

東亞產彎角似鷹爪蝦之族群遺傳結構與地理親緣關係之研究

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摘要

Part sequences of the cytochrome oxidase subunit I (COI) gene were used to elucidate the phylogeography and genetic structure of *Trachypenaeus curvirostris* in East Asia. Five populations including 102 individuals were separately collected from Yilan (YI), Xiamen (XM), Hong Kong (HK), Japan (JP), and Korea (KOR). 102 individuals obtained 32 haplotypes. Haplotype diversity value is 0.837, and nucleotide diversity is 0.0155. The neighbor-joining tree showed 2 clades: clade A included individuals from YI, XM, and HK populations, and clade B included specimens from JP and KOR populations. All  $F_{ST}$  values among populations in clade A showed no significant difference, but the one between JP and KOR in clade B was significant. Both neutrality tests and mismatched distribution analyses suggested all populations except KOR experienced a population expansion.

關鍵字：Trachypenaeus curvirostris, Phylogeography, the genetic structure, COI