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Estimates of Heritabilities of Milk Fat and Milk Protein and Their Correlations with Milk Yield in Sahiwal Cattle of Punjab Pakistan

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ABSTRACT

This study aimed to estimate the genetic parameters for lactation milk yield (LMY), lactation fat yield (LFY), and lactation protein yield (LPY) in the Sahiwal cattle breed of Pakistan. Performance data of 3364 purebred Sahiwal cattle with 9964 herd test records were collected from the public and/or private herds. Various edits were applied, such as herd test day records < 3, unknown calving and drying dates, etc., which reduced the data set to 1039 animals with 4489 herd test records. Lactation yields for milk, fat, and protein were calculated using the test interval method. Preliminary data analysis was performed using PROC MIXED in SAS. The animal model under the REML method was used to estimate the genetic parameters of the milk yield, milk fat, and milk protein. A multivariate model (3-traits) was fitted, which included the fixed effects of parity besides random effects of herd-year-season of calving (HYS), animal and residuals for all three traits. Mean ± SD (kg) of LMY, LFY, and LPY were 1444.07±554.51, 60.48±25.18, and 48.26±19.39, respectively. Parity and HYS significantly varied ($p<0.05$) among cows for all investigated production traits. The estimates of heritabilities with their standard errors for LMY, LFY, and LPY were 0.164±0.065, 0.124±0.061, and 0.181±0.067, respectively. The phenotypic and genetic correlations were high among all three production traits, which ranged between 0.879 to 0.975 and 0.990 to 0.999, respectively, with standard errors ranging from 0.002 to 0.03. Low to moderate heritability estimates for milk component traits obtained in the present study suggest that these traits could be improved through genetic selection.

Keywords: bovine milk fat; bovine milk protein; heritability; Punjab Pakistan; Sahiwal cattle

INTRODUCTION

In Pakistan, almost all cattle breeds are usually raised for draught and/or beef purposes, with the exception of Red Sindhi, Cholistani, and Sahiwal cattle, as these are established as dairy breeds. The production system in Pakistan is usually extensive but with low input. Crossbreds are usually raised under high-input extensive systems at dairy farms to fulfill the demands of the milk, especially in summer when buffalo milk production is quite low. All the local cattle breeds of Pakistan are humped and belong to the *Bos indicus* species. There are several breeds in the country, but Sahiwal and Cholistani cattle are recognized internationally because of their potential as dairy animals. Sahiwal cattle are being sold internationally as pure and crossbred cattle by different countries (Khan, 2022).

Sahiwal is considered as one of the main dairy breeds of Pakistan. It is the Zebu dairy breed with excellent heat and disease-resistant properties. In Sahiwal cattle, the estimates of genetic parameters can be obtained more precisely if the pedigree and performance data related to these traits are recorded accurately. There exists genetic variation related to the milk production in cows, suggesting that the milk yield in Sahiwal cattle can be increased through 2 stages selection approach, the first on the basis of SNP and then on the basis of the first lactation 305d yield (Worku *et al.*, 2022).

Separation of the component of genetic variation from the environmental variation is one of the most difficult steps in the genetic improvement program (Falconer, 1996). The use of a mixed model is a common technique to separate the genetic and the environmental components by estimating environmental effects that are treated as fixed effects and the breeding values of the animals that are treated as random effects (Campos *et al.,* 2015). The use of estimated breeding values as a selection criterion for genetic improvement depends upon the accuracy of these estimated breeding values. The strength of the relationship between the estimated and true breeding values is estimated through the correlation that indicates the accuracy of the estimated breeding values. If the heritability and the correlation that are the genetic parameters are not estimated accurately, then the accuracy of the resulting estimated breeding values will also be not accurate (Daetwyler *et al.,* 2013).

Different genetic improvement programs based on milk yield in buffalo and Sahiwal cattle are ongoing in the country. Research Center for Conservation of Indigenous Breeds (RCCIB) Jhang is leading the genetic improvement program of Sahiwal cattle with selection criteria only based on milk yield. Genetic parameters for milk yield, fat, and protein have already been reported for other breeds (Battagin *et al.,* 2013; Sneddon *et al.,* 2015). However, limited information is available related to the genetic parameters of milk fat and milk protein in Sahiwal cattle. The present study was planned to fill this literature gap. Therefore, the objective of the study was to estimate the genetic parameters for milk, fat, and protein yields based on 305 days of lactation in Pakistani Sahiwal cattle.

MATERIALS AND METHODS

Data Collection

There are five government farms where sufficient numbers of purebred Sahiwal cattle are present, and these farms are working in collaboration with the National Center for Livestock Breeding Genetics and Genomics (NCLBG&G). These farms include Livestock Experimental Station (LES), Khizarabad-Sargodha, LES, Jhangirabad-Khanewal, LES, Rakhghulama-Bhakkar, LES, Kalurkot-Bhakkar, Livestock Production Research Institute (LPRI), Bahadurnagar-Okara, and adjoining private herds. These farms are located in the semi-arid tropical regions of Punjab and generally have a semi-intensive production system.

Performance data of 3364 purebred Sahiwal cattle with 9964 herd test records were collected from the aforementioned herds between September 2020 and June 2022. Data were recorded by the official data recorder by visiting herds on a monthly basis. Samples were collected twice a day, i.e., in the morning and evening. Milk fat and protein percentages were determined using a Lactoscan (SP options) milk analyzer following manufacturer instructions.

Twenty-four hours of milk, fat, and protein yields were calculated as reported elsewhere (ICAR, 2022). In the case of cows with both the morning and evening milk yields recorded, the 24-hour milk yield was obtained by simply adding the morning and evening yields. However, for cows having only morning or evening milk records available due to any reason, the 24-hour milk yield was calculated as follows:

24-hour milk yield= factor * measured milk yield + covariate * (days in milk -158)

Factor and covariate values for morning and evening milking at 12 hours of the interval are 2.000 and 0.000, respectively (ICAR, 2022).

As the fat percentage is affected by the time interval between the milk recordings, the daily fat percentage was calculated with the help of the following equation:

Daily fat percentage= factor for fat percentage * measured fat percentage

The factor value for morning and evening milking at 12 hour of interval is 1.000 (ICAR, 2022).

Where morning fat & protein percentages were given, morning percentages were preferred over the evening for the sake of convenience, and daily fat and protein yield were calculated with the help of the following equations:

DFY = DMY * daily fat percentage
DPY = DMY * daily protein percentage (ICAR, 2022).

Data Editing

Data were subject to editing based on various factors. Editing criteria of all three traits for analysis are specified in (Table 1). For the computation of 305-day lactation yields (kg) of milk, fat, and protein, only cows having at least 3 herd test day records were used. Records on animals with unknown calving and drying dates were also not considered. Furthermore, all duplicate records were removed. Records with < 60 days of lactation were not included and those animals whose lactation milk yield was < 500 kg were also removed. After editing the data, 1039 animals remained.

Lactation yields for all 3 traits, i.e., milk, fat, and protein, were computed from the test day records using the test interval method (ICAR, 2020). The test interval method is believed to be the most authenticated method for calculating lactation yields. The time interval between the successive test records was approximately 35 days. First recordings were taken at least 4 days post-parturition. Lactations of diseased animals and/or those receiving any antibiotic therapy were not included in the analysis.

Lactation milk yield (kg) was calculated using the following equation:

$$LMY = I_0M_1 + I_1 * (M_1 + M_2)/2 + I_2 * (M_2 + M_3)/2 + I_{n-1} * (M_{n-1} + M_n)/2 + I_nM_n \text{ (ICAR, 2020).}$$

Where M_1, M_2, and M_n were the weights of milk yield recorded in 24 hours and given to one decimal place; I_1, I_2, and I_{n-1} were the intervals between recording dates; I_0 was the interval between the start date of the lactation period and the first milk recording date; and I_n was the interval from the last milk recording date to the end of the lactation.

Table 1. Editing detail for all three traits of lactation milk yield, lactation fat yield, and lactation protein yield

Serial No.	Editing criteria	Animals removed	Records removed	Animals remaining	Records remaining
1	Animals with less than 3 HTDs	1797	2276	1567	7688
2	Animals with unknown calving and drying dates and non-consecutive HTDs	462	2569	1105	5119
3	Duplicate records	21	87	1084	5032
4	< 500kg milk production and outliers	45	143	1039	4889

Note: HTDs= herd-test-day records.

Lactation fat yield (kg) was calculated using the following equation:

$$LFY= I_0F_1 + I_1* (F_1 + F_2)/2 + I_2 * (F_2 + F_3)/2 + I_{n-1} * (F_{n-1} + F_n)/2 + I_nF_n \text{ (ICAR, 2020).}$$

Where F_1, F_2, and F_n were the weights of the fat yield calculated by multiplying the milk yield with fat percentage.

Lactation protein yield (kg) was calculated using the following equation:

$$LPY= I_0P_1 + I_1* (P_1 + P_2)/2 + I_2 * (P_2 + P_3)/2 + I_{n-1} * (P_{n-1} + P_n)/2 + I_nP_n \text{ (ICAR, 2020).}$$

Where P_1, P_2 and P_n were the weights of the protein yield calculated by multiplying the milk yield with protein percentage.

Details about the pedigree of animals with records are provided in Table 2. A total of 2058 animals were in the pedigree file. There were a total of 178 sires and 260 dams in the pedigree file. As many as 785 animals had paternal grand sire and 190 animals had paternal grand dam. There were also 154 animals having maternal grandsire and 66 having maternal grand dam.

Table 2. Pedigree structure of animals

Serial No.	Details of the animals	No. of animals
1	Original no. of animals	2058
2	No. of animals after pruning	1350
3	No. of animals with records	1039
4	No. of animals without records	311
5	No. of animals with unknown sire	260
6	No. of animals with unknown dam	913
7	No. of animals with both parents unknown	244
8	No. of sires	178
9	No. of sires with progeny in the data	168
10	No. of dams	260
11	No. of dams with progeny in the data	254
12	No. of animals with paternal grand sire	785
13	No. of animals with paternal grand dam	190
14	No. of animals with maternal grand sire	154
15	No. of animals with maternal grand dam	66

Statistical Analysis

For phenotypic parameter estimates, data were statistically analyzed in SAS on Demand for Academics (www.oda.sas.com) using the PROC MIXED procedure for LMY, LFY, and LPY traits. There were 9 classes of parity and the parity 9 & above were merged into the 9th class of parity. There were 24 HYS levels based on the 6 herds, 2 years, and 2 seasons of calving. A statistical model that was used for milk, fat, and protein yield traits is as follows;

$$Y_{ijk} = \mu + P_i + HYS_j + E_{ijk}$$

Where Y_{ijk} is a 305-day measurement of milk yield or milk fat or milk protein traits of the k^{th} cow belonging to j^{th} herd-year-season class and to i^{th} parity class; μ represents the overall population mean; P_i is the fixed effect of the i^{th} parity (i=9 classes, i.e., 1 to 8 for cows in respective parities whereas 9 for all cows in parity 9 and above); HYS_j refers to the fixed effect of the j^{th} herd-year-season (j=24 classes); and E_{ijk} is the random residual associated with each record.

Heritabilities, as well as phenotypic and genotypic correlations, were estimated for milk yield, milk protein, and milk fat in an animal model under the REML method using WOMBAT software (Meyer, 2007). Parity was treated as a fixed effect, whereas the HYS were treated as random effects in the model for analysis. The following statistical model was used for milk, fat, and protein yield traits;

$$Y_{ijk} = \mu + P_i + HYS_j + Animal_k + E_{ijk}$$

Where Y_{ijk} is a 305-day measurement of milk yield, milk fat, and milk protein traits of the k^{th} cow in the j^{th} herd-year-season class (24 levels) and i^{th} parity class (9 levels). Here, μ represents the overall population mean; P_i is the fixed effect of the i^{th} parity, whereas HYS_j refers to the random effect of the j^{th} herd-year-season. $Animal_k$ is the random additive genetic effect of the k^{th} animal assumed to be distributed as $N \sim (0, \mathbf{A}\sigma^2_a)$, where **A** is the additive genetic relationship matrix among animals and σ^2_a is additive genetic variance; E_{ijk} is the random residual associated with each record, assumed to be normally distributed $N \sim (0, \mathbf{I}\sigma^2_e)$, where **I** is the identity matrix and σ^2_e is residual variance.

RESULTS

Descriptive Statistics

Descriptive statistics of all three traits are given in Table 3. For LMY, LFY, and LPY, mean ± SD (expressed in kilograms) were 1444.07±554.51, 60.48±25.18, and

48.26±19.39, respectively. Average milk fat and protein percentages were 4.18 and 3.33.

Effect of Parity

The cows' parities ranged from 1 to 8, with the last ninth class having cows in parity nine and above. The lactation yields of milk, fat, and protein yield differed significantly ($p<0.05$) among cows for different parities. Least-square estimates of means of LMY, LFY, and LPY for different classes of parity, along with their standard errors, are presented in Table 4. Least-square means of parities ranged from 1216.70 to 1580.15, 49.18 to 64.58, and 41.32 to 53.54, for LMY, LFY, and LPY, respectively.

There was an upward trend for LMY, LFY, and LPY. Milk, fat, and protein yields showed a gradual increase in production with the advanced parities. The daily milk yields were increasing gradually from 1st to 4th lactation, and the parity had a significant effect on the daily milk yield, fat, and protein percentages.

Effect of Herd-Year-Season (HYS)

Overall, there were 24 levels of HYS based on 2 years, 2 seasons, and 6 herds, and the frequencies of all HYS levels are presented in Table 5. HYS was taken as a contemporary group in the analysis. The effect of the HYS contemporary group was significant ($p<0.05$) for milk yield, fat yield, and protein yield. The least-square means (kg) of HYS for LMY, LFY, and LPY ranged from 866.1 to 1897.23, from 35.65 to 73.97, and from 28.12 to 63.47, respectively.

Estimates of Heritabilities

Results of the effect of treating HYS as random on variance components of animal, residual, and phenotypic are given in Table 6. Estimates of heritabilities, along with their standard errors obtained from multivariate analysis of all three production traits, are also given. These estimates of heritability for LMY, LFY, and LPY were 0.164±0.065, 0.124±0.061, and 0.181±0.067, respectively.

Phenotypic and Genetic Correlations Estimates

Phenotypic and genetic correlations of all three production traits are given in Table 7. Among the reported estimates, the highest phenotypic correlation was obtained between the LMY and LPY (0.975±0.002), and the lowest phenotypic correlation was between the LFY and LPY (0.879±0.007). LMY and LFY had a moderate correlation estimate as compared to the correlation estimate between LMY and LPY. Overall, the phenotypic correlations among all three traits are positive and high, indicating strong positive relations among the traits under study.

DISCUSSION

Descriptive Statistics

Average milk yield was a little higher compared to earlier reports by Bilal *et al.* (2008), probably due to the different data sizes and inclusion of cows from many different herds. Average milk and protein percentages are a little higher compared to the percentages reported earlier by Salfer *et al*. (2019) for bovine milk fat and protein (3.73 and 3.10). Fat and protein percentages reported by Mohammadi *et al*. (2014) were lower (3.35 & 3.06, respectively) than our findings.

Effect of Parity

The results of this study indicated that the LMY, LFY, and LPY increased gradually from the first lacta-

Table 3. Overall mean ± SD of lactation milk yield, lactation fat yield, and lactation protein yield in Sahiwal cattle of Punjab, Pakistan

Serial No.	Traits	No.	Mean ± SD	Min	Max	C.V. (%)
1	LMY (kg)	1039	1444.07 ± 554.51	504.75	3356.50	38.40
2	LFY (kg)	1039	60.48 ± 25.18	15.05	152.67	41.64
3	LPY (kg)	1039	48.26 ± 19.39	12.62	119.66	40.19
4	Fat (%)	1039	4.18 ± 0.714	1.789	7.936	17.08
5	Protein (%)	1039	3.33 ± 0.28	1.920	4.798	8.40

Note: SD= Standard deviation, C.V. (%)= Coefficient of variation, LMY= Lactation milk yield, LFY= Lactation fat yield, LPY= Lactation protein yield.

Table 4. Lactation milk yield (kg), lactation fat yield (kg), and lactation protein yield (kg) from 1,039 Sahiwal cows milk samples from Punjab, Pakistan originating from several parities

Traits	Least square means (± SE)									
	Parity 1 (N=249)	Parity 2 (N=180)	Parity 3 (N=145)	Parity 4 (N=165)	Parity 5 (N=108)	Parity 6 (N=87)	Parity 7 (N=55)	Parity 8 (N=29)	Parity 9 (N=21)	Overall *p* value
LMY	1216.70 ± 38.01^{a}	1396.85 ± 46.49^{b}	1329.11 ± 51.45^{abc}	1435.85 ± 49.23^{bcd}	1386.00 ± 57.71^{abcde}	1580.15 ± 62.98^{bdef}	1457.51 ± 75.75^{abcdefg}	1376.17 ± 100.75^{abcdefgh}	1354.70 ± 117.84^{abcdefgh}	<.0001
LFY	49.18 ± 1.71^{a}	57.64 ± 2.09^{b}	55.13 ± 2.32^{abc}	59.32 ± 2.22^{bcd}	57.51 ± 2.60^{abcde}	64.58 ± 2.83^{bcdef}	60.02 ± 3.41^{abcdefg}	55.87 ± 4.53^{abcdefgh}	54.13 ± 5.30^{abcdefgh}	<.0001
LPY	41.32 ± 1.34^{a}	46.63 ± 1.64^{ab}	44.59 ± 1.82^{abc}	47.89 ± 1.74^{bcd}	46.20 ± 2.04^{abcde}	53.54 ± 2.23^{bdef}	49.14 ± 2.68^{abcdefg}	45.68 ± 3.56^{abcdefgh}	44.02 ± 4.17^{abcdefgh}	0.000

Note: SE= Standard error, LMY= Lactation milk yield, LFY= Lactation fat yield, LPY= Lactation protein yield.

Table 5. Frequency and percentage of each of the 24 herd-year-season levels in Sahiwal cattle of Punjab, Pakistan

Serial No.	HYS	Frequency	Percent
1	120201	94	9.05
2	120202	99	9.53
3	120211	69	6.64
4	120212	31	2.98
5	120221	6	0.58
6	220201	70	6.74
7	220202	91	8.76
8	220211	89	8.57
9	220212	31	2.98
10	320201	77	7.41
11	320202	74	7.12
12	320211	60	5.77
13	320212	22	2.12
14	420201	47	4.52
15	420202	61	5.87
16	420211	28	2.69
17	420212	9	0.87
18	520201	20	1.92
19	520202	21	2.02
20	520211	21	2.02
21	520212	6	0.58
22	720201	3	0.29
23	720202	4	0.38
24	720211	6	0.58

Note: HYS= herd-year-season.

tion to the 6th lactation, with the exception of the 3rd and 5th lactation, where these traits took a slight dip in production but almost remained equal to the previous lactation production. These exceptions may be because of the smaller sample size. The production of milk, milk fat, and protein yield decreased gradually from lactation 7 onward.

Milk composition is affected by external factors that include the feeding, season, and milking frequency, and internal factors that include parity, genes, and stage of lactation. Fixed effects of the contemporary group of HYS of calving were common to all three traits (Dunne *et al.,* 2018). A study on the effect of parity on raw milk composition in Chinese Holstein cows by Yang *et al*. (2013) reported that the daily milk yield, fat yield, and protein yield are significantly affected by parity, which is in agreement with our findings. They reported lower daily milk and protein yield in the first lactation as compared to later lactations. The significant effect of parity on protein yield was reported by Sudhakar *et al*. (2013) but not on the fat and milk contents. Nonetheless, the present study showed a significant effect of parity on lactation milk yield along with the fat and protein yields.

Estimates of Heritabilities

These heritability estimates were greater than those presented by Bilal *et al.* (2008) for 305 days of milk production (0.082) based on data from 780 Sahiwal cows. These estimates of the heritabilities were lower for 305 days of milk yield than those reported by Wahinya *et al*. (2020), ranging from 0.22 to 0.35 obtained from different models. Estimates of heritability for LMY, LFY, and LPY were almost similar to the results reported by Sneddon *et al*. (2015), i.e., 0.22, 0.19, and 0.16, respectively, and obtained from bivariate analysis. These were much lower in the univariate analysis (0.19, 0.12, and 0.13, respectively) from 4378 cows. Heritability for LMY and LPY were higher than those reported by Battagin *et al*. (2013) (0.108 and 0.163 for milk and protein yield, respectively), but the heritability for LFY was lower than that of 0.25. In a study by Lembeye *et al*. (2016), the heritability for milk, fat, and protein yields reported were in the ranges between 0.33 to 0.36, 0.21 to 0.26, and 0.22 to 0.25, respectively. These heritability estimates were higher than our findings and that might be because of the large sample size in their study (124,620 to 194,631 milk records). Our heritability estimates for LMY and LFY were also less than those for milk yield and fat yield (0.21 & 0.24) reported by Campos *et al.* (2015), but the protein yield estimates were almost similar.

Heritabilities of the LMY, LFY, and LPY were low yet moderate and could be due to the limited number of samples used in the analysis as milk sample collection twice a day is cumbersome, laboring, time-consuming, and financially demanding because of scattered herds, especially in the context of developing countries where herd size is small and only a few numbers of Sahiwal animals are kept by the farmers. Better estimates would be possible to obtain than those reported in the present study by improving the accuracy and frequency of recording and completeness of pedigree.

Table 6. Estimates of variance components, heritability estimates, and permanent environments for 305- days of lactation in Sahiwal cattle of Punjab, Pakistan

Traits	σ^2 A	σ^2 E	σ^2 P	h^2 (± SE)
LMY	4860.4	22004.1	29625.8	0.164 ± 0.065
LFY	745.428	469.259	602.851	0.124 ± 0.061
LPY	658.565	269.632	364.248	0.181 ± 0.067

Note: σ^2 A= Variance component of animal, σ^2 E= Variance component of environment, σ^2 P= Variance component of phenotype, h^2= Heritability, SE= Standard error, LMY= Lactation milk yield, LFY= Lactation fat yield, LPY= Lactation protein yield.

Table 7. Estimate of phenotypic (above diagonal) and genetic (below diagonal) correlations with standard error among three traits on milk samples obtained from each of 1039 Sahiwal cattle of Punjab, Pakistan

Item	Traits	1	2	3
1	LMY		0.913 ± 0.005	0.975 ± 0.002
2	LFY	0.990 ± 0.029		0.879 ± 0.007
3	LPY	0.999 ± 0.006	0.994 ± 0.040	

Note: LMY= Lactation milk yield, LFY= Lactation fat yield, LPY= Lactation protein yield.

Phenotypic and Genetic Correlations Estimates

The estimates of genetic correlations were strong and positive among all three production traits. The predominant biological reason for the strong genetic correlation could be pleiotropy and linkage (Cai *et al.,* 2020). Our results of the genetic correlation are in agreement with the findings of Borquis *et al*. (2013), i.e., ranging from 0.11-0.99, 0.12-0.99, and 0.05-0.99 between milk, fat, and protein yields, respectively. However, estimates of phenotypic correlation were lower than our findings. There is also a trend that the genetic correlation is lower than the phenotypic correlation, but this was not the case in the present study. High positive phenotypic and genetic correlations between milk, fat and protein yields (0.7 between milk and fat yield, 0.87 between milk and protein yield, and 0.82 between fat and protein yield) on 4378 cows were reported earlier (Sneddon *et al.,* 2015). The trend of correlation was similar in both studies, but in our study, the values of phenotypic and genetic correlation were slightly higher. The high genetic correlation between milk yield and protein yield (0.84-0.85) reported by Lembeye *et al*. (2016) is similar to our findings for the correlation between these two traits. However, the genetic correlation between milk yield and fat yield was moderate in their study (0.35-0.4). The genetic correlation between milk yield and protein yield is 0.89, between milk yield and fat yield is 0.62, and between fat yield and protein yield is 0.72 in dairy cows, as reported by Pritchard *et al*. (2013). The phenotypic correlations were relatively higher than the genetic correlation for these traits in their study. Their results for the correlation between milk yield and protein yield were very similar to our findings for genetic and phenotypic correlations; however, they differed in the other two traits. The genetic correlation estimates among three production traits in the present study are very close to 1.0, probably due to the limited sample size; therefore, estimates may be used with extreme care and may be validated on rather large data before implementation in a breeding program.

CONCLUSION

Lactation milk fat and lactation milk protein displayed low to moderate values of heritabilities in the Sahiwal cattle population of Pakistan. Moreover, the heritabilities of the aforementioned two traits were similar to that of lactation milk yield. Therefore, genetic selection can effectively improve milk fat and milk protein yield in dairy cattle as per industry needs. Furthermore, strong positive phenotypic and genetic associations of lactation milk fat and protein yields with lactation milk yield obtained in the present study suggest that selection for milk yield would have an indirect positive effect on the lactation milk fat and protein yields. The results of the present study have useful implications not only for the genetic improvement of overall milk yield but also for milk components, i.e., fat and protein yields in dairy cattle.

CONFLICT OF INTEREST

We certify that there is no conflict of interest with any financial, personal, or other relationships with other people or organizations related to the material discussed in the manuscript.

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REFERENCES

Battagin, M., C. Sartori, S. Biffani, M. Penasa, & M. Cassandro. 2013. Genetic parameters for body condition score, locomotion, angularity, and production traits in Italian Holstein cattle. J. Dairy Sci. 96:5344-51. https://doi.org/10.3168/jds.2012-6352

Borquis, R. R. A., F. R. de A. Neto, F. Baldi, N. Hurtado-Lugo, G. M. de Camargo, M. Muñoz-Berrocal, & H. Tonhati. 2013. Multiple-trait random regression models for the estimation of genetic parameters for milk, fat, and protein yield in buffaloes. J. Dairy Sci. 96:5923-5932. https://doi.org/10.3168/jds.2012-6023

Bilal, G., M. Khan, I. Bajwa, & M. Shafiq. 2008. Genetic control of test-day milk yield in Sahiwal cattle. Pak. Vet. J. 28: 21-24.

Cai, Z., M. Dusza, B. Guldbrandtsen, M. S. Lund, & G. Sahana. 2020. Distinguishing pleiotropy from linked QTL between milk production traits and mastitis resistance in Nordic Holstein cattle. Genet. Sel. Evol. 52:1-15. https://doi.org/10.1186/s12711-020-00538-6

Campos, R. V., J. A. Cobuci, E. L. Kern, C. N. Costa, & C. M. McManus. 2015. Genetic parameters for linear type traits and milk, fat, and protein production in Holstein cows in Brazil. Asian-Australas. J. Anim. Sci. 28:476. https://doi.org/10.5713/ajas.14.0288

Dunne, F., M. M. Kelleher, S. Walsh, & D. Berry. 2018. Characterization of best linear unbiased estimates generated from national genetic evaluations of reproductive performance, survival, and milk yield in dairy cows. J. Dairy Sci. 101:7625-37. https://doi.org/10.3168/jds.2018-14529

Daetwyler, H. D., M. P. Calus, R. Pong-Wong, G. de Los Campos, & J. M. Hickey. 2013. Genomic prediction in animals and plants: simulation of data, validation, reporting, and benchmarking. J. Genet. 193:347-65. https://doi.org/10.1534/genetics.112.147983

Falconer, D. S. 1996. Introduction to Quantitative Genetics. 4th edition. Pearson Education India, Noida, Uttar Pradesh. https://welcome.oda.sas.com/ [June 15, 2022].

ICAR. 2022. Procedure 1 of Section 2 of ICAR Guidelines - Computing 24-hour Yields. https://www.icar.org/Guidelines/02-Procedure-1-Computing-24-Hour-Yield.pdf [May 28, 2022].

ICAR. 2020. Procedure 2 of Section 2 of ICAR Guidelines - Computing of Accumulated Lactation Yield. https://www.icar.org/Guidelines/02-Procedure-2-Computing-Lactation-Yield.pdf [May 20, 2022].

Khan, M. S. 2022. Cattle breeding in Pakistan – some policy options. J. Anim. Plant. Sci. 32:1168-1176. https://doi.org/10.36899/JAPS.2022.4.0522

Lembeye, F., N. López-Villalobos, J. Burke, & S. Davis. 2016. Estimation of genetic parameters for milk traits in cows milked once-or twice-daily in New Zealand. Livest. Sci. 185:142-147. https://doi.org/10.1016/j.livsci.2016.01.022

Mohammadi, A., S. Alijani, & H. Daghighkia. 2014. Comparison of different polynomial functions in random regression model for milk production traits of Iranian Holstein dairy cattle. Annals Animal Science 14:55-68. https://doi.org/10.2478/aoas-2013-0078

Meyer, K. 2007. WOMBAT—A tool for mixed model analyses in quantitative genetics by restricted maximum likelihood (REML). J. Zhejiang Univ. Sci. B 8:815-21. https://doi.org/10.1631/jzus.2007.B0815

Pritchard, T., M. Coffey, R. Mrode, & E. Wall. 2013. Genetic parameters for production, health, fertility and longevity traits in dairy cows. Animal **7**:34-46. https://doi.org/10.1017/S1751731112001401

Salfer, I. J., C. D. Dechow, & K. J. Harvatine. 2019. Annual rhythms of milk and milk fat and protein production in dairy cattle in the United States. J. Dairy Sci. 102:742-753. https://doi.org/10.3168/jds.2018-15040

Sneddon, N., N. Lopez-Villalobos, S. Davis, R. Hickson, & L. Shalloo. 2015. Genetic parameters for milk components including lactose from test day records in the New Zealand dairy herd. New Zealand Journal Agricultural Research 58:97-107. https://doi.org/10.1080/00288233.2014.978482

Sudhakar, K., S. Panneerselvam, A. K. Thiruvenkadan, J. Abraham, & G. Vinodkumar. 2013. Factors effecting milk composition of crossbred dairy cattle in Southern India. International Journal Food, Agriculture Veterinary Sciences 3:229-233.

Worku, D., G. Gowane, R. Alex, P. Joshi, & A. Verma. 2022. Inputs for optimizing selection platform for milk production traits of dairy Sahiwal cattle. PLoS ONE 17:e0267800. https://doi.org/10.1371/journal.pone.0267800

Wahinya, P., M. Jeyaruban, A. Swan, A. Gilmour, & T. Magothe. 2020. Genetic parameters for test-day milk yield, lactation persistency, and fertility in low-, medium-, and high-production systems in Kenya. J. Dairy Sci. 103:10399-413. https://doi.org/10.3168/jds.2020-18350

Yang, L., Q. Yang, M. Yi, Z. Pang, & B. Xiong. 2013. Effects of seasonal change and parity on raw milk composition and related indices in Chinese Holstein cows in northern China. J. Dairy Sci. 96:6863-6869. https://doi.org/10.3168/jds.2013-6846