COMMUNITY ECOLOGY OF THE CORALLIGENOUS ASSEMBLAGES USING A METABARCODING APPROACH

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Abstract

Coralligenous habitats are bioconstructed, emblematic habitats of the Mediterranean Sea which presents a remarkably complex 3D structure resulting of the permanent dynamics between bioerosion and bioconstructions. This highly complex framework represents an habitat for around 1600 species and is so considered as one of the most important biodiversity hotspot of the Mediterranean Sea. Assessment of species diversity for this very complex habitat is very challenging, here we use a metabarcoding approach to estimate the species richness of 19 different sites of coralligenous habitats in the Bay of Marseille.

Keywords: Mediterranean Sea, Biodiversity, Conservation, Genetics

Coralligenous habitats are bioconstructed, emblematic habitats of the Mediterranean Sea which presents a remarkably complex 3D structure resulting of the permanent dynamics between bioerosion and bioconstruction. The main builders of these habitats are corallines red algae but other marine invertebrates such as bryozoans directly contribute to the frameworks of the habitats as they build their own calcareous skeletons. This highly complex framework represents a habitat for around 1600 species [1] and is so considered as one of the most important biodiversity hotspot of the Mediterranean Sea. It provides many ecosystems services such as : (i) Entertainment, coralligenous habitats are the favorite spot of divers in the Mediterranean Sea, (ii) food production, several species of high commercial values live or feed on these habitats, (iii) jewelry, as it is the habitat were the red coral is harvested, (iv) potential carbon sink as many of the organisms constituting the habitat are calcareous biocontructors. These habitats are threatened by human activities and the global change resulting of them. First mechanical degradation due to anchoring, divers' fins or nets of fisheries are responsible for a direct destructing of the habitats. Many organisms of these habitats are affected by global warming especially gorgonians which encouter mass mortality events correlated with positive thermal anomalies of the seawater. Combination of acidification and warming has been shown to have a deleterious impact on calcareous organisms of the habitats such calcareous red alga or bryozoans [2]. The increasing amount of organic matter due to human activities, invasive species and overfishing are also impacting the composition of the coralligenous communities. Moreover, as coralligenous habitats are found quite deep in the sea they are poorly studied and our lack of knowledge is probably the major constraint to the settup of efficient protection strategies.

Until now the assessment of species richness and monitoring of coralligenous habitats has been mainly conducted using conventional approaches especially direct assessment by scuba diving or based on photographs. These methods can be inefficient in detecting particular taxonomic groups or very small organisms in particular in the very complex framework of coralligenous habitats. Moreover they rely on a very good taxonomic expertise which made them difficult to apply in a monitoring purpose [3]. Metabarcoding is a fast, powerful, potentially cost effective molecular approach to study species diversity [4], and has not yet been used to study ecological communities of the coralligenous habitats.

Fig. 1. Collection of the samples by scuba diving

240 samples from 19 sites of the bay of Marseilles were collected by scuba diving (Figure 1) using a suction sampler and a hammer to extract a 10 square centimeters area of coralligenous habitats. The samples were weighted, examined and a quick counting of the different easily recognizable taxa (Figure 2) was done before crushing them with a blender.

Fig. 2. Examination of the samples in the laboratory

DNA extractions, PCR amplification of a 313 bp fragment of the COI and of the 28S gene were conducted. The first testing sequencing run on Illumina Miseq will allow us to test robustness of our molecular biology protocols by comparing the obtained results with the rapid identification method. Comparison of the results obtained on the 19 different sites and on the different ecological profiles results will allow us to establish connectivity pattern and environmental variables effects on the species diversity. Finally, we will be able to propose new monitoring strategies and indicators to monitor the coralligenous habitats.

References

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