

論文の内容の要旨

MOLECULAR PHYLOGENETIC STUDIES ON JAPANESE
CLAUSILIID LAND SNAILS
(日本産キセルガイ科の分子系統学的研究)

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Clausiliidae is one of the most speciose families in the Japanese land snail fauna with more than 200 nominal endemic species and subspecies being recognized. Clausiliidae is characterized by having a distinctive and very complex structure called the clausilial apparatus (CA) inside the shell. Traditional systems of clausiliid taxonomy have relied heavily on CA morphology. Although 39 generic taxa have been proposed for Japanese clausiliids, the generic classifications are problematic, with the definition of each genus and the hierarchical ranking of subgenera being discordant among authors. In Chapter 2 and 3, I performed a comprehensive molecular phylogenetic analysis of Japanese clausiliids based on mitochondrial and nuclear *ITS* sequences to test traditional morphology-based systems. Almost all Japanese taxa and most Taiwanese taxa constituted a large clade, which is subdivided into seven clades. Phylogenetic relationships among and within the seven clades are largely discordant with the traditional systems. Frequent parallel evolution was also revealed in all taxonomically important characters including CA morphology. Despite the notable discordance between morphology and molecular phylogeny, some tree topologies recovered by this study are congruent with biogeography. As similar phylogeographic patterns have been reported in European clausiliids, local speciations associated with frequent homoplasy

may be a dominant pattern of clausiliid evolution. Two Japanese species, *Mundiphaedusa miyoshii* and *Pliciphaedusa kamoharai*, were placed outside the large clade which includes all other Japanese clausiliids and most of Taiwanese taxa. Instead, these two species were found to be closely related to some Chinese species, suggesting that they are relicts of continental lineage. A new system of generic and subgeneric classification of Japanese and related Taiwanese clausiliids is proposed with description of five new generic taxa: ***Changphaedusa* gen. nov.**, ***Solitariphaedusa* gen. nov.**, ***Dimphaedusa* subgen. nov.**, ***Taiwanphaedusa* subgen. nov.**, and ***Tyrannophaedusoides* subgen. nov.**

Another taxonomic problem on Japanese clausiliids is that the species-level classification is also dubious. In the traditional system, the species-level classification has been based mainly on the shell morphology. In Chapter 2 and 3, I found many cases of discrepancy between the molecular phylogeny and the traditional species classification. In Chapter 4 and 5, I focused on two remarkable cases of such discrepancy between morphology and molecular data, species-level classification of problematic taxa were examined by fine-scale molecular phylogenetic analyses.

In Chapter 4, I performed a phylogeographic analysis on a widely distributed species *Megalophaedusa* (*Pinguiphaedusa*) *pinguis* based on the samples collected from 49 localities. Molecular phylogeny revealed that *Megalophaedusa* (*Pinguiphaedusa*) *pinguis* was not monophyletic. Instead, *M. (P.) pinguis* was shown to be a species complex comprised of eight genetically distinct but geographically confined subclades. Some of the subclades were closely related to different species rather than to other “conspecific” subclades. Genetic divergences among the subclades are very high and some of the inter-subclade distances are equivalent to or higher than the distance between the species verified as biological species. *M. (P.) pinguis* in the traditional sense should be divided into six or eight species.

In Chapter 5, I conducted a fine-scale molecular phylogenetic analysis of *Reinia variegata* and *Reinia ashizuriensis*. *R. variegata* is characterized by the reduction of the lamellae and the absence of clausilium and plicae, while *R. ashizuriensis* has normally developed CA. Due to the remarkable morphological differences, they have been classified as different species belonging to different genera. Molecular phylogeny, however, revealed that *R. variegata* and *R. ashizuriensis* are very closely related to each other with almost no genetic divergence. Haplotype network analysis showed that *R.*

variegata and *R. ashizuriensis* are mutually paraphyletic to each other. It was strongly suggested that *R. variegata* have evolved from *R. ashizuriensis* by independent loss and reduction of CA. Based on the very low level of genetic divergence and probable independent origin of *R. variegata*, *R. ashizuriensis* should be treated as a synonym of *Reinia variegata*.