

GENETIC PARAMETERS OF MILK LACTATION CURVE TRAITS OF THAI DAIRY CATTLE

S. Pangmao¹, P.C. Thomson² and M.S. Khatkar¹

¹Sydney School of Veterinary Science, University of Sydney, 425 Werombi Road, Camden, NSW, 2570 Australia

²School of Life and Environmental Sciences, University of Sydney, 425 Werombi Road, Camden, NSW, 2570 Australia

SUMMARY

The aim of this study was to estimate genetic parameters of lactation traits, viz. 305-day milk yield, peak milk yield, days to peak milk yield and persistency in Thai dairy cattle from three government farms. Milk yield and peak milk yield have moderate heritability suggesting these can be improved by selective breeding while days to peak milk yield and persistency have low heritability which can be improved by adjusting environmental management such as feed and farm management. The genetic correlations of most of these traits across lactations were high suggesting that selection based on the first lactation will improve the first three lactations in these herds.

INTRODUCTION

Lactation curve is important for prediction of milk yield and for feeding management in lactating cows. The inclusion of accurate description of lactation curve can be very useful for breed improvement programs. The test interval method (TIM) is an empirical-based method and is one of the standard methods approved by the International Committee for Animal Recording (ICAR) for calculating 305-day milk yield (ICAR 2019, Schaeffer and Jamrozik 1996). In addition, there are many mathematical models that have been used to describe lactation curves. The Wood model (Wood 1967) has been widely used (Dijkstra *et al.* 2010) due to its simple form and ability to capture key features of the lactation curve (Tozer and Huffaker 1999) and more robust compared to other models when fitting lactation curve to irregular and infrequent test-day sampling regimes (TDSR) (McGill *et al.* 2013). This study used data from three dairy cattle research centres recorded by the Department of Livestock Development of Thailand. The objectives of this study were to estimate the genetic parameters, including heritability, genetic and phenotypic correlations of lactation curve traits across lactations of Thai dairy cattle in three government research farms.

MATERIALS AND METHODS

Description of data and animal management. The data from three Thai government dairy cattle farms provided by the Bureau of Animal Husbandry and Genetic Improvement (BAHGI), Department of Livestock Development (DLD) in Thailand were used for this study. Two farms are located in Chiang Mai province and Nakhon Ratchasima province raised both Holstein-Friesian (HF) and crossbred HF while the third farm located in Sakon Nakhon province raised only crossbred HF. Upgrading local or zebu breeds with HF semen or natural mating with HF bulls has been used to improve productivity and maintain tropical insect and disease tolerance in these herds.

All animals in the three farms were raised under the same guidelines given by BAHGI. Nevertheless, some aspects were different such as feeding and health management because of the differences of locations, weather conditions, feed resources, farm machinery and diseases prevalence. Fresh Ruzi and Napier grass were fed during the rainy season while in the dry season, Ruzi silage and hay were fed (nutrient components of roughage and concentrate feed using in dairy cattle farm as described in Pangmao *et al.* (2017)).

Data and statistical analysis. The data comprised of 25,789 monthly test day milk yield records of 1,468 cattle from lactation 1 to 3 of HF and crossbred HF dairy cattle who calved between 1990 and 2015. The total number of animals, sires and dams in the pedigree file were 4,753; 287 and 1,237, respectively. The records of cows with less than three test day milk yield records were excluded for further analysis. Five breed groups of animals were classified based on the percentage of HF blood as 1 (≤ 75), 2 ($>75 - 87.5$), 3 ($>87.5 - 93.75$), 4 ($>93.75 - 99.99$) and 5 (100), as calculated from the pedigree information. The calving months were grouped into three seasons, namely winter (November to February), summer (March to June) and rainy (July to October). The traits examined were accumulated 305-day milk yield calculated by using the adapted test interval method (Sargent *et al.* 1968) and Wood model (Wood 1967) in the form of non-linear model (MT and MW), peak milk yield (PY), days to peak milk yield (DP) and persistency (PS). The 305-day milk yield calculated by using the adjusted test interval method as follows:

$$MT = I_0 M_1 + I_1 * \left(\frac{M_1 + M_2}{2}\right) + I_2 * \left(\frac{M_2 + M_3}{2}\right) + \dots + I_{n-1} * \left(\frac{M_{n-1} + M_n}{2}\right) + \frac{I_n M_n}{2}$$

where M_1, M_2, \dots, M_n are the milk yields (kg) recorded in the 24 hours of the recording day and given to one decimal place, I_1, I_2, \dots, I_{n-1} are the intervals in days between recording dates, I_0 is the interval in days between the lactation period start date and the first recording date, and I_n is the interval in days between the last recording date and the end of the lactation period. The nonlinear Wood model is as follows:

$$W(t; k, b, c) = \exp(k + b \log_e t - ct)$$

where $W(t)$ is the theoretical or expected milk yield at time t , k is a scalar factor, b is the rate of increase prior to the peak and c is the rate of decrease after the peak. Cumulative milk yield to day T (say day 305) was then obtained as $MW = \int_0^T W(t) dt$. Fitting of the Wood model was conducted using the *nlme* library in R (Pinheiro *et al.*, 2018) and calculation of cumulative milk yield through use of the *pgamma* function in R. The parameters derived from Wood model were used to calculate lactation curve characteristics namely peak milk yield ($PY = e^k(b/c)^b e^{-b}$), days to peak milk yield ($DP = b/c$) and persistency ($PS = -(b+1)\log_e c$).

Estimates of genetic parameters were obtained with an animal model, formulated as a linear mixed model fitted to each of the five traits. Univariate models were used to estimate variance components and heritability estimates of each trait, while bivariate models were used to estimate covariance components and correlations estimates between a trait in two different lactations. Model fitting was conducted using ASReml-R (Butler *et al.* 2009). The univariate model used in the analysis is as follows:

$$y_{ijkl} = \mu + \text{Herd}_i + \text{YSOC}_j + \text{BG}_k + \text{Anim}_l + e_{ijkl}$$

where y_{ijkl} is an observation of trait on animal l ; μ is the overall mean; Herd_i is the fixed effect of herd (level, 1-3); YSOC_j is the fixed effect of year and season of calving (level, 1-78); BG_k is the fixed effect of breed group (level, 1-5); Anim_l is the random animal effect; and e_{ijkl} is the random residual effect.

RESULTS AND DISCUSSION

The descriptive summary of milk yield and lactation characteristic traits for lactation 1 to 3 is shown in Table 1. Both accumulated milk yields (MT and MW) were similar within all the three lactations. The lowest MW in lactation 1 compared with lactation 2 and 3 ($3,348 \pm 1282$ kg vs $3,685 \pm 1,503$ kg and $3,564 \pm 1,317$ kg, respectively) was in agreement with Hossein-Zadeh (2014) ($9,186$ kg vs $10,386$ kg and $10,000$ kg, respectively) which may be due to partition of nutrition for growth and milk production in lactation 1 cows. The highest PS in lactation 1 was in agreement with Gengler (1996) who reported higher persistency in first lactation than the other lactations.

Table 1. Descriptive summaries of the lactation curve traits from lactation 1 to 3 of Thai dairy cattle (mean \pm standard deviation (number of observations))

Traits ^a	lactation 1	lactation 2	lactation 3
MT	3,379 \pm 1,409 (1,301)	3,682 \pm 1,604 (949)	3,599 \pm 1,534 (665)
MW	3,348 \pm 1,282 (1,210)	3,685 \pm 1,503 (906)	3,564 \pm 1,317 (636)
PY	14.95 \pm 4.97 (1,210)	17.52 \pm 6.48 (906)	17.49 \pm 6.09 (633)
DP	49 \pm 26 (1,209)	39 \pm 18 (904)	41 \pm 17 (638)
PS	6.68 \pm 0.48 (1,209)	6.43 \pm 0.39 (906)	6.43 \pm 0.41 (638)

^aMT: milk yield calculated by test interval method; MW: milk yield calculated by Wood model; PY: peak milk yield; DP: days to peak milk yield and PS: persistency

The estimated heritabilities for lactation curve traits of lactation 1 to 3 are shown in Table 2. In general, the heritability estimates of all traits from first parity cows were greater than or equal to those from parities 2 and 3. The heritability estimate of MW was higher in lactation 1 compared to lactation 2 and 3 (0.21 vs 0.01 and 0.08, respectively) while for MT, heritability is similar between lactation 1 (0.19) and 3 (0.19) but lower in lactation 2 (0.12). The heritability estimates of MT and MW in lactation 1 was similar to Mohammed *et al.* (2013) (0.24) but lower compared to the reported in other studies (0.35: König *et al.* 2005 and 0.34: Sarakul *et al.* 2011). The lower milk yield heritability in this study compared to other studies may be due to the low estimate of additive variance and high estimate of residual variance suggesting this trait was highly affected by the environmental factors such as farm and feed management, hot and humid tropical environment. In addition, the different size of the data and the models used for analysis also might have an effect on estimation of variance components and heritability estimates. Nonetheless, milk yield calculated from both methods show the potential of improvement by selection program. Lactation curve traits' heritability estimates (PY, DP and PS) were low to moderate ranging from 0.00 to 0.23 for lactation 1 to 3. The heritability of PY and DP in lactation 1 was similar to Chegini *et al.* (2015) (0.23 vs 0.26 and 0.10 vs 0.10) although PS was higher (0.14 vs 0.05). In general, the heritability estimates of lactation curve traits for all lactations were low except the moderate heritability of PY in lactation 1 and 3 (0.23 and 0.17 respectively) which means only PY can be improved by selective breeding while DP and PS trait may be improved with better management practices.

Table 2. Estimates of heritability (\pm standard errors) of the lactation curve traits from lactation 1 to 3 of Thai dairy cattle

Traits ^a	lactation 1	lactation 2	lactation 3
MT	0.19 \pm 0.06	0.12 \pm 0.07	0.19 \pm 0.10
MW	0.21 \pm 0.06	0.01 \pm 0.05	0.08 \pm 0.09
PY	0.23 \pm 0.06	0.09 \pm 0.07	0.17 \pm 0.10
DP	0.10 \pm 0.05	0.01 \pm 0.05	0.00 \pm 0.00
PS	0.14 \pm 0.06	0.04 \pm 0.06	0.00 \pm 0.00

^aMT: milk yield calculated by test interval method; MW: milk yield calculated by Wood model; PY: peak milk yield; DP: days to peak milk yield and PS: persistency

Table 3 shows the genetic and phenotypic correlation estimates of lactation curve characteristics between lactation 1 to 3. Most of the genetic correlation estimates of the traits were high (0.75 to 0.99). The high genetic correlation estimates of all traits between two different lactations suggested that the selection of animal for first lactation curve traits in these herds will improve traits in the second and third lactation as well, although the phenotypic correlations for most of the traits were low and negative for PS.

Table 3. Genetic and phenotypic correlation (in parenthesis) (\pm standard errors) of lactation curve traits of Thai dairy cattle between traits in two different lactations

Traits ^a	lactation 1 vs lactation 2	lactation 1 vs lactation 3	lactation 2 vs lactation 3
MT	0.96 \pm 0.11 (0.32 \pm 0.05)	0.92 \pm 0.16 (0.28 \pm 0.05)	0.97 \pm 0.26 (0.53 \pm 0.05)
MW	0.99 \pm 0.06 (0.26 \pm 0.05)	0.87 \pm 0.11 (0.29 \pm 0.05)	0.94 \pm 0.07 (0.15 \pm 0.06)
PY	0.99 \pm 0.06 (0.40 \pm 0.04)	0.75 \pm 0.12 (0.26 \pm 0.05)	0.94 \pm 0.11 (0.32 \pm 0.06)
DP	0.92 \pm 1.07 (0.08 \pm 0.05)	NA	NA
PS	0.85 \pm 0.74 (0.06 \pm 0.05)	NA (-0.02 \pm 0.06)	NA (-0.02 \pm 0.06)

^aMT: milk yield calculated by test interval method; MW: milk yield calculated by Wood model; PY: peak milk yield; DP: days to peak milk yield and PS: persistency

CONCLUSIONS

The results from this study suggested that two methods of calculation of accumulated 305-day milk yield were quite similar with moderate heritability estimates for lactation 1 which means that milk yield in these herds can be improved by selective breeding. However, only peak milk yield will respond to selective breeding for lactation curve traits of cows in lactation 1. The high genetic correlation estimates of most lactation traits of the first lactation with the second and third lactation suggested that the selection of animals based on the first lactation could increase the overall milk yield in these three government farms in Thailand.

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