

## 学位論文要旨 Dissertation Abstract

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学位論文題目 : A study on population genetic structure of *Rhynchocypris lagowskii* based on mitochondrial DNA cytochrome *b* analysis  
Title of Dissertation (ミトコンドリアDNAシトクロム*b*解析によるアブラハヤの遺伝的集団構造に関する研究)

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**Chapter I:** Analyses of partial mitochondrial DNA (mtDNA) sequences support the classification of downstream fat minnow *Rhynchocypris lagowskii* from the Sea of Japan and Pacific Ocean. We collected the samples from 29 localities in the Sea of Japan and Pacific Ocean. To investigate genetic population structure, we examine nucleotide sequence of 460 bp of the cytochrome *b* region of mitochondrial DNA was amplified by using two primers, L14391 (5'-ATGGCAAGCCTACGAAAAC-3') and H15551 (5'-GATTACAAGACCGATGCTTT-3'). Total sixty-six haplotypes were provided from 29 localities. Sixty-six haplotypes were greatly divided into three groups. Haplotype 1-36 belong to group 1, haplotype 37-40 to group 2 and haplotype 41-66 to group 3. In this study we found three major geographical groups. Molecular phylogenetic analysis revealed that the haplotype diversity of group 3 showed  $0.8720 \pm 0.0282$ . The group 3 was collected from Chube region. On the other hand, the haplotype diversity of group 2 was  $0.6182 \pm 0.1643$ . The group 2 was collected from the Kamishyou River (Toyama Prefecture) and Hakui River (Ishikawa Prefecture). The haplotype diversity of group 1 was average  $0.7735 \pm 0.0299$ . The haplotype diversity of group 3 was bigger than other two. We compared these average value with the river which flowed through the Sea of Japan and Pacific Ocean. Haplotype diversities in the Sea of Japan were  $0.7838 \pm 0.0339$ . Haplotype diversities in Pacific Ocean were  $0.9295 \pm 0.0100$ . The neighbor-joining tree of the mitochondrial DNA haplotypes for all specimens constructed from the Kimura's two parameter. 29 localities were clustered in to 3 major geographic groups in NJ tree mtDNA segment and NJ tree mtDNA haplotypes. No significant difference for the population pair wise *Fst* was detected by the combination of them in those localities ( $p > 0.05$ ). However the *Fst* values showed a high value between each of three groups. The most parsimonious network of mtDNA haplotype in 29 localities was estimated by using the TCS algorithm. To see their haplotype distribution position we constructed distribution of the 66 haplotypes position of the mitochondrial DNA cyt *b* region in *R. lagowskii* species. Specifically, the populations in group 2 and group 3 showed remarkable differentiation from the group 1 population. On

the other hand, the samples of Asamizu River and Iwai River belong to the group 3, but was distributed over the domain where the group 1 inhabited. This result suggested a creation thing of two possibility for the cause of this, invaded individuals or relicts. From past records, it was suggested that it was move likely to be invaded from group 3 domain.

**Chapter II:** In this chapter our analyses based on mtDNA sequences were undertaken to clarify phylogenetic relationship *Rhynchocypris lagowskii* among various site in Tohoku, Japan. Especially, we have collected 9 locations in Mogami River system and 3 locations in Aka River system. *Rhynchocypris lagowskii* are native to in this region. We found a different type of haplotype for some samples which was caused by former population's interruption. The neighbor-joining tree (NJ) of mtDNA haplotypes shows consistently revealed three deeply diverged groups (Group 1, 2 and 3) of *R. lagowskii*. In this tree we found some invaded fish. Normally Mogami River system were belong to group 1. However we identified some mixed samples of group 1 and group 3 in Mogami River system and Aka River system. Mixing rate of group 3 was 50% at OSH, 16.6% at NY in the Mogami River system and 42.8% at YA in the Aka River system. The OSH and NY were located at the midstream from the stand point of the geographical differentiation. The mixed sample of group 1 and 2 appeared at some spots in the same river system regardless of geographical distribution. It suggested that the group 1 accompanied released Ayu and spread in several localities.