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Abstract

One of the main reasons for establishing networks of marine protected areas (MPAs) is to conserve and manage biodiversity. Of the many elements to biodiversity, representation of species diversity is a common target. As preparing a complete inventory of all marine species is impractical, surrogates to represent species diversity have been sought. One such surrogate is lower taxonomic resolution. Based on the distributions of 977 taxa of fish, invertebrates and plants in a temperate marine bay, we used species richness as a measure of biodiversity to examine the value of using assemblages generated from species, genus, family and class level data as surrogates in a selection process for MPAs. Genus assemblages resulted in selection of areas with a similar number of species to those obtained by using species assemblages, provided the selected set of areas represented 60% or more of the assemblage occurrences. Results

using family and class assemblages varied. Because spatial scale, geographic location and the identity of the taxonomic group are all likely to affect the efficacy of using lower taxonomic resolution as a surrogate for species diversity, we argue that there is no universally preferred level. This requires further study at different spatial scales and among different locations, using a range of taxonomic groups, and we therefore suggest that the use of lower taxonomic resolution survey data to select MPAs should be approached with caution.



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Keywords

Biodiversity; Taxonomic resolution; Marine protected areas; Reserve selection; Surrogate

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