Estimates of genetic and phenotypic parameters for 305-day milk yield in dairy cattle populations in Türkiye

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SUMMARY

The primary goal of breeding organisations focused on sustainable and profitable milk production is to improve milk yield traits in dairy cattle. For this reason, the dairy industry has prioritised improving the genetics of dairy cattle to increase milk yield. The objective of this study was to estimate variance components and genetic parameters for 305-day milk yield (305-dMY), and to determine the effects of environment (calving season)- and animal-based factors (breed and parity) on 305-dMY in Simmental, Holstein, and Brown Swiss cows. The data set consisted of 19,454 records of 305-dMY obtained from 10,282 lactating Simmental, Holstein and Brown Swiss cows and 1,045 sires collected by the Cattle Breeders Association, between 2004 and 2018 in Kastamonu, Türkiye. A mixed ANOVA model was used to determine the effect of breed, parity, calving season and farms on the 305-dMY of cows. The model included three fixed effects: breed, parity and calving season and a random effect: farms. Variance components and breeding values were estimated in a Bayesian JWAS framework, using the conventional model within a Bayesian setting. Genetic parameter estimates were derived from the posterior distributions of the effects, obtained from an Markov Chain Monte Carlo run of 50,000 iterations with a first 5,000-iteration burn-in. The results indicated that 305-dMY was significantly affected by breed, parity, and calving season ($P<0.001$). The highest 305-dMY in Holstein cows was determined to be 5264.16±25.77 kg. The 305-dMY of cows calving in winter was higher than in other seasons (spring, summer and autumn). The mean inbreeding coefficient was found to be 0.091. The estimates of heritability for Simmental, Holstein, and Brown Swiss were 0.061, 0.208 and 0.129, respectively. The genetic trend for estimates of breeding values (EBVs) of 305-dMY was found to be 5.62 kg/year. The repeatability estimates for Simmental, Holstein and Brown Swiss were observed as 0.100, 0.277 and 0.199, respectively. The results indicate that the moderate heritability and repeatability estimate for 305-dMY, suggest that genetic gain can be obtained for these traits through genetic selection of Holstein cows. However, improving the performance traits of Simmental and Brown Swiss cows could be obtained through improving management conditions.

KEY WORDS

Dairy cattle, 305-day milk yield, heritability, repeatability, genetic trend.

INTRODUCTION

The primary targets of breeding organizations that are focused on sustainable and profitable milk production are the enhancement of milk yield traits in dairy cattle (hereafter cows, unless otherwise stated). For the past century, selection programmes have been implemented by both breeding organizations and breeders to increase the milk yield of cows, resulting in improved genetics of cows and increased milk yield.

In many countries, milk samples are collected from cows by breeding organizations, dairy associations and breeders and milk yields are recorded monthly [1]. Milk yield and lactation records are used to perform genetic evaluation of cows for milk yield traits and early selection decisions [2]. The 305-day milk yield (305-dMY) records are a common determinant of milk yield performance in breeding animals [3, 4]. In addition, selection for milk performance in dairy cows is mostly based on 305-dMY [5].

Both genetic and phenotypic differences among cows lead to variations in milk production. In cow husbandry, phenotypic and genetic parameters for milk production traits are essential population parameters [6]. Improvement of both genetic and environmental factors affecting these traits is necessary to increase yield per cow. To determine the genetically superior animals among those reared under suitable environmental conditions, it is necessary to carefully examine the pedigree and yield records; use selection to select the animals with superior yield traits for future generations [4, 7]. The availability of reliable genetic parameter estimates is critical when selecting cows for genetic improvement based on predicted milk yield [6]. Therefore, animal breeding programme must include the calculation of genetic parameters for economically important traits. Genetic parameters, including heritability, repeatability, and genetic correlations, form the basis of breeding programmes for economically important traits in a population [6, 8]. Animal breeding research and the design and implementation of practical breeding programmes depend heavily on

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these genetic parameters [9]. Therefore, genetic evaluation is essential to produce high performing animals and increase future profitability [10].

Heritability describes how much additive genetic variance is associated with observable individual differences [6]. The effect of herd, management, and other environmental factors is lower than that of the genetic background when milk yield traits have higher heritability [11]. Another genetic parameter, repeatability is defined as the capacity of a measured production parameter to maintain a consistent value across subsequent measurements. It is crucial to select and use genetically superior animals in order to increase productivity and profitability. A cow's total genetic capacity for a particular trait is its breeding value. Therefore, the breeding value of an animal is its value for a particular trait in a breeding programme [10]. In selection studies, quantitative genetic methods such as BLUP (Best Linear Unbiased Prediction), which have been widely used to predict breeding value, have greatly increased the influence of genetic factors in estimating milk yield [7]. The role of restricted maximum likelihood (REML) for estimating (co)variance components and genetic parameters is still vital when it comes to the models and algorithms often used in the genetic evaluation of animal breeding data [3, 12].

For the genetic improvement of dairy cows, accurately estimated genetic parameter information is essential for the evaluation of appropriate breeding and selection strategies. To the best of our knowledge, a large body of studies have been conducted on the estimation of phenotypic parameters in dairy cows such as, Holstein Simmental and Brown Swiss. Nevertheless, further studies are required to evaluate the genetic parameters and genetic tendency of the 305-dMY trait of these breeds, as well as the effects of some environmental (calving season)- and animal (breed and parity)-based factors on this milk yield trait. The aims of this study were i) to estimate the variance components and genetic parameters for 305-dMY trait in Simmental, Holstein and Brown Swiss cows and ii) to evaluate the effects of some environmental (calving season)- and animal (breed and parity)-based factors on 305-dMY.

MATERIAL AND METHODS

The data set consisted of 19,454 records of 305-dMY obtained from 10,282 lactating Simmental, Holstein and Brown Swiss cows and 1,045 sires collected by the Cattle Breeders Association, between 2004 and 2018 in Kastamonu, Türkiye. Milk yields were standardised to 305-day lactation length using adjustment factors. Lactation lengths less than 220 days and greater than 550 days were considered to be abnormal and were therefore deleted from the data set. Lactations with fewer than 5 test day records were removed. Pedigree information and sample sizes according to breeds were presented in Table 1. Information on the number of records by breed is also shown in Table 2.

To determine the effect of breed, parity, calving season and farms on 305-dMY of cows, the following mixed ANOVA model was utilised. The model included three fixed effects (parity, calving year, and calving season) and one random effect (farms):

$$Y_{ijklm} = \mu + b_i + p_j + cs_k + (1|f_l) + e_{ijklm}$$

where Y_{ijklm} is the observation value of the trait, μ is the population average, b_i is the effect of the i^th breed (i: Holstein, Simmental, Brown Swiss), p_j is the effect of the j^th parity (j: 1-5), cs_k: is the effect of the k^th calving season (k: winter, spring, summer, autumn,), f_i: is the random effect of l^th farm and e_{ijklm} is the random error.

The 305-dMY was analysed to investigate the effects of certain fixed and random factors using SPSS statistical software (version 21.0; SPSS Inc., Chicago, IL, USA). Before analysis, the normality and homogeneity of variance of the 305-dMY data were assessed using the Kolmogorov-Smirnov and Levene's tests, respectively ($P>0.05$). Descriptive statistics were presented as means and standard errors. The factors were compared using Duncan's Multiple Range Test, with a significance level of $P < 0.05$.

Two different stages were followed to estimate variance components and breeding values. In the first stage, genetic pa-

Table 1 - Information related to pedigree, and sample sizes according to breeds.

	Number of Animals	Number of Observations	Number of Sires	Number of Dams
Simmental	12183	21527	427	6564
Holstein	5243	8692	561	2829
Brown Swiss	2028	3162	155	943
Total	19454	33381	1045	10282

Table 2 - Information related to number of records according to breeds.

	Overall		Simmental		Holstein		Brown Swiss	
	n	%	n	%	n	%	n	%
1 record(s)	11094	57.0	6679	54.8	3111	59.3	2028	64.3
2 record(s)	4704	24.2	2999	24.6	1272	24.3	1304	21.4
3 record(s)	2152	11.1	1459	12.0	499	9.5	433	9.6
4 record(s)	1097	5.6	757	6.2	265	5.1	75	3.7
5 record(s)	407	2.1	289	2.4	96	1.8	22	1.1
Total	19454	100.0	12183	100.0	5243	100.0	2028	100.0

rameters and breeding values were estimated separately for each breed (Holstein, Simmental, Brown Swiss). In the second stage, the breed factor was assumed fixed in addition to other fixed and random effects, and genetic parameters and breeding values were re-estimated.

The variance components and breeding values were estimated using the following model. In the first-stage analyses, the breed effect (b_i) in F_{ijkl} was excluded from the model. In the second stage, the model shown below was employed in its entirety.

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

where $Y_{ijklmno}$ is the observed value for 305-dMY, F_{ijkl} is the fixed ($b_i+p_j+cs_k$) and random (f_i) environmental factors, a_m is the additive gene effect, pe_n is the permanent environmental effect and $e_{ijklmno}$ is the error. Genetic parameters, estimates, and breeding values were estimated in a Bayesian JWAS framework (based on Julia and an interactive Jupyter notebook), using the conventional model within a Bayesian setting [13]. Genetic parameters estimates were based on posterior distributions of the effects, which were calculated using samples from a Markov Chain Monte Carlo (MCMC) that was 50,000 in length with a burn-in of the first 5000 iterations. Genetic parameter estimates were made by calculating the breeding value samples of each individual every 50th iteration of the MCMC. The posterior means of the genetic parameters were derived from the breeding values at the saved iterations. The standard deviation of the parameter values across the saved iterations was used to calculate the standard errors (SE) of the posterior means [13].

The heritability (h^2) and repeatability (r) of the 305-dMY were calculated using the following equation [14]:

$$h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_{pe}^2 + \sigma_e^2} \qquad r = \frac{\sigma_a^2 + \sigma_{pe}^2}{\sigma_a^2 + \sigma_{pe}^2 + \sigma_e^2}$$

where σ_a^2 is the additive genetic variance, σ_{pe}^2 is the permanent environmental variance, and σ_e^2 is the error variance [15], genetic trends were obtained as the average breeding values of animals for each breed, as well as the overall breed value for each birth year.

RESULTS AND DISCUSSION

The effects of breed, parity and calving season on 305-dMY are presented in Table 3. Additionally, in this study, a random effect of the farm was included in the model, and this effect was found to be statistically significant ($P<0.001$). Accordingly, 305-dMY was significantly affected by breed, parity, factor ($P<0.001$). The highest 305-dMY was determined in Holstein cows (5264.16±25.77 kg). Also, it was determined that there were differences between the average 305-dMY values of Simmental (3293.37 ± 7.33 kg) and Brown Swiss cows (3264.71 ± 18.59 kg). In the present investigation, the mean of 305-dMY was found to be lower than that reported in previous studies of Simmental [16], Holstein [17, 18], and Brown Swiss cows [19] raised in Türkiye. This may be explained by the fact that the 305-dMY data of the present study were obtained from cows in intensive, semi-intensive and extensive farming conditions, especially those in extensive farming conditions, which contributed to the lower mean. Furthermore, the variability observed between our results and those of previous studies can be attributed to differences in breed, breeding conditions, feeding strategies, herd management, geographical region and climatic conditions.

The effect of parity on 305-dMY was statistically significant ($P<0.001$; Table 3). The highest 305-dMY was observed in the cows of the 1st parity (4007.36±18.74 kg), while the lowest was found in the cows of the 5th parity (3399.21±20.99 kg). In other words, 305-dMY decreased linearly with advancing parity. Contrary to these findings, previous studies reported that milk yield increased with progressing parity [6, 17, 20]. Similarly, several authors reported that the 305-dMY increased with the advancement of parity from the 1st to 3rd parity [8]. Increasing milk yield with later parity could be explained by the cows' advancing ages, according to some authors [6]. Several authors reported that milk yield may increase due to the increase in body weight of cows until cows reach mature equivalents [21]. However, the same authors underlined that decreases may be observed at older ages due to degeneration of the secretory tissue of the mammary gland and decrease in the physiological activity of the body. These statements do not support the results of our study. However, the result of this study was in close agreement with the result of some authors [17], who found that the highest 305-dMY was found in Simmental cows with 1 parity and 2 parities. The same authors explained the cause of the higher milk production in cows with 1 parity by the fact that these cows maintain their ability to secrete milk for a longer period of time. Furthermore, the authors associated this situation with the fact that cows with 1 parity were less exposed to udder infections compared to cows in subsequent lactations

Table 3 - Effects of environmental factors on 305-dMY.

		n	Mean	SE	F	p
Breed	Simmental	21527	3293.37^b	7.33	198.026	<0.001
	Holstein	8692	5264.16^a	25.77		
	Brown Swiss	3162	3264.71^c	18.59		
Parity	1	10381	4007.36^a	18.74	6.233	<0.001
	2	8616	3938.20^b	20.63		
	3	6227	3708.06^c	21.18		
	4	4470	3539.26^d	21.50		
	5	3687	3399.21^e	20.93		
Calving season	Winter	5770	4213.99^a	26.96	28.820	<0.001
	Spring	10914	3729.11^c	16.37		
	Summer	11187	3549.98^d	14.61		
	Autumn	5510	4037.67^b	24.81		

^{a,b,c}: Different letters indicate a significant difference at $P<0.05$ (Duncan test)

[17]. In another study, the effect of parity on 305-dMY was found to be statistically insignificant [21]. In addition, the variability observed between the results of this study and other studies may be explained by the fact that Holstein, Simmental and Brown Swiss breeds were randomly assigned to each parity group in our study.

The effect of calving season on 305-dMY was found to be statistically significant ($P<0.001$; Table 3). The highest 305-dMY was observed during winter (4213.99±26.96 kg), while the lowest was documented in summer calving cows (3549.98±14.61 kg). The results of the studies reporting that the effect of calving season on 305-dMY was significant [20] and were similar to the results of this study. Several authors reported that the highest 305-dMY was determined in cows born in winter, and the lowest was determined in autumn [20]. Some authors determined that the highest 305-dMY was in winter and spring compared to the other seasons [8]. This result may be due to the fact that winter months are more suitable for the highest milk yield of dairy cows [8]. Several managerial and dietary factors have been associated with lower 305-dMY of cows during the summer season, and the higher ambient temperature also has an adverse influence on the 305-dMY [12]. Seasonal variation in milk yield in different studies could be because of regional and climatic differences [6].

The incidence of harmful or non-detrimental recessive homozygous genotypes in dairy cows is increased by inbreeding, which results in the loss of genetic dominance and other non-additive variables. Inbreeding depression can be reduced by minimizing overall inbreeding and preventing the creation of recessive homozygous offspring [22]. Inbreeding in dairy cows can result in significant reductions in milk yield and composition, thereby negatively affecting productive performance [23]. Moreover, a higher rate of inbreeding also implies a higher risk for the breeding program in terms of genetic gain variance with a lower additive genetic variance expected. In a breeding program, inbreeding is therefore an important parameter to monitor and control [24]. A researcher [25] reported that inbreeding can lead to variable milk yield outcomes, for instance, cows with close inbreeding showed maximum yields (9877.9 kg) compared to those with mild inbreeding (9338.11 kg). Therefore, the coefficient of inbreeding in cattle is a critical measure that reflects the genetic diversity and potential health risks associated with breeding practices.

The study reports an average inbreeding level of 0.117 for Simmental, 0.035 for Holstein, and 0.075 for Brown Swiss cows. The lowest inbreeding coefficient was observed in Holstein cows, while the highest was recorded in Simmental cows. In this study, the mean inbreeding coefficient was determined to be 0.091 (see Table 4). The effect on the relative risk ratios for cows less than 12.5% inbred was minimal compared to the non-inbred cows [26]. Therefore, it can be concluded that a moderate inbreeding coefficient calculated for all breeds in this study does not pose a significant risk to the cows. A study conducted on North American populations revealed that the average inbreeding coefficient for Holstein cows was 0.17, indicating moderate inbreeding [27]. The inbreeding coefficient for Italian Simmental was approximately 0.069, indicating a lower degree of inbreeding compared to Holstein and Brown Swiss [28]. Several authors reported that average inbreeding coefficients were 0.15 for Holstein and 0.14 for Brown Swiss [27].

In the present study, the additive genetic variance estimates for 305-dMY in all breeds were less than residual variance (Table 5). Given the minimal amount of additive maternal genetic effects, on milk yield, these effects do not appear to significantly contribute to phenotypic variance. Additive genetic variation is low in proportion to phenotypic variation, therefore, selection for the improvement of milk would not be effective [5]. The findings of this study indicate that 305-dMY is not a suitable selection criterion for Simmental and Brown Swiss cows; however, it is applicable for Holstein cows. For this reason, a relatively moderate genetic progression is expected for Holstein populations. Some authors reported that this difference is caused by environmental conditions and limited feeding resources [29]. Also, high environmental variance values could be explained by poor management practices and stressful climatic conditions [3]. Therefore, the environmental conditions should be improved to increase milk yield.

The high heritability of traits is a critical metric for evaluating the efficacy of animal breeding programs, as it determines the rate of genetic gain that can be achieved through selection processes [5]. Heritability estimations for 305-dMY in Holstein cows were moderate (0.208; Figure 1) in this study, suggesting that both genetic selection and good environmental and managerial factors could lead to improvement [30]. Howev-

Table 4 - Inbreeding coefficient for Simmental, Holstein and Brown Swiss cows.

	Inbreeding	Inbred Animal Count (n)	Amongst Inbred Animals
Simmental	0.117	62	24.40
Holstein	0.035	8	25.00
Brown Swiss	0.075	7	23.21
General	0.091	77	24.35

Table 5 - Variance components estimates for 305-dMY in Simmental, Holstein and Brown Swiss cows.

Breed	Genetic Variance	Pe Var	Residual Variance	Phenotypic Variance
Simmental	27194.8±2736.4	17157.5±2662.5	400555.7±4690.1	444908.0±4629.4
Holstein	228913.6±19171.1	75805.5±11490.2	793210.2±16110.5	1097929.3±19601.0
Brown Swiss	62600.1±11244.8	34165.0±8552.2	388068.7±13088.1	484833.8±15369.9
General	100236.1±5606.8	28432.6±3317.9	512499.4±5151.1	641168.0±5594.8

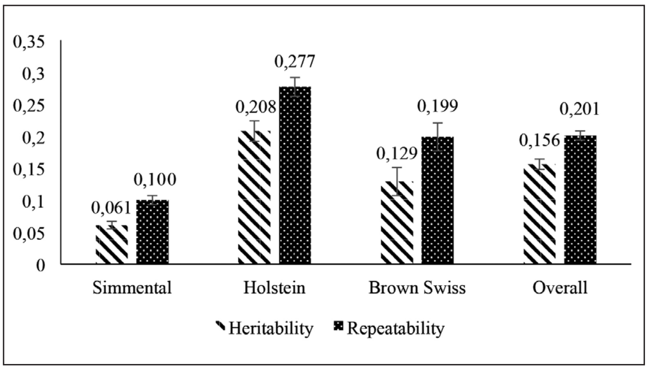

Figure 1 - Heritability and repeatability according to breeds.

er, the heritability determined in Brown Swiss (0.129) and Simmental cows (0.061) was found to be low (Figure 1). The heritability of 305-dMY was low (0.156) in the general model (for all breeds). The lower heritability of 305-dMY for Simmental and Brown Swiss in this study indicated low genetic to environmental variance ratios and reflects differences in the genotypes' response to the existing environmental conditions [31]. Lower heritability estimates can also be explained by reduced additive genetic variance, high environmental variance, and residual variance. High variability in climate, feeding, and management conditions leads to these low heritability estimates [3, 32]. The majority of the variation in 305-dMY for Simmental and Brown Swiss is caused by environmental factors; therefore, a change in environmental conditions, such as feeding and management practices, should result in a significant response. Therefore, 305-dMY might increase when environmental conditions improve. These results suggest that environmental factors, rather than genetic variation, are more responsible for the observed variation [9]. Therefore, direct selection was not practical for increasing milk yield [30].

The heritability determined for the Holstein cows in this study were found to be generally lower than the values reported in previous Holstein studies [5, 21]. However, these heritability values were found to be higher than the results reported in some other studies [15, 31]. Furthermore, the heritability values determined for the Brown Swiss cattle were lower than the values reported by several authors [9]. The current findings indicate that the heritability for 305-dMY was moderate. The study's estimated heritability of 305-dMY differs from the authors' estimates due to several factors, including animal breed, management system, environmental factors, geographic location, data size and structure, analysis model, and statistical techniques used [3-5]. Estimating heritability can differ depending on the size and structure of the data sets and the statistical models for their assessment [3].

The measure of repeatability in cows is the degree of association between repeated records for a trait in a population. This can be used to determine the true producing capacity of individual cows in a herd [4]. The high repeatability of the first lactation performance of the traits is the most reliable indicator for future performance and selection [33]. The overall repeatability determined in this study (0.201) and the repeatability determined for the Holstein (0.277) indicate that both measurements are at a moderate level (Figure 1). The moderate repeatability that was observed for the 305-dMY of Holsteins indicates that cows with parity of 1 data can be used to predict the estimated breeding value in advance for selection purposes. This could be advantageous to improve the overall performance of the herd since good cows would be retained on the farm [12]. However, this cannot be said for Simmental and Brown Swiss due to their low repeatability.

The repeatability determined for the Holstein breed in this study was consistent with the results of a previous study [15], but it was lower than the results of most research [5]. The repeatability determined for Simmental (0.100) and Brown Swiss (0.199) cattle in this study were found to be low. For 305-dMY, low repeatability estimates indicated low ratios of genetic and permanent environmental variances to temporary environmental variances [31]. The low repeatability estimates implied that the 305-dMY variance was more temporary in nature than being a result of cattle genetic influences [12]. Differences in the number of records, the model and methodology used for estimation, and the correction for other environmental factors could all be attributed for the differences in repeatability estimates among various studies [34].

The estimated breeding values of Simmental, Holstein and Brown Swiss cows are shown in Figure 2. The genetic trend for 305-dMY was determined by utilizing a linear regression model of the mean EBVs on birth year. An analysis of the data revealed irregular fluctuations in the 305-dMY of the EBVs. The genetic trend of 305-dMY in this study was positive throughout the period from 2004-2006, then declined until 2014, and rose again in 2015 and 2016, which indicated the effectiveness of selection for improving milk yield, estimated to be 5.62 kg/year for mean EBVs. The variation of EBVs for 305-dMY across years may have been influenced by genetic variability among sires used across years and by management variability across years in this study [32]. The observed variability in the curves' rhythm may be attributable to environmental factors, including (i) changes in climatic conditions, nutrition, hygienic levels, and management practices; (ii) the interaction between genetics and the environment; and (iii) the utilization of sires with diminished breeding value [10]. Positive genetic trends for 305-dMY indicated that there was a genetic improvement in these traits, in the desirable direction during the year, but negative genetic trends indicated a decrease in mean breeding value over the study period. A previous study on Holstein cows [30] reported positive genetic trends for 305-dMY (2.68 kg).

In Türkiye, as well as in Kastamonu province where the present study was conducted, the Holstein breed is among the most commonly raised dairy and combined cattle. Compared to Simmental and Brown Swiss cows, Holstein are typically reared in larger-scale farms. Indeed, feeding, breeding, and other herd management practices tend to be better organized in larger farms. Consequently, environmental factors have a lower influence on the ability of Holstein cows to express their genetic potential for 305-dMY. In other words, better environmental conditions may contribute to higher estimates of heritability and repeatability for 305-dMY, as well as to greater genetic gains in Holstein cows.

CONCLUSION

The findings of this study indicated that the effects of breed, parity, and calving season must be considered when evaluating dairy cows. In general, the 305-dMY obtained for all breeds in this study is lower than the results reported in studies con-

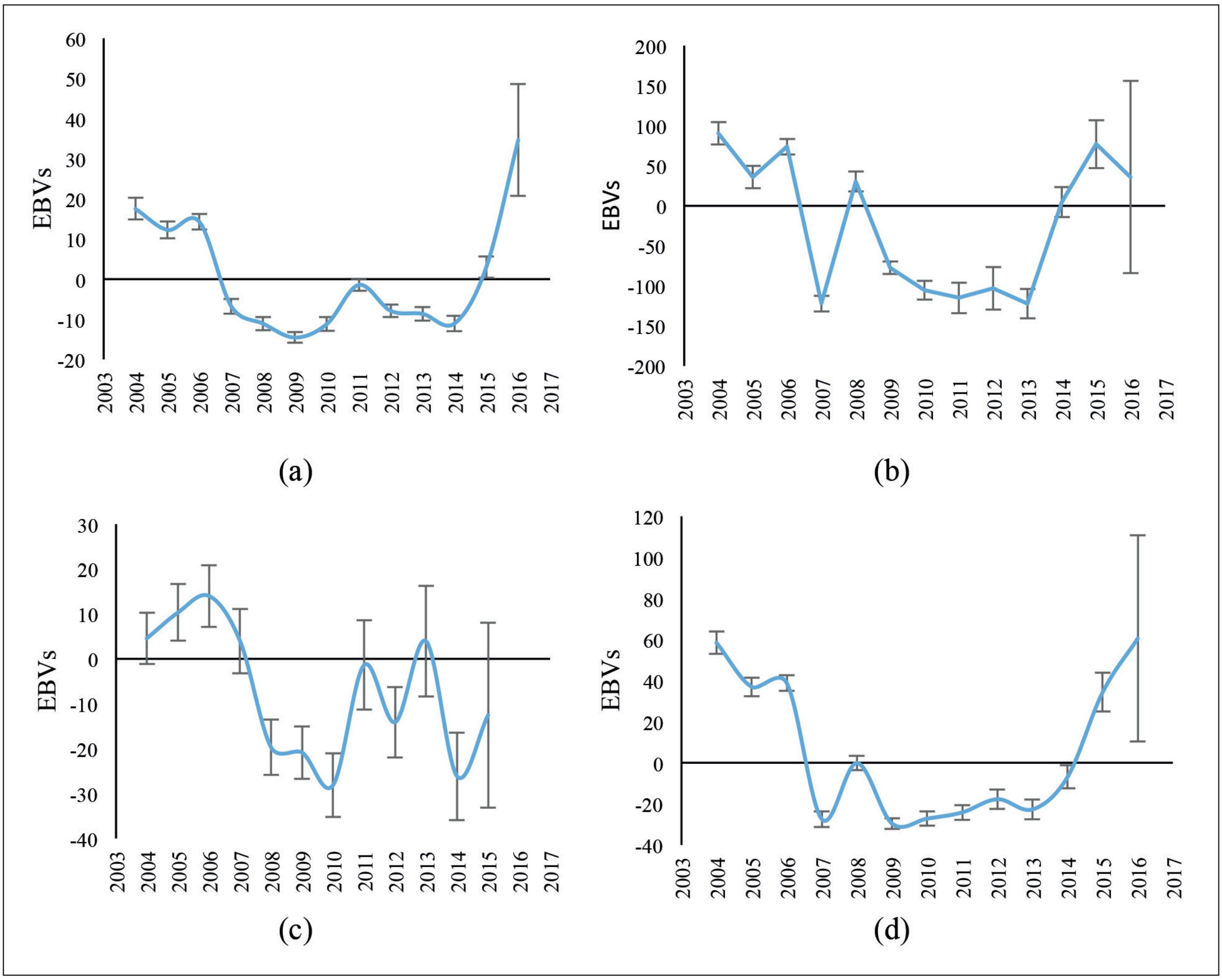

Figure 2 - Mean EBVs for 305-dMY in Simmental (a), Holstein (b), Brown Swiss (c) and mean (d) according to the birth year.

ducted in Türkiye. It has been determined that all breeds possess a moderate inbreeding coefficient, indicating that cows are not at substantial risk. The genetic trend of 305-dMY in this study was positive throughout the period from 2004-2006; then declined until 2014, and rose again in 2015 and 2016. The heritability and repeatability of 305-dMY of Holstein cattle were medium, indicating the future scope for genetic improvement in the herd. However, the heritability and repeatability estimates for milk yield of Simmental and Brown Swiss were low, indicating that these traits are mainly influenced by managerial and environmental effects. The results indicate that the moderate heritability and repeatability estimates for 305-dMY, suggest that genetic gain can be obtained for these trait through genetic selection of Holstein cows.

Ethical approval and consent to participate

The data used in this study consists of recorded data. Therefore, local ethics committee approval is not required.

Author Contributions

SHA: Writing - review & editing, Investigation, Formal analysis, Data curation. **ICO:** Writing - review & editing, Methodology, Data curation, Supervision. **EK:** Writing - original draft, Supervision, Methodology, Investigation, Data curation, Conceptualization.

Conflict of interest

All authors declare no conflict of interest.

Funding

The study received no grants or funds.

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