

博士論文（要約）

**Evolutionary radiation of non-marine
molluscs in East Asia.**

(東アジア産非海産貝類の進化的放散)

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Understanding how phenotypic diversity and diversity patterns have been created is a central subject of evolutionary biology and conservation biology. Non-marine molluscs have been treated as excellent models to investigate causes of morphological evolution, speciation and diversity patterns. East Asia including Japanese Archipelago is known to be a hotspot of land and freshwater snails because of their high species diversity, while there have been few systematic and phylogenetic studies of land and freshwater snails.

In Chapter 2, I documented extensive incongruence between molecular phylogeny and the current taxonomy of the freshwater gastropod family Viviparidae in Japan. A molecular phylogeny for East Asian viviparids comprises three major clades. Among these clades, two are composed of paraphyletic or highly polyphyletic taxonomic species. The observed incongruence between phylogeny and taxonomy may be due to incomplete lineage sorting, introgressive hybridization and/or phenotypic plasticity, suggesting substantial revision is required not only for understanding evolutionary history of these groups but also for developing conservation programs.

In Chapter 3, I reconstructed a molecular phylogeny of the land snail genus *Cyclophorus* using three genes to determine whether their morphological traits and the current taxonomy of the species reflect their phylogenetic relationships. The present results showed that the geographical distributions of the lineages and current taxonomy do not reflect their phylogenetic relationships. In addition, morphological analysis indicated that cryptic species nevertheless shell morphological diversity within species is relatively high in several species. The present study showed that the current zoogeographical boundary lines for animal distribution of the Ryukyu Islands did not reflect evolutionary patterns in *Cyclophorus*. This study suggests that a further taxonomic revision of Japanese *Cyclophorus* is needed for biodiversity conservation.

In Chapter 4, I investigated the molecular phylogeny of the East Asian camaenid land snail genera *Aegista*, *Landouria*, *Trishoplita*, and *Pseudobuliminus* to test whether morphology and current taxonomy reflect phylogenetic relationships. The results documented extensive parallel evolution and substantial incongruence between taxonomy and molecular phylogeny. Many morphological traits were independently gained or lost in a number of lineages. Although genital anatomy reveals phylogenetic conservatism to some extent, love dart and dart-related organs were lost independently. Accordingly, classification of these genera based on morphological traits did not reflect

phylogenetic relationships, and, overall, these genera except for a few species should be tentatively assigned to a single genus as *Aegista*. The present findings suggest that radical revision is required for the taxonomy of camaenid land snails.

In Chapter 5, I investigated the relationship between the shell morphology and habitat use of camaenid land snails of the genus *Aegista* and clarify the causes of the divergence in shell morphology among phylogenetically related species. The results showed that arboreal species have evolved independently from ground-dwelling species at multiple times. A significant association was found between shell shape and habitat use despite of the existence of a certain degree of phylogenetic constraint between these traits. The development of a well-balanced shell shape is one effective method for reducing the cost of locomotion under the force of gravity in each life habitat, resulting in the divergence in shell morphology and the independent evolution of morphologically similar species among different lineages. The present study suggests that ecological divergence is probably the cause of shell morphology divergence in land snails.

In Chapter 6, I described *Aegista hiroshifukudai* n. sp. from Yamaguchi Prefecture, the Chugoku District, western Honshu, Japan. The new species is assigned to *Aegista* based on its morphology and molecular phylogeny. *Aegista hiroshifukudai* n. sp. is phylogenetically distinct from all other closely related species and the shell has a relatively taller spire.

In Chapter 7, I investigated the molecular phylogeny of *Bradybaena* and *Phaeohelix*, to clarify whether morphological traits and the current species taxonomy of these genera reflect their phylogenetic relationships. The results showed that they are genetically divided into three clades, and the geographical distribution pattern of the lineages tends to reflect phylogenetic relationships. In addition, passive long distance dispersal by ocean current influenced their evolutionary history. The nominal species taxonomy was not consistent with their molecular phylogenetic relationships. In addition, present findings showed that *Phaeohelix* should be synonymized with *Bradybaena*. This study suggests that a further taxonomic revision of Japanese Camaenidae is needed.

In Chapter 8, I investigated evolutionary history of the all Japanese *Bradybaena* species with particular focus on dispersal patterns and vicariance events in the Ryukyu Islands, using molecular phylogeny. The inferred mitochondrial and nuclear

gene trees of *B. c. circulus* of the Ryukyu Islands and *B. p. iheyaensis*, *B. pellucida* and *B. similaris* showed incongruence between morphology and phylogeny. All Japanese species were monophyletic, and they are separated into seven major clades. In addition, the geographical distribution of the clades reflected their phylogenetic relationships but not current taxonomy. Particularly almost all subclades of clade 7 showed relatively wide distribution range. In the present study, it is suggested that both vicariance and long range dispersal play a crucial role in creating biogeographical patterns of *Bradybaena* on the Ryukyu Islands.