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Estimation of Genetic Trends for Productive and Reproductive Traits of Holstein Friesian Cows in Turkey

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Abstract: This study investigated genetic trends of some productive and reproductive traits in Holstein Friesian cows kept at five herds in of Turkey. A total number of records used were 6953 during the period from 1980 to 1997. Variance components for 305 day milk yield (305 dMY), Lactation Period (LP) and Calving Interval (CI) were estimated by the Restricted Maximum Likelihood Method, using an animal model. The model included individual, permanent environmental and errors as random effects, herd, month and year of calving and parity as fixed effects. Estimates of heritability were 0.26, 0.07 and 0.09, respectively. Estimated repeatability values were 0.49, 0.17 and 0.23 for 305 dMY, LP and CI, respectively. Means of predicted breeding values for cows, dams and sires according to calving year and the genetic correlations were presented. The estimated of genetic trends of 305 dMY, LP and CI were 44.85 kg/year, 1.3 d/year and -0.95 d/year, respectively.

Key words: Restricted Maximum Likelihood Method, animal model, Holstein, Turkey

INTRODUCTION

The methods of estimation genetic changes in a herd are selection experiments in a constant environment, divergent selection, replication of the same genetic material in successive generations and analysis of field records^[1]. Due to the high costs of keeping farm animals with low reproductive rate and long generation intervals, such as occur with cows, the population parameters of heritability (h^2), repeatability (t), genetic correlations and genetic trend are generally studied from field data or simulation studies^[2]. In addition a goal of dairy cattle breeders is to increase genetic merit for milk traits. To determine the effectiveness of breeding progress, genetic trends in dairy cattle population must be monitored.

The objectives of this study were to estimate heritability, repeatability and genetic correlation coefficients and to study the genetic trends of some productive traits (305 dMY and LP) and reproductive traits (e.g. CI) using field data from different herds of Holstein Friesian cows reared in Turkey.

MATERIALS AND METHODS

Productive and reproductive records of Holstein Friesian cows raised at five herds in Turkey during the period from 1980 to 1997 were used. A total of 6953 normal lactation represented 219 sires were used. All normal records of less than 305 day milk length a long with those

reaching 305 day were included. Traits studied are 305 day milk yield (305 dMY), Lactation Period (LP) and Calving Interval (CI). Animals were fed on silage, concentrates and Alfalfa all the year. Heifers were inseminated when they reached an average of 350 kg body weight, while cows were inseminated during the last heat period after 60 days postpartum. Cows were artificially inseminated by using frozen semen. Assignment of sires to cows was at random.

The records were analyzed by Multiple Trait Derivative Free Restricted Maximum Likelihood (MTDFREML) according to Boldman *et al.*^[3], using repeatability animal model. The multi trait animal model was used to analysis 305 dMY, LP and CI included individual, permanent and errors as a random effects, herd, month and year of calving and parity as a fixed effects. Due to empty cells, then it is difficult to estimates the effects of Herd, Year and Season (HYS). The MTDFREML algorithm was restarted (cold restarted) for the run at least three times after convergence to ensure that the global maximum had been reached. The convergence criterion is a minimum $V (-2 \text{ Log } L)$ of 1×10^{-9} , where, L is the likelihood function and V is the minimum variance of function values. Starting values for 305 dMY, LP and CI were taken from El-Arian *et al.*^[4].

The following general model was adopted.

$$Y = Xb + Za + Wp + e$$

where, Y= observation vector of records, b= fixed effects vector (herds, five herds, month of calving from January to December, year of calving from 1980 to 1997 and parity from 1 to six parties), a= animal direct genetic effect vector, p= permanent environmental effect vector and e= residual effect vector, X, Z and W are incidence matrices and

$$E \begin{bmatrix} a \\ p \\ e \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \end{bmatrix},$$

$$V \begin{bmatrix} a \\ p \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & 0 & 0 \\ 0 & I\sigma_p^2 & 0 \\ 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

To estimate heritability (h^2) and repeatability (t) coefficients, the following equations were used:

$$h^2 = \sigma_a^2 / (\sigma_a^2 + \sigma_p^2 + \sigma_e^2)$$

and

$$t = (\sigma_a^2 + \sigma_p^2) / (\sigma_a^2 + \sigma_p^2 + \sigma_e^2)$$

where, σ_a^2 = additive genetic variance, σ_p^2 = permanent environmental variance and σ_e^2 = temporary environmental variance. Breeding values were calculated from 1803 cows, fathered by 219 sires and mothers by 419 dams. The Mixed Model Equations (MME) for the Best Linear Unbiased Estimate (BLUE) for estimable function for the Best Linear Unbiased Prediction (BLUP) in matrix notation are described in detail by El-Arian *et al.*^[4]. In addition, the accuracy of breeding values and the standard errors are estimated according to Boldman *et al.*^[3].

The genetic trend was obtained by regressing the predicted breeding value for sires on the year of calving.

RESULTS AND DISCUSSION

Unadjusted means and standard deviations for 305 dMY in kg and LP and CI in days were 4659±1386, 301±45.88 and 390±69.71, respectively (Table 1). The present means of 305 dMY and LP are lower than those found by Yener *et al.*^[5] and Atay *et al.*^[6] using another herds of Holstein Friesian cattle in Turkey, being 6777 kg and 5489 kg for 305 dMY and 330 and 333 days for LP, respectively. While, the present means are higher than those reported by Khattab and Sultan^[7], Afifi *et al.*^[8] working on Friesian cattle in Egypt. The present mean of CI are similar to that obtained by Afifi *et al.*^[8] (390 days), working on Friesian cattle in Egypt. While Campos *et al.*^[9]

Table 1: Data structure, unadjusted mean, standard deviations (SD) and coefficient of variability (CV%) for 305 day milk yield (305 dMY), Lactation Period (LP) and Calving Interval (CI)

Traits	Mean	SD	CV%
305 dMY (kg)	4659	1386	29.76
LP (day)	301	45.88	15.27
CI (day)	390	69.71	17.82
Observations			
No. of records	6953		
No. of cows	1803		
No. of Sires	219		
No. of dams	419		
Animals in relationship matrix	2441		
Mixed Model Equations (MME)	12843		
No. of iterations	7261		

Table 2: Estimation of variance components, heritability (h^2), repeatability (t) and genetic correlations (r_g) estimates for 305 day milk yield (305 dMY), Lactation Period (LP) and Calving Interval (CI)

Estimates	Traits		
	305 dMY	LP	CI
σ_a^2	2956.61	59.82	6.310
σ_p^2	5896.90	722.41	55.210
σ_e^2	2736.85	89.59	10.266
h^2	0.26	0.07	0.090
t	0.49	0.17	0.230
r_g 305 dMY with LP,CI		0.96	-0.680
r_g LP with CI			-0.700

r_g : Genetic correlation is corrected for the nongenetic effects

working on Holstein Friesian cattle in Florida found that average CI was 414 days.

Estimates of CV% given in Table 1 showed that variation in 305 dMY was relatively high compared with other traits. Afifi *et al.*^[8] concluded that high variation in productive traits could be attributed to the variation in management decision. The differences between our results and those of other workers could be due to differences in climatic and management conditions and/or genetic differences in herds.

The average number of Mixed Model equations (MME) and iterations were 12843 and 7261, respectively (Table 1). The present results are higher than those estimated from single trait animal model reported by Khattab *et al.*^[10] being 3200 and 1950, respectively. In addition, El-Arian *et al.*^[4] working on Holstein Friesian cattle in Egypt using multi trait animal model, found that the number of MME and iterations were 5787 and 5659, respectively. The higher number of iteration in the present study may be due to using three traits in the same analysis and taking into consideration the genetic, permanent and errors covariances among these traits. In this respect, Dong and Van Vleck^[11] used two samples, each with about 3000 cows, to estimate genetic parameters for milk yield, calving interval and survival for first lactation. The number of iterations allowed was 20 and 23, respectively. While, Albuquerque *et al.*^[12] indicated that some runs stopped after 300 rounds of iterations. In general, number of iterations required to reach

Table 3: Minimum, maximum and range of predicted breeding values (BV) for cows (CBV's) sires (SBV's) and dams (DBV's), their Standard Errors predicted (SE) and accuracy of predicted (r) estimated by multi-trait animal model for 305 day milk yield (305 dMY), Lactation Period (LP) and Calving Interval (CI) for Holstein Friesian cows

Traits	CBV's						SBV's						DBV's					
	Minimum			Maximum			Minimum			Maximum			Minimum			Maximum		
	BV	SE	r	BV	SE	r	BV	SE	r	BV	SE	r	BV	SE	r	BV	SE	r
305 dMY (kg)	3.04	30	0.84	-280	30	0.83	1.65	24	0.89	-223	33	0.80	2.59	44	0.58	-179	44	0.56
LP (day)	3.20	5	0.80	-3.69	5	0.80	2.08	4	0.86	-2.38	5	0.77	3.47	6	0.55	-2.26	7	0.41
CI (day)	3.07	2	0.38	-1.30	2	0.40	2.76	2	0.59	-2.98	2	0.59	1.55	2	0.19	-1.30	2	0.26

convergence could be affected by the number of animals, the number of random effects and traits studies.

Estimates of heritability for 305 dMY, LP and CI were 0.26, 0.07 and 0.09, respectively (Table 2). In this respect, Ulutas *et al.*^[13] working on 853 Holstein cows in Turkey, using animal model, estimated h^2 for 305 dMY and LP, were 0.22 and 0.13, respectively. The present estimates of h^2 for 305 dMY, indicated that genetic change for this trait is possible by selecting the most productive animal. However, the h^2 estimates for LP and CI indicated that the genetic variation among individuals is practically nil. Individual differences with respect to these traits could be reduced by management and breeding practices. Tonhati *et al.*^[2] arrived at the same conclusion. In addition, El-Arian *et al.*^[4] working on Holstein Friesian cattle in Egypt, found that h^2 estimates for 305 dMY and LP are 0.32 and 0.07, respectively. They concluded that more efforts could be made to bring about improvement 305 day milk trait through selection as well as better managerial practices, a low h^2 estimates for LP and CI, indicated that these traits are affected mainly n environmental factors. Improvement of feeding, management, detection of animal in heat and their insemination at proper time by good quality semen would help in improving CI.

In general, h^2 estimates obtained in the present study are lower than those obtained with sire model reported by Atil *et al.*^[14] using the same set of that data, found that h^2 for 305 dMY and LP are 0.38 and 0.13, respectively. In addition, Cue *et al.*^[15] using a sire model with Canadian data, reported h^2 estimates of 0.36 for milk yield.

Cow evaluation and selection are important in herd improvement scheme. The ultimate aim of an evaluation is to enable breeders to compare their animals by the Estimated Producing Ability (EPA) which involves repeatability. The higher estimates of repeatability for 305 dMY (0.49) indicated that the permanent environmental fractions of variance were high. Therefore, the first lactation of each cow would lead to an accurate prediction of future performance, promises efficient selection and also would afford an opportunity for a faster return of sires to service if their evaluation can be made early.

However, the estimated values for LP (0.17) and CI (0.23), this means that LP and CI are to a great extent

under the control of management. Tonhati *et al.*^[2] on Murrah buffaloes arrived at the same conclusion. In addition, Kandiah^[16] concluded that low h^2 and t for CI trait suggested that most of the observed variation in this trait was due to temporary environmental conditions and management. The improvement of this trait may be achieved by better feeding, better management, reduction heat stress, better control of diseases including vaccination programs and wide spread milk recording and testing systems.

The estimated genetic correlations (Table 2) suggests that when milk production is the selected variable there could be an increase of LP and decrease of CI and the selection of animals with short CI might also result in a decrease of LP. In this respect, El-Arian *et al.*^[4] working on Holstein Friesian cows in Egypt arrived at the same results.

The range of cow breeding values for 305 dMY, LP and CI was 584 kg, 6.89 and 4.37 day, respectively and that of SBV's for the above mentioned traits were 388 kg, 4.46 d and 5.74 day, respectively (Table 3). Where was the range of dam breeding values (DBV's) was 438 kg, 5.73 and 2.85 day, for 305 dMY, LP and CI. The present results show large differences among breeding values of cows, sires and dams in different traits studied. In addition, the present results show that predicted breeding values of cows, sires and dams positive values for 305 dMY and LP are in most cases negative values for CI. These results indicate that selection for 305 dMY for top cows, sires and dams will increase LP and decrease CI in the next generation and this is a goal of dairymen. El-Arian *et al.*^[4] and Khattab *et al.*^[17] arrived at the same conclusion on Holstein Friesian and Egyptian buffaloes, respectively. In Table 3, results show the important of cows, since it gave the higher range of breeding values for 305 dMY, LP and CI. Thus, selection of cows for the next generation would lead to higher genetic improvement in the herd. Also, Table 3 shows that the accuracy of sire breeding value was higher than the accuracy of cows and dam breeding values that may be due to the higher number of daughters per sire. In this respect, Khattab *et al.*^[18] found that the greatest sire evaluation for 305 dMY was obtained for a bull with 20 daughters. Low accuracy of predicted breeding values of dams (Table 3), indicating that dams are less important than sires and cows for estimating breeding values.

The estimated genetic trends of 305 dMY, LP and CI obtained by regression of sire breeding values on year of calving were 44.85 kg/year, 1.3 d/year and -0.95 d/year, respectively. Positive genetic trends for 305 dMY and LP and negative genetic trends for CI indicated that the programs of selection of that herd is to selection best sires cows and dams for the next generation would lead to higher genetic improvement for milk traits and decrease reproductive traits, which is the aim of breeders. In addition, the results showed that improvement of milk production through selection is possible. Genetic progress can be achieved if the farms adopt tests for the genetic evaluation of sires. Also, the present results are in agreement with those found by El-Awady^[19] working on Holstein Friesian cattle in Egypt. Weller *et al.*^[20] working on Holstein Friesian cattle found that the genetic trends per year for 305 dMY were positive and highly significant, being 102 kg/year.

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