

Short communication**Genetic analysis of Test Day Milk Yields of Brown Swiss cattle raised at Konuklar State Farm in Turkey, using MTDFREML****U. Zülkadir[#] and İ. Aytekin**

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Abstract

A total of 3696 Test Day Milk Yield (TDMY) records of Brown Swiss cows raised at Konuklar State Farm in the Konya Province of Turkey were used for estimating phenotypic and genetic parameters for TDMY. The phenotypic and genetic parameters were estimated by an MTDFREML programme using a Single Trait Animal Model (STAM). The model included additive direct effects, maternal permanent environment and errors as random effects, parity, year and season of calving as fixed effects, and days in milk (DIM) as a covariate. Genetic parameters and breeding values for TDMY in kg were estimated. The TDMY least square mean was estimated as 15.64 ± 5.82 kg, and the direct heritability (h^2_a), maternal heritability (h^2_m) and the repeatability (r) of TDMY were calculated as being 0.28 ± 0.09 , 0.04 ± 0.54 and 0.31 ± 0.01 , respectively. The effects of parity and year-season of calving on TDMY were significant.

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Selection for milk yield in dairy cattle focuses on the use of 305-d lactation records. Recently, records from single and early test days (TD) have been used to enable earlier selection decisions (Swalve, 1995). The main objective of basing selection on TD was to reduce recording costs and increase accuracy of genetic evaluation (Jensen, 2001; Nigm *et al.*, 2003). The use of test day models for the genetic evaluation of traits related to milk yield has received considerable attention during recent years (Vargas *et al.*, 1998; Jensen, 2001).

Several countries currently have evaluation systems that use TD data that have been adjusted and then combined into a lactation measure (Wiggans & Goddard, 1997). However, Test Day Milk Yields (TDMY) for cows are affected by factors such as breed, region of the country, herd management, season, lactation number, age at calving, month of calving, days in milk, pregnancy status, medical treatments and number of milkings per day. Changes in environment within a 305-d lactation are usually ignored and a simple herd-year-season effect is often used to account for the average of environmental effects on each test day (Jamrozik & Schaeffer, 1997). Genetic evaluations based on test day yields offer many advantages over those based on 305-day lactations including better modelling of factors affecting yields, no need to extend records and possibly greater accuracy of evaluations (Ptak & Schaeffer, 1993).

Animal models take into account differential selection of males and might provide more accurate estimates of parameters than sire models (El-Arian *et al.*, 2003). Suzuki & Van Vleck (1994) indicated that for dairy cattle improvement, prediction of breeding values with an animal model instead of the computation of separate genetic evaluations for cows and bulls is becoming common (El-Arian *et al.*, 2003).

The objective of this study was to estimate the genetic parameters and breeding values of Brown Swiss cattle reared at a farm in Turkey using data for TDMY by using the Single Trait Animal Model (STAM) in the MTDFREML programme.

The data used in this study were collected from Brown Swiss cattle reared at the Konuklar state farm in Turkey. A total of 3696 test day records belonging to 91 cows, 77 dams and 20 sires constituted the pedigree data. Data were analyzed with a derivative-free algorithm (Smith & Graser, 1986) using MTDFREML. To ensure global convergence, the algorithm by Boldman *et al.* (1995) was restarted with estimates until the log likelihood did not change at the fourth decimal. The solutions given are from the

final round of iterations. A maternal permanent environmental effect was included to account for repeated measures. Data were analysed by least square techniques using the general linear models procedure of Harvey (1987). The differences between the factor levels were determined using the Duncan multiple comparison test (Düzgüneş, 1993).

Table 1 shows the estimates of (co)variance components, genetic parameters and data structure, unadjusted mean (kg), standard deviation (s.d.), coefficient of variation (CV%), number of mixed model equations and number of iterations.

Variance components were estimated using the following animal model:

$$Y = X\beta + Za + Wm + Sp + e$$

where;

Y = a vector of the observations,

β = a vector of fixed effects (parity = 1 to 8; year-season of calving = 1 (winter), 2 (spring), 3 (summer) and 4 (autumn))

a = a vector of animal direct genetic effects

m = a vector of random maternal genetic effects

p = a random vector of maternal permanent environmental effects

e = a vector of random error.

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

$$h^2 = \sigma_a^2 / (\sigma_a^2 + \sigma_m^2 + \sigma_{am}^2 + \sigma_p^2 + \sigma_e^2)$$

$$r = \sigma_a^2 + \sigma_p^2 / (\sigma_a^2 + \sigma_m^2 + \sigma_{am}^2 + \sigma_p^2 + \sigma_e^2)$$

The mixed model equation (MME) for the best linear unbiased estimator (BLUE) of estimable functions of **b** and for the best linear unbiased prediction (BLUP) of **a**, **m** and **p** in matrix notation were as follows:

$$\begin{pmatrix} X'X & X'Z & X'W & X'S \\ Z'X & Z'Z + A^{-1}\alpha_1 & Z'W + A^{-1}\alpha_2 & Z'S \\ W'X & W'Z + A^{-1}\alpha_2 & W'W + A^{-1}\alpha_3 & W'S \\ S'X & S'Z & S'W & S'S + I\alpha_4 \end{pmatrix} \begin{pmatrix} \hat{b} \\ a \\ m \\ p \end{pmatrix} = \begin{pmatrix} X'y \\ Z'y \\ W'y \\ S'y \end{pmatrix}$$

Where $\alpha_1 = \sigma_e^2 / \sigma_a^2$, and $\alpha_2 = \sigma_e^2 / \sigma_{am}$, $\alpha_3 = \sigma_e^2 / \sigma_m^2$ and $\alpha_4 = \sigma_e^2 / \sigma_p^2$

The unadjusted mean and s.d. for TDMY were 15.64 ± 5.82 kg, as shown in Table 1. Estimates of the CV% are given in Table 1. The large CV% value for TDMY (34.9%) suggests a large variation between individual TDMY.

The least squares means (LSM), s.d. R^2 value, total and residual sum of squares of TDMY according to parity and calving season are presented in Table 3. The effects of parity and season on TDMY were statistically significant ($P < 0.01$). Similar results were obtained by Nigm *et al.* (2003), using data from Holstein-Friesian cattle in Egypt. The average TDMY was lowest in the first parity, and it increased to the sixth parity and then decreased thereafter. Kaya & Kaya (2003) and Inci *et al.* (2007) reported similar results. The average TDMY obtained for the winter season was the highest (16.55 ± 0.22 kg) followed by the spring season (15.87 ± 0.22 kg). Differences between the average TDMY obtained for the summer and autumn seasons were the least and not significantly different. Table 2 shows mean TDMY, and repeatability and heritability estimates for different breeds, as reported in the literature.

Table 1 Estimation of (co)variance components, genetic parameters and data structure, unadjusted mean (kg), standard deviation (s.d.) and coefficient of variation (CV%), number of mixed model equations and number of iterations for Test Day Milk Yield (TDMY)

Traits	Mean	s.d.	CV%	Estimates	TDMY
TDMY	15.64	5.82	34.92	- 2 log L	15894
Observations				σ_a^2	9.18047
No. of records	3 696			σ_m^2	1.34749
No. of cows	91			σ_{am}	-3.51472
No. of sires	20			σ_p^2	1.25775
No. of dams	77			σ_e^2	25.09282
Animals in relationship matrix (A^{-1})	188			h_a^2	0.28 ± 0.09
Mixed Model Equations (MME)	472			h_m^2	0.04 ± 0.54
No. of iterations	38			r_{am}	-1.00 ± 4.37
				r	0.31 ± 0.01

Table 2 The mean test day milk yield (TDMY), repeatability and heritability estimates reported in the literature

Breed	TDMY (kg)	Repeatability	Heritability	References
Brown Swiss		0.47		Johnson & Corley (1961)
Red Sindhi, Sahiwal, Tharpakar		0.10 to 0.30		Ruvuna <i>et al.</i> (1984)
Holstein			0.10 to 0.15	Nigm <i>et al.</i> (2003)
Portuguese dairy cows	23.70		0.21	Silvestre <i>et al.</i> (2005)
Holstein			0.22	Khattab <i>et al.</i> (2005)
Holstein- Brown Swiss- Red and White	22.12- 18.99- 20.73			Haas <i>et al.</i> (2007)
Italian Brown Swiss	22.4		0.1	Samore <i>et al.</i> (2008)

The heritability and repeatability estimates for TDMY in the present study were calculated to be 0.28 ± 0.09 and 0.31 ± 0.01 , respectively (Table 1). In this study, the direct-maternal genetic exact correlation (r_{am}) value was found to be -1.00 ± 4.37 , indicating that the maternal component should be taken into account in selection. The minimum and maximum predicted breeding values for TDMY for cows, dams and sires ranged from -4.897 and 6.358, -0.936 and 1.153, -2.250 and 2.169, respectively. Accuracies ranged from 0.80 to 0.81 for CBV's, 0.13 to 0.13 for DBV's and 0.50 to 0.72 for SBV's, respectively (Table 3).

Results in Table 3 show the importance of the cow, since it gave the higher range of breeding value for TDMY. Thus, selection of cows for the next generation would lead to higher genetic improvement in a herd. Moderate improvement can be obtained with mass selection for TDMY because of the heritability value ($h^2 = 0.28 \pm 0.09$). Also, the accuracy of the estimates of cow breeding value was higher than the accuracies estimates for dam and sire breeding values. Çilek & Kaygısız (2008) stated that in the genetic

evaluation of dairy cows there were many advantages of using TDMY. Kaya *et al.* (2003) stated that estimated breeding values for TDMY were closely correlated with EBVs for 305-d milk yield.

Table 3 The least squares means (LSM) and standard deviations (s.d.), R² value, total and residual sum of squares of Test Day Milk Yield (TDMY) according to parity and calving season, and range of predicted breeding values of cows (CBV's), sires (SBV's) and dams (DBV's), and their accuracy in predicting TDMY

Trait (Test Day Milk Yield)			Breeding Value Test Day Milk Yield (kg)			
	N	LSM ± s.d.		CBV 's	DBV' s	SBV' s
Parity						
1	525	12.26 ± .25 ^f	Min.	4.897 ± 1.83	-0.936 ± 3.00	-2.250 ± 2.1
2	867	15.94 ± 0.19 ^{cd}	Max.	6.358 ± 1.79	1.153 ± 3.00	2.169 ± 2.62
3	837	16.34 ± 0.19 ^{bc}	Range	11.255	2.089	4.419
4	661	17.07 ± 0.22 ^{ab}	Accuracy	0.80 to 0.81	0.13 to 0.13	0.50 to 0.72
5	349	17.40 ± 0.30 ^a				
6	269	17.49 ± 0.34 ^a				
7	150	15.31 ± 0.46 ^d				
8	38	13.31 ± 0.91 ^e				
Season						
Winter	977	16.55 ± 0.22 ^a				
Spring	873	15.87 ± 0.22 ^b				
Summer	739	14.98 ± 0.24 ^c				
Autumn	1107	15.16 ± 0.21 ^c				
R ²	Sum of sq. (Total)		Sum of sq. (Residual)			
0.091	125415.71		79889.9			

^{a,b} Means in a column with different superscripts differ (P < 0.01).

Genetic parameters for TDMY using the MTDFREML single trait animal model are reported in this study. Evaluations from the test day model are expected to be more accurate because of better accounting for environmental effects. According to results of heritability and repeatability estimates for TDMY in this study, it could be concluded that the genetic improvement in milk yield can be achieved through selective breeding programmes if test day models for the genetic evaluation of cows are adopted for herds.

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