Warangkana Kitpipit 2012: Genetic Evaluation on Milk Production Traits Using Random Regression Test-Day Model in a Thai Multibreed Dairy Cattle Population. Doctor of Philosophy (Animal Science), Major Field: Animal Science, Department of Animal Science. Thesis Advisor: Associate Professor Sornthep Tumwasorn, Ph.D. 120 pages.

Monthly test-day yields of 21,934 records from 2,321 first lactating cows were obtained from the Department of Livestock Development (DLD). Data were collected during the years 1993 and 2003. Test day yield were adjusted by the variation of herd-year-season of calving, Holstein Friesian (HF) breed fractions, calving age and first test-date after calving effects. In the first trial, the four functions included Wilmink exponential (WIL), Wood gamma (WD), Schaeffer and Dekkers (SHE) logarithm, and Legendre polynomials (LEG) functions were used to fit the mean and individual lactation curve. The results found that the WIL gave the best goodness of fit to mean and individual lactation curves and smaller values of residual errors than other functions. Also, WIL was therefore considered to be the most suitable function to describe the lactation curve in this population.

The second trial estimated genetic parameters of 305-d milk yield (305MY) and persistency of milk yield using WIL function. Three measures of persistency were calculated as 1) absolute value of regression coefficient from WIL function or parameter c (PER1), 2) the different of milk yield between days 60 and 280 (PER2) and 3) the ratio between accumulated yield from 201 to 305 days and 305MY (PER3). Multiple-trait animal model was performed using EM-REML to estimate genetic parameters. Heritability of 305MY was found to be 0.12, and persistency traits were low ranging from 0.01 to 0.03. Genetic correlations between 305MY and persistency traits were found to be range from 0.37 to 0.55. Ratio method in our study not only described persistency, but also was highly influenced by 305MY. Genetic correlations among three measurements of persistency were ranged from -0.07 to 0.99. The results showed that PER1 could be considered the suitable method to measure persistency because it was not complicated for computation, interpretation, heritable, and had low correlated with 305MY.

The third trial was carried out to evaluate genetic ability of milk yield using random regression test day model (RR-TDM). The model contained the random effect of herd-test date (HTD), fixed regression, and random regressions on the animal and the permanent environmental effects. The WIL function was nested as sub-models for both fixed and random parts. Residual and HTD variance was assumed constant during lactation. The results showed that heritability of 305MY was 0.47 which was higher than the lactation model (0.12). Heritabilities of daily yields varied from 0.40 to 0.59 and was generally highest at the mid lactation. The correlations of sires and cows occurred between RR-TDM and lactation model were moderate high. These results implied that RR-TDM could be used for routine genetic evaluation instead of lactation model. Moreover, the RR TDM can calculate genetic persistency at the same time. The RR-TDM was therefore suitable for routine evaluations on milk yield and persistency of dairy cattle under small farms and tropical conditions.

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