
Bridging the gap between evolutionary and conservation biology: Postglacial range expansion shapes the spatial genetic structure of a habitat forming octocoral

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Abstract

Understanding how historical and contemporary processes shape and maintain genetic diversity patterns is a central challenge for ecologists with direct implications in biodiversity conservation. Here, we studied the population genetic structure of *Paramuricea clavata* a habitat forming octocoral from the coralligenous, the most diverse but also most threatened biogenic reef in the Mediterranean. Focusing on 13 populations along a latitudinal gradient in the eastern Adriatic and using microsatellite markers, we revealed a pattern of spatial genetic structure combining hierarchical genetic clusters and isolation by distance (IBD). Interestingly, this pattern came along with a significant northward decrease in genetic diversity. While oceanographic barriers to gene flow and restricted dispersal abilities may maintain the IBD and the genetic clusters, the latitudinal genetic gradient raises the question of the legacy of historical processes on the contemporary genetic structure. Implementing extensive evolutionary and demographic history analyses based on approximate Bayesian computations

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and maximum likelihood methods, we demonstrated that a northward "serial founder events range expansion" following the last glacial maximum may explain this latitudinal genetic gradient. Besides, some alleles reach high frequencies at the edge of expansion suggesting the occurrence of allele surfing during this expansion range. Integrating these patterns and processes, we bridge the gap between the evolutionary and the conservation biology of *P. clavata* in the eastern Adriatic and we promote an eco-evolutionary based management plan, which will benefit the associated coralligenous biodiversity.

Keywords: Octocoral, Mediterranean Sea, latitudinal genetic gradient, postglacial range expansion, allele surfing, genetic drift