博士論文要約（Summary）

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タイトル	**STUDY ON GENETIC DIVERSITY OF MYANMAR CATTLE BREEDS**

キーワード（ミャンマー在来牛）　（遺伝的多様性）　（分子遺伝学的手法）

Local cattle breeds are popular in Myanmar because they make excellent draught animals, so it is of fundamental importance that their genetic diversities and population structures are elucidated for breeding and conservation purposes. In this study, I characterized the genetic diversities and population structures of four popular Myanmar local cattle breeds (Pya, Shw, Sha and Ngw) using some molecular genetic approaches such as mitochondrial D-loop sequencing, analyses of autosomal SNP genotypes and Y-chromosomal SNP haplotypes. In addition, I also characterized three measurement traits and the distributions of the SNPs associated with several economically important traits in them.

Firstly, I compared three measurement traits of body height, body length and heart girth between the four local breeds (32 in males and 41 in females) and crossbred population (2 in males and 13 in females). These results showed that the mean height, length and girth ranged from 105.67 ±4.12 cm, 100.33 ±4.97, 126.11 ±6.09 in Sha to 128.38 ±8.29, 126.85 ±5.64, 173.30 ±8.55 in Crossbred (Cro) in adult female. Cro showed significantly larger body than the local breeds, suggesting the significant effect of crossbreeding on improving the local cattle. Among the local breeds, Sha had the significantly small body.

Next, I investigated the genetic diversity and relationship of the local breeds using some molecular genetic analyses. In the D-loop sequencing, 26 polymorphic sites and 27 haplotypes were obtained and belonged to two zebu haplogroups of I1 and I2 by the NJ tree and MJ network. Fifteen novel maternal lineages were found in Myanmar cattle. Sha was significantly different from other breeds, according to the pairwise F_{ST} values.

In the autosomal SNPs genotyping, we characterized the genetic diversities and population structures of four popular Myanmar local cattle breeds and five native cattle populations from neighboring countries

using 21,918 autosomal SNP genotypes on the GeenSeek Genome Profiler 50K array. The mean H_O and expected H_E estimates using pruned datasets ranged from 0.317 and 0.322, respectively, in Cambodia to 0.448 and 0.421, respectively, in Vietnam South. The four Myanmar local breeds exhibited similar levels of genetic diversity. However, AMOVA in nuclear DNA revealed significant genetic differentiation among the four local breeds ($p < 0.00001$), and Neighbor-Net analysis showed that Shan Ngwar Pu was distinct from the other Myanmar local breeds.

For analysis of Y-chromosomal SNP haplotypes, we used 68 bulls from the local breeds and five Y-chromosomal SNPs which discerned between *Bos indicus* and *Bos taurus*. These results showed that 65 bulls had haplotype 1 (H1) which were observed only in *Bos indicus* lineage and three were new haplotype which was 1-base different from H1. These results agreed with my previous results and suggest that Myanmar local breeds were not affected by introgression or gene-flow from taurine cattle in paternal lineage. For distributions of the SNPs associated with several economically important traits, I investigated the distributions of 204 SNPs in the local breeds. *Ppoly* of carcass trait, milk traits occurred in Myanmar cattle. These results may provide useful information for improving beef production and milking use in the Myanmar local breeds. However, further studies are required for the effects of these SNPs on the traits using the local breeds.

In the RAD-Seq analysis, 10,793 SNPs was finally found in 30 cattle from five breeds both of *Bos indicus* and *Bos taurus* cattle. Breed differentiation between *Bos taurus* and *Bos indicus* was clearly identified with phylogenic NJ tree and PCA results. In addition, MDS results showed that the breed origins were reflected according to their geographically location.

In conclusion, the mtDNA sequencing, Bovine 50K SNPs genotyping, GWAS, Y chromosome diversity, genotyping for economic important traits and RAD-Seq methods have been successfully examine on Myanmar cattle breeds for various purposes. The resulting information would be provided implementing national conservation management plans and breeding strategies for sustainable improvement and conservation of cattle genetic resources.