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Sources of variability in functional diversity and uniqueness of the benthic ecosystem

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Abstract

Describing how communities change over time is crucial to better understand and predict ecosystem functioning. In this context, the purpose of this study was firstly to investigate changes in functional diversity and functional redundancy of soft-bottom macrofaunal communities after a quarter of a century, and secondly to determine the main mechanisms structuring these communities (i.e., deterministic *versus* stochastic processes). To achieve this, a large data set was used which included species abundance data collected in 1989 and 2014 from several sampling sites along a transect line (70-160m depth) in Heraklion bay, Crete (south Aegean Sea). A biological trait analysis (BTA) was conducted on the macrofaunal communities to determine their functional role. Functional diversity indices, including functional richness, evenness, as well as uniqueness, i.e., the functional contribution of single species to the overall redundancy of the whole assemblage, were calculated. Significant differences were recorded between the two sampling years. In order to determine the mechanisms that drove these differences, the species co-occurrence networks (based on species abundances) were compared to the functional networks (based on species traits) for the two periods, following a methodological approach based on the network theory and modularity concept. The result of this comparison showed that in 1989, the distribution of species within both networks was not different from a random pattern of distribution, indicating either that stochastic processes were the main factors structuring the community or that there was not a clear dominance of deterministic processes - environmental filtering or competition. In contrast, in 2014, the two networks were similar, indicating that environmental conditions have acted as a major filter on species distribution.

Keywords

macrofauna, functional diversity, species co-occurrence, uniqueness