

Genetic parameters of milk traits of dairy cattle in Thailand

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Summary

The aims of this study were to compare 305-day or less than 305-day milk yield estimated by the test interval method and the Wood model method, and to estimate genetic parameters of 305-day or less than 305-day milk yield estimated by test interval method (MY) and Wood model method (WMY), lactation length (LL), fat percentage (FP) and protein percentage (PP) from first lactation dairy cattle raised in Thailand. The data comprised 11,753 monthly test-day records from 1,300 first lactation of purebred Holstein-Friesian (HF) and crossbred HF with local or zebu animals. Genetic parameters were estimated by univariate and bivariate linear mixed animal model using ASReml-R. The fixed effects were herd, breed group, year of calving, season of calving and the interaction between year and season of calving and the random effects were animal and residual. The estimated heritabilities for MY, WMY, LL, FP and PP were 0.22 ± 0.06 , 0.23 ± 0.06 , 0.09 ± 0.04 , 0.16 ± 0.05 and 0.47 ± 0.07 , respectively. The genetic correlations were high between two milk yield estimates (MY and WMY), and moderate to high between milk yield and LL (0.51 to 0.78), and low to moderate among milk composition (FP and PP) and LL (-0.17 to 0.42). Overall the heritability estimates of all the traits analysed were moderate to high except LL, these indicated that most traits in this herd can be improved by selective breeding.

Keywords: milk traits, lactation length, wood model

Introduction

Milk traits such as milk yield and milk composition are important in dairy cattle breeding improvement globally due to the direct impact on farmers' incomes. Normally, *Bos taurus* breeds in the temperate zone produce more milk and have longer milking periods than *Bos indicus* breeds in the tropical zone. Therefore, many countries in the tropical zone including Thailand have used crossbreeding and upgrading the local or zebu cattle by using Holstein-Friesian (HF) or other temperate breeds to increase milk yield and lactation length. Presently, most of the dairy cattle population in Thailand has more than 75% HF blood (Buaban *et al.*, 2016).

Milk yield and milk composition data of animals in Thailand are typically recorded monthly. These records are used for calculating cumulative 305-day milk yield and milk composition for quantitative genetic analysis or are used directly for quantitative genetic analysis by use of random regression test day models. There are a number of methods for calculating cumulative 305-day milk yield, including the test interval method (TIM) (Sargent *et al.*, 1968), Wood model (Wood, 1967) and Wilmink model (Wilmink, 1987). The TIM and

Wilmink method have been widely used and been the standard method suggested by the International Committee for Animal Recording (ICAR). The Wood model also has been widely used due to requiring fewer parameters and providing good fit of lactation data.

At present, genetic analysis in Thailand mainly relies on quantitative genetic evaluation although molecular genetic evaluation has been conducted and reported recently (Jattawa *et al.*, 2015). However, it will take time before molecular genetic approaches are implemented in Thailand because of the high cost of genotyping. Improvement of the genetics and breeding program in Thailand by accurate and reliable estimates of genetic parameters will help to increase milk production of dairy cattle in Thailand. Thus, the aim of this study was to estimate genetic parameters of 305-day or less than 305-day milk yield estimated by the test interval method (MY) and Wood model method (WMY), lactation length (LL), fat percentage (FP) and protein percentage (PP) from first lactation dairy cattle raised in Thailand.

Material and methods

Animals and management

The animals in this study were raised in three government dairy cattle farms and comprised two main groups of purebred HF and crossbred HF. Upgrading local or zebu breed with HF semen or HF bulls has been used to improve productivity and maintain tropical insect and disease tolerance in these herds. The heifers were bred by both considerations of age (more than 15 months age) and body weight (more than 280 kg). Animals in each farm were raised under the same guidelines given by the Bureau of Animal Husbandry and Genetic Improvement. However, there are some differences in feeding and health management among these farms due to differences in their locations, weather conditions, feed resources, machinery and prevalence of diseases. More details on the feeding and management of these herds can be found in Pangmao *et al.*, (2017)

Data and statistical analysis

The data in this study were provided by the Bureau of Animal Husbandry and Genetic Improvement, Department of Livestock Development, Thailand. Data were recorded using the Dairy Herd Improvement (DHI) program which is used in government dairy cattle farms in Thailand. The data comprised 11,753 monthly test-day milk yield and milk composition records of 1,300 first lactation cattle from HF and crossbred HF dairy cattle that calved between 1991 and 2014. The total numbers of sires, dams and animal in the pedigree file were 287, 1,237 and 4,753 respectively. The data consist of cow number, birth date, calving date, parity, monthly test-day milk yield, fat and protein percentage and lactation length. The records of cow that have less than three monthly test-day milk yield records were excluded. The animals were classified into five breed groups 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). 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 estimated milk yield in 305-day or less, lactation length (LL), fat percentage (FP) and protein (PP) percentage. The 305-day or less milk yield was estimated by an adapted test interval method (MY) Sargent *et al.*, (1968) as given in Equation (1) and the Wood model (WMY) (Wood, 1967) in the nonlinear form as given in Equation (2), the TIM is as follows:

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

where M_1, M_2, M_n are the weights (kg), given to one decimal place, of the milk yielded in the 24 hours of the recording day, I_1, I_2, 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 Wood model is specified as

$$W(t; k, b, c) = \exp(k + b \log_e t - ct) \quad (2)$$

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) is then obtained as $WMY = \int_0^T W(t) dt$. Fitting of the Wood model was conducted using the nlme library in R (Pinheiro *et al.*, 2017) and calculation of cumulative milk yield through use of the pgamma function in R.

Genetic parameters of five traits were estimated using a mixed model in ASReml-R (Butler, 2009), as specified in Equation (3):

$$y_{ijklm} = \mu + H_i + YOC_j + SOC_k + BG_l + YOC : SOC_{jk} + Anim_m + e_{ijklm} \quad (3)$$

where y_{ijklm} is an observation of trait on animal m , μ is the overall mean, H_i is the fixed effect of herd (level, 1–3), YOC_j is the fixed effect of year of calving (level, 1–24), SOC_k is the fixed effect of season of calving (level, 1–3), BG_l is the fixed effect of breed group (level, 1–5), $YOC : SOC_{jk}$ is the fixed effect of interaction between year and season of calving (level, 1–72), $Anim_m$ is the random animal effect and e_{ijklm} is the random residual effect.

Heritabilities were estimated by univariate models as fitted in Equation (3) and genetic and phenotypic correlations were estimated by a series of pairwise bivariate models using the same term of fixed and random effects as univariate models.

Results and Discussion

Overall mean and standard deviation of MY, WMY, LL, FP and PP were $3,376 \pm 1,409$ kg, $3,347 \pm 1,285$ kg, 272 ± 56 days, 3.55 ± 0.67 % and 3.04 ± 0.25 %, respectively. Milk yield estimated by the TIM (MY) and Wood model (WMY) were similar although WMY was approximately 29 kg lower than MY. The BG fixed factor had no significant effect on all traits. Three fixed effects, namely H, YOC and YOC:SOC had significant effects on MY ($P = 3.3E-20$, $P = 5.5E-36$ and $P = 0.034$, respectively), WMY ($P = 1.2E-19$, $P = 1.8E-25$ and $P = 0.0095$, respectively) and FP ($P = 1.8E-6$, $P = 1.6E-31$ and $P = 9.1E-7$, respectively) while H, YOC, SOC and YOC:SOC had significant effects on PP ($P = 1.1E-7$, $P = 9.0E-14$, $P = 0.026$ and $P = 0.013$, respectively). Two fixed effects of YOC and YOC:SOC had significant effects on LL ($P = 5.8E-12$ and $P = 0.020$). Table 1 shows the model-based adjusted means and standard errors for MY, WMY, LL, FP and PP across the three herds. MY and WMY were highest in herd 1 followed by herd 2 and 3. This might be due to a larger proportion of animals in Herd 1 were from Breed Group 5 which tended to produce more

milk as compared to the other groups (Breed Group 1: 2,924 ± 115 kg, Breed Group 2: 3,042 ± 89 kg, Breed Group 3: 3,010 ± 93 kg, Breed Group 4: 3,112 ± 108 kg and Breed Group 5: 3,331 ± 120 kg, respectively). However, BG itself was not significant in this analysis. Herd had no significant effect on LL. Herd 3 has the highest FP but the lowest MY, WMY, LL and PP. The significant effects of herd might be due to different factors such as environment and management factors. SOC had a significant effect only on PP ($P = 0.026$) with the means being rainy season, 3.06 ± 0.02 %, summer, 3.10 ± 0.03 %, and winter, 3.09 ± 0.02 %. YOC and YOC:SOC had a significant effect on all traits (data not shown).

Table 1. Model-based adjusted means and standard errors for test interval milk yield (MY), Wood model milk yield (WMY), lactation length (LL), milk fat percentage (FP) and milk protein percentage (PP) by herd.

Herd	MY (kg)	WMY (kg)	LL (days)	FP (%)	PP (%)
Herd 1	3,595.4 ± 90.8 ^c	3,609.6 ± 87.3 ^c	263.0 ± 3.8	3.42 ± 0.05 ^b	3.18 ± 0.02 ^c
Herd 2	3,209.7 ± 88.6 ^b	3,320.7 ± 85.0 ^b	267.5 ± 3.8	3.30 ± 0.05 ^a	3.08 ± 0.02 ^b
Herd 3	2,445.5 ± 101.9 ^a	2,555.6 ± 98.0 ^a	260.1 ± 4.3	3.60 ± 0.05 ^c	3.00 ± 0.03 ^a

^{a,b,c}Means in the same column with different letters differ significantly ($P < 0.05$)

Estimated additive genetic variances were 253,859 ± 68,865 kg² for MY, 230,771 ± 60,798 kg² for WMY, 270 ± 134 days² for LL, 0.066 ± 0.023 %² for FP and 0.027 ± 0.005 %² for PP. Estimated residual variances were 915,434 ± 64,448 kg² for MY, 770,085 ± 55,818 kg² for WMY, 2,853 ± 161 days² for LL, 0.358 ± 0.024 %² for FP and 0.030 ± 0.003 %² for PP. The heritability estimates for all traits are shown in Table 2. MY and WMY had similar and moderate of heritability estimates (0.217 ± 0.056 and 0.231 ± 0.057, respectively). The heritability estimates of MY and WMY were in the range (0.22 to 0.24) of estimated heritability of milk yield in crossbred dairy cattle in Thailand (Boonkum & Duangjinda, 2015). The heritability estimate for FP was 0.155 ± 0.052 which was lower than the values of 0.22 for FP in multibreed dairy population in Central Thailand (Koonawootrittriron *et al.*, 2009). PP has the highest heritability estimate (0.470 ± 0.069) while LL has the lowest heritability estimate (0.086 ± 0.042).

The estimated genetic and phenotypic correlations for all traits are shown in Table 2. The genetic correlation between MY and WMY was very high (0.987 ± 0.046). This indicated that both test interval method and Wood model method can be used for 305-day or less than 305-day milk yield estimate and provided the similar estimate (3,376 ± 1409 kg vs 3,347 ± 1285 kg) in this herd. Three traits namely MY, WMY and LL had moderate to high genetic correlation (0.505 to 0.987) with each other while FP had low to moderate genetic correlation (0.204 to 0.415) with those three traits. PP had a negative genetic correlation (-0.249 to -0.171) with other traits except with FP (0.301). However, almost of the genetic correlations were only suggestive because of high standard error. The phenotypic correlation was high between MY and WMY (0.714). In contrast, the phenotypic correlations were low (-0.071 to 0.165) between milk composition (FP and PP) and milk yield (MY and WMY) and LL.

Table 2. Estimated heritability (diagonal), genetic correlation (below diagonal) and phenotypic correlation (above diagonal) for test interval milk yield (MY), Wood model milk yield (WMY), lactation length (LL), milk fat percentage (FP) and milk protein percentage (PP).

	MY	WMY	LL	FP	PP
MY	0.217 ± 0.056	0.714 ± 0.014	0.737 ± 0.013	0.165 ± 0.031	0.013 ± 0.034
WMY	0.987 ± 0.046	0.231 ± 0.057	0.340 ± 0.025	0.098 ± 0.032	-0.071 ± 0.035
LL	0.780 ± 0.118	0.505 ± 0.228	0.086 ± 0.042	0.148 ± 0.030	0.123 ± 0.032
FP	0.300 ± 0.223	0.204 ± 0.228	0.415 ± 0.289	0.155 ± 0.052	0.295 ± 0.030
PP	-0.187 ± 0.158	-0.249 ± 0.156	-0.171 ± 0.236	0.301 ± 0.163	0.470 ± 0.069

Overall the heritabilities of all traits were moderate to high except LL, these indicated that most traits in this herd can be improved by using an appropriate mating program and genetic selection. However, breeders should take into consideration the negative genetic correlations between PP and MY, WMY and LL traits. The high genetic correlation between MY and WMY (0.99 ± 0.05) showed that either test interval method or Wood model method can be used for estimate 305-day or less than 305-day milk yield from monthly test-day records in this herd. However, the heritability estimate of WMY is slightly higher. The selection based on an index of milk production traits and WMY can provide maximum genetic gain in overall productivity in these herds.

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