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主論文の要旨

論文題目 Genetic diversity and characterization of Japanese indigenous chicken breeds and their molecular phylogenetic relationship with Thai indigenous chickens and red junglefowls
(育種と保全に向けたセキショクヤケイと比較する日本在来鶏、タイ在来鶏の遺伝的位置づけ)

氏名 秦 彩乃

論文内容の要旨

Chickens have long lived with humans as companion animals for religious, ornamental, food production, or entertainment purposes. Chickens cannot fly or move long distances by themselves, and their introduction history is closely related to the history of human migration and trade. Molecular phylogenetic studies of domestic chickens have been performed for a wide variety of chicken breeds throughout the world to understand their geographical origins and genetic diversities. To understand the evolutionary history of domestic chicken populations, genetic characterization of their wild progenitor, the red junglefowl (*Gallus gallus*), is prerequisite; however, their population genetic surveys are still limited. Indigenous chicken breeds with unique genetic characteristics have been established according to their uses and habitat in the world. Many ancient trade routes across the Eurasian continent played an important role in bringing various chicken breeds to each area, and Japan was one of the eastern ends of trade routes 1000–2000 years ago.

In Chapter I, I conducted a large-scale genetic study using mitochondrial DNA

D-loop sequences and 28 microsatellite DNA markers to investigate the diversity of 298 wild progenitor red junglefowl (*Gallus gallus*) across two subspecies (*G. g. gallus* and *G. g. spadiceus*) from 12 populations and 138 chickens from 10 chicken breeds indigenous to Thailand. Phylogenetic trees were constructed using D-loop sequences obtained in this study and more than 5,000 sequences retrieved from Genbank. Demographic histories of haplogroups of D-loop sequences (e.g. Haplogroup A–I) were inferred by Bayesian skyline plot analysis. Twenty-nine D-loop sequence haplotypes were newly identified: 14 and 17 for Thai indigenous chickens and red junglefowl, respectively. Bayesian clustering analysis with microsatellite markers also revealed high genetic diversity in the red junglefowl populations. In addition, a rare haplogroup-like lineage, which may have separated from other haplotypes around 2,000 years ago, was constructed by one new haplotype found in three red junglefowls. These results suggest that the ancestral populations of Thai indigenous chickens were large, and that a part of the red junglefowl population gene pool was not involved in the domestication process. Thai fighting-cook had the Haplogroup H, which is also found in Japanese fighting cooks (Shamo) in Okinawa, suggesting the possibility that Shamo chicken in Okinawa originated from Thailand.

In Chapter II, Japanese indigenous chickens have a long breeding history, possibly beginning 2000 years ago. Genetic characterization of Japanese indigenous chickens also has been performed using mitochondrial D-loop region and microsatellite DNA markers. Their phylogenetic relationships with chicken breeds worldwide and genetic variation within breeds have not yet been examined. In this study, the genetic characteristics of 38 Japanese indigenous chicken breeds were assessed by phylogenetic analyses of mitochondrial D-loop sequences compared

with those of indigenous chicken breeds overseas. To evaluate the genetic relationships among Japanese indigenous chicken breeds, a STRUCTURE analysis was conducted using 27 microsatellite DNA markers. D-loop sequences of Japanese indigenous chickens were classified into five major haplogroups, A–E, among 15 haplogroups found in chickens worldwide. The haplogroup composition suggested that Japanese indigenous chickens originated mainly from China, with some originating from Southeast Asia. The STRUCTURE analyses revealed that Japanese indigenous chickens are genetically differentiated from chickens overseas; Japanese indigenous chicken breeds possess distinctive genetic characteristics, and Jidori breeds, which have been reared in various regions of Japan for a long time, are genetically close to each other.

In Chapter III, I conducted whole mitochondrial genome sequencing for 282 individuals including red junglefowl, indigenous chickens from Thailand, Japan and other countries to perform highly resolved demographic analysis with 163 mitochondrial genome sequences of chickens deposited on Genbank.

It is well known that the distribution of domestic chickens spread throughout the world by human migration, culture contact, and trade_during the process of chicken domestication. My present results re-confirmed a long history of strong relationship between chickens and humans.