Population Structure and Historical Demography of the Whiskered Velvet Shrimp (Metapenaeopsis barbata) off China and Taiwan Inferred from the Mitochondrial Control Region

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Abstract

Ta-Jen Chu, Daryi Wang, Hsien-Lu Huang, Feng-Jiau Lin, and Tzong-Der Tzeng (2012) Population structure

and historical demography of the whiskered velvet shrimp (Metapenaeopsis barbata) off China and Taiwan

inferred from the mitochondrial control region. Zoological Studies 51(1): 99-107. Sequence analyses of a

344-base-pair segment of the mitochondrial control region were conducted to elucidate the population structure

and historical demography of the whiskered velvet shrimp (Metapenaeopsis barbata) off China and Taiwan. Six

populations including 187 individuals were separately collected from the northern East China Sea (ECS), waters

off Kagoshima (KS, Japan), Taichung (TC, west-central Taiwan), Cheding (CD, southwestern Taiwan), Xiamen

(XM, southern China) and Hong Kong (HK). The haplotype diversity (h) was high for all populations (96.95%),

with values ranging 89.1% (CD) to 98.9% (KS). Nucleotide diversity (π) of all populations was 1.524%, with

values ranging 0.714% (TC) to 1.554% (ECS). All FST values among the 6 populations were significant except

for the ones from the pairs TC-CD, XM-HK, KS-XM, and KS-HK. The haplotype network was divided into 2

clades: clade I included individuals from all populations but YZR, and clade II did not include specimens from

CD or TC. Neutrality tests and mismatch distribution analyses both suggested that this species had experienced

a population expansion. Three distinct groups were yielded by the AMOVA tests, pair-wise FST analyses, and

the UPGMA tree of the 6 sampled areas. The 1st group included the ECS, the 2nd contained TC and CD, and

the 3rd included the KS, XM, and HK populations. Based on the continuity of the geographic position and gene

flow, the 2nd and 3rd groups should be considered a single population.

Keyword: Metapenaeopsis barbata, Mitochondrial DNA, Population structure, Population expansion