Genetic parameters and genetic trend of some yield traits of Holstein Friesian cattle population in Tropical Region (Teke)

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Abstract

This study was conducted to determine the milk yield and reproduction characteristics, genetic trend, and breeding values of Holstein cattle reared in Teke region (Antalya, Burdur, Denizli, and Isparta provinces) of Turkey. In this study, 9844 lactation and reproductive records of Holstein Friesian dairy cattle for the period of 2010 to 2017 were used. For this purpose, variance components and the heritability were calculated based on calving interval (CI) and number of inseminations per conception (NIC) from fertility characteristics and lactation length (LL), 305-day milk yield (305 DMY), and dry period (DP). It was determined that CI, NIC, LL, 305 DMY, and DP were 0.11, 0.10, 0.11, 0.33, and 0.01, respectively. The genetic trend of 305 DMY was 111.5 kg/year. The average breeding value was negative between 2005 and 2009 and positive between 2010 and 2015. In conclusion, the fact that especially 305 DMY heritability was generally higher in this study than the values reported by other studies conducted in Turkey and the genetic trend for 305 DMY was positive and high indicates that breeding value of Holstein cattle in the Teke region is high. Therefore, it can be recommended to continue the pedigree breeding of Holstein cattle in this region, keep pedigree and yield records meticulously, estimate breeding values for selecting animals with superior yield characteristics and using them in future generations, and include current biotechnological methods in breeding program to increase the efficiency in selection.

Keywords Teke region · Heritability · Breeding value · Genetic trend

Introduction

Aiming to increase the yield taken from unit animal, some parameters are needed in order to get successful results and provide the continuation of animal breeding. For this reason, present circumstances and variation should be determined in terms of yield or yields about the subject. The rate of this variation is required to be determined based on rates of genotype or environment. If the genotype has high percentage, it needs to be determined which type of gene effects are

important. Turkey takes place at the forefront in the world in terms of the presence of cattle; however, this is not valid in terms of milk production per animal when compared to the developed countries. According to Turkey's 2018 data, a total of cattle number were 17 042 506 head, and 90.6%, 6.5%, 2.5%, and 0.3% of the 20 million tons milk production constituted as cow, sheep, goat, and buffalo milk, respectively. The number of cattle milked is 6 337 907 heads, and milk yield is determined as 3161 kg/head/year (TurkStat 2020). Milk yield per animal is lower in Turkey compared to the USA and European Union countries.

In order to increase the yield per animal, both the genetic structure and environmental factors affecting the relevant feature should be improved. In order to determine the genetically superior ones among the animals raised under appropriate environmental conditions, it is required to keep the pedigree and yield records meticulously and select the animals with superior yield characteristics in future generations through selection. It is necessary to estimate parameters such as heritability, repeatability, and phenotypic and genetic variance using variance components in order to estimate

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phenotypic and genotypic parameters based on pedigree and yield records (Düzgüneş et al. 1996; Kumlu 2000; Ertuğrul et al. 2002; Ulutaş et al. 2002). These parameters are used for the estimation of breeding values, which are a measure of the animal's performance and are passed down from generation to generation. Today, BLUP (Best Linear Unbiased Prediction) is the common method used for estimating the breeding value accurately (Şahin 2009).

This study, benefiting from the records of Central Association of Cattle Breeders of Turkey, was conducted to determine the genetic parameters, genetic trend, and breeding values of Holstein Cattle in Teke region (Antalya, Burdur, Denizli, and Isparta provinces) through MTDFREML program.

Material and method

Material

The material of the study was the records of Holstein cows between 2010 and 2017 including some fertility and milk yield parameters of businesses in Antalya, Burdur, Denizli, and Isparta provinces obtained from the records of Central Association of Cattle Breeders of Turkey. In the study, LL, 305 DMY, and CI genetic parameters of totally 9844 head Holstein cattle were calculated. In the study, NIC on 9637 cattle and DP on 3663 cattle were determined.

Preparation of the data analysis

In the lactation and year groups, animals which number was less than 100, gave stillbirth, and separated from the herd due to reasons illness and disability were excluded from the evaluation during data preparation. The animals whose lactation length was longer than 600 days and shorter than 220 days were removed. Calving age was less than 20 months and older than 45 months for first lactation and the subsequent lactations, and those except for the ones with 12 months added to previous lowest level and 14 months added to the highest level were excluded from the analysis. In

addition, the data on calving intervals of less than 300 days and more than 675 days were not used.

Standard lactation length was taken as 305 days. Lactation milk yields longer than this period were corrected using conversion factors for 305 days. No change was made in the records of cows which dried out spontaneously in lactations lasting less than 305 days, and actual milk yields were accepted as 305-day milk yield (Alpan 1992). Table 1 summarizes the data numbers used in these evaluations and descriptive statistics.

Method

Statistical analyses

Analysis of variance (General Linear Model, ANOVA) was used to determine lactation period, 305-day milk yield, calving interval, number of inseminations per conception and calving year affecting dry period, calving season, city, and lactation number. Minitab Version 14 and Step-Down Procedure were used in the analysis ($p < 0.10$). Duncan (1955)'s multiple comparison test was used to compare subgroups of important factors.

In the study, the 1st, 2nd, 3rd, 4th and 5th lactations were taken one by one, and the 6th and subsequent lactations were included in the 6th lactation. Genetic and phenotypic parameters were determined using the MTDFREML Animal Model, including fixed factors considered important in preliminary analyses, as well as the direct effect of the animal (Boldman et al. 1995). The breeding value of 305-day milk yield was estimated with Best Linear Unbiased Prediction (BLUP) and genetic trend was determined by years.

Mathematical models of the environmental factors were given.

Model 1:

$$Y_{ijkl} = \mu + a_i + c_j + d_k + f_l + e_{ijkl}$$

where,

Table 1 Data used in evaluation and descriptive statistics

	Traits				
	LL	305 DMY	CI	NSC	DP
Animal	6675	6675	6675	6546	2847
Dam	5630	5630	5630	870	2482
Sire	890	890	890	885	580
All data	9844	9844	9844	9637	3663
$\overline{X} \pm S_{\overline{X}}$	350.90 ± 0.76	9215.2 ± 27.20	418.6 ± 0.77	1.84 ± 0.012	61.90 ± 0.26
CV	21.47	29.25	18.30	63.60	25.08

Y_{ijkl} *i*, calving year; *j*, calving season; *k*, city; *l*, lactation number m. observation value of the cattle (lactation length, 305-day milk yield, calving interval, number of service per conception and dry period)

μ population mean

a_i effect of *i* calving year (*i* 1–8; 2010–2017)

c_j effect of *j* calving season (*j* 1–4; Summer, Autumn, Spring, Winter)

d_k effect of *k* city (*k* 1–4; Burdur, Antalya, Denizli, Isparta)

f_l effect of *l* lactation number (*l* 1–6; 1–6)

e_{ijkl} error (random residual effect)

In addition to direct effect of animal and environmental factors which had significant effects, the permanent environmental factor belonging to the animal was added to the mathematical model (model 2) as a random factor. Variance components, genetic parameters, and mathematic model used on breeding value prediction were given below.

Model 2:where,

$$Y_{ijklmno} = F_{ijkl} + a_m + P_n + e_{ijklmno}$$

$Y_{ijklmno}$ observed values for traits

F_{ijklm} (fixed factors) explained in model 1

a_m additive genetic effect of animal

P_n environmental effect of animal

$e_{ijklmno}$ random residual error

Matrix form is given below:

$$E[y] = [Xb]$$

$$V\begin{bmatrix} a \\ c \\ e \end{bmatrix} = \begin{bmatrix} I\sigma_a^2 & 0 & 0 \\ 0 & I\sigma_c^2 & 0 \\ 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

The genetic trend of 305-day milk yield was determined by calculating the regression between the birth years of the animals and their breeding values. The regression equation is given below:

$$Yij = a + byxXij + eij$$

Yij breeding value

a regression constant

byx genetic trend,

Xij effect of the year

eij random residual error

Results

Table 2 shows variance components and heritability of LL, 305 DMY, CI, NSC, and DP.

Genetic trend and breeding values for milk yield traits

Figure 1 shows the estimated average breeding value belonging to 305 DMY. The 10-year breeding values of Holstein Friesian Dairy Cattle varied between −740.4 and 433.5 kg. While the highest breeding value belonging to cattle calving in the year of 2012 was determined as 433.5 kg, the lowest breeding value was determined as −740.4 kg in 2007. For the Holstein Friesian Dairy Cattle, the genetic trend based on 305 DMY was determined as 111.5 kg/year.

Discussion

The heritability of lactation length (0.11) of Holstein cattle in this study was consistent with the value reported by Sang et al. (1986) as 0.10, Atil et al. (2001) as 0.13, and Naderi (2016) as 0.10 and higher than the value reported by

Table 2 Variance components, heritability of milk, and progeny traits

	Variance Components				Heritability		
	σ_a^2	σ_c^2	σ_e^2	σ_p^2	h^2	c^2	e^2
LL(day)	578.74	4.13	4666.78	5249.65	0.11	<0.001 (0.0079)	0.89
305 DMY (kg)	1,261,501.36	1,293,337.70	1,230,105.91	3,884,944.97	0.33	0.34	0.32
CI (day)	608.24	0.024	4703.20	5311.46	0.11	<0.001 (0.0000045)	0.89
NSC	572,500.48	2,488,736.68	2,437,724.82	5,498,961.98	0.10	0.45	0.44
DP (day)	498,172.12	983,304.47	78,036,050.50	79,517,527.09	0.01	0.012	0.98

LL lactation length, *305 DMY* 305-day milk yield, *CI* calving interval, *NSC* number of inseminations per conception, *DP* dry period

σ_a^2 additive genetic variance, σ_c^2 permanent environmental effect variance, σ_e^2 residual variance (error), σ_p^2 phenotypic variance, h^2 heritability, c^2 rate of permanent environmental variance, e^2 residual error

Fig. 1 Estimated breeding value of 305 DMY according to birth year in Holstein dairy cattle
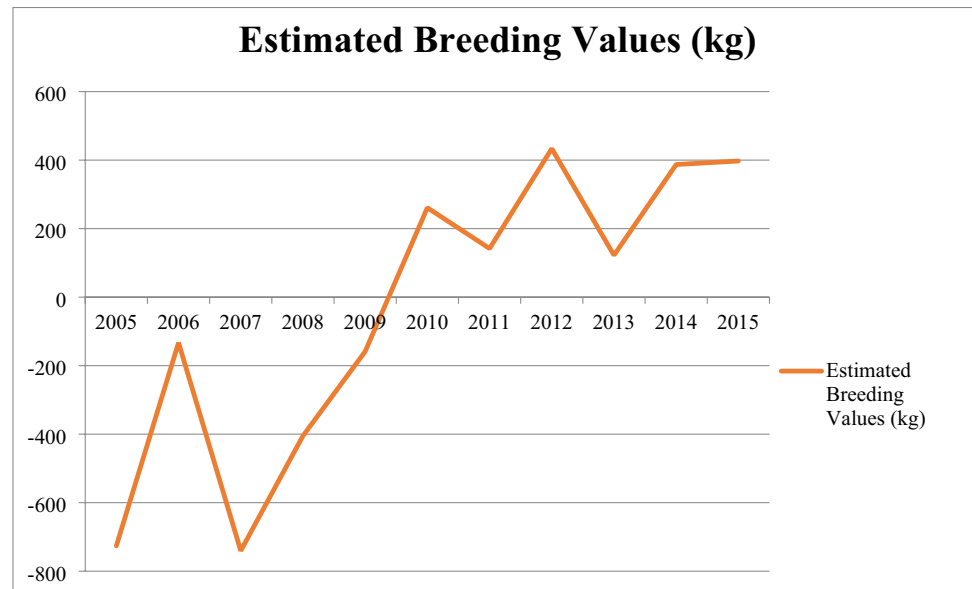
Ertuğrul et al. (2002) as 0.013, Ayalew et al. (2017) 0.03, 0.06 and 0.08, Chegini et al. (2019) as 0.04, 0.03 and 0.04, Genç and Soysal (2019) as 0.01, and lower than the values reported by Bakir et al. (1998) as 0.18, and Atay et al. (1995) as 0.15.

The heritability of 305 DMY (0.33) determined in the study was higher than the values reported by Bakir and Kaygisiz (2009) as 0.10, Şahin and Ulutaş (2010) as 0.23, Konkruea et al. (2017) as 0.149 and 0.147, and Gevrekci et al. (2018) as 0.04, consistent with the values reported by Firat and Kumlu (2002) as 0.3143 and 0.3376 and Sahin et al. (2012) as 0.35 and lower than the values reported by Kadarmideen et al. (2000) as 0.39 and Atil et al. (2001) as 0.38. In general, it was determined that the heritability of 305 DMY of the cattle reared in Teke region was higher than other studies. This indicates that the genetic potential of Holstein cattle raised in this region is higher.

The heritability of calving interval in the study (0.11) was higher than the values reported by Genc and Soysal (2019) as 0.01 <, Şahin (2009) as 0.04, Şahin and Ulutaş (2010) as 0.04, Naderi (2016) as 0.04, and Sarar and Tapki (2017) as 0.02 and consistent with the values reported by Atashi et al. (2019) as 0.11–0.13 and Chegini et al. (2019) as 0.103 and 0.106.

The heritability of NSC determined in this study (0.10) was higher than the values reported by Şahin and Ulutaş (2010) as 0.04, Haile Mariam et al. (2003) as 0.03, and Gonzalez Recio and Alenda (2007) as 0.05 and the same as the values reported by Chagunda et al. (2004) as 0.10.

The heritability (0.01) of DP determined in this study was lower than the value reported by Şahin and Ulutaş (2010) as 0.04, Erdem (1997) as 0.056, and Sarar and Tapkı (2017) as 0.03 and close to the values reported by

Ertuğrul et al. (2002) as 0.017. In general, the fertility in the herds with high milk yield is low. Care, feeding, breeding conditions, and environmental factors such as herd management affecting the related feature should be improved in such herds (Genç and Soysal 2018).

In this study, the genetic trend of 305 DMY was determined as 111.5 kg/year. This value was higher than the values reported by Bakir and Kaygisiz (2009) as 7.99 kg/year, Bakir et al. (2009) as 13.42 kg/year, Şahin et al. (2012) as − 2.46 kg/year, Katok and Yanar (2012) as 3.73 kg/year, and Genc and Soysal (2019) as 7.44 kg/year; close to the values reported by Mohsen et al. (2000) as 112 kg/year in Egypt and Banos et al. (2001) as 116 kg/year; and lower than the values reported by Burnside et al. (1992) as 173 kg/year and Mohsen et al. (2000) as 200 kg/year in Germany. The genetic trend of 305 DMY in this study was higher than studies conducted in Holstein cattle in Turkey as noted above. This indicates that the Holstein cattle raised in Teke region have a good genetic progress over the years in terms of 305 DMY. In this study, it was seen that the average breeding value calculated in Holstein population in Teke region was negative between 2005 and 2009 and positive between 2010 and 2015. It was observed that the high genotypic progression value detected in Holstein in this region had an increasing genotypic tendency as of 2009. Before 2009, average breeding value was determined as negative. This is considered to have a low genotypic nature of the animals used in breeding before this time. Although it shows a fluctuating course, the positive breeding value in the periods after 2009 may be due to the use of the cows and bulls with high breeding value. In the study, the highest breeding value was 433.5 in 2012 and the lowest breeding value was − 740.4 in 2007.

The heritability of the fertility and milk yield characteristics examined in the study was generally similar to and high than most of the literature reports. Genetic progress seems to be possible with selection in terms of features with high heritability. Particularly, 305 DMY heritability was higher than those reported in other studies in Turkey, and this shows a high possibility of success in selection to be made in Teke region according to individual data. It can be recommended to consider both individual yields and relative yields in the selection to be made in this region in terms of relevant features. Since the heritability of the fertility traits is low, it may be advisable to have a more regular order and management of the herd instead of a selection for these traits. In addition, it was found in the study that genetic trend was positive and high in terms of 305 DMY. Therefore, it can be recommended to continue the pedigree breeding of Holstein cattle in Teke region, keep pedigree and yield records meticulously, estimate breeding values for selecting animals with superior yield characteristics and using them in future generations, and include current biotechnological methods in breeding program to increase the efficiency in selection.

Author contribution Y. Öztürk, M. Sarı, and S. Genç conceived and designed research. YO and MS conducted experiment design. SG analyzed data. MS and YO wrote the manuscript. All authors read and approved the manuscript.

Data availability The data obtained from Central Association of Cattle Breeders of Turkey were used in this study. These are available in the archive of Burdur Food Agriculture and Livestock Vocational School, under protection of Yahya Öztürk.

Declarations

Ethics approval and consent to participate We used the data obtained from Central Association of Cattle Breeders of Turkey. The data were produced from cattle breeders. We did not do any procedure on animals. That is why there was no ethical issue.

Consent for publication The authors agree to publish this manuscript without any concern.

Competing interests The authors declare no competing interests.

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