COMMUNITY COMPOSITION OF MACROINVERTEBRATES IN THE MEDITERRANEAN SEA

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Abstract

Artificial sampling units (ASUs) allow for standardized sampling in the marine environment. We deployed ASUs at three sites in the Bay of Marseille for 14 months to measure the diversity and community composition of macroinvertebrates within and among sites. Invertebrates were identified morphologically to the class level. At this resolution, variability within sites was high enough to obscure differences among sites in both taxonomic diversity and community composition. Future work will use metabarcoding techniques to study diversity at the species level, both in the Bay of Marseille and other sites in the Mediterranean and more regional European seas.

Keywords: Biodiversity, Mediterranean Sea, Monitoring

The subtidal environment is an area that is particularly difficult to access for ecological studies. The use of Artificial Sampling Units (ASUs) allows for standardization of the sampling of marine communities. To study community composition and diversity in the Mediterranean Sea, we deployed ASUs in the Bay of Marseille in coralligenous reef habitats. These reefs are important centers of biodiversity in the Mediterranean, but are usually located at greater than 5 m depth and are therefore difficult to sample [1]. Three replicate ASUs were deployed at each of 3 sites. The ASUs were made of four nylon pot scrubbers that were cable-tied together and fixed to the substrate [2]. They were left on the reefs for 14 months. After the ASUs were retrieved by divers, we removed all mobile macroinvertebrates and identified them morphologically to the class level. We then calculated Simpson's diversity index for each replicate, and compared taxonomic diversity among sites using an analysis of variance with Simpson's index as a response variable. We used an analysis of similarity (ANOSIM) and a nonmetric multidimensional scaling (NMDS) analysis to compare community composition across sites. At this level of taxonomic identification, Simpson's index was not different among sites ($F_{2,6} = 2.271$, p = 0.184; Figure 1).
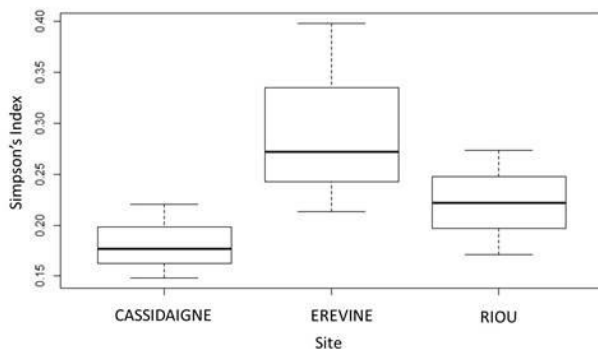

Fig. 1. Boxplots of Simpson's Index of diversity, calculated from three replicate ASUs at each of three sites. There were no significant differences among the sites.

Likewise, the ANOSIM revealed no differences in community composition among sites (R = 0.1276, p = 0.266). Figure 2 shows the NMDS plot of the data.
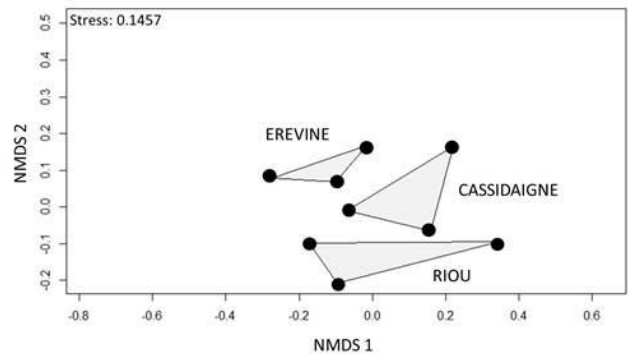

Fig. 2. Nonmetric multidimensional scaling plot of the community composition at three sites. An analysis of similarity showed no differences among the sites.

Although replicates within sites are generally clustered on the plot, the differences among sites are not significant. Future work is underway to use molecular metabarcoding techniques [3,4] to investigate community composition at the species level. We expect that there will be stronger differences among sites when data are collected at the species level. Given the large number of cryptic species found in marine environments [5], we may also uncover previously unknown cryptic diversity by using molecular methods rather than morphological ones. We will also expand this study to other sites in the Mediterranean and across different regional seas of Europe, to study diversity and composition on a larger spatial scale.

References

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