（学位第３号様式）

学 位 論 文 要 旨

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題　目	**Study on genetic diversity of Myanmar indigenous chickens** **ミャンマー在来鶏の遺伝的多様性に関する研究**

[Background] Myanmar indigenous chickens play an important role in providing a protein source for Myanmar people. In recent years, small and medium indigenous chicken farms for meat production have rapidly been developing. However, information on Myanmar indigenous chickens is very limited. In this study, we investigated their genetic characteristics.

[Materials and methods] Blood samples and seven body measurement data of 235 Myanmar indigenous chickens (120 males and 115 females) were collected from April to May 2019. The survey was conducted at the National Chicken Breeding Center, Mandalay, Sagaing, Lashio, Nay Pyi Taw, and Yangon. In Study 1, the characterization of body measurement traits of six populations was investigated using analysis of variance (ANOVA), and calculated the correlation between traits. In Study 2, I analyzed 176 complete mitochondrial D-loop sequences (1,232 bp) to clarify the genetic diversity and phylogenetic relationships. DnaSP software and Network software were used to calculate diversity and median-joining (MJ) network, respectively. In Study 3, ddRAD-Seq of 343 birds was used to clarify the genome-wide genetic diversity and population structure of Myanmar indigenous chickens and evaluated their relationship with Asian indigenous and commercial chickens. The genetic diversity was determined using PLINK software. Principal component analysis (PCA) was performed using SNPRelate R package and ADMIXTURE v1.3.0 was used for admixture analysis. Distinct chicken groups identified from PCA were analyzed for Differentially Selected Regions (DSR) and Gene Ontology (GO) analyses.

[Results] From Study 1, indigenous chickens in Yangon had the largest body weights ($p < 0.05$) and it may be due to feeding commercial broiler feed according to interviews with their owners. Correlation coefficients between phenotypic traits were significant in the range of 0.24 to 0.80 ($p < 0.01$). The highest correlations between body weight and phenotypic traits were found in Height ($R = 0.73$, $P < 0.01$) and Toe to Back Length ($R = 0.71$, $P < 0.01$). From Study 2, 64 haplotypes were observed, and classified as seven haplogroups with the majority being haplogroup F (HF). When 242 HF sequences (79 Myanmar and 163 deposited sequences from Asian countries/region) were analyzed, the highest genetic diversity was observed in Myanmar. Furthermore, Myanmar indigenous chickens and red junglefowls were observed in the center of the star-like MJ network of the 37 HF sequences, revealing Myanmar indigenous chickens as important genetic resources. In Study 3, ddRAD-Seq analysis identified 21,696 SNPs. he heterozygosity values indicated relatively high genetic diversity and population structure analyses suggested that Myanmar indigenous chickens represent a unique genetic cluster comprising three groups; I then identified DSRs among these groups. I identified 71 DSRs between Myanmar fighting and Myanmar indigenous chickens (Comparison-1), 152 DSRs between Myanmar fighting and Asian indigenous chickens (Comparison-2), and 46 DSRs between Myanmar indigenous and Asian indigenous chickens (Comparison-3). The GO analysis revealed that the genes in the DSRs between Comparison-2 and between Comparison-3 were enriched in various GO terms. The results suggested that there are substantial genetic differences between Myanmar and Asian chickens.