

中文摘要

本研究利用粒線體DNA 序列探討兩個主題：(1) 沼蝦屬的分子親緣以及探討東亞沼蝦種群及種化現象；(2) 陸封型粗糙沼蝦在台灣親緣地理和族群遺傳結構。

利用粒線體16S rRNA 序列分析，沼蝦屬包括陸封型和廣鹽型沼蝦，是屬於單一系群，但種間關係並不明確。這結果顯示沼蝦屬為快速輻射演化種群，並證實早先的假設：沼蝦是多次由海水入侵淡水水系，而不同種的陸封型沼蝦幼體發育期縮短，是屬於適應淡水環境的趨同演化結果。傳統分類普遍使用的形質(例如：額角和第二步足)，是在入侵淡水水系時個別演化的特徵。結合16S 和 COI 序列分析，能確定包括不同區域和特有地域的種群，並顯示可能存在5種隱存種和4種未描述種。在東亞，型態相似的種群包括粗糙沼蝦種群有地域性種化現象。在種間屬於保守的外部形質，在同種不同地理區的族群間有時存有很大變異性，使得物種的鑑定上增加困擾。這結果顯示普遍用做分類使用的形質，並非最佳做為沼蝦屬種間親緣分析的依據。隱存種的可能存在，顯示分子生物的技術可以有效做為種的鑑定和瞭解種間親緣關係的工具。本研究結果建議結合分子生物的技術和傳統形質分類，做為研究沼蝦屬物種之間分類研究的好工具。

粗糙沼蝦為陸封型沼蝦，在台灣淡水環境屬於大型的底棲無脊椎動物，數量豐富並廣佈全島。探討台灣粗糙沼蝦的親緣地理和遺傳結構研究發現，顯示粗糙族群在台灣的分佈可以區分成2大群下含4群組，分佈在3個地理區，群組間存在明顯的遺傳差異。進一步利用分子變異分析 "(AMOVA)" 和最短網狀結構圖 "(minimal-spanning network)" 分析顯示，群組間不僅存在明顯遺傳差異，群組內之不同族群間也有明顯遺傳差異，這結果顯示

各個族群具有不同的遺傳結構。根據粗糙族群的親緣地理分析和遺傳差異，推測台灣的粗糙族群至少由 2 個不同的入侵事件所造成。在冰河時期，由大陸藉由海平面下降時形成的陸橋擴散進入台灣，由於中央山脈隆起事件和苗栗堆形成等地理障礙導致族群間基因交流中斷，而逐漸累積族群間遺傳差異。東部族群的高歧異度遺傳結構應是人為多次引入所導致，引入的粗糙沼蝦個體大部分來自西部河川。東部外來族群對當地河川生物的影響，則仍待進一步探討。



Abstract

This study focuses on two subjects by using the mtDNA sequences: (i) molecular systematics of the freshwater prawn genus *Macrobrachium* Bate, 1868 (Crustacea: Decapoda: Palaemonidae) with emphasis on East Asian species; (ii) phylogeography and the genetic structure of the land-locked freshwater prawn *Macrobrachium asperulum* on the continental island of Taiwan.

Based on mitochondrial DNA fragment of the large subunit (16S) rRNA gene, the monophyletic phylogeny of the genus *Macrobrachium*, including land-locked and euryhaline species, was supported. There was, however, poor support for the internal structure. Results suggested that the evolution of this group was marked by rapid radiation. The hypotheses that the prawns originated from marine ancestors and have subsequently migrated towards freshwaters in more than one wave of migration, and the abbreviated larval development of land-locked species represents adaptive convergence are supported. It appears that most of the commonly used morphological characters used in the taxonomy of genus evolved independently during the invasion of inland waters. Based on the 16S and fragment of the cytochrome oxidase subunit I (COI) gene, several species groups, including species from different geographic regions and endemic groups could be recognized from various continents (regions). The presence of five cryptic species is indicated and the identity of four supposedly undescribed species are confirmed. Localized speciation events in East Asia can be correlated with morphological similarities, notably members of the *M. asperulum* species group. Morphological characters tend to be conservative within species-groups but quite variable between geographic distant populations, making species identifications difficult. The present molecular results, combined with morphological datasets, can be used to help reorganize the various species groups in taxonomy.

M. asperulum is a land-locked macroinvertebrate species of freshwater prawn and is

abundant in fresh waters and has a pan-island distribution in Taiwan. In the phylogeography and the genetic structure study of *M. asperulum* in Taiwan. Phylogenetic reconstructions revealed four phylogenetic lineages, with significant genetic differentiation, distributed in three geographical regions; analysis of molecular variance (AMOVA) and minimal-spanning network revealed significant genetic structure across all hierarchical levels, indicating that a major proportion of the genetic divergence is geographically subdivided with a strong population structure. Phylogeographical analyses and an estimation of genetic divergence suggest that such spatial divisions could be correlated with two different colonization routes from the Asian mainland, during the glaciation with low sea level, followed by past fragmentation due to the formation of geographical barriers, such as the Central Mountain Range and Miaoli Plateau in Taiwan, which resulted in rare contemporary gene flow. The high diversity of the genetic structure of eastern populations suggests multiple artificial introductions mainly from rivers of west-central Taiwan. The impacts of the introduced populations on the freshwater ecology in eastern Taiwan require further study.

