

Applying Genomics to Enhance Production Efficiency of Cattle in Tropical Regions

Skorn Koonawootrittriron^{1*}, Mauricio Elzo², Thanathip Suwanasopee¹, Danai Jattawa¹, Bodin Wongpom¹, Pimchanok Yodklaew¹, Tawirat Konkrua¹, Thawee Laodim¹, and Mattaneeeya Sarakul¹

¹Department of Animal Science, Faculty of Agriculture, Kasetsart University, Bangkok, Thailand

²Department of Animal Sciences, University of Florida, Gainesville, Florida, USA

*Corresponding Author's Email: agrskk@ku.ac.th

High temperature and humidity are ubiquitous characteristics in the tropics creating stressful conditions that represent the main challenge to improvements in cattle production efficiency. Thus, a major concern of genetic improvement programs in tropical regions is genetic adaptability of cattle to high temperature and humidity conditions. Crossbreeding between productive *Bos taurus* and adapted *Bos indicus* cattle has been used widely to take advantage of complementarity and heterosis. Increasing our understanding the genomic basis of associations between economically important and adaptability traits under stressful tropical conditions is key to developing genetic programs to enhance production efficiency. Conventional genetic evaluations compute estimated breeding values (EBV) using only phenotypes and pedigree, whereas genomic EBV utilize phenotypes, pedigree, and genotypes, and can have substantially higher accuracies than conventional EBV. The cost of genotyping with high-density chips has decreased markedly in recent years, making it affordable to an increasingly larger number of cattlemen. Thus, widespread genotyping in tropical cattle populations will both increase the accuracy of genomic EBV and yield faster rates of genetic progress for production and adaptability traits. Linkage disequilibrium among SNP markers is used to impute genotypes from cheaper low-density chips to high-density chips, further decreasing costs and increasing the number of genotyped animals. A major advantage of genomic EBV is that animals can be evaluated at much younger ages resulting in shorter generation intervals and faster genetic progress than with conventional EBV. This is particularly advantageous for early selection of artificial insemination sires in dairy cattle. Future research includes identification of large numbers of SNP associated with genes accounting for high percentages of genetic variation affecting production and adaptability traits. These SNP will not only serve as predictors of genomic EBV, but also increase our understanding of the biological function of these genes and their effect on phenotypes in tropical environments.

Keywords: cattle, genetic improvement, genome, production traits, tropical