

琉球大学学術リポジトリ

ウォレス線周辺における海洋生物4種の集団遺伝構造の比較研究

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Abstract

Title

Studies on comparative genetic population structure of four marine organisms across the biogeographical barrier, the Wallace Line

The targeted species in this study are the fiddler crab *Austruca perplexa*, the shallow water shrimp *Acetes sibogae sibogae*, the Javanese ricefish *Oryzias javanicus*, and the Asian monsoon scallops *Amusium pleuronectes* has long been of interest to evolutionary biologist because of the high level of species diversity, its wide geographic distribution, and its economic and ecologically importance. Many of these pressures, including increasing sea-surface temperatures, ocean acidification, pollution, legal and illegal overfishing, destructive fishing methods, water diversions, and other environmental shifts have the potential to result in significant loss of specific biodiversity stock, necessitating careful management wherever possible.

Genetic approaches are one tool that can help inform the conservation and management objectives unique to marine systems. Population genetic tools offer an opportunity to elucidate the genetic level (speciation and diversification), patterns of dispersal (connectivity and migration), and demographics (past and present), to better understand species' responses to ecological changes, anthropogenic stressors, and biogeographical

We compare the patterns of genetic diversity and natural population structure in the target species were investigated to gain a better understanding of its evolutionary history. Samples were collected from Western Pacific Region, especially across the biogeographical barrier, the Wallace line. We characterized sequence variation in an mtDNA control region fragment for all targeted species and microsatellite loci for *O. javanicus*. The genetic diversity result showed the height haplotype diversity and low nucleotide diversity (for *Au. perplexa* and *Am. pleuronectes*), intermediate haplotype diversity and low nucleotide diversity (for *Ac. s. sibogae*), and both low haplotype and nucleotide diversity (for *O. javanicus*). Analysis of molecular variance revealed significant genetic differentiation ($P < 0.0001$) among all sampled sites for both genetic markers accept *Am. pleuronectes*. Furthermore, the mean fixation indices for both genetic markers were relatively high, indicating that dispersal potential among sites was low and that gene flow had been restricted in the past. This pattern of population structure likely reflects a short pelagic larval life and is associated with very limited dispersal potential, leading to isolation by distance, potentially allowing local adaptation to sites that augment any oceanographic, geographic, or biological barriers to gene flow. The patterns of genetic differentiation resulting from this combination of factors represent a source of evolutionary novelty.

Name Eko Hardianto