

学位論文要旨  
Dissertation Abstract

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学位論文題目 : A Study on the Genetic Structure of Tilapia from Ghana  
Title of Dissertation and Japan  
(ガーナと日本におけるティラピアの遺伝的集団構造と遺伝的多様性)

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Tilapia is a freshwater fish with its origin in Africa and has been introduced to other tropical and subtropical regions around the world. In some countries, such as China and other countries in Asia, the aquaculture of tilapia has been a blessing as it has improved the livelihoods of those found in the business and has improved the protein availability in these areas. However, in other areas such as Australia their introduction has caused more problems than benefits. They are considered an invasive species and their culture is prohibited.

1. We identified tilapia species based on mitochondrial DNA. Six species were identified from all samples collected; *O. niloticus*, *S. melanotheron*, *S. galilaeus*, *T. rendalli*, *T. zillii* and *H. elongates*. Wright's  $F$ -statistics ( $F_{ST}$ ) calculated for the *S. melanotheron* populations were high. The Weija Lake recorded only *O. niloticus*, while the Barekese dam showed *S. galilaeus* and *O. niloticus*. The genetic divergence of *S. melanotheron* and *O. niloticus* was suggested between East and West along the coast of the Gulf of Guinea.

2. We wanted to investigate the origin of tilapia populations in Japan. Therefore, Ghana's samples were compared to samples collected from Kochi, Yamaguchi and Thailand (Asia). *Oreochromis* sp., *O. niloticus*, and *O. mossambicus* were identified in Asia with shared haplotypes (Hap5 (*O. niloticus*) and Hap8 (*Oreochromis* sp)) between Kochi and Thailand. Yamaguchi recorded two exclusive

haplotypes, Hap 1 and Hap2, *Oreochromis* sp and *O. mossambicus* respectively. However, there was no shared haplotypes between Ghana and samples from Asia (Japan and Thailand).

3. We continued to identify species from six locations in Japan; Nagoya, Kochi, Yamaguchi, Oita, Kagoshima (2 locations). These samples were analyzed by PCR of the mitochondrial DNA (mtDNA) control region using a different pair of primers. Sequencing of all samples produced a data set of 407bp. A phylogenetic tree showed 51 haplotypes from all six populations. Kagoshima (Tokunoshima Island) population had only *T. zillii* mtDNA type. Nagoya, Kochi and Kagoshima (Minato River) populations had both *O. mossambicus* and *O. niloticus* mtDNA types, whilst Yamaguchi and Oita populations had only *O. mossambicus* mtDNA type. Molecular diversity indices also indicated that the most diverse population for all locations was the *O. mossambicus* type with a value of 0.043, whilst that for *O. niloticus* type was 0.009. However, within population, Kagoshima (Minato River) recorded the highest diversity of 0.04 for *O. mossambicus* and 0.007 for *O. niloticus*.

4. Morphological and meristic characters were measured; weight, standard length, dorsal fin counts and gill raker counts. Initial identification was based on these measures prior to genetic analysis. However, these measures could not differentiate *O. niloticus* from *O. mossambicus* nor the various haplotypes observed. Kagoshima -M recorded the highest weights and lengths within the *O. mossambicus* and *O. niloticus* populations. Kagoshima-M also recorded deformities in the gills albeit the cause is not immediately known. The morphometric measurements did not give conclusive identification.