Abstract T86

Genetic and Phenotypic Trends for Age at First Calving and Milk Yield in Daughters from Imported and Thai Holstein Sires

Age at first calving (AFC) and milk yield (MY; accumulated 305-d milk yield) are important traits for the dairy cattle industry. To genetically improve these traits under tropical conditions in Thailand, both imported Holstein (IH) and Thai Holstein (TH; purebred and crossbred Holstein-Other Breeds) sires have been used for mating with Holstein purebred and Holstein-Other Breeds crossbred cows. The objective of this study was to compare genetic changes in AFC and MY from 1991 to 2013 in first-lactation daughters of IH and TH sires. The dataset included AFC and first-lactation MY from 5,389 daughters of 516 IH and 241 TH sires that calved from 1991 to 2013 in 474 dairy farms. The bivariate animal model considered herd-year-season and Holstein fraction as fixed effects, and animal and residual as random effects. Variance components were estimated using an average information restricted maximum likelihood procedure. Variance component estimates were used to compute heritabilities and correlations. Mean estimated breeding value (EBV) for daughters of IH and TH sires were computed for each calving year. Regressions of mean EBV for AFC and MY on calving years were computed to assess genetic trends. Heritability estimates were 0.19 ± 0.04 for AFC and 0.13 ± 0.04 for MY. Near zero genetic (0.09 ± 0.18) and phenotypic (0.07 ± 0.02) correlations were estimated between AFC and MY. Overall genetic trends were negative for AFC (-0.013 ± 0.003 mo/yr; P < 0.001) and positive for **MY** (1.16 ± 0.30 kg/yr; P = 0.001). However, negative **AFC** genetic trends existed for daughters of **IH** sires (-0.006 ± 0.003). mo/yr; P = 0.06) and **TH** sire (-0.020 ± 0.004 mo/yr; P < 0.001). Conversely, significant positive **MY** genetic trends occurred for progeny of **IH** sires (1.14 ± 0.43 kg/yr; P = 0.008) and **TH** sire (4.40 ± 0.46 kg/yr; P < 0.001). These results indicated that there was genetic improvement in the appropriate direction (negative for AFC and positive for **MY**) in this Thai dairy population, and that **TH** sires brought larger changes than **IH** sires, primarily for **MY**.

INTRODUCTION

Age at first calving (AFC) and milk yield (MY; accumulated 305-d milk yield) are economically important traits for dairy cattle industry. Cows that have early AFC helped the farmers to reduce production costs and increase the opportunity to take advantage in the production system. In addition, cows that have high MY are preferred to increase revenue of the diary business. Thus, reducing AFC and increasing MY of the following generation are considered as objectives of the dairy genetic improvement programs in many countries.

Thailand is a country in Southeast Asia. The weather in country generally has high temperature (average 28 °C; $SD = 2^{\circ}C$) and high humidity (average 74%; SD = 9%), and also two tropical monsoons every year. Commercial dairy production in Thailand was established at around 1957 by a Royal initiative project. To increase **MY** under tropical conditions, both imported Holstein (**IH**) and Thai Holstein (TH; purebred and crossbred Holstein-Other Breeds) sires have been used for mating with Holstein purebred and Holstein-Other Breeds crossbred cows. Currently most of Thai dairy cattle have higher than 75% Holstein breed fractions, and each of them could have one to more than seven distinct cattle breeds (Bos taurus and Bos indicus), which all of them have equal chance to be selected for being as parent of the following generations.

The variability of **AFC** and **MY** over the years in Thai dairy population is the result from genetic differences among animals that they received from their parents (sire and dam), and also environment that they received from management practice of the producer. Thus, knowing the difference of genetic change of **AFC** and **MY** in first-lactation daughters of **IH** and **TH** sires in this Thai multibreed dairy population will be benefit to dairy genetic improvement program under tropical conditions.

MATERIALS AND METHODS

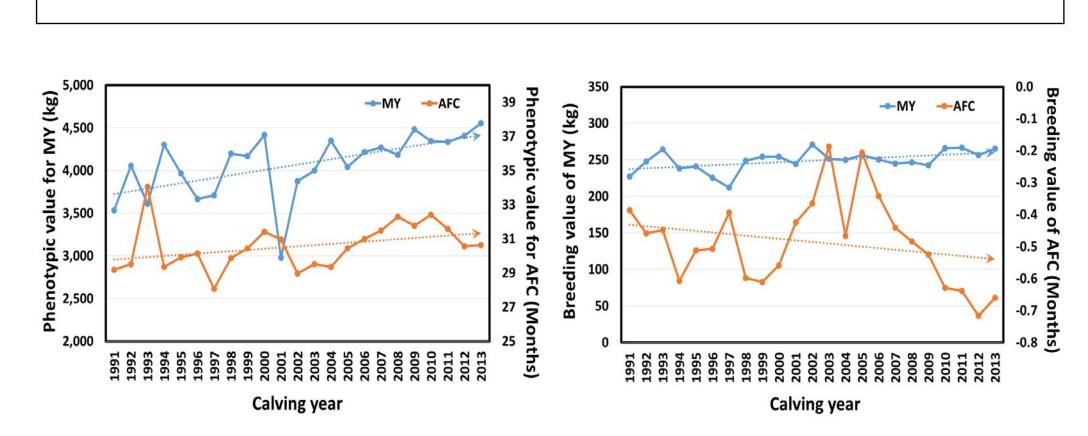
Data, Animals and Traits: The dataset consisted of age at first calving (AFC) and accumulated 305-d milk yield (MY) records of 5,835 first lactation cows raised in 474 dairy farms located across Thailand. These cows had first calving during 1991 to 2013, and they were daughters of 516 imported Holstein (IH) and 241 Thai Holstein (TH) sires that contained purebred Holstein and crossbred Holstein-Other breeds. The pedigree file contained 9,939 animals from 757 males (sires) and 9,182 female (dams and cows). In this dairy population, both purebreds and crossbreds animals had equal chance to be selected for being parent of the next generation (multibreed dairy population; Elzo and Famula, 1985). Cattle breeds presented in this multibreed population were Holstein, Brahman, Brown Swiss, Jersey, Red Dane, Red Sindhi, Sahiwal and Thai Native. However all of them had Holstein breed fraction ranged from 12.5% to 100%. Cows were bred all year round by artificial insemination. Sires were chosen based on their semen availability and their genetic ability for high milk yield and early age at first calving. Culling were done mainly based on their reproductive and health problems.

Tawirat Konkruea*, Skorn Koonawootrittriron*, Thanathip Suwanasopee* and Mauricio A. Elzo† *Department of Animal Science, Kasetsart University, Bangkok 10900, Thailand [†]Department of Animal Sciences, University of Florida, Gainesville, FL 32611-0910, USA

SUMMARY



Means of estimated breeding value (**EBV**) of all cows ranged from -0.72 (0.99) months in 2012 to -0.19 (1.04) months in 2003 for AFC, and from 212.31 (124.98) kg in 1997 to 270.86 (135.11) kg in 2002 for MY. Considering daughters of IH sires, the mean EBV ranged from -0.68 (0.83) months in 2012 to -0.18 (1.16) months in 2001 for AFC, from 242.38 (99.34) kg in 1991 to 306.65 (115.59) kg in 2009 for **MY**. While the means **EBV** of daughters of **TH** sires ranged from -0.86 (0.58) months in 1994 to 0.10 (1.22) months in 2003 for **AFC**, and from 141.76 (101.74) kg in 1997 to 264.37 (111.42) kg in 2011 for MY.



Phenotypic regression coefficient estimate was 0.089 ± 0.016 (P < 0.001) mo/yr for AFC, and 35.32 \pm 3.13 (P < 0.001) kg/yr for MY. The regression coefficient on **EBV** of all cows was -0.013 ± 0.003 mo/yr (P < 0.001) for **AFC**, and 1.16 \pm 0.30 kg/yr (P = 0.001) for **MY**. Genetic trends for **MY** were positive for daughters of IH sires (1.14 \pm 0.43 kg/yr; P = 0.008) and TH sires (4.40 \pm 0.46 kg/yr; P < 0.001). Conversely, genetic trends for AFC were negative for both daughters of IH sires (-0.006 \pm 0.003 mo/yr; P = 0.064) and TH sire (-0.020 ± 0.004 mo/yr; P < 0.001).

The positive genetic trends for **MY**, and the negative genetic trends for **AFC** from both IH and TH sires indicated the favorite genetic improvement for both traits occurred during the study period. However, the genetic change was very slow. Beside, mean EBV for AFC and MY across years of TH sires had larger difference and more fluctuation than those of **IH** sires. The **TH** sires seem to have better AFC, but had lower MY than the IH sires. However, both of IH and TH sires seemed to have close means EBV for both AFC and MY from 2010 to 2013.

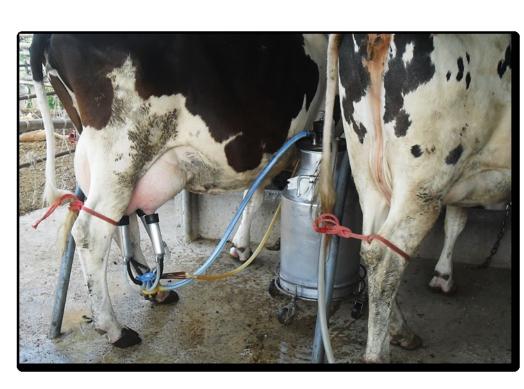
In practice, Thai dairy producers generally choose sires based on semen available and price that they could effort, rather than **EBV** for the considered traits. In dairy genetic improvement programs, **MY** has been considered as the major trait. Thus, fluctuation of mean EBV for AFC and MY of both IH and **TH** sires occurred by chance. However, it could be due to the number of sires with favorite **EBV** for **AFC** and **MY** that were chosen in that particular year. Even though mean **EBV** for **MY** of the **IH** sires is higher than those of **TH** sires, but considering **EBV** for the target important traits of individual animals should be promoted.





Seasons in Thailand were classified as summer (March to June: hot and dry; 29 to 31°C, 69 to 75%RH), rainy season (July to October: hot and humid; 28 to 29°C, 78 to 81%RH), and winter (November to February: cool and dry; 25 to 27°C, 66 to 72%RH). All cattle in this population were raised under openbarns and were milked twice a day. Grasses were fed mainly (direct grazing or cut and carry; 30 to 40 kg/d) and supplemented with concentrate (12 to 15 kg/d; 18 to 22% crude protein). In dry seasons when fresh grasses were limited, the dairy producers fed their cows with silage, rice straw, crop residues, or agricultural by-products (e.g., cassava pulp, brewer grain, soybean meal, corn cob, etc.). Minerals were supplemented to the animals throughout the year.





The study traits were AFC and MY. The AFC was the number of month between the first calving date and birth date, while the **MY** was calculated from monthly test-day samples using test-interval method. In this study, cows that calved in the same herd, year and season (HYS) were assumed to have similar environment and management (contemporary groups).

The used model considered HYS and regression on HF as fixed effects, and animal and residual as random effects. Least squares means (LSM) of AFC and **MY** were estimated for each **HYS** subclasses. Regression coefficients were estimated for **HF**. Variance components were estimated for **AFC** and **MY** using an average information restricted maximum likelihood procedure (AI-REML). The variance component estimates were used to compute heritability, genetic correlation, phonotypic correlation, and phenotypic correlation. Genetic prediction for AFC and MY was performed using a bivariate animal model. Genetic and phenotypic trends were drawn for AFC and **MY** using means of estimated breeding value (**EBV**) of cows and sires of cows that calved in particular years.

RESULTS AND DISCUSSION

The phenotypic mean (standard deviation) was 31.04 (6.10) months for AFC, and 4,302.27 (1,125.25) kg for MY. The mean phenotypic values of cows ranged from 28.08 (4.32) months in 1997 to 34.06 (6.47) months in 1993 for AFC, and from 2,979.98 (2,094.12) kg in 2001 to 4,551.95 (1,178.71) kg in 2013 for MY. Variation of AFC and MY was affected by herd-year-season (P < 0.001), but not Holstein fraction.

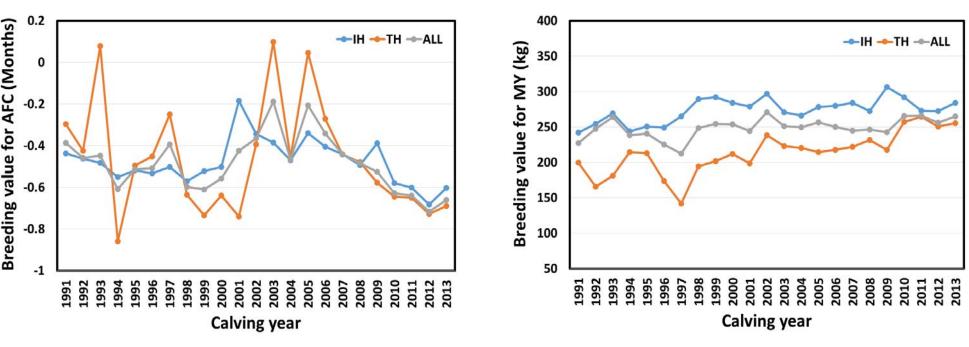


Table 1 Var Trait

> AFC (mo MY (kg

The additive genetic variance was 4.71 ± 1.06 month² for **AFC**, and $89,342 \pm 1.06$ 26,277 kg² for **MY**. The residual variance was 20.64 ± 1.02 month² for **AFC**, and 584,850 ± 26,668 kg² for MY (Table 1). With these variance component estimates, the heritability was 0.19 ± 0.04 for AFC and 0.13 ± 0.04 for MY. The phenotypic correlation (0.07 ± 0.02) and genetic correlation (0.09 ± 0.18) between **AFC** and **MY** were close to zero



The heritability estimates found for **AFC** and **MY** in this Thai multibreed dairy population were lower than those values reported in Thailand (Koonawootrittriron et al., 2006) and the other countries (Ojango and Pollott, 2001; Kheirabadi et al., 2013; Yousefi-Golverdi et al., 2012). These heritability estimates implied the possibility to improve them by genetic selection. However, with low heritability estimates, accurate genetic information of individual animals is needed for genetic selection. Close to zero genetic correlation between AFC and MY (Table 2) implied that selection for increasing **MY** would not significantly affect **AFC**.

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riance component estimates for accumulated 305-d milk yield Y) and age at first calving (AFC)				
ts	Variance Components			
	Additive genetic variance	Residual variance		
onth ²)	4.71 ± 1.06	20.64 ± 1.02		
(g ²)	89,342 ± 26,277	584,850 ± 26,668		

Table 2 Heritability (diagonal), genetic correlations (above diagonal), phenotypic correlations (below diagonal) and standard errors for milk yield (MY) and age at first calving (AFC)

Traits	AFC	MY
AFC	0.19 ± 0.04	0.09 ± 0.18
MY	0.07 ± 0.02	0.13 ± 0.04

FINAL REMARKS

sires had genetic changes larger than **IH** sires for **AFC** and **MY** in multibreed dairy population.

improvement in Thai dairy population has appropriate direction ase of **AFC** and increase of **MY**).

ility estimates for AFC and MY were low, and genetic correlation n AFC and MY was close to zero.

accurate information of the individual animals for the target traits is for selection and genetic improvement programs

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