論文 / 著書情報
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Title(English)	The evolution of egg-eating cichlids – their conservation and ecological adaptation
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（博士課程）
Doctoral Program

論 文 要 旨

THESIS SUMMARY

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要旨（英文 800 語程度）
Thesis Summary (approx.800 English Words)

Cichlids in Lake Victoria, East Africa, represent one of the rapid known cases of adaptive radiation, with approximately 500 endemic species emerging in about 15,000 years. Among the key drivers of this exceptional speciation is their diverse trophic adaptations, with one of the most unique groups being the egg- and fry-eating cichlids, paedophages. Paedophages exhibit a specialized predatory strategy, wherein they attack mouthbrooding mother and steal their eggs and fries. While egg and fry consumption are commonly observed in nature, the behavior of stealing directly from a mouthbrooding mother is unique to cichlids. Therefore, understanding the evolutionary history and molecular mechanisms behind their trophic adaptation process is essential for a comprehensive grasp of cichlid dietary evolution. This study aimed to elucidate the evolutionary history and genetic basis of trophic adaptation in paedophages through genome-wide analyses, focusing on both conservation aspects and molecular mechanisms.

Firstly, I aimed to reveal past demographic events triggered by the expansion of invasive species and the subsequent impacts on the genetic structure of endemic cichlids especially paedophages. The introduction of Nile perch (*Lates niloticus*) into Lake Victoria in the 1950s had profound effects on the lake's ecosystem. By the 1980s, Nile perch population had peaked, resulting in a drastic reduction in endemic cichlids populations and the extinction of nearly 200 endemic species. Previous studies expected that among the most affected were lineages of high trophic level, such as paedophages, whose population size preferentially decreased due to ecological competition with Nile perch. However, comprehensive investigations of which species or dietary groups the most severely had been impacted by Nile perch, intensity of their population loss, and subsequent changes of genetic structure were remained to be elucidated.
To evaluate the genomic impacts on endemic cichlids caused by the Nile perch invasion, large-scale comparative genomics analyses of eight cichlids, including several paedophages were performed. From genetic statistics and estimated demography, multiple signatures of a severe population bottleneck were observed in four of the eight analyzed species. Their bottleneck event was characterized by reduced genetic diversity and population size. These bottleneck events begun during the 1970s and 1980s when the Nile perch population had peaked. Among the affected species, *Haplochromis* sp. "matumbi hunter" (matumbi hunter) the paedophage, exhibited the most severe bottleneck effects. The findings suggested that ecological and unique morphological traits and habitat specificity of matumbi hunter, played a significant role in determining the intensity of predation pressure by Nile perch. The genomic level of evidence of how invasive species can alter the genetic structure and diversity of endemic species populations, offering crucial insights into biodiversity conservation in ecosystems under threat from invasive species.

Secondly, I focused on understanding the molecular mechanisms underlying paedophages' trophic adaptation. Egg and fry are high-nutrient resources mainly composed of proteins and lipids. Thus, physiological ability to effectively process proteins and lipids is expected to be increased in paedophages. In addition, paedophages have craniofacial traits which is suitable for their feeding strategy such as distensible jaws, small number of inner tooth rows, hypertrophy lips, and small embedded tooth. I assumed that both enhancement of metabolic system and gain of craniofacial traits contributed to the evolution of paedophages.
To test this hypothesis, I conducted comparative genomic and transcriptomic analyses between paedophages and their closely related lineage, *Pundamilia* species, which exhibit different dietary preferences. The analyses discovered significant upregulation of genes involved in lipid transport, fatty acid metabolism and biosynthesis pathways in the paedophages. The expression of key enzymes

such as phospholipases, fatty acid desaturases and elongases was found to be significantly increased in paedophages. Upregulations of these enzymes possibly facilitated the efficient digestion of lipid-rich resources like eggs. Surprisingly, genomic regions exhibited the top 1% differentiation statistics between paedophage and *Pundamilia* species, which is defined as highly differentiated regions (HDRs), were observed within or near those lipid and fatty acid related genes. These cis mutations can modulate gene expression, further contributing to intensify lipid metabolism. Moreover, HDRs were also presented in genes regulate craniofacial structure development, inferring that those mutations can alter gene expression, causing the morphological modification. Genes involving the increased lipids metabolisms and evolution of traits suitable for feeding strategy were detected in this study.

This research provides novel insights into the evolutionary history of unique trophic group, paedophages, and genetic basis of their metabolism and feeding strategy. I demonstrated how the introduction and expansion of invasive species, can lead to population bottlenecks and subsequent alteration of genetic structure, emphasizing the vulnerability of endemic species to ecological changes. These results have implications for conservation biology, particularly in designing strategies to protect biodiversity in ecosystems facing similar threats from invasive species. Furthermore, discovering genes underlying dietary specialization sheds light on the genetic basis of trophic adaptation, a key driver of speciation and ecological success in cichlids. These insights may promote the enforcement of new conservational rules, and further understanding of explosive trophic adaptation of African cichlids.