

CONTENTS

Acknowledgement-----	I
Chinese Abstract-----	II
Abstract-----	IV
Chapter 1: General Introduction-----	1
Chapter 2: Molecular systematics of the freshwater prawn genus <i>Macrobrachium</i> Bate, 1868 (Crustacea: Decapoda: Palaemonidae) inferred from mtDNA sequences, with emphasis on East Asian species	
Introduction-----	6
Materials and Methods	
(1) Collection of materials-----	9
(2) DNA extraction, PCR amplification and sequencing-----	9
(3) Data analyses-----	10
Results	
(1) Sequence characteristics and variations-----	12
(2) Phylogenetic analyses-----	13
(3) Analysis of the combined dataset-----	16
Discussion	
(1) Phylogenetic relationships-----	17
(2) Taxonomic implications-----	19
Chapter 3: Phylogeography and the genetic structure of the land-locked freshwater prawn <i>Macrobrachium asperulum</i> (Decapoda: Palaemonidae) on the continental island of Taiwan	
Introduction -----	25
Materials and Methods	

(1) Sample collection-----	27
(2) DNA extraction and amplification-----	28
(3) Sequence alignment and phylogenetic analyses -----	28
Results	
(1) Genetic characteristics and variations-----	30
(2) Phylogenetic analyses of mtDNA sequences-----	31
(3) Genetic structuring among and within lineages-----	33
(4) Statistical tests of neutrality-----	33
(5) Population divergence-----	34
Discussion	
(1) Population genetic structure and differentiation -----	34
(2) Phylogeography and demographic history-----	36
(3) The introduced populations of east Taiwan-----	39
Chapter 4: General Conclusion-----	41
References-----	44
Tables-----	58
Figures-----	63

Table Contents

Table 1. Species list in molecular systematics study-----	58
Table 2. Sources of additional 16S sequences-----	59
Table 3. Sampling localities, sample size (n), haplotype number (hn), nucleotide diversity (π) and haplotype diversity (h) of <i>M. asperulum</i> -----	60
Table 4. Hierarchical analysis of molecular variance (AMOVA) among <i>M. asperulum</i> populations in Taiwan-----	61
Table 5. Pairwise F_{ST} values and exact test of population differentiation -----	62



Figure Contents

Fig. 1. Saturation test of 16S-----	63
Fig. 2. Saturation test of COI-----	64
Fig. 3. Phylogenetic relationships based on 16S sequences-----	65
Fig. 4. Phylogenetic relationships based on COI sequences-----	66
Fig. 5. Phylogenetic relationships based on combined 16S and COI data-----	67
Fig. 6. Sampling localities of <i>M. asperulum</i> and the geographical regions-----	68
Fig. 7. Neighbour-joining tree based on combined 16S and COI sequences-----	69
Fig. 8. Minimum-spanning network obtained from <i>M. asperulum</i> populations-----	70
Fig. 9. Pairwise F_{ST} values among populations plotted against their straight-line geographical distances (km)-----	71
Fig. 10. Mismatch distribution of pairwise differences among mtDNA haplotypes-----	72
Fig. 11. Two incursive colonization and one back dispersal scenarios-----	73