

Use of Young and Proven Sires with Genomic Evaluations for Improving Milk Yield in Thai Multibreed Dairy Cattle

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Dairy cattle genetic evaluation in Thailand was changed from conventional to genomic since 2016. This is expected to increase selection accuracy and shorten generation in dairy breeding program. The objective was to investigate the genomic estimated breeding values (GEBV) and prediction accuracy for 305-d milk yield (MY) of young sires (had no or < 10 daughters) and proven sires (had ten daughters or more) in 2016 to 2018 Thai dairy genomic evaluations. Three single-step genomic evaluations were constructed using datasets that were used to make the genomic evaluations in 2016, 2017 and 2018. Pedigree and phenotypes for 2016, 2017 and 2018 evaluations were accumulated from 9,339, 10,345, and 11,383 first-lactation cows, respectively. In addition, genomic data included actual and imputed 74,396 SNP from 2,661 animals in 2016, 2,961 animals in 2017 and 3,261 animals in 2018. Animal GEBV for MY were computed using variance components estimated with AIREMLF90. Single-step genomic models included herd-year-season, calving age, heterosis as fixed effects, and additive genetic and residual as random effects. Standardized GEBV for MY of only top 100 sires evaluated in particular year were investigated. Results showed that 69% of sires in 2016, 65% of sires in 2017 and 64% of sires in 2018 that were ranked in top 100 for MY were young sires. Moreover, GEBV LSmeans for MY of top 100 sire tended to increase for + 290.62 kg in 2016, + 300.37 kg in 2017, and + 312.12 kg in 2018. The similar trends were found for young sires and proven sires. GEBV LSmean trended to increase from +278.83 kg (in 2016) to +307.41 kg (in 2018) for young and from +302 kg (in 2016) to +316 kg (in 2018) for proven sire. Similarly, LSmeans of prediction accuracy trended to increase from 29.27% (in 2016) to 30.29% for young sires and from 65.49% to 70.08% for proven sires. These results indicated the achievement of sire production in Thailand due to the increment of GEBV and prediction accuracy of superior sires. Wider utilization of superior sires would help speed up genetic progress for MY in Thai dairy population.