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Use of Multiple Traits Animal Model for Genetic Evaluation of Milk Yield and Age at First Calving of Holstein Friesian Cattle in Turkey

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Abstract: A total of 1780 normal first lactation records of Holstein Friesian cows kept at five herds in West Turkey during the period from 1981 to 1997 were used in this study. Genetic and phenotypic parameters for 305 day milk yield (dMY) and Age at First Calving (AFC) were estimated by MTDFREML using multi trait animal model. The model included individual and error terms as random effects, herds, season and year of calving as fixed effects and the effect of AFC on 305 dMY as a covariate. Estimates of heritability were 0.20 and 0.75 for 305 dMY and AFC, respectively. The genetic correlation between 305 dMY and AFC was negative (-0.22). Predicted breeding values for cows, dams and sires were presented.

Key words: Animal model, genetic evaluation, Holstein, Turkey

INTRODUCTION

Estimation of breeding values for milk traits are based on first lactation records, all lactation records or some combination of first and later lactations records. Performance of first lactation has been the standard of evaluation for most genetic studies with dairy cattle. First records are available sooner or more cows and are less susceptible to error from selection, injury, previous days dry and mastitis than are later records.

Age at first calving and the first lactation yield are expected to contribute a good deal towards the producing capacity of an animal during her lifetime and consequently needs an important consideration in selecting cows[1]. In addition, age at first calving influences the reproductive life of cows, the generation interval and the efficiency of progeny testing of bulls. It also affects the productive performance of cattle, particularly first lactation production. A reduction in age at first calving will minimize the cost of raising the heifers, shorten the generation interval and maximize the number of lactation per cow[2]. The genetic relationship between first milk yield and age at first calving was found to be negative in many investigations[2-6]. The objective of this study was to estimate the genetic parameters and breeding value using all available sources of pedigree. Cows, sires and dams for first 305 day milk yield and age at first calving in different herds of Holstein Friesian cows in Turkey, by using multivariate analysis (Multi Trait Animal Model).

MATERIALS AND METHODS

Data of 1780 normal first lactation records of Holstein Friesian cows raised at five herds in Turkey (i.e. Tahirova, Dalaman, Turkgeldi, Sarmisakli and Menemen) were used in the present study. Records covered the period from 1981 to 1997. Abnormal records affected by diseases or by abortion were excluded. Heifers were inseminated when they reached on an average of 350 kg body weight. Animals were fed on silage, concentrates and Alfalfa all the year. Cows were machine milked twice a day. Milk yield recorded to the nearest 0.2 kg, for each cow. Cows producing more than 15 kg a day and those in the last two months of pregnancy were supplemented with extra concentrate rations. Traits studied were 305 day milk yield (dMY) and age at first calving (AFC). Genetic analysis included the sires, which have at least 10 daughters. Artificial insemination (AI) was used.

Data were analyzed by Multiple Trait Derivative Free Restricted Maximum Likelihood (MTDFREML) according to Boldman *et al.*[7] using multiple trait analysis. Table 1 shows the data structure considered in the analysis as well as the means of 305 dMY (kg) and AFC in months. The DF algorithm was restarted (cold restarts) for the run at least three times after convergence to ensure that the global maximum had been reached. The convergence criterion was a minimum V (-2 log L) of $1x10^{-9}$, where L is the likelihood function and V is the minimum variance of function values. Starting values for iteration for 305 dMY

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Table 1: Data structure, means, standard deviation (SD) and coefficient of variation (CV%) for 305 day milk yield (305 dMY) and age at first calving (AFC)

Traits	Mean	SD	CV%
305 dMY, kg	4642.00	1382.00	29.77
AFC, mo	28.80	3.61	12.53
Observations			
No. of records			1780
No. of cows			1780
No. of sires			219
No. of dams			401
Animals in relationship matrix (No. A^{-1})			2400
Mixed model equations (No. of MME)			4860
No. of iterations			5249

and AFC were taken from Khattab *et al*.[6]. The Multi Trait Animal Model was used to analyze 305 dMY and AFC included, individual and errors as random effects, month and year of calving and herds as fixed effects and the effect of AFC on 305 dMY as a covariate.

In matrix notation the animal model used was:

$$Y = Xb + Xg + e$$

where, Y= observations vector of animals, b= fixed effects vector (i.e. month of calving, 1,…,12; year of calving, 81,…,97 and herds, 1,…,5), g= animal direct genetic effect vector and e= residual effect vector, X and Z are incidence matrices and

$$E\begin{pmatrix} a \\ e \end{pmatrix} = \begin{pmatrix} 0 \\ 0 \end{pmatrix}$$

$$V\begin{pmatrix} a \\ e \end{pmatrix} = \begin{pmatrix} A\sigma^2_{a1} & A\sigma^2_{a12} & 0\ 0\ 0 & 0 \\ A\sigma^2_{a21} & A\sigma^2_{a2} & 0\ 0\ 0 & 0 \\ 0 & 0 & 0\ 0\ I\sigma^2_{e1} & I\sigma^2_{e2} \end{pmatrix}$$

To estimate heritability (h^2) coefficient, the following equations was used:

$$h^2 = \sigma^2_a(\sigma^2_a + \sigma^2_e)$$

where:
σ^2_a = additive genetic variance and σ^2_e= temporary environmental variance.

Breeding values were calculated from 1780 cows, fathered by 219 sires and mothered by 401 dams. The Mixed Model Equations (MME) for the Best Linear Unbiased Estimator (BLUE) for Estimable Function for the Best Linear Unbiased Prediction (BLUP) was in matrix notation are described by El-Arian *et al*.[8] and Khattab *et al*.[6].

RESULTS AND DISCUSSION

Unadjusted mean and standard deviation (SD) for 305 dMY and AFC were 4642±1382 kg and 28.80±3.61 mo, respectively (Table 1). The present mean of 305 dMY was lower than those reported by Atay *et al*.[9], Bakir and Sogut[10] using another herds of Holstein Friesian cows in Turkey, being 5480 and 6964 kg, respectively. Also, the present mean was lower than those found by Abdel-Salam *et al*.[11] and El-Arian *et al*.[8] working on Holstein Friesian cattle in Egypt, being 7128 and 5021 kg, respectively. The mean of AFC was lower than the estimate found by Ashmawy[2] (32 mo) and Khattab and Sultan[4] (31.3 mo). The coefficient of variability for 305 dMY and AFC are lower than those reported by Khattab *et al*.[6] on Egyptian buffaloes. The differences between present results and those of the other workers could be due to differences in climatic and management conditions and/or genetic differences in herds.

The average number of equations and iterations recorded were 4860 and 5249, respectively (Table 1). Results of the present study are higher than those estimated from single trait animal model reported by Khattab *et al*.[12] being 3200 and 1950, respectively. The higher number of iterations in the present study may be due to using two traits in the same analysis and taking into consideration the genetic and errors covariances among these traits. El-Arian *et al*.[8] concluded that the number of iterations required to reach convergence could be affected by the number of animals, the number of random effects in the models and traits studies.

The heritability estimates were 0.20 and 0.75 for 305 dMY and AFC, respectively (Table 2). Similarly, Atay *et al*.[9] and Ulutas *et al*.[13] working on Holstein Friesian cattle in Turkey, found that h^2 for 305 dMY were 0.26 and 0.22, respectively.

According to moderate h^2 estimates for 305 dMY, it can be concluded that the genetic improvement in milk yield can be achieved through selective breeding program. The present estimate of h^2 for AFC was higher than those estimates reported by Gopal and Bhatnagar[1] (0.36), Basu *et al*.[3] (0.24), Khattab and Sultan[4] (0.38) and Atil *et al*.[5] (0.57). In this respect, Abubaker *et al*.[14] opined that the large sire variance in AFC is due to confounding of sire with management. Tonhati *et al*.[15] on Murrah buffaloes in Brazil found that h^2 for total milk yield and AFC were 0.38 and 0.20, respectively. The present study concluded that the genetic change for these traits is possible by selecting the most productive animals.

Table 2: Estimates of variance and covariance components, heritability (h^2) and genetic correlation (r_g) for 305 day milk yield (305 dMY) and age at first calving (AFC)

Estimate	Traits	
	305 dMY (kg)	AFC (mo)
Additive variances and covariances		
σ^2_a	2810.00	11.17
σ_a 305 dMY with AFC		-38.40
Environmental variances and covariances		
σ^2_e	10930.00	3.70
σ_e 305 dMY with AFC		3.14
h^2	0.20	0.75
r_g 305 dMY with AFC		-0.22

Table 3: Range of predicted breeding values of cows (CBV's), sires (SBV's) and dams (DBV's) and their accuracy for 305 day milk yield (305 dMY) and age at first calving (AFC)

	Traits	
CBV's	305 dMY (kg)	AFC (mo)
Minimum	-1475±4	-5.23±1
Maximum	1049±4	12.71±1
Range	2524	17.94
Accuracy	0.65 to 0.74	0.87 to 0.95
SBV's		
Minimum	-1027±3	-6.61±1
Maximum	1159±3	7.70±2
Range	2186	14.31
Accuracy	0.80 to 0.85	0.89 to 0.96
DBV's		
Minimum	-558±5	-3.46±3
Maximum	1028±5	5.63±3
Range	1586	9.09
Accuracy	0.44 to 0.46	0.40 to 0.55

The genetic correlation between 305 dMY and AFC was negative and significant (-0.22) and suggested that selection for high yielding cows would cause a correlated decrease in their age at first calving. Therefore, a reduction of AFC is a desirable goal of dairymen and will help in minimizing the cost of raising breeding heifers and maximizing the number of lactation per cow. In this respect, Basu *et al.*[3] found negative genetic correlation between milk yield and AFC (-0.43) and they concluded that, direct selection for milk yield would result in moderate decline (improvement) in age at first calving. The selection index involving AFC, milk yield and lactation period (RIH 0.69) would give an expected genetic gain change 257.74 kg as against 255.19 kg from direct selection for milk yield. In addition, Ashmawy[2] concluded that selection on the basis of first 305 dMY and AFC would lead to an increase in the length of herd life and cows would produce more offspring. The early selection is essential for minimum generation interval and subsequently maximum genetic progress. Gopal and Bhatnagar[1] came to the same conclusion. On the other hand, Tonhati *et al.*[15] found that the genetic correlation between milk yield and AFC was 0.63. They suggested that, when milk yield is the selection target there could be an increase of AFC. Their results revealed that milk yield and AFC could be considered independently in planning buffalo selection programs.

The range of cow breeding values for 305 dMY and AFC were 2524 kg and 17.94 mo, respectively and that of SBV's for the above mentioned traits were 2186 kg and 14.31 mo, respectively. While, the range of dam breeding values (DBV's) were 1586 kg and 9.09 mo, respectively (Table 3). The present results show large differences among breeding values of cows, sires and dam in both traits studied. Thus, the improvement of milk production and age at first calving through selection is possible. Genetic progress can be achieved if the farms adopts test for the genetic evaluation of sires and cows. El-Arian *et al.*[8], Khattab *et al.*[6] and Abdel-Salam *et al.*[11] arrived at the same conclusion. In addition, the present results show that predicted breeding values of cows, sires and dams positive values for 305 dMY are also in most cases negative values for AFC. These results indicate that selection for 305 dMY for top cows, sires and dams will decrease AFC in the next generation and this is a goal of dairymen. Ulutas *et al.*[13] working on another herd of Holstein Friesian cows in Turkey, estimated breeding values for 305 dMY, by using animal model. They concluded that, involving of BLUP procedure to herd management with increasing number of records and selection based on EBV's of each animal might help to improve genetic gain for herd.

On the other hand, Tonhati *et al.*[15] on Murrah buffaloes, estimated breeding values of cows, dams and sires for milk yield and AFC, by using single trait animal model, concluded that the average breeding values of cows, sires and dams for different traits studied were around zero, which indicated that selection in such cases was not effective.

Results in the present study (Table 3) show that the importance of cows, since it gave the higher range of breeding values for 305 dMY and AFC. Thus, selection for cows for the next generation in maternal line would place emphasis on good genetic maternal effects in addition to good estimates of breeding value. Khattab *et al.*[6] arrived at the same results on Egyptian buffaloes. Also, Table 3 shows that the accuracy of the estimates of sire breeding value was higher than the accuracy of cow and dam breeding values, which may be due to the higher number of daughters per sire. Then it is necessary to depend on sire for estimated breeding value and low accuracy of predicted breeding values of dams, indicate that dams are less important than sire and/or cows for estimating breeding values.

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