Functional and phylogenetic diversity of copepod communities among Mediterranean ecoregions

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Abstract

The diversity of natural communities is classically estimated through species identification (taxonomic diversity) but can also be estimated from the ecological functions performed by the species (functional diversity), or from the phylogenetic relationships among them (phylogenetic diversity). Estimating functional diversity requires the definition of specific functional traits, i.e., phenotypic characteristics that impact individual fitness and are relevant to ecosystem functioning, such as size or trophic regime. Estimating phylogenetic diversity requires the description of phylogenetic relationships using molecular tools. In the pelagic environment, the distribution of plankton diversity is driven by complex interactions between environmental factors, ecological interactions, and dispersal constraints. However, the distribution of the different facets of plankton diversity and its interplay with ocean dynamics and biogeochemical provinces is poorly documented.

In the present study, we aimed to compare functional and phylogenetic diversity of copepod communities among different ecoregions. Ecoregions are defined as geographical entities with relatively homogeneous hydrodynamical and biogeochemical characteristics. Since the boundaries between ecoregions mainly result from oceanographic constraints, how could they

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influence the distribution of plankton diversity? To address this question, we compiled an unprecedented dataset of copepod abundances recorded at the species level over the entire Mediterranean Sea. We computed the taxonomic, functional, and phylogenetic diversity of copepod surface communities within each of the recently defined consensus ecoregions of the Mediterranean Sea. Functional diversity was estimated using a specific trait database for the most commonly-sampled and abundant copepod species of the Mediterranean Sea. It included four traits encompassing diverse ecological functions. Secondly, we reconstructed a phylogenetic tree using the available sequences of 18S rRNA. Our tree included 154 of the analyzed Mediterranean copepod species. Comparing the different facets of copepod diversity among ecoregions allows to relate oceanographic features to the distribution of plankton diversity at a regional scale.