Genome-wide association analysis for milk yield, fat yield, and age at first calving in the Thai multibreed dairy population

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The objective in this research was to identify sets of SNP markers and genes associated with milk yield (MY), fat yield (FY), and age at first calving (AFC) in the Thai multibreed dairy population. Genotype data included 74,144 actual and imputed GGP80k SNP makers from 2,661 animals. A 3-trait genomic-polygenic model was used to estimate SNP genetic variances for MY, FY, and AFC. Fixed effects were contemporary group (herd-year-season), breed regression, and heterosis regression. Random effects were animal additive genetic and residual. Individual SNP explaining at least 0.001% of the genetic variance for MY, FY, and AFC were used to locate genes or nearby genes in the NCBI database using R package Map2NCBI. Ontologies of genes associated with these three traits were performed using program PANTHER. There were 26,576 SNP associated with MY, 26,399 SNP with FY, and 26,655 SNP with AFC. Forty-four percent of these SNP were located inside or within 2,500 bp of genes for MY and FY, and 38% for AFC. Genes associated with the three traits (n = 3,436) were located in all chromosomes. These genes explained 26% of the additive genetic variance for MY and FY, and 25% for AFC. Genes associated with all traits were primarily involved in binding and catalytic activities related to cellular processes. Important genes in the Thai multibreed dairy population differed substantially from those reported in *Bos taurus* breeds in temperate environments. This indicated that studies to identify sets of genes relevant to MY, FY, and AFC in this and other populations subject to a variety of environmental conditions need to continue because predicted SNP values will likely differ across cattle populations and changing environmental conditions over time.

Keywords: SNP genetic variation, genome, dairy cattle, tropical regions

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