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主論文の要約

博士の専攻分野の名称：博士（水産科学）　　氏名：　北　村　志　乃

学 位 論 文 題 目

Molecular phylogenetic studies on the Odontoceti, with special reference to the family Ziphiidae and Delphinidae

（ハクジラ亜目鯨類の分子系統学的研究－特にアカボウクジラ科とマイルカ科について）

Extant cetaceans are known to include two distinct groups, Mysticeti with 14 species of six genera from four families, and Odontoceti with 72 species of 34 genera from 10 families by their morphology. As the number of species shows, the Odontoceti exhibit a greater diversity than the Mysticeti, in terms of the body size, morphology, habitats, and their life history. Identification of species or stocks and their taxonomical clarification are essential to conservation and effective management of target cetaceans. However, previous morphological and/or molecular genetic studies had failed to infer unified phylogenetic relationships, especially within genera in the family Delphinidae and Ziphiidae, the two largest families in the Odontoceti.

In the present thesis, nuclear α-2-actin gene first intron (nuDNA ACTA2I) and mitochondrial DNA control region (mtDNA CR) were used to examine the phylogenetic relationships among 458 individuals, 68 species from 34 genera of ten Odontoceti families, with particular reference to the family Ziphiidae to estimate the genetic diversity of the genus *Berardius*, and *M. stejnegeri*, and Delphinidae.

In Chapter 1, each family of the Odontoceti was shown to be monophyletic with both nuDNA ACTA2I and mtDNA CR markers as reported previously, although intergeneric relationships were still unresolved, particularly for the genera of the Delphinidae, in the present study. Monophyly of the four families of river dolphins was not supported on the CR trees, but Pontoporiidae and Iniidae formed a sister clade on both trees. Relationships among Delphinidae, Monodontidae, and Phocoenidae were inconsistent between both trees, as Monodontidae and Phocoenidae formed a sister clade on nuDNA tree, in agreement with the previous report using Bayesian method (May-Collardo and Agnarsson 2006), but Monodontidae and Delphinidae were sister on mtDNA tree.

In Chapter 2 Part I, both DNA markers supported the monophyly of the Ziphiidae with substantial statistic support, but gave somewhat different intrageneric relationships each other, mainly owing to disparate positioning of the species in the genus *Mesoplodon*. With the ACTA2I marker, five genera *Berardius*, *Hyperoodon*, *Indopacetus*, *Tasmacetus*, and *Ziphius* were monophyletic with moderate statistic support, besides a large cluster of the genus *Mesoplodon*. With the CR marker, however, the cluster of the genus *Mesoplodon* included three other genera except for the genus *Berardius* with low statistic support. On the other hand, both the ACTA2I and CR trees clearly separated the genus *Berardius* into three sister clades with substantial statistic support, namely two groups of *B. bairdii* and *B. arnuxii*, showing the same topology. The observed genetic divergence between the two groups of *B. bairdii* was even larger than the interspecific divergence between *B. bairdii* and *B. arnuxii*. The two groups of *B. bairdii* included five individuals from the Sea of Okhotsk and the rest of them. Although no ocean stocks among the Sea of Okhotsk, the Sea of Japan and Pacific Ocean were genetically apparent, the present analysis with ACTA2I and mtDNA CR distinguished two groups of *B. bairdii* phylogenetically, suggesting the occurrence of a cryptic species in the genus *Berardius*.

In Chapter 2 Part II, 97 individuals of *M. stejnegeri* collected around Japan Seas were analyzed with two DNA markers. Both tree supported the sister clades with *M. densirostris*. In *M. stejnegeri*, gene diversity was higher than haplotype diversity. No other species in cetacean were reported that gene diversity was higher than haplotypes. No genetic differences between regions were suggested in both DNA markers. The estimates of molecular diversities also conformed to HWE and the results favor a probable single panmixic population of *M. stejnegeri* around Japan, although this must be confirmed with a larger scale ecological study using more specimens from different regions of the distribution range.

In Chapter 3, the ML tree with ACTA2I as well as the CR tree supported the monophyly of the Delphinidae with substantial statistic support, although the topology of these trees was notably different and not resolved in mtDNA CR marker. To clarify paraphyletic situation in *S. coeruleoalba*, both nuDNA ACTA2I and mtDNA CR sequences were used to estimate substitution sites within species. In ACTA2I alignmented sequences, 21 bp indel was observed and their allelic combinations were not available for population identification in *S. coeruleoalba*.