Genes Involved in Cellular Responses to Heat Stress in Thai Multibreed Dairy Cattle

Laodim, T.¹, Koonawootrittriron, S.^{1*}, Suwanasopee, T.¹, & Elzo, M.A.² ¹Department of Animal Science, Faculty of Agriculture, Kasetsart University, 50 Ladyao, Chatuchak, Bangkok 10900, Thailand ²Department of Animal Sciences, University of Florida, Gainesville, Florida, United States of America *E-mail: agrskk@ku.ac.th

Dairy producers in tropical environments expect their cattle to be both adapted and productive under hot and humid conditions. Single nucleotide polymorphisms (SNPs) could be associated with milk yield (MY) directly through genes that increase MY or indirectly through genes that increase adaptability to high heat and humidity allowing dairy cattle a fuller expression of their MY genetic ability under tropical conditions. Thus, the objective of this study was to identify a subset of genes associated with MY that were also involved in cellular responses to heat stress in the Thai dairy multibreed population. Milk yield phenotypes were from 8,361 first-lactation cows in 810 farms located in Northern, Northeastern, Central, Western, and Southern Thailand. All cows had complete phenotypic and pedigree information. Genotypic data included 74,144 imputed and actual SNPs from 2,661 animals (89 sires and 2,572 dams). Single-step genomic best linear unbiased predictions were utilized to estimate SNP variances for MY. Fixed effects included contemporary group (herd-year-season), breed regression, heterosis regression, and calving age effects. Random effects were animal additive genetic and residual. SNPs explaining 0.001% or more of the genetic variance for MY, were selected to identify genes in the NCBI database. Biological functions of genes associated with MY, were extracted from the Gene Cards database. There were 29 genes associated with MY involved in cellular response to heat stress. These genes were located in chromosomes 1, 5, 6, 7, 11, 12, 13, 15, 16, 17, 18, 19, 20, 22, 23, 25, 26, and 28. The high number and widespread location of SNP across the genome support the quantitative nature of adaptability to heat stress. The importance of these genes will likely vary depending on animal breed composition and adaptability of Holstein and other breeds in the Thai population. Further, breed composition and environmental conditions vary across locations and years, thus this study will need to be periodically repeated to have a more complete understanding of the adaptability and productivity of dairy cattle in Thailand.