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Research Article

A Research on The Milk Yield Traits of Brown Swiss, Simmental, Holstein Friesian Cattle and Their Crossbreeds Registered in The Herdbook System in Türkiye

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Abstract: This study was conducted to examine the milk yield traits of Holstein Friesian (HF), Brown Swiss (BS), and Simmental (SM) breeds, as well as their crossbreeds raised in enterprises registered in the herdbook system in Türkiye. With this study, the performances of cattle breeds and their crossbreeds widely raised in Türkiye were compared in terms of milk yield characteristics based on agricultural regions of Türkiye. The data used in the study included the completed lactation records of 22 331 heads of cattle for the years 2000-2014. The GLM ANOVA method was used in the statistical analysis of the effects of breed, genotype, and region on traits related to milk yield. Across the herd, the mean and standard deviation values were determined as 7551±2771 kg for lactation actual milk yield (AMY), 4.2±1.8 for total lactation number (TLN), and 382.9±9.2 days for lactation period (LP). The effects of genotypes and regions were found to be significant or very significant ($p<0.05$ or $p<0.001$) for all three studied traits, region x genotype interaction was found to be very significant for AMY and TLN ($p<0.001$), and not significant for LP ($p=0.184$). As a result, it was revealed that the interaction effects of genotype, region, and genotype x region should be taken into account in determining the milk yield traits of cultured breed and crossbreed cows that are widely raised in Türkiye. Accordingly, it was concluded that the interaction findings should be evaluated in determining the breed preferences by the regions.

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1. Introduction

The animal production sector has strategic importance in terms of economic and social aspects, such as adequate and balanced nutrition of the population, successful rural development, reducing unemployment in the agricultural field, and preventing migration from villages to cities (Ekmen, 2017; Alev, 2018). In this respect, it is important to ensure the sustainability of agricultural production and animal production (Kaygısız et al., 2022). Cattle breeding is a production area where human communities on a small or large scale carry out activities for milk, meat, and their derivatives. The main source of these products is cattle (Akbulut and Yılmaz, 2013). Globally, the milk consumed by humans is largely (83.1%) obtained from cattle (Faye and Konukpayeva, 2012).

Approximately 90% of red meat production and 91% of milk production in Türkiye are met from cattle (TİGEM, 2019). In the livestock sector, between 2002 and 2019, the presence of cultured cattle increased by 360%, the presence of cultured crossbreed cattle increased by 73%, and the presence of native cattle decreased by 56% (ESK, 2019).

Today, the Holstein Friesian (HF) cattle breed ranks first in the world cattle presence and is intensively raised. This breed is also preferred in breeding and selection studies due to its high milk yield (Jasirowski et al., 1987; Akbulut et al., 2001; Genç and Karaağaç, 2019). After the HF breed, Simmental (SM) is in second place, and Brown Swiss (BS) breed is in third place (Yavuz and Yeniyurt, 2022).

The main aim in cattle breeding is to obtain the highest yield most economically, as in the breeding of other species. To achieve this, it is necessary to ensure the sustainability of the positive contribution of the genetic structure of the animal and the environmental conditions (Erdem et al., 2007). In other words, first of all, it is necessary to determine the cattle genotype suitable for the macro-environmental conditions (climate, altitude, fauna, etc.) and improve the necessary breeding conditions (shelter, feeding, etc.) for this breed. In addition, genetic breeding studies should be carried out simultaneously (Bıyıkoğlu, 2009).

In Türkiye, priority is HF, BS, and SM breeds in breeders' preference of cattle genotype. In the enterprises registered in the Herdbook system, the ratio of HF breed is 72.46%, while the ratio of Simmental (SM) and Brown Swiss (BS) breeds is 19.94% (CBAT, 2020). However, in the study conducted by Şahin et al, (2022), breeders declared that they preferred the SM breed primarily (31.2%). The preference rates of breeders for other breeds were 27.9% for HF, 14.8% for BS, and 5.0% for Jersey.

HF, SM, and BS breeds, which are of European origin, are raised on almost all continents of the world. In countries with advanced animal husbandry, sub-genotypes of these breeds (line, breed) have been developed depending on the breeding program of that country. The yield performances of the mentioned breeds and lines differ based on the conditions of the country and region where they are raised (Jasirowsski et al., 1987; Akbulut et al., 2001). Therefore, the countries that import these breeds have to make breed preferences by taking into account region and market conditions. The most important guiding information in this preference is to know the yield performance of the breed or genotype whose breeding is being considered in that region and, more specifically, in enterprises. In this context, a large number of studies examining the milk and meat yield traits of HF, SM, and BS breeds and crossbreeds have been conducted in Türkiye. The results of 73 studies conducted with HF and BS breeds were evaluated analytically by Akbulut (1998a and 1998b). In addition, the original research results examining the milk yield and fertility traits of these breeds in Türkiye were compiled by Şahin (2021).

Studies examining some yield traits of HF cattle population registered in herdbook system (or in CBA herd) in Türkiye have been conducted (Kumlu and Akman, 1999; Özkök and Uğur 2007; Genç and Soysal, 2018). In this context, a study covering all breeds was carried out by Özyürek and Tüzemen (2015) in the province of Erzurum.

In this study, the comparison of milk yield traits of HF, SM, and BS cattle breeds, as well as their crossbreeds registered in the herdbook system in Türkiye on the basis of breed and genotype, was made and the change in their performance by region was discussed. It is expected that the obtained results will guide breeders and possible policies. In addition, this study will be useful in terms of determining the level reached by the current yield performances of cattle breeds and crossbreeds that are widely raised in Türkiye.

2. Material and Methods

2.1. Material

In this research, herd records between the years 2000-2014 were used for the milk yield traits of herds registered in the herdbook system in Türkiye. The cattle whose yield records were evaluated were born in Türkiye and completed their development in Türkiye. The data of Holstein Friesian (HF), Brown Swiss (BS), and Simmental (SM) cattle breeds, as well as Holstein Friesian crossbreed (HFX), Brown Swiss crossbreed (BSX), and Simmental crossbreed (SMX) cattle, were evaluated in the study. Abbreviations of breeds and crossbreeds were made based on the BCSM (2022) coding standard.

In the analysis of yield records, i) animals with first calving age less than 700 days and longer than 1500 days, ii) animals with lifetime milk yield less than 1000 kg, and iii) animals whose milking time or lactation period was less than 100 days and longer than 660 days were excluded from the evaluation.

In the measurement of milk yield, as the main milk yield traits, i) actual milk yield (AMY), which is an indicator of milk yield during lactation, ii) lifetime number of lactations or total lactation number (TLN) and mean lactation period (LP) traits were analyzed.

2.2. Methods

Statistical analyzes of the data were made by the SPSS package program (SPSS, 2013). The GLM ANOVA method was used to analyze the effects of race or genotype and region on the traits related to milk yield. The linear statistical model with interaction used in data analysis is as follows:

$Y_{ijk}=\mu+g_i+b_j+(gb)_{ij}+e_{ijk}$

where;

Y_{ijk}: The observation value of the studied trait ($Y_{ijk}\sim N(\mu, \sigma^2)$)

μ: The general mean of the examined trait,

g_i: The effect of breed or genotype

b_j: Effect of the geographical region,

$(gb)_{ij}$: The effect of breed/genotype and region interaction,

e_{ijk}: Random error ($e_{ijk}\sim N(0, \sigma_e^2)$).

As descriptive statistical measures, the mean of the central location measure and the standard deviations of the variability measures were used. Since it was aimed to determine the magnitude of the variability in the studied traits, the standard deviation was presented. To determine the different subgroups of the factor (genotype or region) found to be significant for any trait, Duncan's Multiple Range test (DMRT) was used (Yıldız and Bircan, 1994).

3. Results

The results of the analysis of variance for the effects of genotype and geographical region on the studied traits are given in Table 1. Descriptive statistics and Duncan's Multiple Range test results for AMY, TLN, and LP traits by genotypes and regions are given in Table 2, Table 3, and Table 4.

As seen in Table 1, significant (P<0.01) and very significant (p<0.001) differences were detected between the genotypes in terms of AMY and LP traits, while differences were not found significant in terms of TLN. It was found that the effect of the region factor on all the examined traits was significant (P<0.01 or P<0.001). On the other hand, whereas the genotype-region interaction was not significant in the LS trait, it was significant in the other two traits (Table 1).

Table 1. Summary table of statistical significance test for milk yield traits

Variation Source[1]	Df	AMY		TLN		LP	
		F	P	F	P	F	P
G	5	23.047	<0.001	2.202	0.051	3.178	<0.007
B	6	40.225	<0.001	6.463	<0.001	3.623	<0.001
Interaction (G x B)	30	2.935	<0.001	2.038	<0.001	1.225	0.184
Error	22289						
A-R^2		0.891		0.850		0.952	

[1] AMY: Actual milk yield; TLN: total lactation number; LP: Lactation period; Df: Degrees of freedom; G: Genotype; B: Geographic region; A-R^2: Adjusted coefficient of determination.

Table 2. Descriptive statistics for AMY by race and region, and Duncan's Multiple Range test results

		MR	AG	CA	MD	BLS	EA	SEA	BRD
HF	n	8029	3551	7141	584	445	28	107	19885
	x̄±Sd	8165±3070	7706±2623	7428±2326	7305±2238	6021±2732	5970±2113	7138±2130	7737±2739^{a}
BS	n	73	128	222	6	123	22	7	581
	x̄±Sd	6520±2388	7216±3010	6372±2235	7737±2406	3816±1435	3368±2030	5416±896	5924±2637^{c}
SM	n	97	238	274	48	144	25	14	840
	x̄±Sd	7252±2601	6116±2090	6079±1785	7532±1904	4191±1805	4401±1453	6456±2078	5941±2211^{c}
HFX	n	127	104	276	14	23	2	20	566
	x̄±Sd	8276±3190	7299±2544	6716±2266	7159±2237	4612±1683	4966±1799	5508±1427	7049±2644^{b}
BSX	n	7	20	44	1	15	37	2	126
	x̄±Sd	6707±1383	6711±3109	5918±2102	3265± -	2977±1004	1826±953	6036±709	4517±2768^{e}
SMX	n	42	56	123	9	52	44	7	333
	x̄±Sd	7210±2431	6289±2360	5795±1794	6099±1407	3750±1390	3034±2134	4325±4680	5350±2362^{d}
REG	n	8375	4097	8080	662	802	158	157	22331
	x̄±Sd	8136±3063^{k}	7564±2636^{l}	7296±2327^{l}	7300±2211^{l}	5110±2517^{n}	3558±2255^{o}	6653±2094^{m}	7551±2771

HF: Holstein Friesian (Black and White), HFX: Holstein Friesian Crossbreeds, BS: Brown Swiss, BSX: Brown Swiss Crossbreeds, SM: Simmental, SMX: Simmental Crossbreeds; a, b, c, d: Use to geographic region ($p<0.05$); k, l, m, n, o : Use to breed-genotype ($p<0.05$); BRD: Breed; REG: Region; MR: Marmara region; AG: Aegean region; CA: Central Anatolia region; MD: Mediterranean region; BLS: Black sea region; EA: East region; SEA: Southeast region.

Table 3. Descriptive statistics for TLN by race and region, and Duncan's Multiple Range test results

		MR	AG	CA	MD	BLS	EA	SEA	BRD
HF	n	8029	3551	7141	584	445	28	107	19885
	x̄ ±Sd	4.0±1.8	4.4±1.8	4.3±1.7	4.5±1.8	4.0±1.8	3.7±1.9	3.3±1.4	4.2±1.7^{cd}
BS	n	73	128	222	6	123	22	7	581
	x̄±Sd	3.8±1.9	4.6±2.1	4.5±1.8	4.3±2.3	4.5±2.4	3.2±1.5	2.9±1.4	4.4±2.0b^{c}
SM	n	97	238	274	48	144	25	14	840
	x̄±Sd	4.2±2.2	5.2±2.1	4.6±2.0	3.9±1.8	4.7±2.1	3.6±1.8	4.4±1.8	4.7±2.1^{a}
HFX	n	127	104	276	14	23	2	20	566
	x̄±Sd	3.5±1.6	4.3±1.7	4.2±1.7	5.1±2.0	4.2±1.9	3.5±0.7	3.3±1.7	4.1±1.8^{d}
BSX	n	7	20	44	1	15	37	2	126
	x̄±Sd	4.3±1.8	4.7±2.2	4.5±1.9	3.00± -	5.5±2.6	4.0±1.7	5.0±4.2	4.5±2.0^{ab}
SMX	n	42	56	123	9	52	44	7	333
	x̄±Sd	4.1±2.0	4.7±2.1	4.7±2.0	4.6±2.8	4.8±2.1	4.0±1.9	3.0±1.4	4.5±2.0^{ab}
REG	n	8375	4097	8080	662	802	158	157	22331
	x̄±Sd	4.0±1.8^{l}	4.5±1.9^{k}	4.3±1.7^{k}	4.5±1.9^{k}	4.3±2.0k	3.8±1.8^{l}	3.4±1.5^{m}	4.2±1.8

HF: Holstein Friesian (Black and White), HFX: Holstein Friesian Crossbreeds, BS: Brown Swiss, BSX: Brown Swiss Crossbreeds, SM: Simmental, SMX: Simmental Crossbreeds; a, b, c, d: Use to geographic region ($p<0.05$); k, l, m : Use to breed-genotype ($p<0.05$); BRD: Breed; REG: Region; MR: Marmara region; AG: Aegean region; CA: Central Anatolia region; MD: Mediterranean region; BLS: Black sea region; EA: East region; SEA: Southeast region.

Differences between geographical regions and races for AMY and TLN treatments were found to be statistically significant ($p<0.05$).

If the interaction finding is interpreted in a more explicit way, it can be said that a genotype with a high yield in a region in terms of AMY and TLN traits may not be highly efficient in all regions. The same can be expressed for a genotype that has a low yield in a region. The fact that genotype-region interaction is found to be significant in terms of any trait requires the evaluation of interaction findings in determining breed preference by region.

Differences between geographical regions and races for LP treatment were found to be statistically significant ($p<0.05$).

Table 4. Descriptive statistics for LP (Day) by race and region, and Duncan's Multiple Range test results

		MR	AG	CA	MD	BLS	EA	SEA	BRD
HF	n	8029	3551	7141	584	445	28	107	19885
	x̄ ±Sd	375.4±8.4	387.9±9.5	392.8±9.3	380.4±8.4	370.0±8.3	387.6±9.1	379.9±9.9	383.9±9.2^{c}
BS	n	73	128	222	6	123	22	7	581
	x̄±Sd	389.7±99.2	396.8±96.6	391.0±83.1	342.3±80.5	351.6±65.0	339.9±90.5	366.6±78.7	381.0±87.0^{bc}
SM	n	97	238	274	48	144	25	14	840
	x̄±Sd	363.7±84.5	374.4±84.9	365.2±79.6	364.8±71.9	359.3±80.7	341.2±50.1	383.9±82.0	366.2±80.9^{a}
HFX	n	127	104	276	14	23	2	20	566
	x̄±Sd	366.6±95.5	394.0±79.5	390.9±91.9	348.7±63.9	383.4±79.6	329.0±45.3	365.6±100.	383.5±90.3^{c}
BSX	n	7	20	44	1	15	37	2	126
	x̄±Sd	389.9±43.0	394.5±64.5	377.4±89.1	317.0±-	351.5±60.2	337.1±89.6	366.0±73.5	365.2±81.9^{a}
SMX	n	42	56	123	9	52	44	7	333
	x̄±Sd	366.7±90.5	370.4±73.8	375.9±80.5	306.8±42.2	380.7±95.6	351.0±91.6	387.4±56.6	369.7±85.7^{ab}
REG	n	8375	4097	8080	662	802	158	157	22331
	x̄±Sd	375.2±84.8^{lm}	387.3±85.6^{kl}	391.4±88.0^{k}	377.2±82.3^{l}	366.0±77.5^{lm}	350.8±85.4^{n}	378.0±85.1^{lm}	382.9±9.2

HF: Holstein Friesian (Black and White), HFX: Holstein Friesian Crossbreeds, BS: Brown Swiss, BSX: Brown Swiss Crossbreeds, SM: Simmental, SMX: Simmental Crossbreeds; a, b, c, d: Use to geographic region ($p<0.05$); k, l, m, n, o : Use to breed-genotype ($p<0.05$); BRD: Breed; REG: Region; MR: Marmara region; AG: Aegean region; CA: Central Anatolia region; MD: Mediterranean region; BLS: Black sea region; EA: East region; SEA: Southeast region.

4. Discussion

Lactation Actual Milk Yield (AMY)

In the study, the general mean and standard deviation of the AMY trait for the examined genotypes (HF, BS, SM, HFX, BSX, and SMX) were found to be 7 551±2 771 kg. The general mean values of AMY for the same breeds and genotypes were reported as 3 834 liters for herds registered to the Cattle Breeders' Association (CBA) of the Erzurum province (Özyürek and Tüzemen, 2015).

According to the results of the Duncan's Multiple Range test, the highest AMY was determined as 7 737±2 739 kg in the HF breed. This breed was followed by the HFX genotype with a yield of 7 049±2 644 kg. Among these six genotypes, the lowest AMY was determined as 4 517±2 768 kg in the BSX genotype.

In terms of AMY, the highest yield was found in the Marmara region (8 136±3 063) and the lowest yield was found in the Eastern Anatolia region (3 558±2 255). In the Aegean, Central Anatolia, and Mediterranean regions, the mean yield in question was similar, and they were followed by the Southeastern Anatolia region, which had a lower yield level (Table 2).

When the genotype-region subgroups were examined, it was observed that the highest yield was obtained in the HFX in the Marmara region and it was followed by the HF breed in the same region (8 276 and 8 165 kg, respectively). The lowest yield, on the other hand, was determined in BSX animals in Eastern Anatolia and the Black Sea regions (1 826 and 2 977 kg). The yield of the HFX genotype in the Marmara region was 4.5 times the yield of the BSX genotype in the Eastern Anatolia region and approximately 2.8 times the yield of the same genotype in the Black Sea region. Hundreds of studies have been conducted in Türkiye on the milk yield traits of HF, BS, and SM breeds as well as their crossbreeds raised in different regions and enterprises. In this context, the milk yield of HF and BS breeds by agricultural regions was evaluated in a study conducted by Akbulut (1998a). The findings of this study revealed that AMYs of both breeds showed significant differences in agricultural regions.

According to the results of 23 studies, the mean AMY for the HF breed varied between 2 657 kg and 8 264 kg, and the highest yield was reported as 7 340 kg in the Middle North agricultural region. For the BS breed, this yield varied between 1 571 and 6 045 kg, and the lowest mean value was found in the Northeastern agricultural region (2 318 kg) (Akbulut, 1998a). In this context, another review study was conducted by Şahin (2021). In this review study, milk yield was reported in the range of 4 398-7 892 kg in HF breed cattle, 2 243-8115 kg in BS breed, and 3 412-7 693 kg in SM breed.

The findings obtained in this current study were higher than the values reported by Akbulut (1998a) and similar to the reports of Şahin (2021). In addition, the milk yield values found by Tüzemen and Özyörük (2015) in herds registered to Erzurum CBA were compatible with the results found in this study for the eastern Anatolia region.

When examining the mean lactation milk yield reported by some studies conducted in other countries, it was observed that Mellado (2011) reported this mean value between 10071 ± 281 and 14680

± 642 kg for HF cattle breed with lactation between <2 and >6 in northern Mexico, respectively. In a study where the mean number of lifetime lactations of animals in SM-breed cattle was found to be 3.61±0.04 in Serbia, Petrović et al. (2015) reported the amount of milk given by cows for life as an average of 14 604 kg. This means that an average of 4 045 kg (14 604 kg/3.61 pieces) of milk was obtained per lactation. In another study conducted in Bulgaria, the mean actual lactation milk yield of SM breed cattle was reported as 5478±112 kg (Karamfilov and Nikolov, 2019).

Total Lactation Number (TLN)

In this study, the mean total lactation number (TLN) and its standard deviation were found as 4.2±1.8 for all examined genotypes (HF, BS, SM, HFX, BSX, and SMX) (Table 3).

According to the results of the Duncan's Multiple Range test, the highest TLN was found to be 4.7±2.1 in the SM breed. This breed was followed by BSX and SMX genotypes with a yield of 4.5±2.0. Among these six genotypes, the lowest TLN was found in the HFX genotype as 4.1±1.8.

In terms of TLN, the highest value was found in the Aegean and Mediterranean regions with the same value (4.5±1.9), while the lowest value was found in the Southeastern Anatolia region (3.4±1.5). The mean TLN was similar in the Central Anatolia and Black Sea regions, and these regions were followed by the Eastern Anatolia region, which had a lower TLN (Table 3).

When the Genotype-Region subgroups were examined, it was seen that the highest TLN was obtained in the BSX genotype in the Black Sea region, and it was followed by the SM and HFX genotypes in the Aegean and Mediterranean regions (5.5±2.6, 5.2±2.1 and 5.1±2.0, respectively). The lowest TLN was found in the BS breed in the Southeastern Anatolia region (2.9±1.4). The TLN of the BSX genotype in the Black Sea region was 1.9 times higher than the TLN of the BS breed in the Southeastern Anatolia region and about 1.8 times higher than its TLN in the Eastern Anatolia region.

Many studies have been conducted on the milk yield and fertility traits of HF, BS, and SM breeds as well as their crossbreeds raised in different regions and enterprises in Türkiye. However, there was no study in Türkiye that examined these animals' total lactation numbers (TLN) that they give during the time they are used in production.

Moreover, in studies conducted in some countries other than Türkiye, the mean TLN in HF breed was reported as 5.5±1.4 in Egypt by Afifi et al. (2004), 2.88±1.8 in South Africa by Theron and Mostert (2009), 2.94 in the United States (USA) by Hare et al. (2006), 2.3±1.3 in Sweden by Hagnestam-Nielsen et al. (2009), 4.35 in Ethiopia by Goshu and Sing (2013), and 3.6 in Ireland by McNamara et al. (2003). Hare et al. (2006) reported the mean TLN in BS cattle as 2.89 in the USA. As for Simmental cattle, Petrović et al (2015) reported the mean lactation number of animals from three different farms in Serbia as 3.38±0.06, 3.72±0.09, and 3.76±0.07 for Dobričevo, Zlatiborski Suvati, and Kotraža, respectively. The mean of these numbers was 3.61±0.04. Martens and Bange (2013) found that the mean lactation number in the HF breed varies between 3.5 and 4.5 in Germany.

The TLN values obtained in this current study in HF breed were 1.3 times lower than the values reported by Afifi et al. (2004), while they were 1.2 times higher than the value reported by McNamara et al (2003), and 1.5 times higher than the values determined by Theron and Mostert (2009) and Hare et al. (2006).

Lactation Period (LP)

In the studied genotypes (HF, BS, SM, HZX, BSX, and SMS), the overall mean and standard deviation of the LP trait was found to be 382.9±9.2 days. The overall mean LP values for the same breeds and genotypes were reported as 304.12±1.5 days in cattle herds registered in the CBA of the Erzurum province (Özyürek and Tüzemen, 2015).

As a result of Duncan's Multiple Range test, the highest LP was found to be 383.9±9.2 days in HF breed. This breed was followed by the HFX genotype with 383.5±90.3 days and the BS breed with 381.0±87.0 days. Among these six genotypes, the lowest LP was detected as 365.2±81.9 days in the BSX genotype.

In terms of regions, the highest LP value was found in the Central Anatolia region (391.4±88.1 days) and the lowest value was found in the Eastern Anatolia region (350.8±85.4 days). In the Marmara, Aegean, Mediterranean, and Southeastern Anatolia regions, the mean lactation period in question was obtained close to each other (Table 4).

When the Genotype-Region subgroups were examined, it was observed that the highest LP values were obtained in BS and BSX breeds in the Aegean region (396.8±96.6 and 394.5±64.5 days, respectively). On the other hand, the lowest LP values were obtained in SM and BSX animals in the Mediterranean region (306.8±42.2 and 317.0±0.0 days, respectively). In addition, when the regions other than the Mediterranean region were compared, the lowest values for all breeds and genotypes, except for the SA breed, were found in animals bred in the Eastern Anatolian regions.

Numerous studies have been conducted on the lactation period traits of HF, BS, and SM breeds and their crossbreeds raised in different regions and enterprises in Türkiye. In this context, the lactation period of HF and BS breeds by agricultural regions was examined in a study conducted by Akbulut (1998a). According to the findings of this study, the LP values of both breeds showed significant differences in agricultural regions. According to the results of 23 studies, LP for the HF breed varied between 240 days and 355 days, and the highest period was reported as 334 days in the Northeastern agricultural region.

For the BS breed, the LP varied between 214 and 376 days, and the lowest mean was determined in the Northeastern agricultural region (258 days). In this context, in a study conducted by Özyürek and Tüzemen (2015), the lactation period of HF, BS, and SM breeds for herds registered in the CBA of the Erzurum province was reported as 308.1±7.6 days, 298.2±5.6 days, and 288.2±8.7 days, respectively. In the same study, LPs for HFX, BSX, and SMX cattle were reported as 315.2±11.8 days, 291.9±4.4 days, and 303.2±8.0 days, respectively. In a review study conducted by Şahin (2021), LP values were reported in the range of 299-358 days for the Holstein Friesian, 266-356 days for the BS breed, and 300-337 days for the SM breed. Tankal and Tüzemen (2022) reported that the mean lactation period in HF cows raised at Gökkale Agricultural Enterprise in Türkiye was 357.5±1.3 days.

The LP value obtained in this research was determined to be higher than the values obtained for the same breeds and genotypes in the cattle herd registered to the Erzurum CBA by Özyürek and Tüzemen (2015) and the LP value reported by Şahin (2021).

When the mean lactation periods reported in some studies conducted in other countries were examined, it was seen that in HF cattle breed with lactation orders between <2, 2-4, 4-6, and >6 in Northern Mexico, the LP values were reported as 414±9, 502±11, 479±9 and 483±19 days (Mellado, 2011). In Bulgaria, on the other hand, Karamfilov and Nikolov (2019) reported the mean lactation period in SM-breed cattle as 342.60±6.18 days.

Conclusion

In this study, it was determined that the milk yield traits had the desired values in cattle breeding enterprises. The obtained mean milk yield is higher than the mean of Türkiye and meets the expectations. However, it is possible to say that the fact that the mean milk yield is high is due to the length of the lactation period. The fact that the lactation period is higher than the value of 305 days reduces the number of highly productive days and also does not meet the expectation of "one offspring per animal per year" in cattle breeding enterprises.

The obtained results showed that the effect of genotype x region interaction was significant on milk yield traits. As a result, it was concluded that in determining the breed preference by region, it is necessary to evaluate the interaction findings and take these findings into account in decision-making.

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Ethical statement

Milk yield records registered in the Herdbook system were used.

Conflict of Interest

As authors, we declare that there is no conflict of interest between us.

Contributions of authors

OŞ, IY and ÖA designed the study. OŞ collected the data. ÖA made the statistical analysis. The article was written by OŞ, IY, and ÖA. All authors contributed to the critical revision of the article.

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