

Thawee Laodim 2015: Genomic Variation for Dairy Production Traits in a Multibreed Dairy Cattle Population in Thailand. Master of Science (Animal Science), Major Field: Animal Science, Department of Animal Science. Thesis Advisor: Assistant Professor Skorn Koonawootrittriron, Ph.D. 83 pages.

Single nucleotide polymorphisms (8,810 SNPs) were obtained from 1,413 cows representing 195 farms located in Central (78 farms), Southern (67 farms) and Northeastern (50 farms) regions of Thailand. A total of 8,573 SNPs were chosen based on their call rate ( $> 90\%$ ) and known physical location in each chromosome (autosomes and sex chromosome). The selected SNPs were analyzed in terms of genomic variation and extent of linkage disequilibrium (LD) in a Multibreed dairy cattle population in Thailand. Analyses included distribution of SNPs, distance between SNPs, density of SNPs, and minor allele frequencies (MAF) within chromosomes. The SNPs that had known physical location in autosomes and had  $MAF \geq 0.05$  were linked using an SNP map and the pedigree of cows with the Haploview software and LD estimated using parameters  $D'$  and  $r^2$ . The results indicated that SNPs of Thai multibreed dairy cattle were unevenly distributed within autosomes and the sex chromosome and they tended to be clustered in some chromosome regions. The distribution of LD in each autosome was affected by distance between pairs of SNPs, MAF, and sample size. High levels of the LD were found in autosomes, particularly between SNP pairs at distances between 40 to 50 kb ( $D' = 0.694 \pm 0.007$  and  $r^2 = 0.202 \pm 0.003$ ). The minimum sample size of Thai multibreed dairy cattle required to obtain accurate measurement of LD was more than 177 for  $D'$ , and 89 for  $r^2$ . Differences between results obtained here and from other cattle populations support the need to conduct genome-wide association studies in Thai multibreed populations to improve their genetic potential under local environmental conditions.

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