Research article

Genetic and non-genetic factors affecting test day milk yield and milk composition traits in crossbred dairy cattle in Ethiopia

Rekik Bekele[1,2*], Mestawet Taye[1], Girma Abebe[1] and Selam Meseret[3]

[1]School of Animal and Range Sciences, College of Agriculture, Hawassa University, Hawassa, P.O. Box 05, Ethiopia
[2]Department of Animal Science, College of Agriculture and Natural Resource Sciences, Debre Berhan University, Debre Berhan, P.O. Box 445, Ethiopia,
[3]Livestock Genetics, International Livestock Research Institute, Addis Ababa, P.O. Box 5689, Ethiopia

Abstract

This study evaluated the effects of genetic group (GG), lactation number (LN), lactation length (LL), calving season (CS), and calving year (CY) on the milk yield and composition traits of four hundred twenty lactating crossbred dairy cows in 13 districts of three regions in Ethiopia. Test day milk yield (TDMY), protein (P), fat (F), lactose (L), solid not fat (SNF), density (D), total solids (TS), total protein (TP), casein (CN), whey (W), salts (S), and freezing point (FP) were determined using standard procedures. The data were analyzed using generalized linear models (GLM) using R software. TDMY was highest in high-grade cows (> 87.5% exotic blood) that calved in the rainy season of 2022, mid-lactation (101-200 days), and the 2nd LN. GG, LL, CS, CY, and LN significantly (P<0.05) influenced F, SNF, and TS. F was higher in cows with a genetic group ≤ 50%, in early and late lactation, in the dry season, in 2020, in the 1st and ≥ 4th LN than their counterparts. Proteins were affected by GG, LL, and CY but not by CS and LN (P<0.05). All milk proteins had a higher value in cows with ≤ 50% genetic group and in early lactation. In this study, milk yield and composition were affected by genetic and non-genetic factors, providing an opportunity for crossbreeding programs to balance the quality and quantity of milk by manipulating the level of the exotic gene found in cows, choosing the best climatic conditions, and improving the level of management.

Keywords: Crossbred, Genetic, Milk Composition, Milk Yield, Non-Genetic

Corresponding author: Rekik Bekele, Department of Animal Science, College of Agriculture and Natural Resource Sciences, Debre Berhan University, P.O. Box, 445 Debre Berhan, Ethiopia. Email: rekikbekele@gmail.com.

INTRODUCTION

Ethiopia has diverse agroecological and climatic conditions that favor improved and high-yielding breeds for dairy production. The daily livelihood of farmers in the study areas depends mostly on dairy farming, which also has the potential to do more to improve nutrition and reduce poverty in the nation (Duguma, 2022; Zemarku et al., 2022). The capacity of Ethiopia's dairy sector still needs to be improved to produce sufficient quantities of milk and dairy products to meet domestic demand (Gebreyohanes et al., 2021). The dairy industry has issues with a lack of high-yielding improved genetics and poor extension and marketing services (Pragna et al., 2017; Mekonen et al., 2022). Improving the genetic potential of dairy cows by crossbreeding Bos taurus with Bos indicus (local zebu) is recognized as a quick way to increase milk productivity. Crossbreeding has been used as an essential tool for the genetic improvement of dairy cattle in urban areas of Ethiopia (MOA, 2019). Crossbreeding in Ethiopia has been widely used to combine the adaptability, hardiness, disease resistance, and heat tolerance of local zebu with the high milk-producing potential and faster growth rate of exotic breeds (Tadesse et al., 2022).

Milk is a crucial product that contains many vital nutrients, such as body-building proteins, fat, energy-providing lactose, health-providing vitamins, bone-forming minerals, and milk fat that affect animal and human health. The composition of milk has economic significance to milk producers and processors in addition to reflecting the quality of the milk, the health of dairy cows, the nutritional value, and the technological properties of milk (Amenu and Deeth, 2007). Genetic and environmental factors such as breed, feeding, health status, and climatic conditions influence milk yield and composition. Furthermore, some physiological factors, such as the lactation number and length, affect milk yield and composition (Sudhakar et al., 2013; Sabek et al., 2021; Oloo et al., 2022). Evaluating the milk yield and milk composition performance of crossbred dairy cattle in different production environments provides clues for selecting a more productive cattle genotype in a given environment. It is crucial for decision-making on continuing the existing synthetic dairy cattle breed development in Ethiopia. The present study was therefore undertaken to study the milk yield and milk composition of crossbred dairy cattle under various environmental factors in Ethiopia.

MATERIALS AND METHODS

Data Source and Study Area

Data for this study were collected from 13 districts in the central (six), southern (three), and northeastern (four) regions of Ethiopia. Their geographical location ranges from 6°49' to 9°54' latitude and 37°44' to 39°47' longitude. All selected sites had binomial rainfall distribution. Study areas were selected based on the availability of genotyped lactating dairy cows.

Vet Integr Sci *Bekele et al. Vet Integr Sci. 2023; 21(3): 717 - 733*

718

Animal and Management

A total of 420 cows were included in the current study, and of these, 320 cows were genotyped using the 50K Illumine Bovine Bead Chip array, while the remaining 100 cows were not genotyped. The breed composition of genotyped individual cows was determined using the clustering method implemented by the program Admixture v1.3.0 (Alexander et al., 2009). The genetic groups of non-genotyped cows were obtained from dairy producer records. The breed composition of Ethiopian cattle has been largely influenced by Holstein Friesian and to a lesser extent Jersey breeds, which have long been imported into the country as live animals or through artificial insemination (AI) to improve the native cow breed (Chebo and Alemayehu, 2012).

Data were divided into four different genetic groups based on the exotic blood level and its distribution: ≤ 50%, 50.5-75%, 75.5-87.5%, and ≥ 88% (Haile et al., 2008). In this study, range values were used instead of point values. Lactation stages were grouped into early (≤ 100 days), mid (101-200 days), late (201-305 days), and extended lactation (>305 days) (Lambert et al., 2015; Yang et al., 2016; Niozas et al., 2019; Sehested et al., 2019). Lactation numbers of cows were divided into four groups: 1st, 2nd, 3rd, and 4th and above (Yang et al., 2016; Sahu et al., 2018; Kuczyńska et al., 2021). All lactation numbers four and above were pooled together. The calving seasons were grouped into three: long rainy (June–September), short rainy (October–January), and dry (February–May) (Rosell, 2011; Yalew et al., 2011). Calving years were classified into 2020, 2021, and 2022 years (Verma et al., 2017).

The studied dairy farms were found in urban and peri-urban production systems. Natural pasture, hay, and a concentrated mixture of wheat bran (*Triticum vulgare*), nug cake (*Guizotia abyssinica*), and salt were the primary feed sources for cattle. The concentrat feed was supplemented based on body weight, productivity, and physiological stage, with clean tap water available at all times.

Milk Yield Measurement and Sample Collection

Milk yield was recorded during morning and evening milking on the sampling day. Milk yield was measured using graduated buckets or cups from each cow in the morning and evening; milk data were added to get the daily milk yield on the measurement day. Raw milk samples were collected directly from each cow's teats after cleaning and drying the udder and teats with towels. Approximately 100 ml of morning or evening milk was aseptically collected in sterile sample bottles after discarding the first three to five milk strands. The samples were labeled and immediately placed in an icebox and either transported to the Central Biotechnology Laboratory of Hawassa University (CBLHU) or kept at -20 °C until later transportation to the CBLHU for analysis. Dairy farm records were also used to collect information about each cow's calving date, lactation length, lactation number, estimated exotic blood levels, and farm management practices.

Milk Sample Preparation for Analysis

Milk samples were removed from the refrigerator and allowed to thaw at room temperature for 30–45 minutes, then gently mixed by hand, then warmed and slowly shaken in a water bath at 35–45 °C for 10 minutes. To determine total milk protein, casein, and whey, 30 ml milk sample was centrifuged at 5000 rpm for 20 minutes at 4 °C, the upper-fat layer was scraped off with a spatula, and the lower aqueous phase (skimmed milk) was transferred to another tube with a filter.

Milk Analysis

Milk compositional analysis was carried out at the CBLHU. Fat, protein, lactose, total solids, density, solids-non-fat, freezing point, and salt were analyzed using a near-infrared instrument (Milkotronic-ultrasonic milk analyzer, Milkotronic Ltd) (Mekonen et al., 2022). The concentration of total milk protein was determined using the Bradford method (Krauspe and Scheer, 1986). Briefly, Coomassie blue reagent was prepared by combining 5 mg of Coomassie Brilliant Blue G 250 with 25 ml of 95% ethanol, 50 ml of 88% phosphoric acid, and 425 ml of ultrapure water. In a 96-well plate, 5 µl of milk was mixed with 250 µl Coomassie Blue reagent and incubated and shaken at room temperature for 15 minutes. Absorbance was measured at 595 nm on a microplate reader (Multiskan™ GO) controlled by SkanIt RE 6.1.1 software. The absorbance readings for a series of increasing bovine serum albumin (0, 10, 20, 40, 60, 80, and 100 µl) were plotted on a graph to create a standard curve; this was done in duplicate. Casein was determined by the isoelectric precipitation method, Briefly, 20 ml of skim milk was transferred into a beaker to separate casein and whey proteins by precipitation at their isoelectric point (pH 4.6) by adding dropwise 1N hydrochloric acid (8.33 ml HCL to 100 ml H_2O) with constant stirring, checking the pH, and allowing it to sediment. Casein precipitated, and the supernatant was decanted using 45µm filter paper and a funnel. The precipitate was washed with distilled water to remove the salts and then with ethanol to remove the remaining fats then dried and weighed (Jabeen et al., 2020). Whey protein was obtained by subtracting casein from total protein.

Statistical Analysis

Data points of milk production traits were coded and checked for outliers and normal distributions. All studied traits were analyzed using the General Linear Model (GLM) of the R software procedure. The model accounted for the effects of genetic groups, lactation length, lactation number, calving season and calving year. The effect of class variables was expressed as Least Square Means (LSM) ± Standard Error (SE). The mean comparison test was done using Duncan's multiple range test. A correlation analysis was used to determine the relationships between milk yield and milk composition. Correlation coefficients were plotted using the corrplot package in R software (Taiyun and Viliam, 2021).

Vet Integr Sci *Bekele et al. Vet Integr Sci. 2023; 21(3): 717 - 733*

720

The following model was used:

$$Y_{ijklm} = \mu + GG_i + CS_j + LN_k + CY_l + LL_m + e_{ijklm}$$

Where:

Y_{ijklm} : - all milk production traits (TDMY, P, F, L, SNF, D, TS, TP, CN, W, S, and FP)

μ: - the overall mean;

GG_i: - the effect of ith genetic group (≤ 50, 50.5-75, 75.5-87.5, and ≥ 88);

CS_j: - the effect of jth calving season (dry, short rainy and long rainy);

LN_k: - the effect of kth cow lactation number (1, 2, 3, and ≥ 4);

CY_l: - the fixed effect of lth calving year (2020, 2021 and 2022);

LL_m : - the fixed effect of mth lactation length (early, mid, late, and extended);

e_{ijklm} : - random residual term.

RESULTS

The range of the coefficient of variation for milk production traits was from 6.20% to 39.30%. The model utilized in this study fits the data well and has a high predictive ability but poor findings for lactose. The descriptive statistics for the data and the coefficient of variation and R^2 values are shown in Table 1.

Table 1 Descriptive statistics and the coefficients of variation (CV%) and R^2 value of milk production traits in crossbred cattle in Ethiopia.

Traits	N	Min	Max	Mean	SD	CV (%)	R^2
Test Day Milk Yield (TDMY)	420	5	22	13.8	3.7	33.8	0.9
% Protein (P)	420	2.37	4.3	3.27	0.4	12.1	0.5
% Fat (F)	420	1.62	4.97	3.21	0.9	26.7	0.8
% Lactose (L)	420	2.82	5.86	4.45	0.6	14.8	0.1
% Solid Not Fat (SNF)	420	4.33	10.1	7.64	1.3	19.8	0.8
% Density(D)	420	18.4	38.7	28.79	4.4	17	0.4
% Total Solid (TS)	420	8.79	12.3	10.85	0.7	6.2	0.6
Total Protein (TP)	420	24.7	52	36.38	7.9	21.70	0.6
Casein (CN)	420	21.7	41.3	29.89	5.7	18.60	0.6
Whey (W)	420	2.94	10.7	6.49	2.3	39.30	0.6
Salt (S)	420	0.44	0.88	0.67	0.1	13.90	0.4
Freezing Point (FP)	420	-0.68	-0.34	-0.52	0.1	12.60	0.4

Effect of Genetic Group

The genetic group of the cows had a significant effect on all milk production traits except lactose (P < 0.05). The least-square means, and standard errors of the milk production traits for the effect of the genetic group are presented in Table 2. Cows with an exotic blood level above 87.5% had the highest test day milk yield (18.72 ± 0.12 litters/day) than those with a lower exotic blood level. The percentage values of P (3.58 ± 0.04), F (4.29 ± 0.05), TP (47.21 ± 0.76), CN (37.77 ± 0.54), W (9.44 ± 0.22), and FP (-0.51 ± 0.01) were higher in the ≤ 50% genetic group than in other genetic groups. While percentages of SNF (5.65 ± 0.08), D (24.27 ± 0.48), TS (9.94 ± 0.06), and salt (0.65±0.01) were lower in ≤ 50% of the genetic group than in other genetic groups. Figure 1 shows that the fat percentage decreased for each genetic group as the volume of test-day milk yield increased.

Table 2 Least square means ± standard errors for the effect of genetic groups on milk production traits.

Traits	Genetic Group				P value
	≤ 50 %	>50 ≤ 75 %	>75 ≤ 87.5%	>87.5 %	
	N = 55	N =131	N=123	N=111	
	LSM±SE	LSM±SE	LSM±SE	LSM±SE	
TDMY	7.99±0.17[d]	12.98±0.11[c]	15.51±0.11[b]	18.72±0.12[a]	***
P	3.58±0.04[a]	3.36±0.02[b]	3.19±0.03[c]	2.94±0.03[d]	***
F	4.29±0.05[a]	3.66±0.03[b]	2.41±0.03[d]	2.48±0.03[c]	***
L	4.42±0.08[ns]	4.46±0.05[ns]	4.47±0.05[ns]	4.46±0.06[ns]	NS
SNF	5.65±0.08[d]	7.65±0.05[c]	8.9±0.05[a]	8.35±0.06[b]	***
D	24.27±0.48[c]	28.62±0.3[b]	30.82±0.32[a]	31.45±0.34[a]	***
TS	9.94±0.06[c]	11.31±0.04[a]	11.31±0.04[a]	10.83±0.04[b]	***
TP	47.21±0.76[a]	36.44±0.47[b]	31.73±0.5[c]	30.15±0.54[c]	***
CN	37.77±0.54[a]	29.75±0.34[b]	26.45±0.35[c]	25.61±0.38[c]	***
W	9.44±0.22[a]	6.69±0.14[b]	5.29±0.14[c]	4.54±0.16[c]	***
S	0.65±0.01[c]	0.67±0.01[b]	0.67±0.01[ab]	0.69±0.01[a]	**
FP	-0.51±0.01[a]	-0.52±0[ab]	-0.53±0.01[b]	-0.53±0.01[b]	*

[a-d] Means within rows with different superscripts are significantly different at *$P<0.05$; ** ($P<0.01$); *** ($P<0.001$) for genetic effect.

Abbreviation: TDMY = Test day milk yield (litters/day); P = protein percentage; F = fat percentage; L = lactose percentage; SNF = solid not fat percentage; D = density (g/cm^3); TS = total solid percentage; TP = total protein (mg/ml); CN = casein (mg/ml); W = whey protein (mg/ml); S = salt percentage; FP = freezing point (^{o}C).
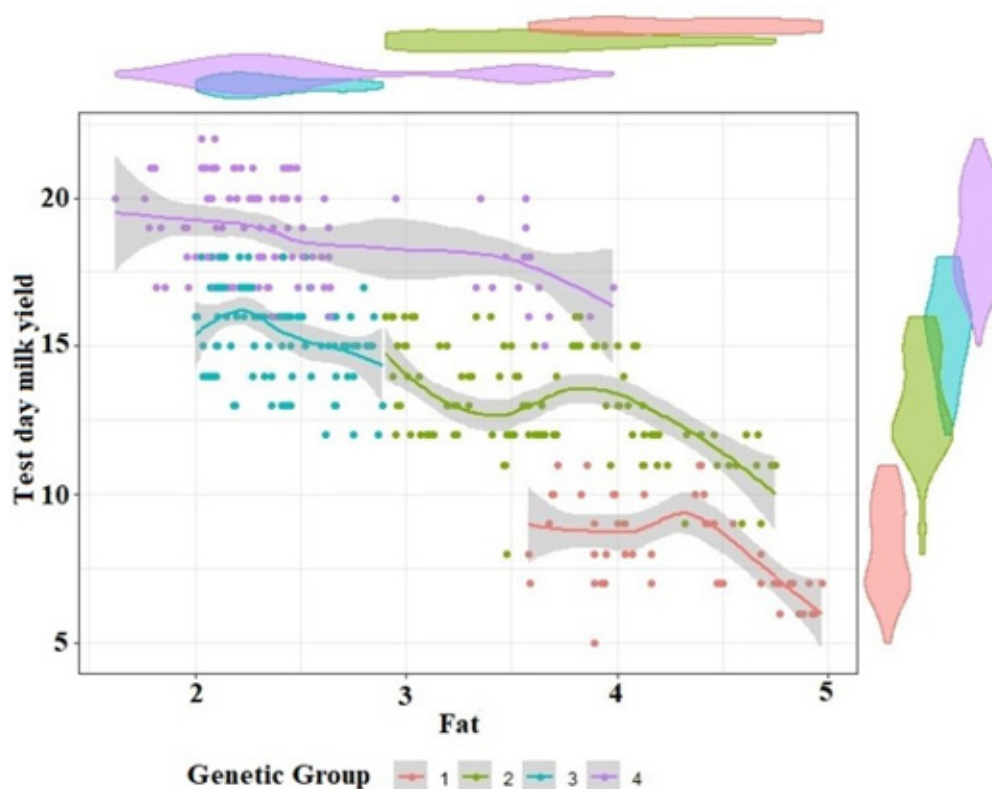
Figure 1 TDMY and F in different genetic groups (1= 0-50; 2= 50.5-75; 3 =75.5-87.5: 4 = 88-100).

Vet Integr Sci Bekele et al. Vet Integr Sci. 2023; 21(3): 717 - 733

722

Effect Lactation Length

The results showed that all milk production traits except L, D, S, and FP were significantly affected by lactation length (P<0.05). The least-square means, and standard errors for the effect of lactation length on milk production traits is reported in Table 3. Cows in early lactation recorded the lowest milk yield, which tended to increase in cows in the second and third lactation lengths and then decreased in the fourth lactation group of cows. Fat percentages were higher in early and extended lactation and lower in mid and late lactation. The milk proteins (P, TP, CN, and W) were higher in early and mid-lactation, then tended to decrease in late and extended lactation.

Table 3 Least square mean ± standard errors of milk yield and milk composition across lactation length.

Traits	Lactation Length				P Value
	Early	Mid	Late	Extended	
	N = 96	N = 86	N = 125	N = 113	
	LSM±SE	LSM±SE	LSM±SE	LSM±SE	
TDMY	13.46±0.13^b	14.27±0.12^a	14.23±0.13^a	13.84±0.16^{ab}	***
P	3.33±0.03^a	3.31±0.03^a	3.22±0.03^b	3.21±0.04^b	*
F	3.46±0.04^a	2.83±0.04^c	3.05±0.04^b	3.5±0.04^a	***
L	4.46±0.06^{ns}	4.49±0.06^{ns}	4.43±0.06^{ns}	4.43±0.07^{ns}	NS
SNF	7.27±0.06^c	8.17±0.06^a	7.82±0.06^b	7.29±0.07^c	***
D	28.12±0.37^{ns}	28.65±0.34^{ns}	29.06±0.37^{ns}	29.32±0.43^{ns}	NS
TS	10.73±0.05^b	11±0.04^a	10.87±0.05^a	10.79±0.05^b	***
TP	37.75±0.59^a	37.4±0.54^a	35.4±0.58^b	34.98±0.68^b	***
CN	30.83±0.42^a	30.62±0.38^a	29.22±0.41^b	28.91±0.48^b	*
W	6.93±0.17^a	6.78±0.16^a	6.18±0.17^b	6.07±0.2^b	**
S	0.66±0.01^{ns}	0.67±0.01^{ns}	0.67±0.01^{ns}	0.68±0.01^{ns}	NS
FP	-0.5±0.01^{ns}	-0.53±0.01^{ns}	-0.52±0.01^{ns}	-0.54±0.01^{ns}	NS

$^{a-d}$ Means within rows with different superscripts are significantly different at *P<0.05; ** (P<0.01); *** (P<0.001) for lactation length effect.
Abbreviation: TDMY = Test day milk yield (litters/day); P = protein percentage; F = fat percentage; L = lactose percentage; SNF = solid not fat percentage; D = density (g/cm³); TS = total solid percentage; TP = total protein (mg/ml); CN = casein (mg/ml); W = whey protein (mg/ml); S = salt percentage; FP = freezing point (°C).
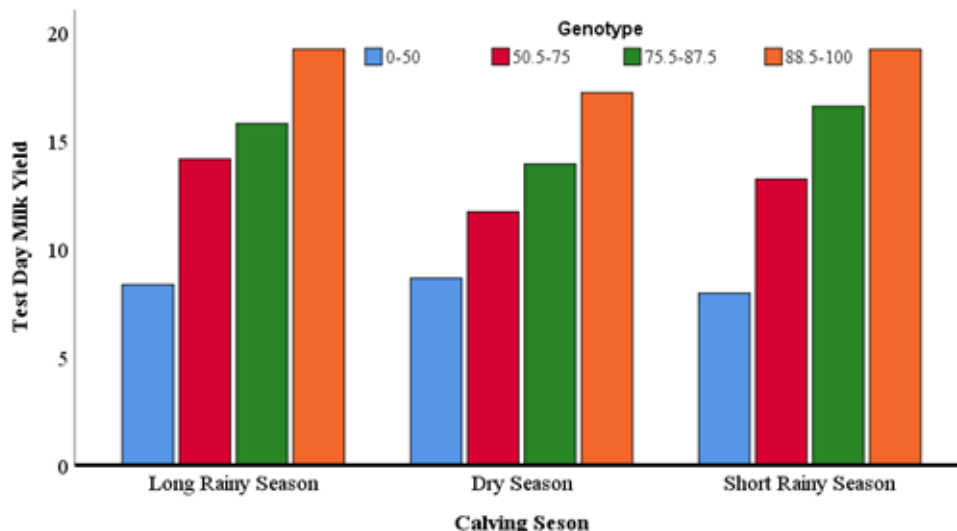
Effect of Calving Season

The season in which the cows have calved significantly affected test-day milk yield (P<0.05). The effect of calving seasons on test-day milk yield, fat, protein, total solid, solid not fat, density, lactose, salt, and freezing point of milk is shown in Table 4. Cows that calving during the long (June-September) and short (October-January) rainy seasons produced higher milk yields of 14.43 liters/day and 14.60 liters/day, respectively, compared to 12.37 litters/day in the dry (February-May) season. The least-square means of lactose content and SNF were significantly higher during the long rainy season than in other seasons (P<0.05). Figure 2 shows that TDMY was low during the dry season and high during the short and long rainy seasons in all genetic groups.

Table 4 Least square means ± standard errors for effects of the calving season on milk production traits

Traits	Calving Season			P value
	Dry	Short Rainy	Long Rainy	
	N = 142	N = 123	N = 155	
	LSM±SE	LSM±SE	LSM±SE	
TDMY	12.37 ± 0.12^b	14.43 ± 0.11^a	14.6 ± 0.11^a	***
P	3.27 ± 0.03^{ns}	3.24 ± 0.03^{ns}	3.23 ± 0.03^{ns}	NS
F	3.26 ± 0.03^{ns}	3.23 ± 0.03^{ns}	3.14 ± 0.03^{ns}	NS
L	4.26 ± 0.05^c	4.39 ± 0.05^b	4.71 ± 0.05^a	***
SNF	7.49 ± 0.06^c	7.65 ± 0.05^b	7.78 ± 0.05^a	**
D	28.71 ± 0.33^{ns}	28.57 ± 0.31^{ns}	29.09 ± 0.32^{ns}	NS
TS	10.75 ± 0.04^{ns}	10.88 ± 0.04^{ns}	10.92 ± 0.04^{ns}	NS
TP	37.32 ± 0.52^a	35.47 ± 0.48^b	36.36 ± 0.5^{ab}	*
CN	30.6 ± 0.37^a	29.22 ± 0.34^b	29.86 ± 0.36^a	*
W	6.72 ± 0.15^{ns}	6.26 ± 0.14^{ns}	6.5 ± 0.14^{ns}	NS
S	0.66 ± 0.01^b	0.69 ± 0.01^a	0.67 ± 0.01^b	**
FP	-0.51 ± 0.01^a	-0.53 ± 0^b	-0.52 ± 0.01^b	**

[a-c] Means within rows with different superscripts are significantly different at *$P<0.05$; ** ($P<0.01$); *** ($P<0.001$) for calving season effect.

Abbreviation: TDMY = Test day milk yield (litters/day); P = protein percentage; F = fat percentage; L = lactose percentage; SNF = solid not fat percentage; D = density (g/cm^3); TS = total solid percentage; TP = total protein (mg/ml); CN = casein (mg/ml); W = whey protein (mg/ml); S = salt percentage; FP = freezing point (°C).

Figure 2 Calving season effect on test day milk yield in various genetic groups.

Effect of Calving Year

The year of calving had a significant effect (P<0.05) on all milk production traits except lactose. The least-square means, and standard errors for the effect of the calving year on milk production traits is shown in Table 5 The test day milk yield was significantly higher in the calving year 2022 than in the calving years 2020 and 2021. The fat percentage, proteins (protein percentage, total protein, casein, and whey), and FP were higher in 2020. Solid not fat, density, total solid, and salt were higher in 2022.

Table 5 Least square means ± standard errors of milk production traits across the calving year.

Traits	Calving Year			P value
	2020	2021	2022	
	N = 182	N = 115	N = 123	
	LSM±SE	LSM±SE	LSM±SE	
TDMY	13.21 ± 0.1^c	13.88 ± 0.13^b	14.31 ± 0.15^a	***
P	3.37 ± 0.02^a	3.23 ± 0.03^b	3.2 ± 0.04^b	***
F	3.35 ± 0.03^a	3.17 ± 0.04^b	3.11 ± 0.04^c	***
L	4.5 ± 0.05^{ns}	4.47 ± 0.06^{ns}	4.39 ± 0.07^{ns}	NS
SNF	7.38 ± 0.05^c	7.74 ± 0.06^b	7.8 ± 0.07^a	***
D	27.31 ± 0.28^b	29.42 ± 0.37^a	29.63 ± 0.43^a	***
TS	10.73 ± 0.04^b	10.91 ± 0.05^a	10.91 ± 0.05^a	**
TP	38.08 ± 0.44^a	36.38 ± 0.58^b	34.69 ± 0.68^c	***
CN	31.11 ± 0.32^a	29.91 ± 0.41^b	28.67 ± 0.48^c	***
W	6.97 ± 0.13^a	6.48 ± 0.17^b	6.02 ± 0.2^c	***
S	0.61 ± 0.01^c	0.68 ± 0.01^b	0.72 ± 0.01^a	***
FP	-0.48 ± 0^a	-0.53 ± 0.01^b	-0.56 ± 0.01^b	***

[a-c] Means within rows with different superscripts are significantly different at *$P<0.05$; ** ($P<0.01$); *** ($P<0.001$) for calving year effect.
Abbreviation: TDMY = Test day milk yield (litters/day); P = protein percentage; F = fat percentage; L = lactose percentage; SNF = solid not fat percentage; D = density (g/cm³); TS = total solid percentage; TP = total protein (mg/ml); CN = casein (mg/ml); W = whey protein (mg/ml); S = salt percentage; FP = freezing point (ºC).

Effects of Lactation Number

Lactation number significantly affected the TDMY, fat, solid not fat, TS, salt, and FP of milk ($P < 0.05$). The least-square means, and standard errors for lactation number effect on milk production traits is reported in Table 6. The TDMY was higher for lactation numbers two and three than in one and four. In lactation number one and four and above, cows had a higher fat percentage than cows at second and third lactation. The percentage of solid not fat and total solid and salts were significantly ($P < 0.05$) higher at lactation number two and three. All milk proteins, lactose, and density were not significantly affected by lactation number.

**Table 6** Least square means ± standard errors for the effect of lactation number on milk production traits

Traits	Lactation Number				P value
	1	2	3	≥4	
	N = 82	N = 121	N = 66	N = 151	
	LSM±SE	LSM±SE	LSM±SE	LSM±SE	
TDMY	13.44 ± 0.14^b	14.55 ± 0.11^a	13.79 ± 0.16^a	13.43 ± 0.1^b	***
P	3.29 ± 0.03^{ns}	3.28 ± 0.03^{ns}	3.24 ± 0.04^{ns}	3.25 ± 0.02^{ns}	NS
F	3.24 ± 0.04^a	3.11 ± 0.03^b	3.21 ± 0.05^b	3.27 ± 0.03^a	**
L	4.41 ± 0.06^{ns}	4.45 ± 0.05^{ns}	4.5 ± 0.07^{ns}	4.47 ± 0.05^{ns}	NS
SNF	7.49 ± 0.07^b	7.8 ± 0.05^a	7.69 ± 0.07^a	7.59 ± 0.05^b	**
D	28.34 ± 0.39^{ns}	28.62 ± 0.32^{ns}	29.09 ± 0.44^{ns}	29.1 ± 0.29^{ns}	NS
TS	10.73 ± 0.05^b	10.91 ± 0.04^a	10.9 ± 0.06^a	10.86 ± 0.04^b	*
TP	37.41 ± 0.61^{ns}	35.95 ± 0.5^{ns}	36.03 ± 0.7^{ns}	36.14 ± 0.46^{ns}	NS
CN	30.6 ± 0.44^{ns}	29.59 ± 0.35^{ns}	29.68 ± 0.5^{ns}	29.71 ± 0.33^{ns}	NS
W	6.81 ± 0.18^{ns}	6.36 ± 0.14^{ns}	6.35 ± 0.2^{ns}	6.43 ± 0.13^{ns}	NS
S	0.67 ± 0.01^b	0.68 ± 0.01^a	0.67 ± 0.01^a	0.66 ± 0.01^b	*
FP	-0.53 ± 0.01^a	-0.53 ± 0.01^a	-0.51 ± 0.01^b	-0.51 ± 0^b	*

[a-d] Means within rows with different superscripts are significantly different at *$P<0.05$; ** ($P<0.01$); *** ($P<0.001$) for lactation number effect.

Abbreviation: TDMY = Test day milk yield (litters/day); P = protein percentage; F = fat percentage; L = lactose percentage; SNF = solid not fat percentage; D = density (g/cm³); TS = total solid percentage; TP = total protein (mg/ml); CN = casein (mg/ml); W = whey protein (mg/ml); S = salt percentage; FP = freezing point (ºC).

Correlation Between Test Day Milk Yield and Milk Composition Traits

TDMY strongly and negatively correlated with F, whereas SNF and density correlated with TDMY positively and strongly. Proteins (P, TP, CN, and W) were also negatively correlated with TDMY. Proteins were strongly and negatively correlated with SNF and density. Milk fat percentage had a strong and negative correlation with SNF. The correlation coefficient of test day milk yield and milk composition traits is shown in Figure 3.

Vet Integr Sci *Bekele et al. Vet Integr Sci. 2023; 21(3): 717 - 733*

726
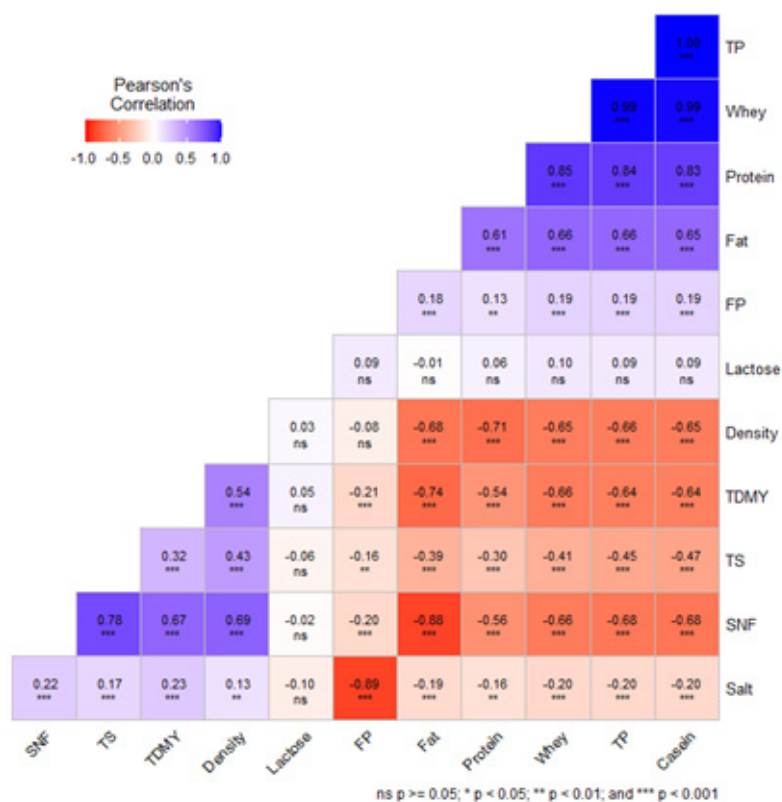
Figure 3 Person correlation coefficient for test day milk yield and milk composition traits. The intensity of the color describes the degree of association, i.e., how strong or weak the association is between two milk production traits. Also, it includes the r and p values in each square.

DISCUSSION

One of the main interests of this study was to assess the effect of genetic groups derived from Single Nucleotide Polymorphisms (SNPs) on milk production traits. Using DNA markers to characterize bovine genomic structure is very helpful when pedigree records are unavailable or incomplete. Knowledge of breed composition is important for genomic selection, an adaptation of breeds to production environments, prediction of heterosis, identification of pure breeds for conservation purposes, and understanding the trends of dairy cattle development (Ceruiyot et al., 2018).

Effect of Genetic Group

The results of this study have shown that genetic groups significantly impact test-day milk yield. A previous study also reported that various proportions of exotic genotype cows had significant differences in test-day milk yield (Ojango et al., 2019). According to Ojango et al. (2019), cows with a genetic makeup containing >87.5% exotic blood levels had a higher mean TDMY than those with a lower proportion, similar to this study; this may be due to the genetic makeup of the exotic cows. It is known that Holstein Friesian

cattle have been selected and established as a high milk-producing dairy breed. As a result of this merit, it is widely used in crossbreeding programs in many developing countries, including Ethiopia. The larger the infusion of the Holstein Friesian gene into the indigenous cattle populations, the higher the milk yield of crosses. The test day milk yield for the >87.5% genetic group in this study was 18.72 litters/day, which is comparable to a previous 18.60 kg/day study in Holstein Friesian cattle in Ethiopia during the third lactation (Meseret and Negussie, 2017). The fact that this genetic group is producing more milk implies that the management condition at the farm was acceptable because it allowed the cows to express their genetic potential more effectively in a given managements. There are instances where high-grade dairy cattle have performed lower than crosses due to poor feeding management practices (Britt et al., 2021).

Genetic groups also had a significant effect on milk composition traits. This study found that when the proportion of the exotic gene increased, the percentages of milk constituents decreased significantly (P <0.05), which is consistent with earlier findings by Haile et al. (2008) and Ceruiyot et al. (2018). The volume of milk produced is inversely proportion to the milk constituents. As the exotic blood level increases, the volume of the milk increases, while the constituents in milk decreases (Haile et al., 2008). The protein percentage was 2.93 in the ≥ 87.5% genetic group was lower than 3.13 in 87.5% of the Holstein crossbreds in Ethiopia (Haile et al., 2008); However, it was higher than 2.66 Holstein Friesian crosses in Ethiopia (Yoseph et al., 2022). This may be due to the variation of dam breeds. The mean value of the milk protein percentage of the ≤ 50% genetic groups is lower than the 3.8% reported by Kebede (2018) for 50% crossbred dairy cows and higher than the 2.76 % reported by Mekonen et al. (2022) for Holstein Friesian crossbred dairy cows in Ethiopia. Fat percentage was highest for the ≤ 50% genetic group, but a decline was observed as the proportion of exotic genes increased; similar to a previously study (Ceruiyot et al., 2018).

The total protein, casein, and whey proteins were significantly affected by genetic groups (P<0.05); which is in line with Abraham and Gayathri (2015). TP, CN, and W were higher in the lower exotic gene group and decreased with increasing exotic gene levels. The total value of protein previously reported was 40 mg/ml by Cozma et al. (2011) for milk from Romanian cows and 39.10 mg/ml by Neide et al. (2020) for skim milk in Brazil. This result is higher than the 30.15 mg/ml found in the >87.50% and lower than the 47.21 mg/ml found in the ≤ 50% genetic group of cows in this study. The content of casein previously reported was 28.26 mg/ml by Cozma et al. (2011), 32.66 mg/ml by Maurmayr et al. (2018), and 28.36 ml/ml by Amalfitano et al. (2020), all the reported values being less than ≤ 50% group of cows (37.77 mg/ml), while greater than 25.61 mg/ml was found in the >87.5% group of cows in this study. Jabeen et al. (2020) reported 4.91g (49.1 mg/ml) using acid precipitation methods in cow's milk in Pakistan; this is greater than the current study reported for all genetic groups. The value of whey protein previously reported was 6.99 mg/ml by Maurmayr et al. (2018) and 5.42 mg/ml by Amalfitano et al. (2020); both reported results lower than 9.44 mg/ml found in ≤ 50% and higher than 4.54 mg/ml found in >87.5% of cows in this study. The variation between the different reports could be attributed to the management type and level, exotic breed, environment and animal factors among others.

Effect of Lactation Length

Lactation length had a significant (P < 0.05) impact on TDMY, P, F, SNF, TS, TP, CN, and W in this study. The test-day milk yield was low during early lactation and extended lactation, with the highest test-day milk yield occurring in mid-lactation, in accordance with Cardak (2016) and Sabek et al. (2021). Fat percentage was high during early and late lactation; this aligns with Cardak (2016) but contradicts Sabek et al. (2021), who reported that the fat percentage increased with increasing lactation length. The variation among the results may be explained by the fact that fat is the most variable component among milk constituents and can easily be influenced by short-term feeding practices, regardless of the stage of lactation. Solids-not-fat increased with increasing lactation length; this result agrees with Jozwik et al. (2012) and Sabek et al. (2021), who recorded higher SNF in the mid-lactation of milk than in early lactation. Lactose was not significantly affected by lactation length; this aligns with Cardak (2016).

Effect of Calving Season

The calving season significantly impacted test-daily milk yield; this is similar to what Tadesse and Dessie (2003) observed in Ethiopia for the daily milk yield of Holstein Friesians and their crosses. According to Sipahi (2022), there was a seasonal effect on the test-day milk yield of Holstein Friesian cows in Turkey. Although milk yield was high during the rainy season, Desyibelew and Wondifraw (2019) reported higher levels of the milk constituents during the dry season; this is similar to the current study except for lactose and density; all milk constituents are numerically high, which may be due to the low water content of the feed. The percentages of SNF, lactose, total protein, casein, salt, and freezing point were significantly affected by the calving season, except for protein, fat, density, total solids, and whey.

Effect of Calving Year

The year of calving had a significant effect on all the studied milk production traits except lactose (P<0.05). Tadesse and Dessie (2003), Beneberu et al. (2020), and Getahun et al. (2020) reported that the calving year significantly affected daily milk yield in Holstein Friesians and their crosses in Ethiopia; this is similar to this study. However, Verma et al. (2016) found that the calving year did not affect test-day milk yield. The variation in test day milk yield observed across years reflects the level of management as well as environmental effects. Test day milk yield in 2022 was higher than in 2020 and 2021, which probably indicates that management conditions have improved over the years due to experiential learning. The year of calving had a significant effect (P<0.05) on all milk composition traits except lactose. Similar findings were reported for the effect of calving year on milk composition in different cattle breeds (Nyamushamba et al., 2014; Verma et al., 2016).

Effects of Lactation Number

Lactation number is one of the important non-genetic sources of variation in milk yield. This study shows that lactation number significant affected test-day milk yield (P<0.05). The test day milk yield from cows in the second lactation was higher than those in the first, third, and fourth and above

Vet Integr Sci *Bekele et al. Vet Integr Sci. 2023; 21(3): 717 - 733*

729

lactation number; this perhaps suggests most of the cows in this study reach peak milk production during the second lactation. This result is similar to the previous findings of Tadesse and Dessie (2003) and Sabek et al. (2021), who reported that the trend of test day milk yield increased from lactation number one to lactation number three and slightly decreased from lactation number three to lactation number four and above. The first lactation cows produce low test day milk yield, which might indicate the maturity of the mammary gland and the growth of the udder of the cows. Lactation number significantly (P< 0.05) affected the percentages of fat, SNF, total solids, salt, and freezing points. Fat was higher in cows in lactation one and four and above. Therefore, cows' first and fourth and above lactation numbers produced milk richer in fat. SNF and TS were high in the first lactation number and tended to decrease in the second, with a slight increase again in the fourth and higher lactation numbers.

Correlation Between Test Day Milk Yield and Milk Composition Traits

The correlation coefficient among milk production traits ranges from positive 0.05 to 1.00 and negative 0.02 to 8.8. Test-day milk yield was strongly and inversely correlated with fat percentage and milk proteins. SNF, density, and TS were positively correlated with test-day milk yield. Protein percentage correlated strongly and positively with F, TP, CN, and W while negatively correlated with SNF, density, and TS. The fat percentage had a strongly positive correlation with P, TP, CN, and W and was negatively correlated with SNF, density, and TS. However, the traits that showed a direct negative correlation indicate that an increase in one trait tends to decrease the other. The correlations reported here are all phenotypic. Depending on the available data, analyzing for genetic correlation will provide a basis for selection.

CONCLUSIONS

The performance level of cows belonging to different genetic groups and kept on farms has been investigated by measuring milk production and composition traits; cows with a higher exotic blood-level performed better than those with lower. Based on the results, it is concluded that higher levels of exotic breeds would be better suited for the liquid milk market, as current milk prices are often based on milk volume. On the other hand, crossbred cows (50% exotic genes) produce low milk with higher fat content. Thus, this group of animals will be preferred for low-input dairy systems and those away from the milk market, where household butter production and marketing are the norms. As a follow-up to this study, it would be essential to have a repeated measurement (at least three times during lactation) to have a complete picture of the genetic group's performance.

Vet Integr Sci Bekele et al. Vet Integr Sci. 2023; 21(3): 717 - 733

730

AUTHOR CONTRIBUTIONS

Corresponding author participated in the collection, analysis and interpretation of data, as well as the writing of the manuscript. All authors have participated in the conception and design of this work, in the research report editing and reviewing of the article, and in the decision to submit the article for publication.

CONFLICT OF INTEREST

The authors declare that they have no known competing interests that could have appeared to influence the work reported in this paper.

REFERENCES

Abraham, B.L., Gayathri, S., 2015. Milk composition of crossbred and desi cattle maintained in the sub-tropical high ranges of kerala. Ind. J. Vet. Anim. Sci. Res. 44(1), 53-55.

Alexander, D.H., Novembre, J., Lange, K., 2009. Fast model-based estimation of ancestry in unrelated individuals. Genome. Res. 19(9), 1655-1664.

Amalfitano, N., Stocco, G., Maurmayr, A., Pegolo, S., Cecchinato, A., Bittante, G., 2020. Quantitative and qualitative detailed milk protein profiles of 6 cattle breeds: Sources of variation and contribution of protein genetic variants. J. Dairy. Sci. 103(12), 11190-11208.

Amenu, B., Deeth, H., 2007. The impact of milk composition on cheddar cheese manufacture. Aust. J. Dairy. Technol. 62(3), 171-184.

Asimwe, L., Kifaro, G.C., 2007. Effect of breed, season, year and parity on reproductive performance of dairy cattle under smallholder production system in Bukoba district, Tanzania. Livest. Res. Rural. Dev. 19(10).

Assan, N., 2014. Factors affecting yield and milk composition in dairy animals. Academic Publishing, United Kingdom, pp. 129-132.

Beneberu, N., Shibabaw, W., Getahun, K., Alemayehu, K., 2020. Effect of non-genetic factors on milk production traits of pure jersey dairy cattle in Central Highland Ethiopia. Food sci. qual. manag. 103, 7-12.

Bondan, C., Folchini, J.A., Noro, M., Quadros, D.L., Machado, K.M., González, F.H.D., 2018. Milk composition of holstein cows: a retrospective study. Ciencia Rural. 48(12), 565–576.

Britt, J.H., Cushman, R.A., Dechow, C.D., Dobson, H., Humblot, P., Hutjens, M.F., Jones, G.A., Mitloehner, F.M., Ruegg, P.L., Sheldon, I.M., Stevenson, J.S., 2021. Review: Perspective on high-performing dairy cows and herds. Animal. 15, 100298.

Cardak, A., 2016. Effects of somatic cell count, parity and lactation stage on yield and components of milk in holstein-friesian cows. Harran. Üniv. Vet. Fak. Derg. 5(1), 34-39.

Cheruiyot, E.K., Bett, R.C., Amimo, J.O., Mujibi, F.D.N., 2018. Milk composition for admixed dairy cattle in Tanzania. Front. Genet. 9, 142.

Chebo, C., Alemayehu, K., 2012. Trends of cattle genetic improvement programs in Ethiopia: challenges and opportunities. Livest. Res. Rural. Dev. 24(7), 1–17.

Cozma, A., Andrei, S., Miere, D., Filip, L., Loghin, F., 2011. Proteins profile in milk from three species of ruminants. Not. Sci. Biol. 3(1), 26-29.

Desyibelew, W., Wondifraw, Z., 2019. Evaluation of milk composition in zebu× hf crossbred dairy cows in different seasons and stage of lactations in amanuel town. Ethiopia J. Agr. Sci. Food. Res. 10(1), 6-9.

Duguma, B., 2022. Milk composition, traditional processing, marketing, and consumption among smallholder dairy farmers in selected towns of jimma zone, oromia regional state, Ethiopia. Food. Sci. Nutr. 10(9), 2879-2895.

Vet Integr Sci *Bekele et al. Vet Integr Sci. 2023; 21(3): 717 - 733*

731

Gebreyohanes, G., Yilma, Z., Moyo, S., Okeyo Mwai, A., 2021. Dairy industry development in Ethiopia: Current status, major challenges and potential interventions for improvement. ILRI, Nairobi, Kenya.

Getahun, K., Tadesse, M., Hundie, D., Tadesse, Y., 2020. Productive performance of crossbred dairy cattle. Ethiopia. J. Agric. Sci. 30(2), 55-65.

Haile, A., Joshi, B.K., Ayalew, W., Tegegne, A., Singh, A., Yilma, Z., 2008. Genetic evaluation of Ethiopian Boran cattle and their crosses with Holstein Friesian for milk constituent traits in central Ethiopia. J. Cell. Anim. Biol. 2(10), 171–176.

Jabeen, M., Anwar, M., Fatima, W., Saleem, A., Rehman, K., Masood, M., Iqbal, N., Anjum, S., Zafar, A.M., Aslam, N., 2020. Quantitative estimation of casein in different milk samples. Sci. j. anal. chem. 8(3), 107.

Jóźwik, A., Krzyzewski, J., Strzałkowska, N., Poławska, E., Bagnicka, E., Wierzbicka, A., Niemczuk, K., Lipińska, P., Horbańczuk, J.O., 2012. Relations between the oxidative status, mastitis, milk quality and disorders of reproductive functions in dairy cows - a review. Anim. Sci. Pap. Rep. 30(4), 297–307.

Kebede, E., 2018. Effect of cattle breed on milk composition in the same management conditions. J. Agric. Sci. 28(2), 53–63.

Krauspe, R., Scheer, A., 1986. Coomassie brilliant blue G-250 dye-binding technique for determination of autolytic protein breakdown in Euglena gracilis and comparison to other methods of autolysis measurement. Anal. Biochem. 153(2), 242–250.

Kuczyńska, B., Puppel, K., Gołębiewski, M., Wiśniewski, K., Przysucha, T., 2021. Metabolic profile according to the parity and stage of lactation of high-performance Holstein-Friesian cows. Anim Biosci. 34(4), 575–583.

Maurmayr, A., Pegolo, S., Malchiodi, F., Bittante, G., Cecchinato, A., 2018. Milk protein composition in purebred holsteins and in first/second-generation crossbred cows from swedish red, montbeliarde and brown swiss bulls. Animal. 12(10), 2214-2220.

Mekonen, T., Tolera, A., Nurfeta, A., Bradford, B., Yigrem, S., Vipham, J., 2022. Effects of pigeon pea leaves and concentrate mixture on feed intake, milk yield, and composition of crossbred dairy cows fed native pasture hay. Animal. 16(10), 100632.

MOA, 2019. Agricultural and rural transformation in Ethiopia obstacles, triggers and reform considerations policy working paper (Issue January).

Niozas, G., Tsousis, G., Malesios, C., Steinhöfel, I., Boscos, C., Bollwein, H., Kaske, M., 2019. Extended lactation in high-yielding dairy cows. II. Effects on milk production, udder health, and body measurements. J. Dairy Sci. 102(1), 811–823.

Nyamushamba, G.B., Chikwanda, D., Matondi, G.H.M., Marandure, T., Mamutse, J., Tavirimirwa, B., Banana, N.Y.D., Dhliwayo, M., 2014. The effect of non-genetic factors on milk yield and composition of Red Dane cattle in Zimbabwe. Livest. Res. Rural. Dev. 26(5), 17.

Ojango, J.M.K., Mrode, R., Rege, J.E.O., Mujibi, D., Strucken, E.M., Gibson, J., Mwai, O., 2019. Genetic evaluation of test-day milk yields from smallholder dairy production systems in Kenya using genomic relationships. J. Dairy Sci. 102(6), 5266–5278.

Oloo, R.D., Ekine-Dzivenu, C.C., Ojango, J.M., Mrode, R.A., Chagunda, M., Okeyo Mwai, A., 2022. Effects of breed exoticness, agro-ecological zone and their interaction on production and fertility traits of multibreed dairy cattle in Kenya. Available online: https://hdl.handle.net/10568/118429

Pragna, P., Archana, P.R., Aleena, J., Sejian, V., Krishnan, G., Bagath, M., Manimaran, A., Beena, V., Kurien, E.K., Varma, G., Bhatta, R., 2017. Heat stress and dairy cow: impact on both milk yield and composition. Int. J. Dairy Sci. 12(1), 1–11.

Ríos-Utrera, Á., Calderón-Robles, R.C., Galavíz-Rodríguez, J.R., Vega-Murillo, V.E., Lagunes-Lagunes, J., 2013. Effects of breed, calving season and parity on milk yield, body weight and efficiency of dairy cows under subtropical conditions. Int. J. Anim. Vet. Adv. 5(6), 226-232.

Rosell, S., 2011. Regional perspective on rainfall change and variability in the central highlands of Ethiopia, 1978-2007. Appl. Geogr. 31(1), 329–338.

Sahu, J., Bhonsle, D., Mishra, S., Khune, V.N., Dutta, G.K., 2018. Effect of parity on milk composition traits of kosali cows. J. Pharm. Innov. 7(7), 518–520.

Sehested, J., Gaillard, C., Lehmann, J.O., Maciel, G.M., Vestergaard, M., Weisbjerg, M.R., Mogensen, L., Larsen, L.B., Poulsen, N.A., Kristensen, T., 2019. Review: extended lactation in dairy cattle. Animal. 13(S1), A65–A74.

Vet Integr Sci Bekele et al. Vet Integr Sci. 2023; 21(3): 717 - 733

732

Sipahi, C., 2022. The Effect of Different Environmental Factors on Milk Yield Characteristics of Holstein Fresian Cattle Raised with Different Production Scale on Teke Region of Turkey. Sustainability. 14(21), 13802.

Sudhakar, K., Panneerselvam, S., Thiruvenkadan, A., Abraham, J., Vinodkumar, G., 2013. Factors effecting milk composition of crossbred dairy cattle in Southern India. Int. j. food agric. vet. sci. 3(1), 229-233.

Tadesse, M., Dessie, T., 2003. Milk production performance of Zebu, Holstein Friesian and their crosses in Ethiopia. Livest. Res. Rural. Dev. 15(3), 28–37.

Tadesse, M., Getahun, K., Hunde, D., Gelmessa, U., 2022. Analysis of the non-genetic factors influencing the performance of high-grade and inter se mated crossbred dairy cows at holetta dairy research farm, Ethiopia. J. Dairy. Foods. Home. Sci. 41(1), 38-42.

Verma, M.K., Sachdeva, G.K., Yadav, A.K., Gautam, S., Ali, M.M., Bindal, S., 2016. Effect of genetic and non-genetic factors on milk yield and milk constituents on sahiwal cattle. Indian. J. Anim. Res. 50(5), 808–810.

Verma, M.K., Sachdeva, G.K., Yadav, A.K., Gautam, S., Ali, M.M., Kumar, S., 2017. Effect of genetic and non-genetic factors on milk yield and milk constituents in Murrah buffalo. Indian. J. Anim. Res. 51(2), 387–390.

Yalew, B., Lobago, F., Goshu, G., 2011. Calf survival and reproductive performance of Holstein-Friesian cows in central Ethiopia. Trop. Anim. Health Prod. 43(2), 359–365.

Yang, L., Yang, Q., Yi, M., Pang, Z.H., Xiong, B.H., 2013. Effects of seasonal change and parity on raw milk composition and related indices in Chinese Holstein cows in northern China. J. Dairy Sci. 96(11), 6863–6869.

Yang, Y., Fan, W., Mao, Y., Yang, Z., Lu, G., Zhang, R., Zhang, H., Szeto, C., Wang, C. (2016). Bovine leukemia virus infection in cattle of China: Association with reduced milk production and increased somatic cell score. J. Dairy Sci. 99(5), 3688–3697.

Yasmin, I., Iqbal, R., Liaqat, A., Khan, W.A., Nadeem, M., Iqbal, A., Chughtai, M.F.J., Rehman, S.J.U., Tehseen, S., Mehmood, T., Ahsan, S., Tanweer, S., Naz, S., Khaliq, A., 2020. Characterization and comparative evaluation of milk protein variants from Pakistani dairy breeds. Food. Sci. Anim. Resour. 40(5), 689-698.

Yoseph, D., Didanna, H.L., Ayza, A., 2022. Household characteristics, production and quality of bovine milk from crossbred dairy stock in the rural dairy production system of Ethiopia. J. Agric. Res. 10, 100453.

Zemarku, Z., Senapathy, M., Bojago, E., 2022. Determinants of adoption of improved dairy Technologies: the case of Offa Woreda, Wolaita Zone, Southern Ethiopia. Adv. Agric. 2022, 35–49.

How to cite this article;

Rekik Bekele, Mestawet Taye, Girma Abebe and Selam Meseret. Genetic and non-genetic factors affecting test day milk yield and milk composition traits in crossbred dairy cattle in Ethiopia. Veterinary Integrative Sciences. 2023; 21(3): 717 - 733.

Vet Integr Sci *Bekele et al. Vet Integr Sci. 2023; 21(3): 717 - 733*

733