

Population structure and expansion of kuruma shrimp (*Penaeus japonicus*) in the adjacent waters of Taiwan inferred from intron sequences
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Abstract

Sequence analyses on the specific intron from the elongation factor-1 α gene were conducted to examine the population genetic structure and expansion of kuruma shrimp (*Penaeus japonicus*) off Taiwan. Five populations including 119 individuals were separately sampled from the north of East China Sea (ECS), west of Taiwan Strait (WTS), east of Taiwan Strait (ETS), South China Sea (SCS) and adjacent waters of Kagoshima (JAN). The gene diversity (h) was high for all populations (99.9%), with values from 99.7% (ETS) to 1. Nucleotide diversity (π) for all populations was 0.0421, with values from 0.0368 (JAN) to 0.0437 (ETS). Neighbor-joining tree and network of all alleles showed no significant genealogical structure. Analyses of molecular variance and F_{ST} also revealed no significant genetic structure among five populations, but the F_{ST} value between ECS and ETS was significant. Fu's F statistics and analysis of mismatch distribution for overall alleles suggested that this species in the studied waters had experienced population expansion.

Keyword : Intron of elongation factor-1 α gene, *Penaeus japonicus*, population genetic structure, population