

Chapter 4: General Conclusions

In the phylogenetic study demonstrates that based on molecular data, *Macrobrachium* species have resulted from a monophyletic group and processed a rapid radiation; multiple origins of *Macrobrachium* fauna on various continents (or regions) are inferred. Early studies from biogeography, larval development models, larval development characters, adult and larval salinity-freshwater tolerance, inter-and intra-specific allozyme data and as well as molecular genetic data in this study have conformed that the *Macrobrachium* species is polyphyletic in this genus.

Morphological conservation by *Macrobrachium* species might have been the result of rapid radiation. Land-locked species, suggesting that they likely originated from multiple marine ancestors and have subsequently migrated towards fresh waters through more than one wave of migration. The adaptive convergence result of larvae's abbreviated development is a process derived from the selection pressures for becoming established in freshwater environments rather than to the geographic association. The morphological characters (such as the unequal second pereiopod, big robust claws, spine, etc.) developed independently through the invasion of inland waters, and also helps explain the taxonomic difficulty in morphological characters of the genus.

The natural species group contains a mixture of the euryhaline and land-locked species may represent evolution of the species group from a single ancestral lineage. The species group of *M. nipponense*/ *M. formosense* and *M. hainanense* may be represented to the ongoing freshwater invasion and recent speciation in East Asia. The cryptic species suggested here challenge the effectiveness of using the traditional morphological-taxonomic methods, more caution should be exercised in taxonomic or phylogenetic studies with more specimens or populations, and also suggest that molecular techniques will yield great resolution for delimiting species and recover their relationships.

The overall results of this study confirm the importance of considering evidence from

different types of data from both systematics and evolutionary studies. Further study, in using more species, other mitochondrial or nuclear sequence data, and new data on the biology and ecology of these species and their habitats, and updated knowledge of the paleogeographical history is obviously required to ultimately conform to their evolutionary history and help clarify the possibility of microhabitat and behavioral specialization giving rise to the radiation of freshwater prawns.

In the study of phylogeography and the genetic structure of the land-locked freshwater prawn *M. asperulum* reveals a high degree of phylogeographically related genetic structure and significant genetic differentiation existed among populations.

Two major groups contain four lineages with significant genetic breaks, belonging to three geographical regions were identified. Regional differentiation is associated with geographical barriers. Population differentiation within regions is correlated with geographical distances and is consistent with the model of “isolation by distance”. Rare contemporary gene flow occurs among population in same river system or even in the same river indicated that the freshwater prawn with land-locked life cycle has limited dispersal ability.

High-level population diversity in *M. asperulum* can be maintained if the population is large enough and stable for a long period of time in rivers with stable hydrological factors. Some populations showed highly divergent genetic structures among localities and low levels of genetic variability within populations suggesting the result of bottleneck event. The Tadu River may be presented a hybrid zone for populations of two lineages (II and III) which survived the ice ages. Four eastern populations studied here indicating that multiple introductions by human have occurred recently in eastern Taiwan and the introduced prawns were primarily from west-central Taiwan.

The biogeographical pattern of *M. asperulum* suggests that it resulted from two colonization events from China and then followed by isolation, lineage sorting, and allopatric

fragmentation. The dispersal scenario correlated well with current concepts regarding the tectonic evolution of Taiwan and subsequent palaeoclimatic oscillations of glaciations. The population of the Mulan River suggests a more-recent back dispersal from Taiwan to China during the Pleistocene. Intensive sampling of more populations from Asian mainland is required to infer their exact biogeographical histories and to define geographic barriers to dispersal.

