

Genetic differentiation and signatures of local adaptation revealed by RADseq for a highly-dispersive mud crab *Scylla olivacea* (Herbst, 1786) in the Sulu Sea

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Abstract

Connectivity of marine populations is shaped by complex interactions of biological and physical processes across the seascape. The influence of environmental features on the genetic structure of populations has key implications to the dynamics and persistence of populations, and an understanding of spatial scales and patterns of connectivity is crucial for management and conservation. This study employed a seascape genetics approach combining larval dispersal modeling and population genomic analysis based on RADseq to examine environmental factors influencing patterns of genetic structure and connectivity for a highly-dispersive mud crab, *Scylla olivacea* (Herbst, 1796) in the Sulu Sea. Dispersal simulations reveal widespread but asymmetric larval dispersal influenced by persistent southward and westward surface circulation features in the Sulu Sea. Despite potential for widespread dispersal, significant genetic differentiation was detected among eight Sulu Sea populations based on 1,655 single-nucleotide polymorphism (SNP) markers ($F_{ST} = 0.0057$, $p = 0.001$) and a subset of 1,643 putatively neutral SNP markers ($F_{ST} = 0.0042$, $p = 0.001$). Oceanography influences genetic structure, as redundancy analysis (RDA) revealed significant contribution of asymmetric ocean currents to neutral genetic variation ($R^2_{adj} = 0.133$; $p = 0.035$). Genetic structure may also reflect demographic factors, with divergent populations characterized by low effective population sizes ($N_e < 50$). Pronounced latitudinal genetic structure was recovered for loci putatively under selection ($F_{ST} = 0.2390$, $p = 0.001$), significantly correlated with variability in mean sea surface temperatures during peak spawning months of *S. olivacea* ($R^2_{adj} = 0.763$; $p = 0.041$), suggesting putative signatures of selection and local adaptation of early life history stages to thermal clines. This study contributes to the growing body of literature documenting population genetic structure and local adaptation for highly-dispersive marine species, and provides information useful for spatial management of the fishery resource.

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