

琉球大学学術リポジトリ

東アジア産エラブウミヘビ亜科とウミヘビ亜科を対象とした集団遺伝学的解析と分類に関する研究

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論 文 要 旨

Abstract

論 文 題 目

Title Population genetics and taxonomic study of laticaudine and hydrophiine sea snakes in the islands of East Asia

This study is divided into two main parts, concerning two different groups of sea snakes, namely laticaudine sea kraits (Elapidae: Laticaudinae) and hydrophiine sea snakes (Elapidae: Hydrophiinae). First, sequences of mitochondrial cytochrome *b* gene were examined to infer the population genetic structures among the amphibious, laticaudine sea kraits, *Laticauda laticaudata* (n=136) and *L. semifasciata* (n=177), in the Ryukyu-Taiwan region. The results of the molecular analyses revealed a total of 4 (Lati-1 to 4) and 16 (Semi 1 to 16) haplotypes for *L. laticaudata* and *L. semifasciata*, respectively. The pairwise F_{ST} values revealed distinct genetic structures between subregions, suggesting that deep waters serve as obstacles for dispersal and gene flow in both species. In *L. laticaudata*, the results of the analysis of molecular variance (AMOVA) further revealed genetic structures among islands within the same subregion, suggesting differences in dispersal abilities and terrestrial affinities between the two laticaudine species. Based on these findings, the mitochondrial cytochrome *b* sequences obtained from putative migrants, including one specimen of *L. laticaudata* from Yamaguchi Prefecture and 2 specimens *L. semifasciata* from Oita and Mie Prefectures, confirmed the occurrences of accidental drifters, most probably transported to the main islands of Japan by the Kuroshio Current.

Secondly, genetic assessments were conducted to resolve taxonomic confusions and verify the taxonomic status of 2 species of hydrophiine sea snakes, *Hydrophis melanocephalus* and *H. cyanocinctus*, in the Ryukyu Archipelago. Mitochondrial cytochrome *b* sequences obtained from *Hydrophis* spp. specimens from the Central and Southern Ryukyus, and Thailand (n=37) were compared with published sequences from DDBJ/EMBL/GenBank and a phylogenetic tree was constructed. The results revealed two separate taxonomic entities in the Ryukyu Archipelago. Base on the molecular results, examinations of external morphological characteristics revealed overlapping trends, suggesting that these characteristics are unsuitable for distinguishing the two clades in the Ryukyus and examinations of additional morphological characters are needed.

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