Estimation of Covariance Components and Prediction of Additive Genetic Effects for First Lactation 305-d Milk and Fat Yields in a Thai Multibreed Dairy Population[1]

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Abstract

Estimates of covariance components and predicted additive genetic effects for accumulated 305-d milk yield (MY) and accumulated 305-d fat yields (FY) were obtained by using production records of 610 purebred and crossbred first lactation cows in a Thai multibreed dairy population. Covariance components were estimated using average information restricted maximum likelihood procedures and two two-trait additive genetic animal models with different genetic grouping strategies. The BTBI model accounted for *Bos taurus* (BT) and *Bos indicus* (BI) fractions, whereas the HO model considered Holstein (H) and Other breeds (O) fractions. Heritability estimates obtained using the BTBI model were 0.45 for MY and 0.24 for FY, and those obtained using the HO model were 0.46 for MY and 0.25 for FY. Genetic, environmental, and phenotypic correlations between MY and FY obtained from these two models were high (0.89 to 0.99). The estimates of BT additive genetic group effects, as deviations from BI, were 149 kg for MY and -26 kg for FY. The estimate of H additive genetic group effects, as deviations from O, were 18 kg for MY and -21 kg for FY. Expected breeding values (EBV) of sires and dams were evenly spread across BT (BTBI model) and H (HO model) fractions. The top 10% and the bottom 10% of sires for MY and FY were purebred H sires (91% of all sires were 100% H). The highest dam EBV for MY was from a crossbred dam (5/8 H) and the lowest one was from a 100% H dam. The EBV here suggest that BT (or H) crossbred animals can potentially yield better MY and FY than purebred BT or H animals under Thai tropical conditions. One drawback of the additive group regression models used here is that they ignored nonadditive genetic effects. In particular, interbreed nonadditive genetic effects need to be studied in Thai dairy cattle populations. To assess the importance of these genetic effects, multibreed genetic evaluation procedures that account for additive and nonadditive genetic effects could be used.

Key words: Dairy cattle, Milk yield, Fat yield, Multibreed, Genetic group, Genetic evaluation

Introduction

The current Thai dairy cattle population has more than ten different breeds represented in both purebred and crossbred forms. Most animals in this population are crossbred, and composed of up to seven different breeds.

A large-scale dairy genetic evaluation program was created through a collaboration between the Dairy Farming Promotion Organization of Thailand (DPO) and Kasetsart University in 1996 (D.P.O., 1996). Since that year, genetic predictions of sires used in the multibreed dairy population controlled by DPO have been published for milk and fat yield every year. Currently, genetic predictions are computed based on a best linear unbiased prediction (BLUP) procedure using a single-trait animal model (Henderson, 1975; Quaas and Pollak, 1980). This single-trait animal model includes the components of a contemporary group as main effects (i.e., interactions among location, year, and season are *ignored*), and subclass genetic group effects based on ranges of accumulated *Bos taurus* (BT) and *Bos indicus* (BI) fractions as defined by Vinther (1974). This model has several aspects that could be modified to produce genetic predictions of higher accuracy given the available information supplied by DPO.

Firstly, location in the DPO model is defined as clusters of herds (amphurs). This definition of location assumes that sires of all genetic values will be used in all herds within an amphur. However, this may not happen if more intensively managed herds use sires of higher predicted genetic values than more extensively managed herds. If this happens, the resulting predicted genetic values will overestimate the genetic value of sires in intensively managed herds by referring them to the amphur's lower mean than that of their own herds, and vice versa. Thus, it seems preferable to use herds than amphurs as the definition of location.

Secondly, if interactions among location, year, and season were important in the DPO population ignoring them would cause biases in genetic evaluations. Further, if regression procedures could be used to explain genetic group effects, they would be more accurately estimated because information from all animals in the population would contribute to their estimation. As with the current DPO model, genetic evaluations using a model with these modifications can be readily obtained using available computer packages (e.g., ASREML, Gilmour et al., 2000).

Thirdly, the genetic basis that genetic predictions are deviated from could be defined in a way that reflects more closely the breed composition of the DPO population. The most represented breed in this population is Holstein (H). In fact, almost every dairy animal in the DPO multibreed population contains some H fraction. Thus, an alternative genetic grouping strategy to the current DPO strategy would be to consider H and Other Breed (O) fractions, where O would include fractions of any other breed (BT or BI) present in an animal.

Consequently, the objectives of this study were: 1) to develop multiple-trait additive group regression animal models that account for interactions among contemporary group components, and use regression to describe either BT and BI fractions (BTBI model), or H and O fractions (HO model), 2) to estimate covariance components and genetic parameters for these two models for 305-d milk and 305-d fat yields, and 3) to compare the expected breeding value (EBV) of sires and dams of all available BT (BTBI model) and H (HO model) fractions under Thai tropical conditions.

Materials and Methods

Animals and Records

The initial data set used consisted of 12,505 monthly test-day milk yields and 10,042 monthly test-day fat yields of 921 first lactation purebred and crossbred cows that calved from 1991 to 2000 provided by DPO. These records were from 68 farms in central Thailand. Calving seasons were classified as winter (November to February), summer (March to June), and rainy season (July to October).

Breeds represented in this Thai multibreed data set were Holstein, Brahman, Jersey, Red Dane, Red Sindhi, Sahiwal, and Thai Native. However, preliminary descriptive statistical analyses revealed that the distribution of numbers of sires, dams, and females with records was severely skewed towards Bos taurus, and in particular, Holstein, and that most of these breeds were represented only as small fractions in crossbred animals. The small size of the dataset and the unbalancedness of the breed composition of animals in this DPO dataset made it impossible to consider all breed groups for genetic analyses. Thus, these ten distinct breeds were re-defined as *Bos taurus* (BT) and *Bos indicus* (BI) breeds for the analysis using the BTBI model, and Holstein (H) and Other Breeds (O) for the analysis using the HO model.

The dataset used in the analyses was prepared in two steps: 1) cow accumulated 305-d milk yields (MY) and 305-d fat yields (FY) were predicted using monthly test-day milk and fat samples, respectively, and 2) connectedness was determined by considering the representation of sires across contemporary groups. Then, the largest connectedness dataset was used for the genetic evaluation and the estimation of covariance components.

Prediction of MY and FY

To predict MY and FY, test-day samples that were collected on months after reaching 305-d in lactation of each animal were ignored, and animals that did not have consecutive monthly test-day milk and fat yield records within the first ten months after calving were discarded.

Monthly production yields (milk and fat) were computed using two consecutive test day production samples, and then these monthly production yields were used to compute the accumulated 305-d productions. Unfortunately, the DPO had not recorded dates of measurement of those monthly test-day samples in the database, and this information could not be retrieved. Thus, the number of days between two consecutive production samples could not be calculated. Monthly production samples were collected by DPO primarily during the last week of each month. Thus, it was assumed that these test-day samples were collected the last day of every month. Consequently, the new estimation equation was,

$$TPY = (P_1 \times D_1) + \sum_{i=2}^{k}[(\frac{P_i + P_{i-1}}{2}) \times D_i] + (P_{k+1} \times D_{k+1}) \qquad [1]$$

where TPY is the total production yield of an individual animal, P_1 is the test-day production yield sample in the first month after calving, D_1 is the interval between five days after calving and the last day of the fist sampling month, P_i is the test-day production yield sample in month i (i = 2, … , k), D_i is the interval between the last day of month i - 1 and i (i = 2, … , k), P_{k+1} is the test-day production yield sample in the last month of reaching 305-d in lactation, and D_{k+1} is the interval between the 305-d of lactation and the last day of the month before reaching 305-d in lactation. To predict MY and FY in this step, statements in the data step of the SAS program (SAS, 1990) were used.

Finding the Largest Genetic Connected Dataset

Connectedness between management units or contemporary groups can influence the accuracy of genetic evaluation or selection when selection is among animals raised in different environments (Kennedy and Trus, 1993). Preliminary analysis of this data set reconfirmed that the calving herd $\times$ year $\times$ season subclass had important effects (P < 0.01) on milk and fat production. Thus, contemporary groups here were defined as groups of cows that calved in the

same herd, year, and season (HYS). A FORTRAN program was written (Elzo, 2000) to find the largest connected data set using the connections between sires and contemporary groups. The largest connected data set consisted of 610 MY and 487 FY from 610 purebred and crossbred cows representing 214 sires from 178 contemporary groups (Table 1).

Table 1. Description of the largest connected data set

Characteristic	Value
Number of sires	214
Number of cows	610
Number of animals in the population	1,319
Number of contemporary groups	178
Number of 305-d milk yield records	610
Number of 305-d fat yield records	487
Average 305-d milk yield (kg)	3,925
Average 305-d fat yield (kg)	149

A description of the largest connected data set in terms of numbers of sires, dams, and cows with records by BTBI breed-group-of-sire × breed-group-of-dam combination is shown in Table 2, and by HO breed-group-of-sire × breed-group-of-dam combination in Table 3. These tables clearly show the extreme unbalancedness of the distribution of animals in the DPO population. *Bos taurus* sires accounted for 93% of all sires represented in this data set, and 83% of all dams in this data had a 60% or higher BT fraction. The vast majority of the BT sires were H (98%), and 77% of all dams in the 60% or higher BT fraction had H alleles. This reflects a suggestion of the Thai government to preferably use H semen on the existing cow population during this period (1991-2000).

Table 2. Numbers of sires, dams, and calves by BTBI breed-group-of-sire × breed-group-of-dam combination

	Breed-group-of-sire	
Breed-group-of-dam	*Bos taurus*	(0.00-0.99)BT (1.00-0.01)BI [1]
(0.6-1.0)BT (0.4-0.0)BI	183 [2]	15
	462 [3]	36
	513 [4]	36
(0.4-0.6)BT (0.6-0.4)BI	32	3
	37	6
	43	6
(0.0-0.4)BT (1.0-0.6)BI	12	-
	12	-
	12	-

[1] BT = *Bos taurus* (Holstein, Jersey, Red Dane), BI = *Bos indicus* (Native, Brahman, Red Sindhi, Sahiwal); [2] Number of sires; [3] Number of dams; [4] Number of females with records.

Table 3. Numbers of sires, dams, and calves by HO breed-group-of-sire × breed-group-of-dam combination

	Breed-group-of-sire	
Breed-group-of-dam	Holstein	(0.00-0.99)H (1.00-0.01)O [1]
(0.6-1.0)H (0.4-0.0)O	158 [2]	12
	356 [3]	28
	394 [4]	28
(0.4-0.6)H (0.6-0.4)O	84	6
	114	8
	130	8
(0.0-0.4)H (1.0-0.6)O	38	4
	41	6
	44	6

[1] H = Holstein, O = Other breeds (Native, Brahman, Red Sindhi, Sahiwal, Jersey, Red Dane);
[2] Number of sires; [3] Number of dams; [4] Number of females with records.

Estimation of Covariance Components

Covariance components were estimated by a restricted maximum likelihood procedure (REML) using the average information (AI) algorithm (ASREML; Gilmour et al., 2000). The starting values for the two-trait ASREML analyses were the estimates of variance components obtained from the initial single-trait genetic analyses using the same data set.

The models used here were two-trait (MY and FY) animal models. Each trait was assumed to have only direct additive genetic effects. Fixed environmental effects were contemporary group and calving age (mo). Regression additive genetic group effects were (BT - BI) for the BTBI model and (H - O) for the HO model. The random effects in these models were additive animal genetic effects, and residual.

The BTBI and the HO models for two traits can be described using the following generic matrix notation:

$$y = Xb + Z_{ga}g_a + Z_a a_a + e \qquad [2]$$

with
$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix}\begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_{ga_1} & 0 \\ 0 & Z_{ga_2} \end{bmatrix}\begin{bmatrix} g_{a_1} \\ g_{a_2} \end{bmatrix} + \begin{bmatrix} Z_{a_1} & 0 \\ 0 & Z_{a_2} \end{bmatrix}\begin{bmatrix} a_{a_1} \\ a_{a_2} \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix} \qquad [3]$$

where

y = vector of MY and FY ordered by cows within traits.
b = vector of contemporary groups (HYS) and calving age (mo),
g_a = vector of regression additive genetic group deviations, i.e., (BT - BI) for the BTBI model and (H - O) for the HO model,
a_a = vector of animal additive genetic effects,
e = vector of residuals,
X = matrix of 1's and 0's that relates cow records to elements of b,
Z_{ga} = matrix of expected fractions of BT alleles (BTBI model) and of H alleles (HO model) that relates cow records to elements of g_a,
Z_a = matrix 1's and 0's that relates cow records to elements of a_a,

subscript 1 = MY, and
subscript 2 = FY.

It was assumed that

$$
\begin{bmatrix} y \\ a_a \\ e \end{bmatrix} \sim MVN\left(\begin{bmatrix} Xb + Z_{ga}g_a \\ 0 \\ 0 \end{bmatrix}, \begin{bmatrix} Z_aG_aZ'_a + R & Z_aG_a & R \\ G_aZ'_a & G_a & 0 \\ R & 0 & R \end{bmatrix} \right)
$$

[4]

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 $\otimes$ represents direct product (Searle, 1982), and

R = residual covariance matrix.

Prediction of Genetic Effects

Solutions of genetic effects were obtained by solving the mixed model equations using the estimated variance components obtained at convergence. The additive genetic value (EBV) of animal ij is:

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

[5]

where $\hat{u}_{a_{ij}}$ is the additive genetic value of animal ij, p_{ij} is the fraction of BT alleles in the BTBI model, and of H alleles in the HO model for animal ij, $\hat{g}^{\circ}_{a_i}$ is the regression additive genetic group effect (BT - BI in the BTBI model, and H - O in the HO model) , and $\hat{a}_{a_{ij}}$ is the random additive genetic effect of animal ij.

Results and Discussion

Regression Additive Genetic Evaluation Models

The models used here accounted for herd-year-season subclass effects and used regression to describe differences between BT and BI genetic effects (BTBI model), and between H and O genetic effects (HO model). These models were based on the one used in the DPO genetic evaluations between 1996 and 1999. The BTBI and HO model differ from the DPO model in the way contemporary groups (i.e., HYS) and genetic group effects are defined. These differences are discussed below.

Contemporary Groups. In dairy genetic evaluations, animals are compared in groups maintained under similar environmental conditions. These comparison groups are commonly formed by fitting factors such as herd, year, and season of calving (VanVleck, 1987; VanBebber et al., 1997). The model used by DPO included the *components* of a contemporary group (i.e. location, year, and season of calving) as main effects, but it ignored the interactions among them. In that model, herds were grouped according to administrative locations (amphur), and then amphurs were used in place of herds in the DPO model. The mean of an amphur for any trait will be lower than that of the better-managed herds and higher than that of the poorer managed herds.

Assuming that better managed herds bought semen of higher EBV sires, using groups of herds (amphurs) instead of single herds as part of a contemporary group may have biased the EBV of genetically better sires upwards because their daughters were compared to the amphurs' lower means than those of their herds of origin. Contrarily, lower EBV sires may be biased downwards. To avoid these potential biases, dairy cattle genetic evaluation models in Thailand should use herds instead of amphurs.

Ignoring interactions among contemporary group components may result in biased DPO genetic evaluations. Dairy cattle genetic evaluation models normally include these interactions because they have usually been found to be significant (e.g., VanVleck, 1987; Schmitz et al., 1991). Preliminary analyses of the DPO data set here reconfirmed this fact. Two- and three-way interactions among herds, years, and seasons were significant ($P < 0.01$). Thus, HYS subclasses should be used in genetic evaluation models for the DPO data set.

Genetic Group Effects. The purpose of genetic group effects in dairy genetic evaluation is to account for genetic differences among subpopulations (Quaas and Pollak, 1981). Genetic group effects in a genetic prediction model can be viewed from a subclass or a regression viewpoint. Regression grouping strategies are better suited to multibreed populations than subclass grouping strategies because regression components (e.g., *Bos taurus*) are estimated using information from all animals containing that component in their genotypes, and they can be used to predict any subclass genetic group effect, including those not represented in the data set. Contrarily, subclass-grouping strategies use only information from a particular subclass to estimate the genetic group values of that subclass (less accurate than an estimate using regression group components), and they cannot be used to predict group subclasses not in the data set. The 1999 DPO model created subclass genetic groups based on ranges of accumulated fractions of BT and BI as defined by Vinther (1974). If interbreed BT $\times$ BI nonadditive genetic effects were important for the 1999 genetic evaluation, they would have been an integral part of the estimated DPO subclass group effects, and the random portion of the EBV would have been deviated from *a function of additive and nonadditive genetic group components*. In the 1999 sire summary, however, DPO published only the *random* part of sire EBV, which contained only additive genetic effects. Thus, the 1999 published EBV permitted unbiased comparisons among sires of the *same* BT-BI composition; comparison among bulls of different BT-BI composition would be biased.

Ideally additive and nonadditive genetic effects should be estimated separately to help improve selection and mating decisions in a multibreed population. Unfortunately, the structure and size of the DPO multibreed data set here prevented a separate estimation of BT $\times$ BI interbreed nonadditive genetic group effects. Consequently, the genetic value of a sire was defined here to be the sum of an additive genetic group part and of an additive random genetic part (equation [5]). Data-permitting, however, these nonadditive genetic effects must be included in future larger and more complete Thai multibreed data sets.

The second regression grouping strategy used here, HO, is a step further in the development of regression breed oriented multibreed models for Thailand. Holstein was chosen as the identifiable breed because it is the most popular base breed for dairy crossbreeding purposes in Thailand. Regression breed oriented multibreed models are likely to become more feasible in the future as more data becomes available on a few major breeds in Thailand.

Estimates of Covariance Components and Genetic Parameters

Additive genetic and environmental variance components, heritability estimates, and their standard errors for MY and FY using the BTBI and the HO model are presented in Table 4. The genetic base of the BTBI model was the set of BI alleles in the population. On the other hand, the

genetic base of the HO model was the set of non-H alleles in the population. Estimates of additive genetic variances were similar in the BTBI (327,544 kg^2 for MY and 237 kg^2 for FY) and the HO model (335,235 kg^2 for MY and 250 kg^2 for FY). Environmental variance estimates were also similar for MY and FY in these two models. Thus, heritability estimates were almost identical in the BTBI (0.45 for MY and 0.24 for FY) and the HO model (0.46 for MY and 0.25 for FY). The close similarity of heritability estimates between the BTBI and the HO model probably occurred because the breed composition of the base genetic groups for these two models differed very little. In fact, 88% of the alleles in this data set were *Bos taurus*, and 91% of them were from Holstein. As expected, because of the small size of the multibreed data set, standard errors were large for variances and heritabilities, particularly for FY additive genetic variances and heritabilities in both models.

Table 4. Additive genetic and environmental variance components, and heritabilities for accumulated 305-d milk (MY) and fat yields (FY) by the BTBI and the HO model

Parameters	MY	FY
BTBI model		
Genetic variance (kg^2)	327,544 (132,380)[1]	237 (189)
Environmental variance (kg^2)	393,429 (126,913)	766 (184)
Heritability	0.45 (0.18)	0.24 (0.18)
HO model		
Genetic variance (kg^2)	335,235 (148,334)	250 (195)
Environmental variance (kg^2)	386,998 (134,842)	747 (190)
Heritability	0.46 (0.19)	0.25 (0.19)

[1] Standard error

The heritability estimates for MY and FY obtained here were similar to others obtained in tropical environments. Misra et al. (1979) reported MY heritability estimates of 0.48 for Sahiwal, 0.36 for Red Sindhi, and 0.44 for Friesian × BI crossbreds in India. Heritability estimates for Holstein were 0.24 for MY and 0.20 for FY in Australia (Visscher and Goddard, 1995), 0.28 for MY and 0.26 for FY in New Zealand (Ahlborn and Dempfle, 1992), 0.25 for MY and 0.22 for FY in Brazil (Costa et al., 2000), and 0.20 to 0.44 for MY and 0.18 to 0.42 for FY in USA (Miszta l et al., 1992; Dematawewa and Berger, 1998).

Heritability estimates for MY and FY here were lower than those reported in other Thai multibreed studies. Differences in the multibreed field data sets used, editing procedures, and genetic evaluation models are likely to account for a large portion of these different estimates. Kanloung *et al.* (1999) computed heritability estimates of 0.53 for MY and 0.50 for FY using a model that considered amphur-year-season subclass as contemporary groups. Kuha (1999) obtained heritability estimates of 0.55 for MY and was 0.58 for FY using a model that had only year and season as main effects (i.e., no herds or amphurs), and no contemporary group subclass. Both studies included a version of Vinther's (1974) BT subclass groups. These two studies are likely to have overestimated the heritability estimates for both MY and FY. Inclusion of amphur as part of the definition of a contemporary group may lead to upward biases in estimates of genetic variances as discussed earlier. Ignoring herds (or amphur) will increase the likelihood and size of these biases.

Table 5 shows genetic covariances, and genetic, environmental, and phenotypic correlations between MY and FY using the BTBI and HO model. The *estimated* genetic correla tion between MY and FY was high (0.99) for both the BTBI and the HO model. Estimates

of environmental and phenotypic correlations for MY and FY were also high and positive as additive genetic correlations. Standard errors for these correlation estimates were all

Table 5. Genetic covariances, and genetic, environmental, and phenotypic correlations between accumulated 305-d milk (MY) and fat yields (FY) for the BTBI and the HO models

Parameters	BTBI model	HO model
Genetic covariances (kg^2)	8,751 (3,835)[1]	9,076 (5,291)
Genetic correlation	0.99 (0.09)	0.99 (0.07)
Environmental correlation	0.89 (0.04)	0.93 (0.04)
Phenotypic correlation	0.90 (0.01)	0.90 (0.01)

[1] Standard error

low (0.01 to 0.09). High genetic correlations between MY and FY have been reported in H (0.62 to 0.79; Misztal et al., 1992; Visscher and Goddard, 1995; Dematawewa and Berger, 1998; Costa et al., 2000). These high genetic correlations between MY and FY indicated that selection to improve one of these traits (MY or FY) would also improve the other. They also reflect the part-whole correlation that exist between MY and FY (FY=MY*Fat percentage).

Regression Genetic Group Effects

The estimate of the MY regression additive genetic group effects was higher in the BTBI model (149 ± 532 kg) than in the HO model (18 ± 363 kg). It is unclear why there was such a large difference between the BTBI (149 kg) and the HO (18 kg). However, these values should be considered with caution because of their extremely large standard errors. The small HO difference in MY might be an indication that non-H alleles performed in similar fashion to H alleles, but this needs to be reconfirmed with a substantially larger multibreed data set.

The estimates for FY regression additive genetic group effects were similar in both models (BTBI: -26 ± 21; HO: -21 ± 14 kg), and had much smaller standard errors than those for MY. These regression values would suggest superiority for FY of the *Bos indicus* breeds represented in this multibreed population.

Additive Genetic Predictions

The number and breed composition of sires and dams represented in the multibreed data set was substantially different. Sires represented only 16% of the evaluated animals in the data set. Most sires were straightbred H (91%), whereas the majority of dams (88%) were crossbred with a high H fraction (5/8 H and higher). Because of these differences, ranges and figures of EBV were constructed for both sires and dams.

Table 6 shows the range of EBV for sires, dams, and for all evaluated animals in the Thai data set. The range of EBV values for MY was smaller for sires than for dams in both the BTBI (-567 kg to 1,009 kg for sires, and -1,394 kg to 1,298 kg for dams) and the HO (-638 kg to 888 kg for sires, and –1,564 kg to 1,248 kg for dams) models. The same pattern occurred for FY. The larger range of EBV values in dams may be a reflection of their larger variability in breed composition as well as their lower accuracies of genetic predictions compared to those of sires.

The distribution of EBV for sires and dams by models (BTBI and HO) is presented in Figure 1 for MY and in Figure 2 for FY. Sires and dams were ordered by EBV value within BT fraction (BTBI model) and H fraction (HO model). These figures provide a clear depiction of the predicted additive genetic ability of sires and dams of different breed composition. Of particular

Table 6. Range of expected breeding values (EBV) for accumulated 305-d milk (MY) and fat yields (FY) by the BTBI and HO model for sires and dams

Range of EBV (kg)	BTBI model	HO model
MY sires	-567 (332)[1] to 1,009 (572)	-638 (333) to 888 (579)
FY sires	–45 (9) to –3 (15)	–39 (9) to 7 (16)
MY dams	-1,394 (389) to 1,289 (572)	-1,564 (391) to 1,248 (579)
FY dams	-67 (11) to 7 (15)	-65 (10) to 22 (16)
MY all animals	-1,394 (331) to 1,289 (572)	-1,564 (333) to 1,248 (579)
FY all animals	-67 (9) to 7 (15)	-65 (9) to 22 (16)

[1] Standard error

interest is the comparison of the additive genetic ability of straightbred or crossbred animals of high H fraction (7/8 H or 224/256 in the figures) with crossbred animals of H fraction below 7/8H (i.e., below 224/256 in the figures). The figures clearly show that in this Thai multibreed population there were animals of high and low EBV across all fractions of BT (BTBI model) or H (HO model). In fact, the lowest dam EBV for MY and FY occurred in dams that were 100% H, and the highest dam EBV were crossbred.
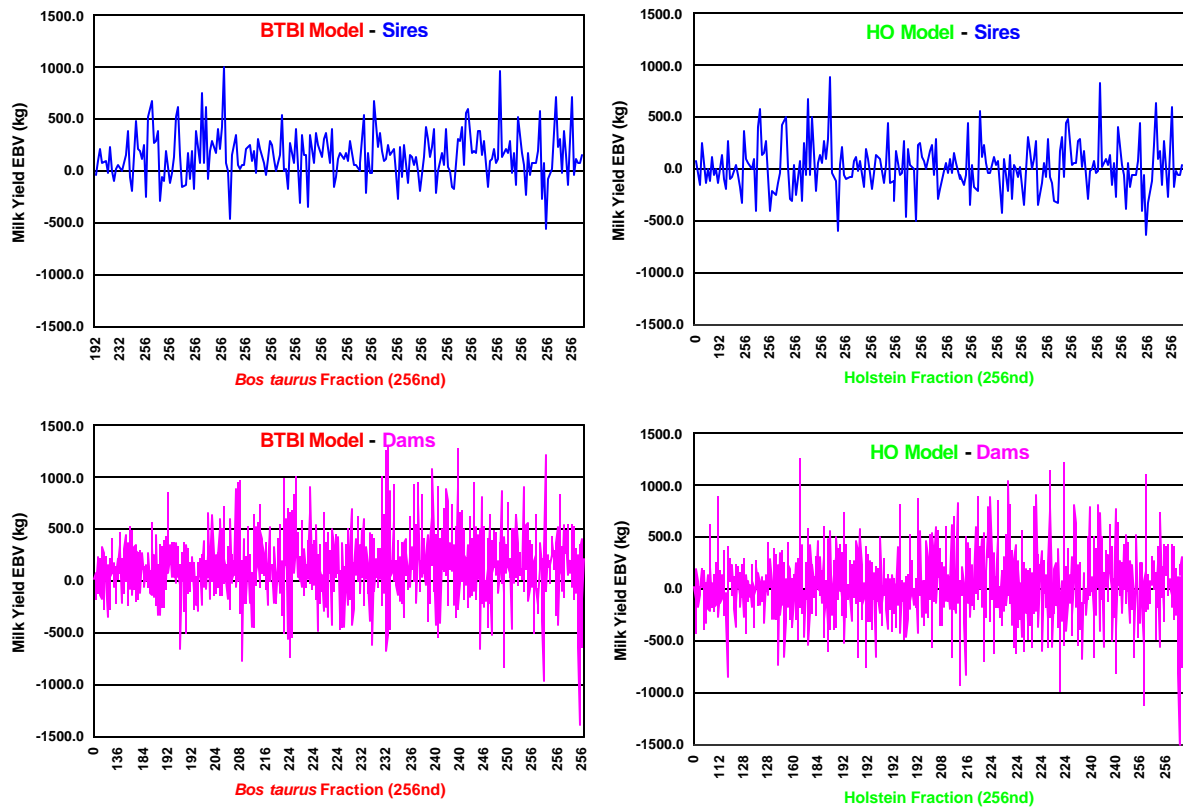

Figure 1. Milk yield (MY) EBV for sires and dams ordered by EBV within BT (BTBI model) and H (HO model) fraction

Sire EBV showed a similar pattern for MY and FY (the high FY EBV sires with no H fraction were from three Jersey sires used between 1992 and 1994). This pattern of EBV suggests that, under the environmental conditions of the animals in this multibreed data set, crossbred animals of various BT or H fractions were as good or better than straightbred H for MY and FY. Purebred BT animals from temperate breeds like H are known to be less adapted than BT $\times$ BI crossbred animals in tropical environments. Tropical parasites and insects in Thailand will cause BT cattle to loose weight and to decrease milk production (Madsen and Vinther, 1975; Trisanarom et al., 1990; Markvichitr et al., 1995). These known BT adaptability concerns and the EBV obtained here suggest that BT and H crossbred sires and dams should continue to be used as the main source of breeding animals for this population. Thus, straightbred H should be considered only in herds capable of providing the demanding nutritional, management, and environmental conditions necessary for the expression of their MY and FY genetic potential.
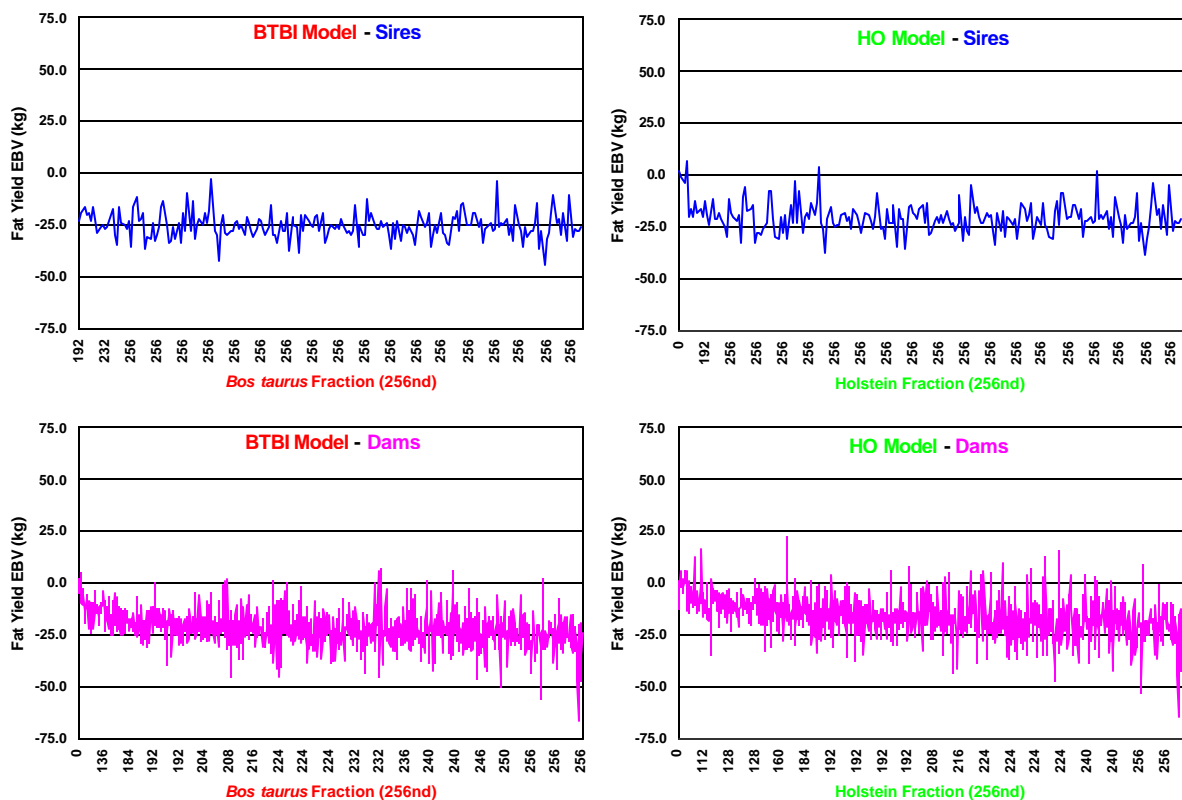

Figure 2. Fat yield (FY) EBV for sires and dams ordered by EBV within BT (BTBI model) and H (HO model) fraction

The additive group regression models used here provided a reasonable approximation to the underlying set of genetic effects. Their main drawback was that they ignored nonadditive genetic effects (group and random), particularly nonadditive interbreed. However, most dams in this data set were 75% H or higher and most males were 100% H, thus the expected fraction of interbreed nonadditive genetic effects was small (25% in most matings). Thus, group interbreed nonadditive genetic effect may be large, and ignoring even a small fraction may cause biases in additive genetic predictions. Further, ignoring random interbreed nonadditive genetic effects will

increase the size of the standard errors of prediction of additive genetic evaluations. These two aspects need to be addressed in future studies, particularly because of the continued use of crossbred BT × BI sires in Thailand. Mating of BT × BI crossbred sires (e.g. 50% , 75% BT) to non-BT and BT × BI crossbred dams will guarantee the existence of a substantial number of animals with BT fractions lower than 50% in Thai dairy cattle populations. Multibreed genetic models that include additive and nonadditive genetic effects (Elzo, 1983; Elzo and Famula, 1985) will need to be used to account for both additive and nonadditive genetic effects in such multibreed populations. The estimates of variance and covariance components and the genetic evaluations obtained here will serve as a comparison base for more complex future multibreed genetic evaluation models and procedures in Thailand.

Conclusions

The results of this study showed the feasibility of using additive group regression models for the genetic evaluation of Thai multibreed dairy populations. Genetic predictions and covariance component estimates obtained here were reasonable considering the small size and the extreme unbalancedness of the dataset. It should be emphasized, however, that inferences from this study can be made only to the region and the population studied here. To make inferences of national relevance, a substantially larger multibreed data set that contains information from all regions of Thailand will be needed. Thus, this study needs to be repeated with a suitably large and nationally distributed data set. Because of the use of crossbred animals as parents, the national Thai population will continue to be multibreed in the foreseeable future. Thus, national genetic evaluation models would need to include additive as well as nonadditive genetic effects. Several alternative multibreed models containing additive and nonadditive genetic effects would need to be developed and compared for their suitability for the Thai multibreed population before a final model is chosen to conduct national genetic evaluations. This is a dynamic process. Thus, future changes in the structure and composition of the national Thai multibreed population will need to be closely monitored to make appropriate changes to the current multibreed models and computational procedures.

Acknowledgements

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