

ABSTRACT
PHYLOGEOGRAPHY AND POPULATION GENETIC OF THE
ORANGE MUD CRAB, *SCYLLA OLIVACEA*, IN PHILIPPINE WATERS

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Scylla olivacea, the orange mud crab, is regarded as an important fishery resource due to high demand and high market value. However, natural mud crab populations are threatened by overexploitation and habitat degradation, and would benefit from resource management interventions. This study examined patterns of genetic diversity and connectivity of orange mud crab populations across the Philippines, for the purpose of inferring population structure and identifying putative management units. In addition, this study examined phylogeography and demographic history of the orange mud crab, whose life history offers an opportunity for dispersal and widespread connectivity against a backdrop of complex archipelagic waters and geologic processes. A total of 417 *Scylla olivacea* individuals were collected from ten locations representing marine biogeographic regions. Mitochondrial DNA control region (mtDNA-CR) sequences from 293 individuals revealed cryptic genetic diversity within *Scylla olivacea* specimens, with five mitochondrial lineages recovered. Mitochondrial DNA cytochrome c oxidase I (mtDNA-CoI) sequences however, did not reflect the phylogenetic diversity of the control region. Consequently, the hypervariable mtDNA-CR offers better resolution for uncovering intraspecific diversity relative to the more conserved CoI marker. Demographic history of Philippine orange mud crab populations is characterized by recent expansion and potential admixture. *Scylla olivacea* populations exhibit high haplotype diversity (mean $h = 0.991$) and nucleotide diversity (mean $\pi = 3.48\%$), which may be indicative of a large, stable population within Philippine archipelagic waters. Analysis of molecular variance based on mtDNA-CR sequences revealed that Philippine populations do not constitute a single genetic stock ($\phi_{ST} = 0.004$, $p < 0.001$). Significant population structure was also revealed by eleven microsatellite loci (overall $R_{ST} = 0.015$, $p < 0.05$). Several individual-based assignment approaches such as factorial correspondence, discriminant analysis of principal components, and Bayesian model-based clustering analyses, were used to infer clusters of genetically similar individuals to estimate population genetic structure. Both mtDNA-CR sequences and multilocus microsatellite genotypes revealed significant population genetic structure. However, there was no underlying geographical pattern, which may be caused by *Scylla olivacea* populations not being at equilibrium due to demographic expansion. The implications of these results on resource management are discussed.