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 present a remarkably complex 3D structure resulting from the permanent dynamics between bioconstruction and bioerosion. The main builders of these zones are coralline red algae but other marine invertebrates such as bryozoans directly contribute to the structure of the habitats as they build their own calcareous skeletons. This highly complex framework shelters about 1600 species and for this reason it is considered one of the most important biodiversity hotspot of the Mediterranean Sea. Until now the assessment of species richness and monitoring of coralligenous habitats has mainly been conducted using direct assessment by scuba diving or based on photographs. These methods can be inefficient in detecting particular taxonomic groups or very small organisms and this is particularly true in the very complex structure of coralligenous habitats. Moreover they require good taxonomic expertise which impairs their use for monitoring. Metabarcoding is a fast, powerful, potentially cost effective molecular approach to study species diversity, and has not yet been used to study ecological communities of the coralligenous habitats. Here we present assessment of the species diversity of 240 samples from 19 sites of the bay of Marseilles using meta-barcoding for the classical barcode gene COI (for metazoans) and on a fragment of the 28S ribosomal DNA designed for calcareous red algae.

Keywords: metabarcoding, coralligenous habitats, community ecology

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