and abundant organisms by co-occurrence network analysis.

Conclusions

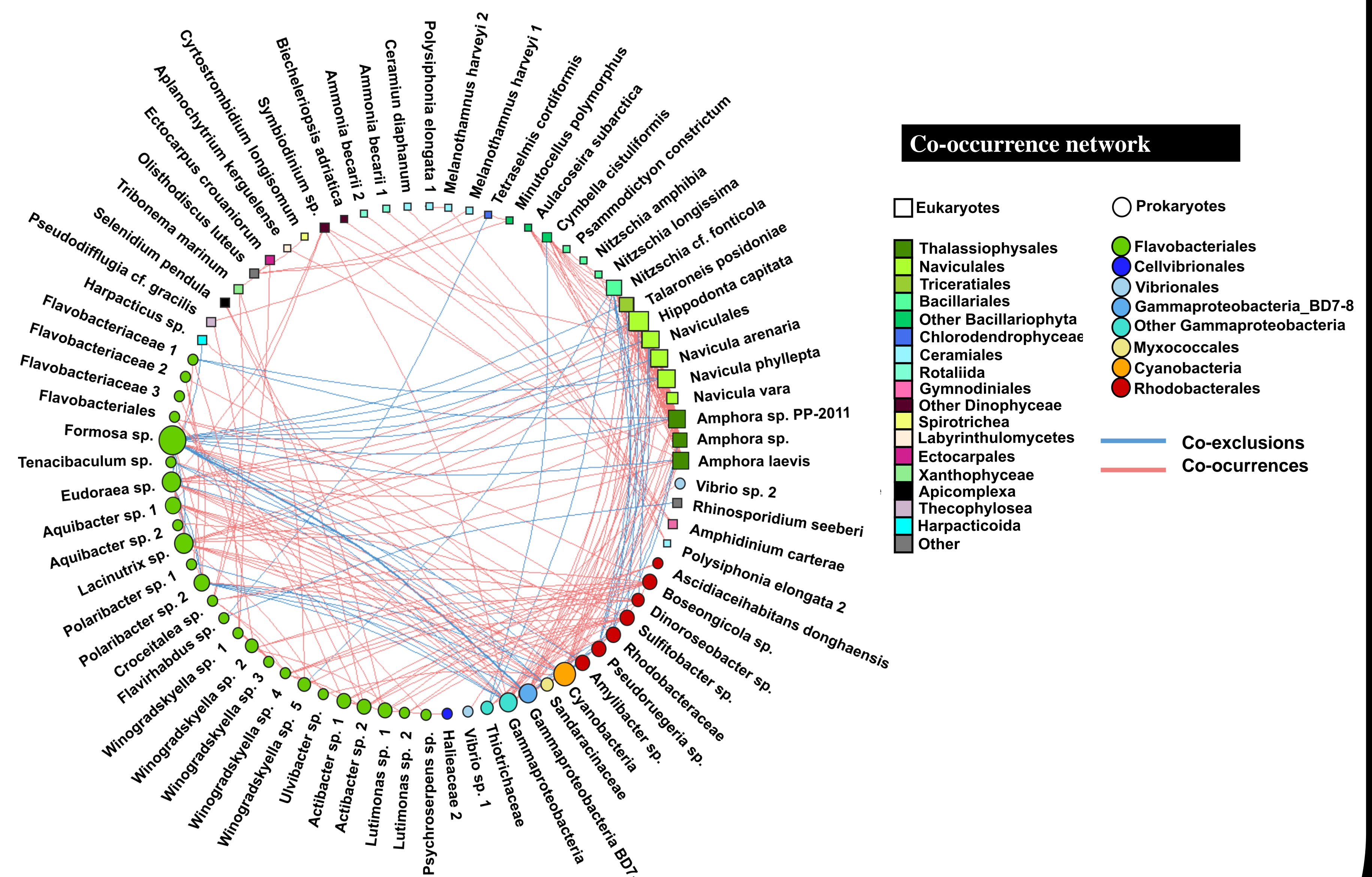
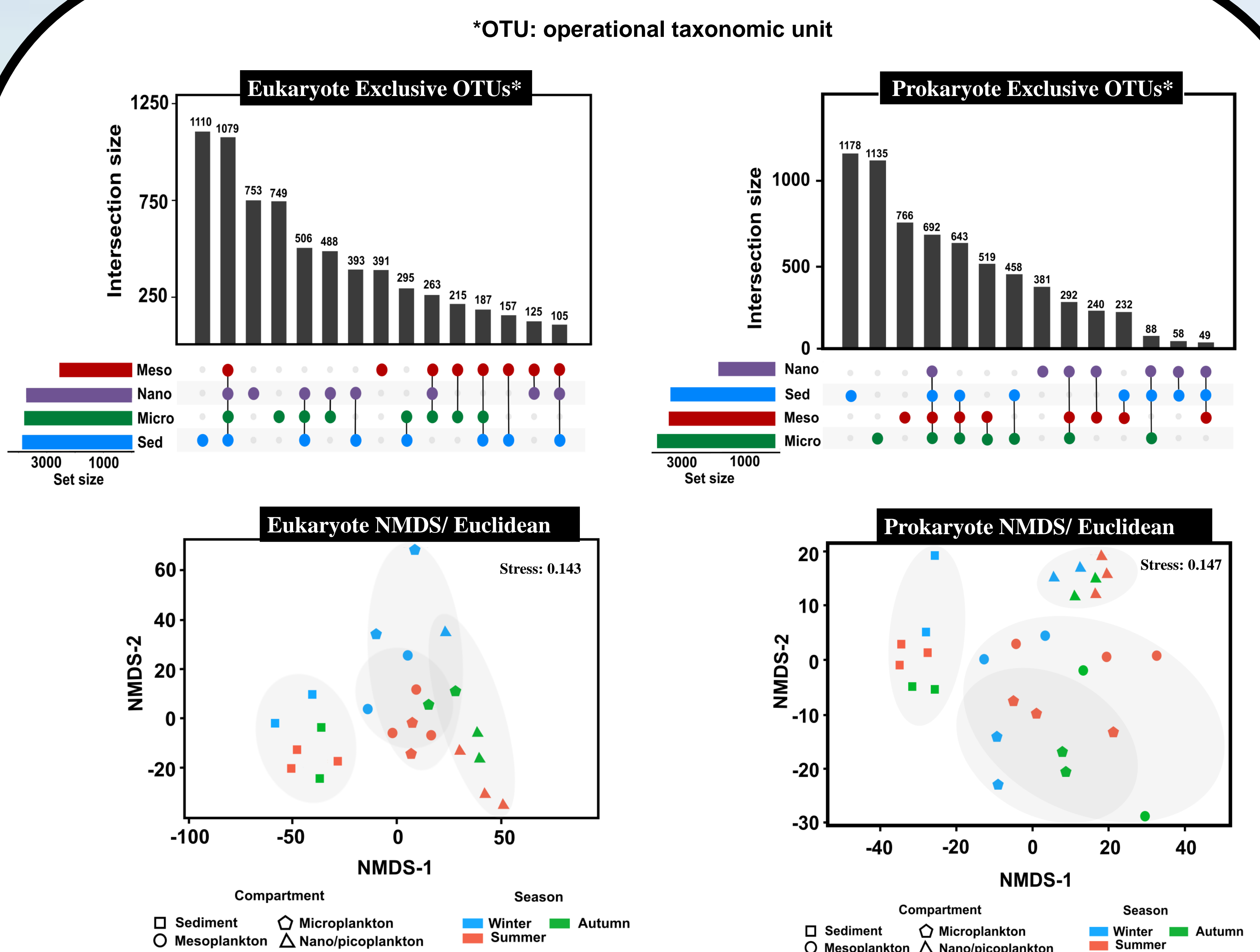
- Significant differences among eukaryote and prokaryote communities were found between sediment and plankton samples.
- High percentage of exclusive operational taxonomic units (OTUs) were associated with each compartment, especially from sediment.
- Shared water-sediment taxa suggested a relatively meaningful exchange of organisms between both environmental compartments.
- Significant co-occurrences were mainly obtained between prokaryotes (41%), followed by eukaryotes-prokaryotes (32%) and between eukaryotes (27%).
- The abundant and strong positive correlations between organisms suggested an essential role of biotic interactions as community-structuring factors in shallow waters where beneficial associations likely prevail.
- The high diversity obtained and the detection of predominantly coexisting interactions among organisms from sediment and the overlying water column suggest a movement of species between both habitats and therefore confirms the importance of integratively studying shallow marine ecosystems.
- DNA metabarcoding approaches could be useful tools for the integrative and systematic monitoring of diversity as well as for detecting potential biotic interactions among organisms in shallow marine environments, which are some of the most endangered areas in the context of global change.

Methodology



Sediment and size-fractionated plankton samples were collected in Meira, Galicia (NW, Spain) Lat: 42° 17' 6.72"; Long: 8° 43' 18.8

Results



Undirected network that represents all the links among organisms (prokaryote-prokaryote, eukaryote-eukaryote, and eukaryote-prokaryote). Significant co-occurrences or co-exclusions (p value < 0.01) were represented with a Spearman $\rho > 0.7$. Red edges represent positive correlation (co-occurrences), whereas blue edges represent negatives (co-exclusions). The size and colour of the nodes represent the degree of each taxonomic group.