

東亞產日本沼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 *Macrobrachium nipponense* in East Asia. Eight populations including 270 individuals were separately collected from Japan (JJCH), Korea (KOCH), north of Fukien (NFJM), south of Fukien (SFJK), Chinmen (YML), Shihmen reservoir (SR, northern Taiwan), Mingte reservoir (MTR, west-central Taiwan) and Chengchinghu reservoir (CCHR, southern Taiwan). 270 individuals obtained 83 haplotypes. Haplotype diversity value was 0.926, and nucleotide diversity was 0.0176. Neighbor-joining tree for all individuals showed 2 clades: clade A included individuals from KOCH、NFJM、SFJM、YML、MTR and SR populations, and clade B included specimens from JJCH、MTR、CCHR、YML、NFJM and SFJM populations. All  $F_{ST}$  values among populations were significant. Neutrality tests suggested KOCH, MTR and CCHR populations experienced a population expansion.

關鍵字： *Macrobrachium nipponense*, Phylogeography, the genetic structure, COI