

Genetic diversity and historical demography of kuruma shrimp (*Penaeus japonicus*) species complex off China based on mitochondrial DNA analysis  
Chun-Han Shih, Hsien-Lu Haung, 朱達仁, Ying-Chou Lee, Ching-Ming Wang, Tzong-

Der Tzeng

Leisure and Recreation Management

Tourism

tajen@chu.edu.tw

### Abstract

Two varieties (I and II) of kuruma shrimp (*Penaeus japonicus*) were found in the north of South China Sea (SCS) and Taiwan Strait (TS). To estimate the demographic history and genetic diversity of this species complex off China, 141 individuals were collected from the East China Sea (ECS), TS and SCS and 27 variety 2 specimens from SCS were also sampled for comparison. Sequence analyses on fragments of 454-bp at 5' end of mitochondrial DNA control region were conducted. Neighbor-joining tree and network of all populations yielded two clades; one included variety I individuals, the other comprised variety II. The variety II could also be found in ECS. The haplotype diversity ( $h$ ) for variety I was high for all populations (99.9%), with values from 99.3% (ECS) to 1 (SCS). Nucleotide diversity ( $d$ ) for variety I was low for all populations (0.0321), with values from 0.0285 (TS) to 0.0361 (ECS). The  $h$  and  $d$  for variety II were 1 and 0.0446, respectively. Analyses of molecular variance and  $F_{ST}$  revealed no significant genetic structure for variety I populations. Neutrality tests and mismatch distribution analyses suggested a late Pleistocene population expansion for both variety I (62,132 to 86,605 years ago) and variety II (94,464 to 146,655 years ago) of kuruma shrimp off China.

Keyword : Mitochondrial DNA, *Penaeus japonicus*, historical demography, control region.