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Genetic trends in a Holstein × Other Breeds multibreed dairy population in Central Thailand

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Abstract

Genetic variability and genetic trends for 305-d milk yield (MY), 305-d fat yield (FY), and average 305-d fat percent (FP) were evaluated using monthly test-day records from first-lactation cows collected from 1991 to 2005 in 92 farms located in Central Thailand. Estimates of variance and covariance components and breeding values (EBV) were obtained using a multiple-trait animal model. Fixed effects were contemporary group (herd-year-season), calving age, additive genetic group as a function of Holstein fraction, and non-additive genetic group as function of heterosis effect. Random effects were animal and residual. Program ASREML was used to perform computations. Estimates of heritabilities were 0.38 ± 0.10 for MY, 0.25 ± 0.11 for FY, and 0.22 ± 0.11 for FP. Although the difference between the mean MY for cows in 1991 and 2005 was 324.1 kg, the regression of mean cow EBV for MY on year was 6.5 kg/yr. Differences between mean cow EBV for FY and FP in 1991 and 2005 and their corresponding regressions of mean FY and FP on year were all near zero. Similarly, mean EBV for sires and dams of cows also showed near zero trends during these years. A factor contributing to the near complete absence of genetic trends was likely the variety of criteria used by producers to choose sires and to keep dams in addition to EBV (e.g., availability of semen, reproductive ability, adaptation to hot and humid conditions). It also appears that high percent Holstein cows failed to reach their production potential under the management, nutrition, and hot and humid climatic conditions in this tropical region. Changes in nutrition and management would be needed for high percent Holstein cows to show an upward trend in Central Thailand.

Keywords: Cattle; Dairy; Genetic trends; Thailand; Tropical

1. Introduction

There has been a concerted effort to increase milk production in Thailand for the past 35 years. This effort has been a combination of government policies, importation and widespread use of Holstein semen, and extensive use of high-percent Holstein sires generated in Thailand. This mating strategy has resulted in a multibreed dairy population where 90% of animals are 75% Holstein or greater (Department of Livestock Development, 2006).

Central Thailand is the most important dairy region. In 2005, it contained approximately 60% of dairy farms (12,253 farms), 70% of dairy cows (145,912 cows), and it produced 66% of raw milk per day (805,083 kg) in Thailand (Department of Livestock Development, 2006). The large concentration of dairy farms led to the establishment of 27 dairy cooperatives and 13 private milk collection centers in this region.

The Dairy Farming Promotion Organization of Thailand (DPO) has been collecting dairy production, breed composition, and pedigree records in Central Thailand since 1991. To help dairy producers with their selection decisions for economically important traits, Kasetsart University began to conduct annual genetic evaluations with the DPO dataset in 1996. Currently, estimated breeding values for purebred and crossbred animals are computed for milk yield, fat yield, fat percentage, and age at first calving using multibreed mixed model procedures (Koonawootrittriron et al., 2002). These evaluations are published and distributed to farmers in the yearly DPO Sire and Dam Summary (Dairy Farming Promotion Organization, 2006).

It is important to evaluate changes over time in the DPO dairy population for economically important dairy traits, particularly since genetic evaluations began in 1996, to obtain information on the impact of the selection and mating strategies used by farmers and on aspects that need to be improved. Thus, the objective of this research was to assess genetic variability and genetic trends for first lactation 305-d milk yield (MY), 305-d fat yield (FY), and average 305-d fat percent (FP) in the DPO dairy cattle population in Central Thailand from 1991 to 2005.

2. Materials and methods

2.1. Animals and Data

The original dataset consisted of 17,085 monthly test-day records from 2,034 first lactation cows. All cows had their sire and dam identified. However, 657 (32.3%) of them needed to be eliminated because they had incomplete or no information of breed composition, birth date, calving date, and drying-off date. Thus, the resulting edited dataset had 15,260 monthly test-day records from 1,377 first-lactation cows collected from 1991 to 2005 in 92 farms in Central Thailand. These cows were the progeny of 378 sires and 1,176 dams.

Breeds represented in the multibreed dairy population were Holstein, Brahman, Jersey, Red Dane, Red Sindhi, Sahiwal, and Thai Native. However, the majority of animals in the population were composed of a large Holstein fraction, and a small fraction of other breeds. Thus, two breed groups were defined: Holstein (H) and Other breeds (O), where O included all breeds other than Holstein. Table 1 presents numbers of cows by breed group of sire × breed group of dam combination. Most cows (86 %) were sired by purebred Holstein, 13% of cows were produced by crossbred Holstein sires ($0.50 \leq H < 1.0$), and 1% of cows were daughters from 5 Jersey sires. Ninety one percent of cows (1,255 of 1,377 cows), 91% of dams (1,070 of 1,176 dams), and 10% of sires (35 of 378 sires) in the population were crossbred. The breed composition of the DPO population was similar to the breed structure of the dairy cattle population in Thailand reported by the Department of Livestock Development (2004).

Test-day samples were measured for milk volume and analyzed for fat content (fat percentage) monthly. Monthly test-day fat volume was computed as the product of test-day milk volume and fat content. Monthly test-day samples were used to compute MY and FY using the test-interval method (Sargent et al., 1968; Koonawootrittriron et al., 2001). Monthly production yields (milk and fat) were computed using two consecutive test-day production samples, and then added to obtain the accumulated 305-d productions. Computations were performed using an in-house-written SAS program (SAS, 2003).

2.2. Climate, Nutrition, and Management

Weather in Thailand is heavily influenced by tropical monsoons. Central Thailand has daily temperatures ranging from 19° to 36° Celsius, relative humidity ranging from 48 to 94 %, and rainfall is approximately 1,232 mm per year (Meteorological Department, 2004). Seasons were winter (November to February: cool [21° to 32° Celsius] and dry [70% RH, precipitation 124 mm/year]), summer (March to June: hot [25° to 36° Celsius] and dry [69% RH, precipitation 187 mm/year]), and rainy season (July to October: hot [24° to 33° Celsius] and humid [79% RH, precipitation 903 mm/year]).

Grasses used in dairy farm pastures of Central Thailand were Guinea (*Panicum maximum*; 9% to 12% CP and 50% to 52% TDN, DM basis), Ruzi (*Brachiaria ruziziensis*; 10% to 12% CP and 57% to 59% TDN, DM basis), Napier (*Pennisetum purpureum*; 11% to 12% CP and 53% to 54% TDN, DM basis), and Para (*Brachiaria mutica*; 10% to 11% CP and 53% to 55% TDN, DM basis). To increase the nutritive value of pastures, some farmers planted mixtures of grasses and legumes such as Verano stylo (*Stylosanthes hamata* cv. Verano; 16% to 20% CP and 50% to 56% TDN, DM basis), Thapra stylo (*Stylosanthes guianensis CIAT 184*; 14% to 18% CP and 48% to 55% TDN, DM basis), and Leucaena (*Leucaena leucocephala*; 18% to 22% CP and 55% to 73% TDN, DM basis). Grasses in this region usually grow faster than legumes (Mclovor, 1978; Haynes, 1980; Nakamanee et al., 2004). Thus, the composition of pastures was approximately 90% grasses (e.g., Guinea or Ruzi) and 10% legumes (e.g., Thapra stylo).

Concentrate feed for cows was either produced by the farmers themselves, or purchased from dairy cooperatives and local companies (e.g., Charoen Pokphand Foods Public Co. Ltd., Bangkok, Thailand; Betagro Agro Group Co. Ltd., Bangkok, Thailand). Concentrate mixtures contained from 15% to 19% of CP and from 70% to 75% of TDN (DM basis). Ingredients used in the concentrate were: 1) a protein source (10% to 40% CP), e.g., soybean meal, brewer’s grain, cotton seed meal, Para-rubber seed meal, Leucaena; 2) an energy source (63 to 83% NFE), e.g., corn, cassava, broken rice, rice bran, fat from animals and plants; and 3) a mineral and vitamin source, e.g., premixes such as MT MIX, Mahthong Co. Ltd., Bangkok, and SMART MIX, BETTER PHARMA Co. Ltd., Bangkok).

Feeding was based on concentrate (12 to 15 kg/d, or considering 1 kg of concentrate for 2 kg of milk), and fresh grass (direct grazing or cut and carry; 30 to 40 kg/d) from farmers own land (90% of farmers) or from public areas (small holders). However, availability of forage in Thailand is limited. Except for a period of 4 months (July to October), there is insufficient fresh grass for dairy cows the rest of the year. During this 8-month period (November to June) when fresh grass is limited, farmers feed dairy cows rice straw (2 to 5% CP, 40 to 44% TDN, DM basis), urea-treated rice straw, and crop residues (cassava leaves, corn cobs, peanut leaves) as sources of fiber coupled with large amounts of concentrate to compensate for the lack of good quality forage. A free-choice mineral supplement was available throughout the year.

Cows were housed in open barns. Less than 10% of farmers used fans to reduce heat stress. Nearly all dairies milked their cows twice a day. Cows were bred all year round by artificial insemination. Reasons for culling cows were mainly health (e.g., Brucellosis, Paratuberculosis, Foot and Mouth Disease, and Anaplasmosis; National Institute of Animal Health, 2006) and reproductive problems (e.g., delayed estrus, non-return to estrus, silent heats, and long days open).

2.3. Genetic Parameters

A multiple-trait multibreed animal model was used to obtain estimates of breeding values (EBV) and of variance and covariance components. Variance and covariance components were estimated using restricted maximum likelihood procedures and computed with an average information algorithm (ASREML; Gilmour et al., 2000).

Estimates of variances and covariances were subsequently used to compute heritabilities for and genetic correlations among MY, FY, and FP.

The multiple-trait animal model was as follows:

$$y = Xb + Z_{ga}g_a + Z_{gn}g_n + Z_a a_a + e$$

where

y = vector of MY, FY, and FP ordered by traits within cows,

b = vector of contemporary groups (herd-year-season; HYS) and a covariate for calving age (mo),

g_a = vector of regression additive genetic group deviations (i.e., H - O),

g_n = vector of interbreed intralocus non-additive genetic group deviations (i.e., heterosis effects; ½ (HO + OH – HH – OO),

a_a = vector of animal additive genetic effects,

e = vector of residuals,

X = incidence matrix that relates cow records to elements of vector b,

Z_{ga} = matrix of expected fractions of H alleles that relates cow records to elements of vector g_a,

Z_{gn} = matrix of probabilities of interbreed intralocus configurations (= prob (H alleles in sire) × prob (O alleles in dam) + prob (O alleles in sire) × prob (H alleles in dam) relating cow records to elements of vector g_n,

Z_a = matrix 1's and 0's that relates cow records to elements of vector a_a, and

subscript 1 = MY, subscript 2 = FY, and subscript 3 = FP.

The assumptions of the model were:

$$\begin{bmatrix} y \\ a_a \\ e \end{bmatrix} \sim \text{MVN}\left(\begin{bmatrix} X\beta \\ 0 \\ 0 \end{bmatrix}, \begin{bmatrix} Z_a G_a Z_a' + R & Z_a G_a & R \\ G_a Z_a' & G_a & 0 \\ R & 0 & R \end{bmatrix} \right)$$

where

G_a = $G_o \otimes A$, where G_o is the matrix of additive genetic covariances, A is the numerator relationship matrix (Henderson, 1976), and ⊗ represents direct product (Searle, 1982), and

R = residual covariance matrix.

The EBV were computed as a weighted sum of additive group genetic effects and random effects. Thus, the EBV for animal ij was (Koonawootrittriron et al., 2002):

$$\hat{u}_{a_{ij}} = p_{ij} g^{\circ}_{a_i} + \hat{a}_{a_{ij}}$$

where $\hat{u}_{a_{ij}}$ is the EBV of animal ij, p_{ij} is the fraction of H alleles for animal ij, $\hat{g}^{\circ}_{a_i}$ is the estimate of the regression additive genetic group deviation (H - O) , and $\hat{a}_{a_{ij}}$ is the prediction of the random additive genetic effect for animal ij.

2.4. Genetic Trends

Weighted yearly means of EBV of cows, sires, and dams were plotted against year. Weights for cow yearly means were equal to 1, and weights for sire and dam yearly means were equal to their respective numbers of daughters per year. In addition, unweighted means were computed for sires and dams. Differences between weighted and unweighted means would help explain differences in sire usage and dam representation per year in the population. These differences would give an indication of the type of sires and dams that were predominantly chosen as parents in the population, and their impact on genetic yearly means.

Linear regressions of EBV yearly means on years were computed for each trait using the REG procedure of the SAS program (SAS, 2003). Pearson correlation coefficients among cow, sire, and dam EBV were also estimated using the CORR procedure (SAS, 2003).

3. Results and discussion

3.1. Least Squares Means

Least squares estimates and SE for MY, FY, and FP were computed using the mixed procedure of SAS with single-trait fixed models that contained the same fixed effects as the multiple-trait animal model used to compute EBV and variance components. Table 2 shows the least squares means for MY, FY, and FP per breed group of cow. Milk yield tended to increase from cows with 50% H or less to cows (3,508.7 ± 340.7 kg) to 96.87% H and above but less than 100% (4,185.2 ± 118.8 kg). Milk yield for purebred H cows (3,810.6 ± 120.0 kg) was between the milk production of $0.50 \leq H < 0.75$ cows (3,643.5 ± 119.1 kg) and that of $0.75 \leq H < 0.875$ cows (3,911.3 ± 64.4 kg). Fat yield was highest in the $0.75 \leq H < 0.875$ group of cows (144.4 ± 3.3 kg), and lowest in less than 50% H cows (117.3 ± 17.5 kg); purebred H cows had the second lowest fat yield (121.0 ± 6.2 kg). Lastly, $0.50 \leq H < 0.75$ cows had the largest fat percentage (3.44 ± 0.11 %) and purebred H the lowest (2.95 ± 0.11 %).

The LS means and their SE for the H - O breed deviation were 1,010.0 ± 870.8 kg ($P = 0.15$) for MY, 38.7 ± 49.8 kg ($P = 0.07$) for FY, and -0.64 ± 5.28 % ($P = 0.11$) for FP. Least squares means and SE for heterosis were 412.1 ± 481.5 kg ($P = 0.26$) for MY, 23.4 ± 27.8 kg ($P = 0.07$) for FY, and 0.03 ± 0.29 % ($P = 0.81$) for FP. The large SE of the estimates of H - O and of heterosis were likely due to the poor representation of O in the DPO dairy population. The DPO is currently expanding its recorded population of dairy cows, thus, it is likely that more accurate estimates of breed group differences and of heterosis effects would be obtained in the near future.

Overall, the H - O estimates in this population suggest that cows with larger H fractions tended to produce more milk and fat, but they had lower fat percentage. Similarly, the estimates of heterosis indicate that nonadditive genetic effects tended to increase milk yield and fat yield. To attain these high levels of production under the tropical conditions in Thailand, purebred H and high fraction H cows must receive appropriate nutrition, management, and health care. High H fraction or purebred H cows that do not get appropriate nutrition, management, and health care show health problems (e.g., thin cows, weak calves, tick fever, laminitis, and ephemeral fever) and reproductive problems (silent heats, low conception rates, long days-open, and long calving intervals) as well as lower levels of milk and fat yields (Markvichitr et al., 1995; Punyapornwithaya et al., 2005). The levels of MY (lower than that of $0.75 \leq H < 0.875$ cows), FY (lower than $0.50 \leq H < 0.75$ cows), and FP (lowest of all breed groups of cows) of purebred H suggest that the level of nutrition, management, health care cows received was insufficient for them to express their genetic potential.

Dairy production in Thailand is based on a combination of concentrate and tropical grasses. However, because good quality forage is unavailable in Central Thailand most of the year, a way for high percent H and purebred H cows to achieve high milk and fat yields is by consuming large amounts of concentrate, which most dairy farmers in Thailand cannot afford (Tumwasorn et al., 1995). Thus, most Thai farmers prefer cows that have an H fraction no larger than 90% in order to maintain the profitability of their operations.

3.2. Genetic Variances and Genetic Parameters

Estimates of additive genetic variances were 255,068.0 ± 69,690.7 kg^2 for MY, 451.6 ± 193.0 kg^2 for FY, and 0.038 ± 0.02 $\%^2$ for FP. Phenotypic variances were 663,652.0 ± 31,610.0 kg^2 for MY, 1,781.6 ± 89.5 kg^2 for FY, and 0.18 ± 0.09 $\%^2$ for FP. Heritability estimates were 0.38 ± 0.10 for MY, 0.25 ± 0.11 for FY, and 0.22 ± 0.11 for FP. Estimates of additive genetic and phenotypic variances for MY in the DPO multibreed population were lower than estimates for H cows in Brazil (Ceron-Muñoz et al., 2004; Costa et al., 2000), Colombia (Ceron-Muñoz et al., 2001, 2004; Stanton et al., 1991), and Mexico (Cienfuegos-Rivas et al., 1999; Stanton et al., 1991). However, the estimate of heritability for MY was higher than corresponding values in all these countries because of the much smaller estimate environmental variance in the DPO dataset than in the H datasets used in those studies. Differences in breed composition of animals in the DPO (multibreed, high percent H) and the H populations in Brazil, Colombia, and Mexico likely account for a portion of the differences in genetic and environmental variation between these populations. However, genetic and environmental variances for MY in the DPO population were more similar to corresponding variances in cows from herds classified as having low variability (Ceron-Muñoz et al., 2004; Cienfuegos-Rivas et al., 1999; Costa et al., 2000). Considering that 90.6% of cows in the DPO dataset were 75% H and higher, the lower estimates of genetic and environmental variation may be an indication that feeding regimes and management practices are limiting the genetic potential for MY in the DPO population. On the other hand, estimates of additive genetic and phenotypic variances and heritability for FY in the DPO population were somewhat higher than estimates (Costa et al., 2000) from a Brazilian H population. Genes from other breeds present in the DPO population (e.g., Jersey) may be partly responsible for these differences as well as differences among sires used in Thailand and in Brazil.

Estimates of additive genetic covariances were 8,277.6 ± 3,111.9 kg^2 between MY and FY, -420.0 ± 271.0 kg*% between MY and FP, and -0.846 ± 1.365 kg*% between FY and FP, and their corresponding additive genetic correlation estimates were 0.77 ± 0.12 between MY and FY, -0.43 ± 0.24 between MY and FP, and -0.20 ± 0.36 between FY and FP. These estimates of heritabilities and genetic correlations were within the range of values reported in previous Thai studies (Department of Livestock Development, 2004; König et al., 2005; Chanvijit et al., 2005).

3.3. Mating Patterns, Sire Usage, and Dam Representation

To visualize mating patterns in the DPO population in terms of the EVB of sires and dams, mean EBV for MY, FY, and FP for cows, their sires and their dams were computed by breed group of cow. Similar patterns were observed for MY, FY, and FP. Thus, only mean EBV for MY are shown (Table 3) and discussed here. The sires with the highest EBV for MY (982.1 ± 13.6 kg to 1,012.0 ± 25.6 kg) were mated to dams whose breed composition ranged from 87.5% to less than 100% H (second to fourth breed groups in Table 3). The dams with the highest mean EBV in the DPO population were 96.87% H (1,031.7 ± 21.0 kg), whereas purebred H dams were second highest (969.1 ± 20.8 kg). These mating patterns clearly indicate that Thai farmers mated the highest EBV H sires not to purebred H dams, but to upgraded dams that had some non-Holstein fraction, perhaps due to their perceived superior adaptability to purebred H dams as suggested by their higher milk and fat yields, or perhaps simply due to their desire to mate their highest milk producing cows to the best available sires. Mean EBV for cows, sires, and dams for MY, FY, and FP were also computed by breed group of dam x year to try to detect differences in mating strategies across breed groups of dams over time. None were found.

To assess whether higher EBV bulls had been more frequently used as sires, and whether higher EBV dams were more represented in the cow population within years, unweighted yearly EBV means were computed for sires and dams, and compared to their corresponding weighted yearly EBV means. A larger weighted than unweighted sire EBV mean in a given year indicates a heavier use of high EBV sires. Similarly, a larger weighted than unweighted dam EBV mean suggests a larger number of daughters from high EBV dams in a particular year. Patterns of sire usage and dam representation in the DPO dataset were similar for MY, FY, and FP, thus only those for MY are discussed here (Fig. 1). As expected from the larger number of progeny per sire than per dam, differences between weighted and unweighted yearly EBV means were larger for sires than for dams. There was, however, a similar number of years when the difference between weighted and unweighted EBV mean was positive (7 years for sires and dams) and negative or zero (8 negative years for sires; 3 negative and 5 zero years for dams). This pattern of positive and negative weighted vs. unweighted yearly EBV means suggests that there was no consistent strategy for choosing either sires or dams as parents. This supports the contention that Thai dairy farmers chose parents using a variety of determining factors (e.g., availability of semen, cost, pedigree for sires; health, reproductive ability for dams), and that EBV may not have been the most important one.

3.4. Genetic Trends

Fig. 2 shows the trends for yearly EBV means of cows, their sires, and their dams for MY, FY, and FP from 1991 to 2005. Genetic trends for sires were negative for MY (-5.0 ± 3.5 kg/yr; $P = 0.18$) and FY (-0.3 ± 0.1 kg/yr; $P < 0.03$), but positive for FP (0.004 ± 0.001%/yr; $P < 0.01$). Contrarily, genetic trends for cows and dams were positive for MY (6.5 ± 2.1 kg/yr for cows and 17.7 ± 2.0 kg/yr for dams; $P < 0.01$) and FY (0.2 kg/yr for cows and 0.7 kg/yr for dams; $P < 0.05$), and they were negative for FP (-0.004 ± 0.001 %/yr for cows and -0.011± 0.001 %/yr for dams; $P < 0.01$). Cow genetic trends in the DPO population showed a similar pattern to the one reported by the Department of Livestock Development (2004) using records from a large segment of the Thai dairy population (MY: 3.3 kg/yr; FY: (0.05 kg/yr; FP: -0.002 %/yr).

Weighted yearly means of sire EBV were higher than those of dams for MY and FY, but they were lower than those of dams for FP from 1991 to 2005 (Fig. 2). The magnitude of the difference between weighted yearly mean EBV for sires and dams decreased from 1991 to 2005. These differences were 387.8 kg in 1991 and 142.2 kg in 2005 for MY, 14.5 kg in 1991 and 3.5 kg in 2005 for FY, and 0.27 % in 1991 and 0.08 % in 2005 for FP. Cow EBV yearly means were more highly associated to dam weighted EBV yearly means (r = 0.73, P = 0.0018, for MY; 0.69, P = 0.0042, for FY; and 0.82, P = 0.0002, for FP) than to sire weighted EBV yearly means (r = 0.36, P = 0.1903, for MY; 0.29, P = 0.2852, for FY; and -0.12, P = 0.6713, for FP).

The genetic trends for MY, FY, and FP observed in the DPO population were likely due to the upgrading of dairy cattle to Holstein promoted by the Thai government rather than selection. The small genetic trends for MY, FY, and FP suggest that sires and dams in this population were chosen based on considerations other than their EBV for these production traits. Most Thai dairy farmers may have considered information on cost, health, reproductive ability, and pedigree, in addition to production traits when selecting sires and dams. Further, the availability of EBV for imported sires under Thai conditions was limited, and those available had low accuracies due to small numbers of progeny. This suggests the need for a comprehensive national dairy genetic evaluation to increase both accuracy of genetic evaluation and availability of Thai and imported sires for artificial insemination.

Another factor for the low genetic trends may have been genotype by environment interaction. Indirect evidence in this regard was suggested by the low levels of genetic and environmental variation for MY found in the DPO multibreed population compared to those from H populations in other tropical and subtropical countries (Brazil, Colombia, and Mexico) discussed in section 3.2. The high % H (75% or more) of most cows (90.6%) in the DPO population suggests that they may have the genetic potential to produce high levels of MY. However, least squares means for MY for high % and purebred H cows in the DPO population were lower than adjusted and unadjusted means reported for Brazil (Ceron-Muñoz et al., 2004; Costa et al., 2000), Colombia (Ceron-Muñoz et al., 2001, 2004; Stanton et al., 1991), and Mexico (Cienfuegos-Rivas et al., 1999; Stanton et al., 1991). Further, cows between 75% H and less than 100% H in the DPO population had higher MY, FY, and FP than purebred H (Table 2). These aspects suggest that purebred Holstein cows failed to reach their production potential under the management, nutrition, and hot and humid climate conditions in this tropical region. Unfortunately specific information on management practices, feeding regimes, nutritional value of diets, and information on other traits (cow weights, body condition) that would have helped characterize the existence of genotype by environment interaction in the DPO population were unavailable. However, efforts to improve data collection, nutrition, management, and health aspects as well as increase the number of farms and animals with records in this population are being pursued. The economic situation of most dairy farmers in Thailand makes it unlikely for rapid improvement of environmental conditions to occur. Thus, one alternative to help improve dairy production in Thailand would be to include adaptability traits (e.g., heat and humidity tolerance, tolerance to insects), reproduction, and production traits in dairy selection programs. This would permit the identification of animals that are both well adapted and productive under Thai production conditions.

Economically, the most important dairy traits in Thailand are MY and FP. Milk price in Thailand is primarily determined by amount of milk produced, with additions and deductions due to milk components (FP, solids-non-fat) and milk quality (bacterial score, somatic cell count; Rhone et al., 2007; Sangjan and Koonawootrittriron, 2007). Dairy farm revenues could be substantially increased if there were a consistent strategy to choose sires from year to year. Given a price range that a farmer could afford, artificial insemination sires could be chosen based on high EBV for MY and FP. Another aspect that needs to be improved is the accuracy of animal evaluations. This implies that a substantially larger number of dairy herds and cows should provide individual animal information for genetic evaluation purposes. Currently, only two organizations produce dairy genetic evaluations in Thailand: the DPO and the Department of Livestock Development. The number of cows providing information to these two organizations is only 23, 000, which represents only 11% of the total number of dairy cows (208,831 cows; Department of Livestock Development, 2006) in Thailand. Thus, to substantially increase the accuracy of Thai genetic evaluations, it is imperative to increase the number of cows that participate in genetic evaluation programs. A national dairy genetic evaluation system would need to be implemented to optimize the use of the information from the various subpopulations, and achieve the maximum genetic trends feasible under Thai environmental conditions.

4. Conclusions

Genetic trends in the Holstein × Other Breeds dairy cattle population in Central Thailand from 1991 to 2005 were small for MY, and near zero for FY and FP. A National Sire Evaluation needs to be implemented to improve the accuracy of genetic evaluations and to increase the availability of Thai and imported sires evaluated under Thai conditions for artificial insemination. The pricing system for milk may need to be changed to stimulate herd size growth and to increase the number of dairy farms willing to participate in genetic improvement programs in Thailand.

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Table 1

Number of cows by breed group of sire × breed group of dam combination

Breed group of dam	Breed group of sire							
	Holstein (338)[1]	$0.9687 \le H < 1.0$ (0)	$0.9375 \le H < 0.9687$ (3)	$0.875 \le H < 0.9375$ (12)	$0.75 \le H < 0.875$ (17)	$0.50 \le H < 0.75$ (3)	Other Breeds (5)	Total (378)
Holstein (H) (108)[1]	122	0	2	0	7	0	1	132
$0.9687 \le H < 1.0$ (28)	26	0	0	2	1	0	2	31
$0.9375 \le H < 0.9687$ (88)	91	0	1	2	8	1	0	103
$0.875 \le H < 0.9375$ (228)	221	0	6	19	13	4	3	266
$0.75 \le H < 0.875$ (383)	384	0	11	21	23	11	4	454
$0.50 \le H < 0.75$ (275)	271	0	4	28	8	3	3	317
$H < 0.50$ (66)	68	0	2	1	3	0	0	74
Total (1,178)	1,183	0	26	73	63	19	13	1,377

[1] Numbers of animals in parenthesis

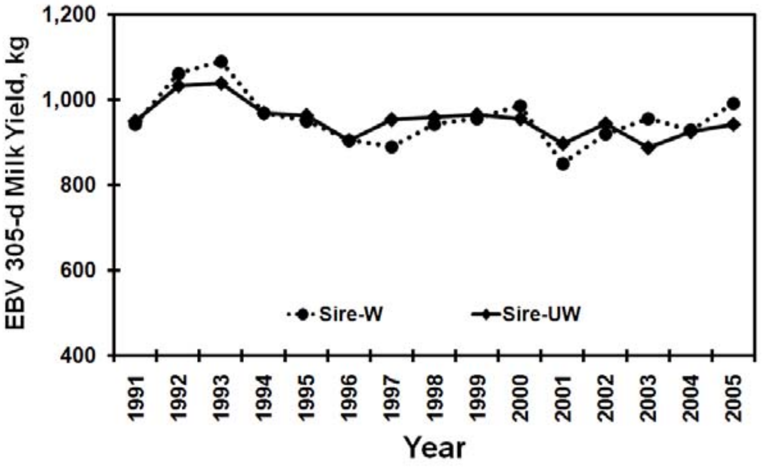
Table 2
Cow least squares means ± SE for 305-d milk yield, fat yield, and fat percentage by breed group of cow

Breed group of cow	No. Cows	Milk yield (kg)	Fat yield (kg)	Fat percentage (%)
Holstein	122	3,810.6 ± 120.0	121.0 ± 6.2	2.95 ± 0.11
$0.9687 \leq H < 1.0$	119	4,185.2 ± 118.8	142.5 ± 6.1	3.23 ± 0.11
$0.9375 \leq H < 0.9687$	222	4,011.7 ± 85.3	141.9 ± 4.4	3.14 ± 0.08
$0.875 \leq H < 0.9375$	422	3,890.3 ± 60.6	140.6 ± 3.1	3.29 ± 0.06
$0.75 \leq H < 0.875$	362	3,911.3 ± 64.4	144.4 ± 3.3	3.42 ± 0.06
$0.50 \leq H < 0.75$	117	3,643.5 ± 119.1	137.0 ± 6.1	3.44 ± 0.11
$H < 0.50$	13	3,508.7 ± 340.7	117.3 ± 17.5	3.15 ± 0.32
Total	1,377	3,781.1 ± 1040.5	131.2 ± 53.5	3.19 ± 0.97

Table 3

Mean EBV ± SE of cows and their sires and dams for 305-d milk yield by breed group of cow

Breed group of cow	No. Cows	Cow EBV	No. Sires	Sire EBV	No. Dams	Dam EBV
Holstein	122	933.4 ± 25.7	66	957.6 ± 25.3	100	969.1 ± 20.8
$0.9687 \le H < 1.0$	119	1,035.9 ± 26.0	71	1,012.0 ± 25.6	99	1,031.7 ± 21.0
$0.9375 \le H < 0.9687$	222	965.1 ± 19.1	113	1,018.8 ± 18.7	177	896.6 ± 15.3
$0.875 \le H < 0.9375$	422	894.9 ± 13.8	190	982.1 ± 13.6	345	807.7 ± 11.1
$0.75 \le H < 0.875$	362	772.5 ± 14.9	168	909.9 ± 14.7	309	628.9 ± 12.1
$0.50 \le H < 0.75$	117	551.7 ± 26.3	73	788.5 ± 25.8	104	344.1 ± 21.3
$H < 0.50$	13	451.9 ± 78.7	5	130.4 ± 77.4	12	747.3 ± 63.3
Total	1,377	856.3 ± 283.8	378	944.9 ± 285.4	1,176	769.6 ± 231.3



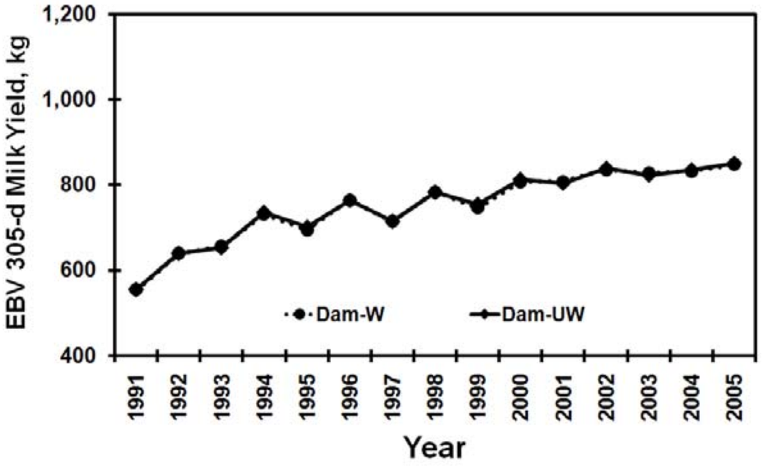


Fig. 1. Weighted (W) and unweighted (UW) yearly means of sire and dam EBV for 305-day milk yield

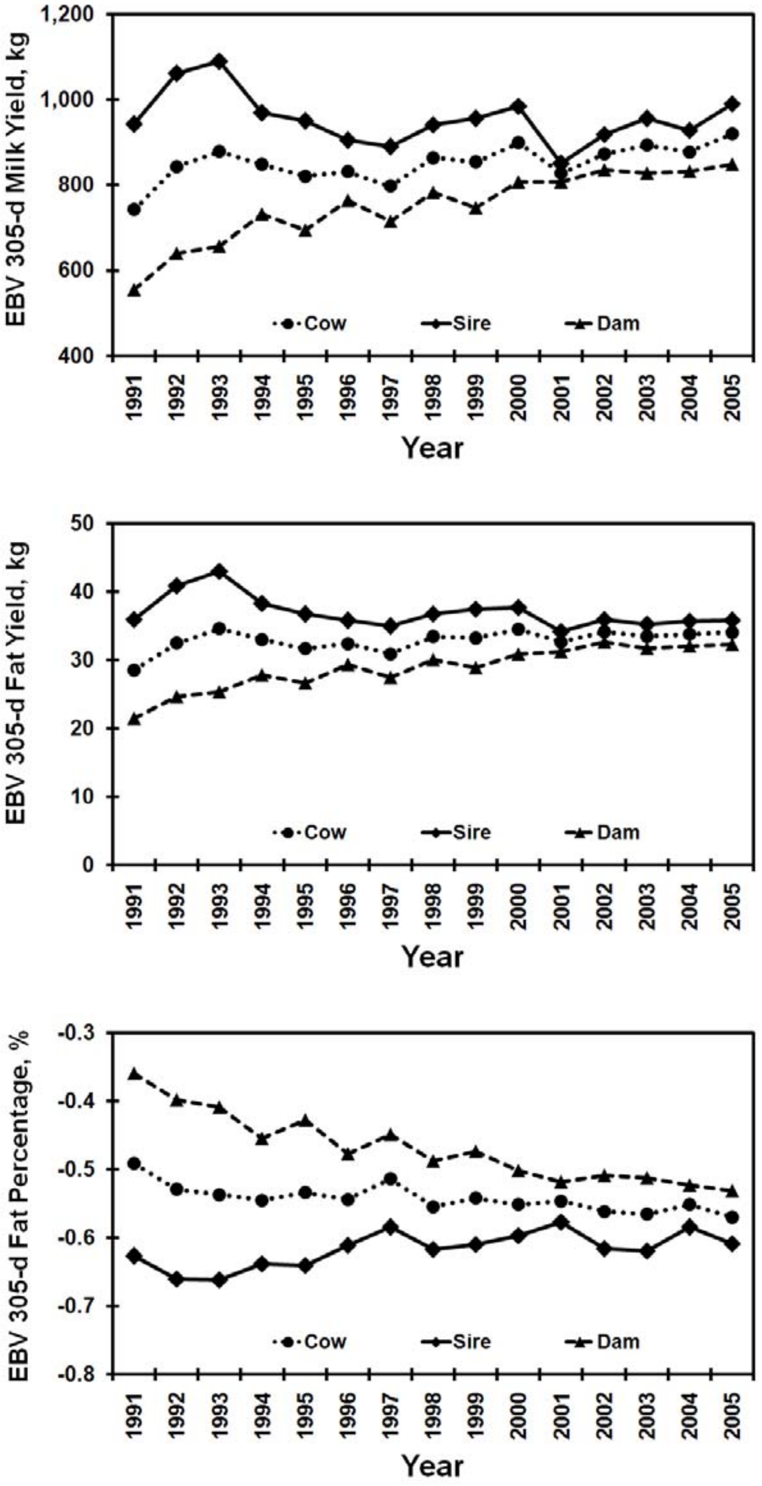


Fig. 2. Genetic yearly means of cow, sire (weighted), and dam (weighted) EBV for 305-day milk yield, fat yield, and fat percentage