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Original Article

Milk yield, fat yield and fat percentage associations in a Thai multibreed dairy population



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A R T I C L E I N F O

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ABSTRACT

Milk yield (MY), fat yield (FY) and fat percentage (FP) are important traits for dairy cattle selection and dairy farm profitability in Thailand. Most dairy cattle in Thailand are multibreed, comprising multiple breeds (three from eight breeds per animal). This multibreed composition of dairy animals has generated a large amount of variation in dairy traits among cows raised under farm, tropical environmental conditions across the country. Effective genetic evaluation and selection programs for dairy traits in this population require reliable variance components and genetic parameters estimated under the management, nutritional, health, and climatic conditions in Thai dairy farms. Thus, the objective of this study was to estimate genetic parameters for MY, FY and FP in a Thai dairy multibreed dairy cattle population using farm-collected information. The dataset consisted of pedigree and phenotypic data for MY, FY and FP from 6596 first lactation cows from 687 farms. The data were analyzed using a three-trait (MY, FY and FP), animal mixed model. Fixed effects were herd-year-season, Holstein fraction, heterozygosity and age at first calving. Random effects were animal and residual. An average, information-restricted, maximum likelihood procedure was used to estimate variance components, which in turn were used to compute heritabilities and genetic correlations. Means (SD) were 4315.43 kg (1112 kg) for MY, 157.41 kg (50.42 kg) for FY and 3.59% (0.56%) for FP. Heritability estimates were 0.22 \pm 0.06 for MY, 0.17 \pm 0.06 for FY and 0.24 ± 0.07 for FP. Genetic correlations were 0.47 ± 0.16 between MY and FY, -0.30 ± 0.20 between MY and FP, and 0.30 \pm 0.21 between FY and FP. These estimates of genetic parameters indicated that Thai dairy producers would achieve reasonable amounts of genetic progress if they selected dairy animals based on MY and either FY or FP.

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Introduction

Dairy milk contains many nutrients necessary for humans and is an excellent source of protein, fat, lactose, vitamins and minerals that are vital for body growth, health maintenance and disease prevention (Bauman et al., 2006; German and Dillard, 2006). Commercial dairy production was established in Thailand in the late fifties; however, national milk production has yet to meet the domestic demand (Office of Agricultural Economics, 2014). The most important trait for Thai dairy producers is volume of milk or milk yield because it is directly associated with the amount of income. In addition, milk composition traits such as fat percentage have been used as indicators of milk quality and considered in the determination of price paid for raw milk sold by producers, with a high content of fat in milk being generally preferred in dairy processing plants (Thai Milk Board, 2016).

Crossbreeding local cattle with improved dairy temperate breeds (for example, Holstein, Brown Swiss and Jersey) has been widely used in Thailand as a means of increasing milk production (Koonawootrittriron and Elzo, 2010). An upgrading program to Holstein has been promoted by the government for over 40 yr and purebred Holstein and crossbred Holstein with representation of various other breeds have been used as parents, thus creating a multibreed dairy population with a wide range of breed compositions (Koonawootrittriron et al., 2009). This crossbreeding mating strategy has likely increased the amount of genetic variation for MY, FY and FP among cows in the Thai dairy population. Accurate estimation of variance components and genetic parameters in the

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Thai multibreed population would benefit dairy genetic improvement programs and lead to the design of optimum breeding programs. Thus, the objective of this research was to estimate the variance components and genetic parameters for 305 d first lactation milk yield (MY), 305 d fat yield (FY), and average 305 d fat percent (FP) using all available phenotypic and pedigree information from the Thai dairy population from 1989 to 2013.

Materials and methods

Data, animals and traits

The dataset consisted of monthly test-day milk yields, monthly test-day fat yields and monthly test-day fat percentages from 6596 first-lactation cows that calved from 1989 to 2013. These cows were from 687 farms located in Central, Northern, Northeast and Southern Thailand and were the progeny of 1013 sires and 4727 dams. Breeds represented in the multibreed dairy population were Holstein, Brahman, Jersey, Red Dane, Red Sindhi, Sahiwal and Thai Native. Holstein was represented in the vast majority of animals in the population, with 92% of all animals in the population being at least 75% Holstein and the Holstein percentage within animals ranged from 12.5% to 100%.

Traits were 305 d first lactation milk yield (MY), 305 d fat yield (FY) both measured in kilograms and average 305 d fat percentage (FP). Test-day milk yields were taken from each individual cow once a month beginning after calving and continuing until dry off. Monthly cow test-day milk samples were sent to a laboratory for determination of the fat percentage for a given month. Monthly test-day milk yields were used to compute MY using the test-interval method (Sargent et al., 1968; Koonawootrittriron et al., 2001). FP was computed as a weighted average of monthly fat percentages over the lactation of a cow. FY was computed as the sum of the products of milk yield for each interval multiplied by the fat percentage for that interval, over all intervals within a lactation.

Climate, management and nutrition

The weather in Thailand is influenced by the southwestern and northeastern monsoons; daily temperature ranges from 17.5 °C to 36.2 °C, humidity fluctuates between 63% and 84% and the average rainfall is 1587.7 mm/yr (Thai Meteorological Department, 2014a). Seasons are classified into winter (November to February; cold and dry), summer (March to June; hot and dry), and rainy (July to October; hot and humid).

Dairy cattle in this population were managed differently across farms. Cows were fed different amounts of concentrate depending on their daily milk production (1 kg of feed per 2 kg of milk produced). Roughage consisted mainly of fresh grasses (*Penicum maximum*, *Brachiaria ruziziensis*, *Pennisetum purpureum* and *Brachiaria mutica*). Fresh grass was limited during the dry season (November to June) because of the limited availability of stored water and underground water supplies. Other sources of fiber that farmers fed their cows included rice straw and agricultural byproducts such as corn cobs, cassava leaves and corn silage.

Cows were raised in open barns and milked twice a day. The first milking was in the morning (0400–0500 h) and the second milking was in the afternoon (1400–1500 h). Farmers used a bucket system or a pipeline system for milking. Raw milk was collected in bulk tanks and transported to a dairy cooperative or to a private milk collection center after each milking session. Cows were mated all year round using artificial insemination. Sires were chosen on the basis of high milk yield of their offspring and availability of semen.

Estimation of variance component and genetic parameters

The variance and covariance components for MY, FY and FP were estimated using an average information restricted maximum likelihood procedure with the program ASREML (Gilmour et al., 2006). The data were analyzed using a 3-trait animal model. Fixed effects were herd-year-season, Holstein fraction of cow, heterosis of cow as a function of heterozygosity (the probability of having alleles of different breeds within loci) and cow age at first calving. Random effects were animal additive genetic effects and residual. Heritabilities, genetic correlations and phenotypic correlations were computed using the variance component estimated with ASREML. The 3-trait animal model in matrix notation is shown in Eq. (1):

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z}\mathbf{a} + \mathbf{e} \tag{1}$$

where **y** is a vector of MY, FY and FP, **b** is a vector of fixed effects (herd-year-seasons, Holstein fractions, heterozygosities of cows and cow ages at first calving), **a** is a vector of random animal additive genetic effects, **e** is a vector of random residual effects, **X** is an incidence matrix relating records in **y** to fixed effects in **b** and **Z** is an incidence matrix relating records in **y** to animal additive genetic effects in **a**.

The assumptions of the 3-trait animal model are presented in Eq. (2):

$$\begin{bmatrix} \mathbf{y} \\ \mathbf{a} \\ \mathbf{e} \end{bmatrix} \sim MVN \left(\begin{bmatrix} \mathbf{X}\mathbf{b} \\ \mathbf{0} \\ \mathbf{0} \end{bmatrix}, \begin{bmatrix} \mathbf{Z}_{\mathbf{a}}\mathbf{G}_{\mathbf{a}}\mathbf{Z}'_{\mathbf{a}} + \mathbf{R} & \mathbf{Z}_{\mathbf{a}}\mathbf{G}_{\mathbf{a}} & \mathbf{R} \\ \mathbf{G}_{\mathbf{a}}\mathbf{Z}'_{\mathbf{a}} & \mathbf{G}_{\mathbf{a}} & \mathbf{0} \\ \mathbf{R} & \mathbf{0} & \mathbf{R} \end{bmatrix} \right)$$
(2)

where G_a is equal to $G_0 \otimes A$ where G_0 is the matrix of additive genetic covariances among the 3 traits (MY, FY, and FP), A is the numerator relationship matrix, \otimes is a Kronecker product, R is equal to $R_0 \otimes I$, where R_0 is the matrix of residual covariances among the three traits (MY, FY and FP), and I is an identity matrix. Multivariate normal distribution (*MVN*) was assumed for all considered variables.

Results and discussion

Mean values for cows in the Thai multibreed dairy population were 4315.4 kg (SD = 1112.0 kg) for MY, 157.4 kg (SD = 50.4 kg) for FY and 3.6% (SD = 0.6%) for FP. The ranges in values were from 1103 kg to 9562 kg for MY, from 29 kg to 635 kg for FY and from 1.2% to 6.3% for FP. The means were within the ranges reported in previous studies in Central and Northern Thailand (Chongkasikit et al., 2002; König et al., 2005; Koonawootrittriron et al., 2009; Department of Livestock Development, 2010; Dairy Farming Promotion Organization, 2012).

Factors affecting milk yield, fat yield and fat percentage

Herd-year-season and calving age were important for MY and FY (p < 0.01). Holstein fraction only influenced MY (p < 0.05). Fat percentage was affected by herd-year-season (p < 0.01) but not by Holstein fraction, heterozygosity and calving age. Herd-year-season least squares means (LSM) estimates and standard errors ranged from 1143.6 ± 788.4 kg to 9580.5 ± 788.5 kg for MY, 34.8 ± 35.8 kg to 636.2 ± 35.8 kg for FY and 1.2 ± 0.4% to 5.8 ± 0.4% for FP. These ranges in differences were the outcome of the combined effects of climate conditions, herd management, feeding, health care and cow Holstein fractions across herd-year-season subclasses. The LSM by year-season across herds tended to increase for MY (3.86 ± 1.71 kg/ year-season, p < 0.05), and to decrease for FY (-0.25 ± 0.12 kg/year-season, p < 0.05) and FP ($-0.007 \pm 0.001\%$ /year-season, p < 0.01).

Lastly, trait LSM across year-seasons within herds ranged from 2070.6 kg to 7078.0 kg for MY, 47.3 to 300.4 kg for FY, and 1.85% to 5.07% for FP.

Yeamkong et al. (2010a) reported that year-season and farm location-farm size affected the monthly milk yield and milk quality per farm and per cow in dairy cattle in Thailand. Variation in MY, FY and FP among herd-year-seasons was expected because of the variability in feeding regimens, management strategies and the breed composition of cows. Furthermore, Thailand is a tropical country where seasonal climatic conditions are influenced by the southwestern and northeastern monsoons (Thai Meteorological Department, 2014b). Thus, seasonal differences in temperature, humidity and rainfall affect the abundance of forage, which is associated with the ability to produce milk in dairy cows. The current results confirmed that variation in yearseasons and herds affected milk production in the Thai multibreed dairy population.

The Holstein fraction affected MY (p < 0.05; Table 1). The regression coefficient of MY on Holstein fraction was 13.19 ± 5.68 kg (p < 0.05). This regression coefficient estimate indicated that cows with higher Holstein fractions would have higher MY. However, upgraded crossbreds with a high percentage of Holstein may fail to reach their production potential under the hot and humid climatic conditions in Thailand (Koonawootrittriron et al., 2009; Seangjun et al., 2009). In addition, sensitivity to heat stress was found to be higher in crossbred Holstein cows with Holstein fractions higher than 93.7% (Boonkum et al., 2011). Thus, to achieve high milk production levels with very high Holstein-fraction cows, dairy producers would also need to further improve their management practices (housing and feeding) to better match the dairy genetic production ability of their cows.

Heterozygosity was not significant for any trait (Table 1). However, Thai dairy cattle can be composed of fractions of up to eight breeds (Koonawootrittriron et al., 2002; Ritsawai et al., 2014). An increase in the Holstein fraction was found to be associated with an increase in the milk yield, whereas an increase in the Thai Native and Jersey fractions was associated with a decrease in the milk yield (Ritsawai et al., 2014). Holstein was the most highly represented breed in this population. However, 99% of cows were crossbred involving three breeds; hence, heterozygosity should be considered in genetic prediction models used for genetic improvement in the Thai multibreed dairy population.

Calving age was important for MY and FY (p < 0.01; Table 1). The estimated regression coefficients were 11.73 ± 2.78 kg for MY (p < 0.01) and 0.55 ± 0.16 kg for FY (p < 0.01). These regression coefficient estimates indicated that cows calving at older ages would have higher MY and FY. Mostert et al. (2001) also reported the cows calving at older ages had higher milk yields than cows calving at younger ages in Holstein and Jersey populations. The development of the mammary gland is the primary factor affecting milk production, and a well-developed mammary gland with many secretory cells, good blood supply and strong connective tissue will be highly productive over a long time (Strucken et al., 2015). Moreover, 80% of mammary cells are formed during pregnancy and calving (Wall and McFadden, 2012). The optimum age at first calving to produce the highest, first-lactation milk

yields in Holstein heifers was in the range 23-24.5 mth (Ettema and Santos, 2004; Teke and Murat, 2013). However, the average age at first calving was 30.3 ± 5.3 mth in the Thai multibreed dairy population (Koonawootrittriron et al., 2006). Thus, reducing the age at first calving in Thai dairy cattle through management and nutrition could reduce costs and increase cow lifetime milk production.

Variance component estimation, heritability and genetic correlations

Estimates of the additive genetic variances were $144,485 \pm 39,803 \text{ kg}^2$ for MY, $233 \pm 90 \text{ kg}^2$ for FY and $0.48 \pm 0.15\%^2$ for FP. Estimates of residual variances were 498,004 \pm 36,698 kg² for MY, 1082 \pm 87 kg² for FY and for 1.48 \pm 0.14%² for FP. The heritability estimates were moderate for all traits (0.22 ± 0.06 for MY, 0.17 ± 0.06 for FY and 0.24 ± 0.07 for FP; Table 2). These heritability estimates were lower than the values of 0.29–0.41 for MY, 0.29 to 0.39 for FY and 0.47 to 0.50 for FP in a Dutch Holstein-Friesian population (Stoop et al., 2008; Schopen et al., 2009). Heritabilities for MY and FY here were also lower than in UK Holstein-Friesian populations (Pollott, 2009; Eaglen et al., 2013). However, cows in these studies were purebred as opposed to the multibreed composition of cows in the current study. Cows in the Thai dairy population can be composed of up to eight different breeds-Holstein, Brahman, Jersey, Red Dane, Red Sindhi, Sahiwal, Brown Swiss and Thai native (Koonawootrittriron et al., 2002; Ritsawai et al., 2014). Furthermore, Thai dairy farmers were reported to be small holders with less than 10 milking cows per day (Yeamkong et al., 2010b). Thus, differences in variances and heritabilities were probably related to differences in breed composition as well as in the production conditions in tropical Thailand and in temperate European countries.

Estimates of correlations between FY and FP were positive for both the genetic correlation (0.30 ± 0.21) and the phenotypic correlation (0.40 ± 0.01) , whereas there was a negative genetic correlation (-0.30 ± 0.20) and a negative phenotypic correlation (-0.15 ± 0.02) between MY and FP (Table 2). Similarly, Koonawootrittriron et al. (2009) in Thai multibreed and Toghiani (2012) in Holstein cattle populations also found negative genetic correlations between MY and FP. Estimates of genetic and phenotypic correlations between MY and FY were high and positive (genetic correlation = 0.47 ± 0.16 and phenotypic correlation = 0.70 ± 0.01 ; Table 2). Similarly, high genetic correlations between MY and FY were also obtained in Thai dairy cattle (0.77; Koonawootrittriron et al., 2009), Canadian Holstein (0.56; Miglior

Table 2

Heritabilities (diagonal) and genetic correlations (above diagonal) and phenotypic correlation (below diagonal) among first-lactation 305 d milk yield (MY), 305 d fat yield (FY) and 305 d fat percentage (FP) in dairy cows.

Trait	МҮ	FY	FP
MY	0.22 ± 0.06	0.47 ± 0.16	-0.30 ± 0.20
FY	0.70 ± 0.01	0.17 ± 0.06	0.30 ± 0.21
FP	-0.15 ± 0.02	0.40 ± 0.01	0.24 ± 0.07

Table 1

Regression coefficient estimates (b) and their standard errors (SE) of Holstein fraction, heterozygosity and calving age on milk yield, fat yield and fat percentage.

Factors	Milk yield	Milk yield		Fat yield		Fat percentage	
	b ± SE	<i>p</i> -value	b ± SE	<i>p</i> -value	b ± SE	p-value	
Holstein fraction Heterozygosity Calving age	13.19 ± 5.68 5.69 ± 3.34 11.73 ± 2.78	0.017 0.0882 <0.0001	73.20 ± 37.79 0.39 ± 0.21 0.55 ± 0.16	0.0529 0.0606 <0.0001	$\begin{array}{c} 0.21 \pm 0.46 \\ 0.0023 \pm 0.0026 \\ 0.00001 \pm 0.00200 \end{array}$	0.6376 0.3662 0.9738	

et al., 2007) and in Californian and New York Holsteins (0.52–0.63; Albuquerque et al., 1995). The negative genetic correlation between MY and FP may not be of immediate concern to Thai dairy producers because the revenue from Thai dairy farms depends mostly on yield traits.

The estimates of variance components and genetic parameters here indicate that dairy producers should consider the positive association between MY and FY and the negative association between MY and FP in their genetic improvement programs. In addition, to increasing the level of expression of dairy traits in animals with a high Holstein fraction, housing conditions, feeding regimes and health care will likely need to be upgraded. If dairy producers wanted to increase both MY and FP, then a selection index based on estimated breeding values for MY and FP suitable to their selection goals would need to be utilized. Thus, the variance components and genetic parameters obtained here will help dairy producers develop genetic improvement programs and breeding plans tailored to their goals. Utilization of estimates of variance components and genetic parameters for genetic evaluation and selection would help optimize Thai dairy genetic improvement and mating programs.

In conclusion, the heritabilities for MY, FY and FP were moderate, indicating that selection for these traits would be expected to make reasonable progress. Genetic correlations between MY and FY and between FY and FP were low and positive, and between MY and FP were low and negative. These genetic correlations indicated that genetic progress for MY and FY could be achieved by selecting for these traits directly. Conversely, increasing both MY and FP would require an index with weights appropriate to dairy producer selection goals. These genetic parameters estimated under Thai environmental conditions would help optimize dairy genetic improvement and mating programs.

Conflicts of interest

The authors declare that they have no conflict of interest.

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