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Kapil Dev

Veterinary Surgeon, Department of Animal Husbandry & Dairying, Haryana, India

Manjeet

Veterinary Surgeon, Haryana Veterinary Training Institute, Hisar, Haryana, India

SS Dhaka

Professor, Department of Animal Genetics and Breeding, Lala Lajpat Rai University of Veterinary and Animal Sciences, Hisar, Haryana, India

AS Yadav

Professor & Head, Department of Animal Genetics & Breeding, Lala Lajpat Rai University of Veterinary and Animal Sciences, Hisar, Haryana, India

CS Patil

Assistant Professor, Department of Animal Genetics & Breeding, Lala Lajpat Rai University of Veterinary and Animal Sciences, Hisar, Haryana, India

Corresponding Author Kapil Dev Veterinary Surgeon, Department of Animal Husbandry & Dairying, Haryana, India

Estimates of genetic and phenotypic correlation among production performance and test day milk records in Hardhenu crossbreed cattle

Kapil Dev, Manjeet, SS Dhaka, AS Yadav and CS Patil

Abstract

Data from 1997 to 2016, pertaining to production performance traits and test day milk record from TD1 TO TD₁₀ on 862 Hadhenu cattle sired by 63 were collected from history cum pedigree sheets maintained at Cattle Breeding Farm (CBF), Lala Lajpat Rai University of Veterinary and Animal Sciences, Hisar over a period of 20 years from 1997 to 2016. Analysis of variance done by restricted maximum likelihood method of Harvey (1990) using mixed linear model in which fixed effect of period, season of calving and random effect of parity was taken into consideration. The genetic and phenotypic correlations among production performance traits were low to high ranged from -0.70 (LL and DP) to 0.99 (LMY-305 and SP) and -0.55 (MSC and DP) to 0.96 (LMY and LMY-305). The genetic and phenotypic correlations of MSC with all production performance traits were moderate to high ranged from 0.28 (SP) to 0.90 (LMY) and 0.28 (SP) to 0.90 (AMY), respectively barring some exceptions. The genetic and phenotypic correlations among test day milk yields ranged were positive and high. The highest correlations were found between contiguous test day milk records and the correlations decreased as interval between tests days increased. Genetic correlations between test day milk records and production performance traits were positive and low to high ranged from 0.01 to 0.99 except negative association ship of AFC with all test day milk records ranged from -0.38 to -0.16. Estimates of phenotypic correlations of test day milk records with all production performance traits (LMY, LMY-305, LL, PY, AMY, MCI and MSC) were significant (p<0.01), high and positive barring few exceptions. Critical appraisal among genetic and phenotypic correlations between production performance traits, it may be inferred that selection based on milk yield per day of age at second calving that had high estimates of heritability (0.50) and appreciably high genetic and phenotypic correlations with production performance traits, would not only improve production performance but also take care of reproductive performance.

Keywords: Crossbreed cattle, genetic factors, non-genetic factors, production performance traits

1. Introduction

India occupies pre-eminent position in milk production with an annual output of 165.40 million tonnes accounting for 18.5 per cent of world production. Out of which, share of milk production by exotic/crossbred cows was 25% and that of indigenous/non-descript was 20%. Out of the 190.90 million cattle population, crossbred population was 19.42 million while that of indigenous was 48.12 million (19th Livestock census). Crossing Zebu cattle (Bos indicus) with temperate breed (Bos Taurus), undertaken for improving the milk production to cater the needs of ever increasing human population has led to the synthesis of several new crossbred strains of cattle. During late nineties Frieswal bulls were also used on synthetic dams having a composition of Friesian and indigenous Haryana cattle at Lala Lajpat Rai University of Veterinary and Animal Sciences (LUVAS) formerly CCS, HAU, Hisar, animal farm. The principle objective was identification of superior breeding bulls and faster multiplication of their progenies in rural and urban farmers of Haryana state in particular and whole of country in general. Hardhenu, is a cross between North American Holstein Friesian, Haryana and Sahiwal breeds with an inheritance ratio of exotic to indigenous as 62.5%: 37.5%.

In fact, the economy of dairy industry mainly rely upon the performance parameters of dairy animals, therefore, it becomes more relevant to tackle out the means for ameliorating the performance parameters by developing certain guidelines for selection. In most of the genetic improvement programmes in the country selection has been focused on production traits and fertility performance of the animal has not been given the due emphasis. Though such selection would slow down the rate of improvement in productivity of dairy cattle, however such reduction can be more than compensated by simultaneous improvement in fertility traits. Further, multi trait selection has been advocated under Indian conditions due to small number of daughters per sire; as such selection will improve the accuracy and efficiency of sire evaluation (Sahana and Gurnani, 1999)^[28]. Therefore, including fertility along with production traits in sire evaluation would enable genetic improvement in production potential along with improvement in fertility traits. Critical appraisal among genetic and phenotypic correlations between production based on milk yield per day of age at second calving that had high estimates of heritability (0.50) and appreciably high genetic and phenotypic correlations with production performance traits, would not only improve production performance.

2. Materials and methods

The data on 862 crossbreed cattle pertaining to production performance traits up to five lactations were collected from history cum pedigree sheets maintained at Cattle Breeding Farm (CBF), Lala Lajpat Rai University of Veterinary and Animal Sciences, Hisar over a period of 20 years from 1997 to 2016 were analysed to study the genetic parameters. Animals having lactation shorter than 100 days, suspected outliers on the basis of histograms and abnormal records like abortion, mastitis and chronic illness were excluded from present study. Following production performance traits was recorded up to fifth lactations: LMY (Lactation milk yield in kg), LMY-305 (305 days milk yield in kg), LL (Lactation length in days), PY (Lactation peak milk yield in kg/day), AMY (Average daily milk yield = LMY/LL in kg/day), MCI (Milk yield per day of calving interval in kg/day), MSC (Milk yield per day of age at second calving in kg/day), persistency (Persistency in days), age at first calving (AFC), SP (Service period in days) and CI (Calving interval in days) and DP (dry period in days). In addition to this, Persistency (lactation milk yield/ peak yield) and test days of first lactation milk yield from TD₁ to TD₁₀ were also recorded. First test day milk yield was recorded from 7th day after calving and total of 10 test day milk records were taken at every 4 week interval viz., TD_1 to TD_{10} .

Assuming that there is not much variation in adjacent years, entire period of twenty years was divided into five equal periods from 1997-2000, 2001-2004, 2005-2008, 2009-2012 and 2013-2016. Each year was further delineated into 4 seasons of calving according to the prevailing agro-climatic conditions in the region viz., Summer (April to June), Rainy (July to September), Autumn (October to November) and Winter (November to March). In order to overcome nonorthogonally of the data due to unequal subclass frequencies, least squares and maximum likelihood computer program of Harvey (1990) was utilized to estimate the effect of various tangible factors on production performance traits. The following statistical model will be used to explain the underlying biology of the traits included in the study.

$Y_{ijklm} = \mu + S_i + P_j + C_k + R_l + e_{ijklm}$

Where, $Y_{ijklm} = m^{th}$ record of individual calved in jth period, kth season and lth parity pertaining to ithsire, μ = is the overall population mean, S_i = is the random effect of ith sire, P_j = is the fixed effect of jth period of calving, C_k = is the fixed effect of kth season of calving, R_1 = is the fixed effect of lth parity, e_{ijkl} = is the random error associated with each and every observation and assumed to be normally and independently distributed with mean zero and variance σ^2 e. The standard error of genetic correlation was estimated using formula given

by Robertson (1959) ^[27]. The standard error of phenotypic correlation was obtained by formula by Panse and Sukhatme (1967) ^[25].

3. Results and discussion

3.1 Among production performance traits

Genetic and phenotypic correlations among production performance traits indicated that LMY and LMY-305 had high genetic correlations with all production performance traits except negative association ship with AFC and DP. On the other hand, phenotypic correlations of LMY and LMY-305 with all the production performance traits were found to be low to high ranging from 0.08 (AFC) to 0.96 (LMY-305) and 0.06 (AFC) to 0.90 (MCI), respectively except moderately negative association ship with DP (Table 1). On the contrary, Mukherjee (2005) reported moderate estimates of genetic correlations of LMY with AFC and similarly, negative estimates of genetic correlations of LMY with AFC. While, low but negative estimates of genetic and corresponding phenotypic correlations were reported by Divya (2012) and Cayo et al. (2018) ^[13, 3]. On the other hand, corresponding high estimates of genetic and phenotypic correlations were obtained by Dash. Similarly, Lakshmi, et al. (2009) ^[19] and Singh et al. (2011) ^[19, 30] reported that the genetic and phenotypic correlation between lactation milk yield and lactational milk yield-305 was highest and significant in crossbred cattle. Likewise, Kumar (2000) ^[17] and Lakshmi, et. al. (2009)^[19] also reported significantly high genetic and phenotypic correlations between LMY and LL in crossbreed cattle. However, high genetic and phenotypic correlations between lactation milk yields (LMY) with peak yield (PY) were reported by Patond and Bhoite (2014) and Verma et al. (2016) ^[24, 31] in crossbreed cattle. Whereas, the genetic and corresponding phenotypic correlations between lactation milk yield and peak yield were low to moderate to the tune of 0.03 to 0.25 as reported by Lakshmi et al. (2009) ^[19]. Similarly, Dhawan *et al.* (2015) ^[12] reported moderate to high significant genetic and corresponding phenotypic correlations of LMY with AMY, MCI and MSC. However, Verma *et al* (2016) ^[24] also reported high genetic and phenotypic correlations of LMY with MSC. Seangjun *et al.* (2009) and Sahito *et al.* (2016) ^[28, 27] also reported moderate to high genetic correlations between LMY and persistency to the tune of 0.56 to 0.61 and corresponding phenotypic correlations to the tune of 0.38 in Sahiwal cross and Red-Sindhi cattle. Similarly, Deb, et al. (2008) [8] reported highly negative estimates of genetic correlation of LMY, LL and MCI with DP. Likewise, Singh et al. (2011) [19] reported similar high estimates of genetic and corresponding phenotypic correlations of LMY-305 with LL. Lakshmi et al. (2009) and Patond and Bhoite (2014) [19, 24] reported similarly moderate to high estimates of genetic and phenotypic correlations of LMY-305 with PY. Similar, estimates of genetic and phenotypic correlations of LMY-305 with AMY and MCI were reported by Dash in Karan-Fries cattle. Similarly, high genetic correlations of LMY-305 with persistency and moderate estimates of phenotypic correlations was reported by Boujenane and Hilal (2012)^[2] in H.F cattle. The positive association of LMY with SP explains that with increase in service period the phase of pregnancy will shift and thus production will increase. Since this association is not favourable, an optimum service period needs to be decided so that favourable trend in it does not adversely affect the production performance of individual.

 Table 1: Estimates of heritability (diagonal), genetic correlation (below diagonal) and phenotypic correlation (above diagonal) among various production performance traits

Trait	LMY	LMY-305	LL	PY	AMY	MCI	MSC	Persistency	AFC	SP	CI	DP
LMY	0.41 ± 0.11	0.96**±0.01	0.68**±0.10	0.52**±0.12	$0.80^{**\pm}0.05$	0.91**±0.08	$0.85^{**\pm 0.03}$	0.76**±0.17	0.08 ± 0.21	$0.42^{**\pm 0.62}$	0.44**±0.24	-0.27**±0.36
LMY-305	0.90 ± 0.01	0.36 ± 0.11	$0.54^{**\pm}0.14$	0.48**±0.13	$0.88^{*\pm}0.03$	$0.90^{**\pm}0.08$	$0.89^{*\pm}0.02$	$0.75^{*\pm}0.17$	0.06 ± 0.21	$0.28^{*}\pm 0.71$	0.29**±0.28	-0.29**±0.37
LL	0.79 ± 0.10	0.72 ± 0.14	0.26 ± 0.09	0.55 ± 0.15	0.15 ± 0.22	0.56**±0.17	0.36**±0.16	$0.50^{**\pm 0.24}$	0.07 ± 0.24	$0.66^{**\pm}0.40$	0.69**±0.17	-0.31**±0.44
PY	0.59 ± 0.12	0.58±0.13	0.42 ± 0.15	0.44±0.16	0.39**±0.15	0.51**±0.12	0.43**±0.14	-0.09 ± 0.20	$0.01{\pm}0.20$	$0.25*\pm0.51$	0.27**±0.26	-0.16 ± 0.28
AMY	0.93 ± 0.05	0.96 ± 0.03	0.50 ± 0.22	0.96 ± 0.03	0.30 ± 0.10	0.79**±0.09	0.90**±0.03	$0.64^{**\pm}0.20$	0.06 ± 0.20	0.02 ± 0.78	0.02 ± 0.36	-0.44 ± 0.37
MCI	0.75 ± 0.08	0.78 ± 0.08	0.48 ± 0.17	0.60 ± 0.12	0.76 ± 0.09	0.31±0.10	$0.83^{*\pm}0.10$	$0.66^{*}\pm 0.22$	0.09 ± 0.21	-0.07 ± 0.12	-0.08 ± 0.38	-0.09 ± 0.31
MSC	0.90 ± 0.03	0.50 ± 0.22	0.75 ± 0.16	0.59 ± 0.14	0.94 ± 0.03	0.73±0.10	0.50±0.12	$0.66^{**\pm}0.18$	-0.23*±0.19	$0.30^{*}\pm 0.88$	0.28**±0.28	-0.55 ± 0.44
Persistency	0.51 ± 0.17	0.51 ± 0.17	0.29 ± 0.24	-0.41 ± 0.20	0.46 ± 0.20	0.16±0.22	0.50 ± 0.18	0.26 ± 0.09	0.11 ± 0.22	0.30**±0.53	0.31**±0.35	-0.35 ± 0.39
AFC	-0.11±0.21	-0.19 ± 0.21	-0.03 ± 0.24	-0.23 ± 0.20	-0.08 ± 0.20	0.06±0.21	-0.45±0.19	0.11±0.22	0.45 ± 0.20	-0.02 ± 0.01	0.02 ± 0.01	-0.07 ± 0.01
SP	0.94 ± 0.62	0.99 ± 0.71	0.66 ± 0.40	0.57 ± 0.51	0.85 ± 0.78	0.18±0.12	0.28 ± 0.88	0.37 ± 0.53	-0.48 ± 0.10	0.04 ± 0.01	0.94**±0.25	$0.44^{**\pm}0.10$
CI	0.72 ± 0.24	0.64 ± 0.28	$0.84{\pm}0.17$	0.56 ± 0.26	0.49 ± 0.36	0.62 ± 0.38	0.51±0.28	0.23±0.35	-0.36±0.10	0.07 ± 0.01	$0.10{\pm}0.07$	$0.43^{**\pm0.10}$
DP	-0.57±0.36	-0.51±0.37	-0.70±0.44	-0.32 ± 0.28	-0.19*±0.37	-0.31**±0.31	-0.53** ±0.44	-0.22**±0.39	-0.37±0.22	-0.69±0.20	-0.53±0.15	0.11±0.07

Where (** P < 0.01)

LL and PY had moderate to high genetic correlations with all production performance traits ranging from 0.29 (persistency) to 0.84 (CI) and 0.56 (CI) to 0.96 (AMY), respectively except low and negative associations of both traits with AFC (-0.03), (-0.23) and DP (-0.70), (-0.32). While, negative genetic correlations of PY with persistency (-0.41). Likewise, LL and PY had varied magnitude i.e low, moderate to high significantly positive phenotypic correlations ranging from 0.07 (AFC) to 0.69 (CI) and 0.01 (AFC) to 0.55 (LL), respectively except negative associations with DP (-0.31), (-0.16). Likewise, association ship of PY with persistency was low and negative (-0.09). However, Dangar and Vataliya (2015) ^[6] reported moderate to high estimates of genetic and phenotypic correlations between LL and AFC. Verma et al. (2016)^[24] reported low and negative estimates of genetic and phenotypic correlations between PY and DP. While, low genetic correlations to the tune of 0.07 and negative phenotypic correlations to tune of -0.07 between PY and AFC was reported by Dangar and Vataliya (2015)^[6] in Gir cattle. On other hand, low genetic correlations to the tune of 0.01 and corresponding phenotypic correlations to the tune of 0.15 were reported by Lakshmi et al. (2009) [19]. However, negative estimates of genetic and phenotypic correlation was reported by Patond and Bhoite (2014) [24]. Likewise, reported high genetic correlations of LL with AMY and MCI and corresponding low to moderate phenotypic correlations. Verma et al (2016) ^[24] also reported high genetic and phenotypic correlations between LL and MSC. Similarly, Sahito et al. (2016)^[27] also reported high genetic correlations between LL and persistency in Red-Sindhi cattle. In addition to this, Verma et al (2016) [^{24]} also reported higher estimates of genetic and phenotypic correlations of PY with AMY, MCI and MSC in Frieswal cattle. Also, Seangjun et al. (2009) [28] reported moderate to high genetic and phenotypic correlations of PY with persistency. The negative genetic and phenotypic correlations of production performance traits with DP is in desirable direction because unproductive life of the animal decreases by decrease in dry period and increase in economic traits viz. lactation length, lactation length, peak yield etc. Similar findings were also supported by Deb et al. (2008), Ulutas and Sezer (2009) and Verma et al. (2016) [8, 30, 24].

The genetic correlations of AMY and MCI with production performance traits varied from low to high ranging from 0.46 (persistency) to 0.96 (LMY-305) and 0.06 (AFC) to 0.78 (LMY-305) except negative correlations of AMY with AFC (-0.08) and correlations of MCI with DP (-0.19). While, phenotypic correlations of AMY and MCI varied from low to high ranging from 0.02 (CI) to 0.90 (MSC) and 0.09 (AFC) to

0.91 (LMY), respectively except negative associations of AMY with DP (-0.44) and of MCI with SP (-0.07), CI (-0.08) and DP (-0.09). The genetic correlations of MSC and persistency with production performance traits were moderate to high ranging from 0.28 (SP) and 0.94 (AMY) and 0.11 (AFC) to 0.51 (LMY), (LMY-305), respectively except association ship of MSC with AFC (-0.45) and DP (-0.53), which were of highly negative in magnitude. On the contrary, genetic correlations of persistency were moderate to high and negative with PY (-0.41) and DP (-0.22).

The phenotypic correlations of MSC and persistency varied from low to high ranging from 0.28 (CI) to 0.90 (AMY) and 0.11 (AFC) to 0.76 (LMY) except negative association ship of MSC with AFC (-0.23) and DP (-0.55). While negative association ship of persistency with PY (-0.09) and DP (-0.35). Verma *et al.* (2016) ^[24] reported low but positive estimates of genetic correlations of AMY and MCI with AFC. Dhawan *et al.* (2015) ^[12] reported higher estimates of genetic and phenotypic correlations between AMY with MCI. Similarly, Dhaka, *et. al.* (2002) ^[10], Dhaka *et al.* (2009) and Dhawan *et al.* (2015) ^[11, 12] reported higher estimates of genetic and phenotypic correlations of AMY and MCI with MSC. Dhaka also reported moderate estimates of genetic and phenotypic correlations of MCI and MSC with persistency.

AFC had low to moderate and negative genetic correlations with all production performance traits ranged from -0.48 (SP) to -0.03 (LL) except low and positive relationship with MCI (0.06) and Persistency (0.11). Whereas, low and positive phenotypic correlations of AFC ranging from 0.01 (PY) to 0.11 (Persistency) except low and negative association ship with MSC (-0.23), SP (-0.02) and DP (-0.07). Similar estimates were reported by Verma et al. (2016)^[24] in Frieswal cattle. However, Dangar and Vataliya (2015) [6] reported low but positive estimates of genetic and phenotypic correlations between AFC and DP in Gir cattle. Also, SP had moderate to high genetic correlations with production performance traits ranged from 0.18 to 0.99, with the highest value to the tune of 0.99 (LMY-305) except association ship of SP with AFC which was highly negative (-0.48). Similar estimates were reported by Dash and Dubey. Whereas, SP had moderate to high and significant phenotypic correlations with various production performance traits ranging from 0.25 (PY) to 0.94 (CI) except low correlation with AMY (0.02) and negative correlations with MCI (-0.07). Verma et al. (2016) [24] also reported similar estimates of genetic and phenotypic correlations in Frieswal cattle. Likewise, CI had moderate to high genetic correlations with all production performance traits ranged from 0.23 (Persistency) to 0.84 (LL) except high

negative association hip with DP (-0.53). However, opposite results to present study were reported by Ulutaş and Sezer (2009) ^[30] in Simmental cattle. Similarly, low to highly positive phenotypic associations of CI with all production performance traits ranged from 0.02 (AFC) to 0.94 (SP) except negative association with MCI (-0.08). DP had varied range of genetic correlations ranged from -0.70 (LL) to -0.19 (AMY) i.e. low to highly negative associations with production performance traits. Likewise, DP had low to highly negative phenotypic correlations ranged from -0.55 (MSC) to -0.07 (AFC) except highly positive significant associations with SP (0.44) and CI (0.43). Likewise, Verma et al. (2016) ^[24] also reported similar estimates of genetic and phenotypic correlations in Frieswal cattle. Similar results were obtained by Deb et al. (2008) and Cayo et al. (2018)^[8, 3] in GI Rolando cattle. Critical appraisal of heritability estimates, genetic and phenotypic correlations between production performance traits, it may be inferred that selection based on milk yield per day of age at second calving (MSC) that had high estimates of heritability (0.50) and appreciably high genetic and phenotypic correlations with production performance traits, would not only improve production performance but also take care of reproductive performance. Therefore, selection based on MSC would result in improvement in desirable direction through positive correlated response in all the traits under study. Milk yield per day of age at second calving (MSC) can be used as an index

trait in selection programme as it is associated with AFC and milk yield, which is an important trait that determines the economic merit.

3.2 Among test day milk records

The genetic correlation among test day milk yields ranged from 0.56 to 0.99. The lowest value of correlation was found between most distant (Ist to 10th) test day milk records being 0.55. The phenotypic correlations between test day milk records ranged from 0.55 to 0.75. The phenotypic correlation among all test day milk records were highly significant (P<0.01). (Table 2). Similar, results were reported by Lidauer et al. (2003)^[20], Ilatsia et al. (2008) and Kokate et al. (2013) ^[15, 16]. Highest correlation between adjacent test day milk records were supported by Pander et al. (1992) [22], Deb and Gurani (1994) and Kokate et al. (2013)^[9, 16]. Whereas, Kumar (2015) reported low to high estimates of genetic and phenotypic correlations among test day milk records ranged from 0.12 to 0.82 and 0.11 to 0.75, respectively, and the highest correlations were found between adjacent test day milk records and the correlations decreased as interval between test days increased. As additive genetic and permanent environment variances were higher for test-day milk yields at both ends of lactation, the residual variance was observed to be lower than the permanent environment variance for all the test-day milk yields.

 Table 2: Estimates of heritability (diagonal), genetic correlation (below diagonal) and phenotypic correlation (above diagonal) amongst test day milk records

Traits	TD ₁	TD ₂	TD ₃	TD ₄	TD5	TD ₆	TD ₇	TD8	TD9	TD ₁₀
TD ₁	0.37±0.20	0.90 ± 0.03	0.88 ± 0.06	$0.84{\pm}0.08$	0.81 ± 0.09	0.78 ± 0.11	0.73 ± 0.14	0.70 ± 0.14	0.67 ± 0.14	0.55±0.12
TD ₂	0.91±0.03	0.45 ± 0.19	$0.94{\pm}0.02$	0.91±0.03	0.88 ± 0.04	$0.84{\pm}0.07$	0.79 ± 0.09	0.75 ± 0.09	0.72 ± 0.10	0.59±0.10
TD ₃	0.85 ± 0.06	0.96 ± 0.02	0.34±0.17	0.97 ± 0.01	0.93 ± 0.02	0.89 ± 0.04	0.83 ± 0.06	0.78 ± 0.06	0.74 ± 0.08	0.58±0.11
TD ₄	0.78 ± 0.08	0.92 ± 0.03	0.99 ± 0.01	0.47±0.16	0.95 ± 0.01	0.92 ± 0.02	0.86 ± 0.05	0.80 ± 0.05	0.77 ± 0.08	0.58±0.11
TD ₅	0.76 ± 0.09	0.91 ± 0.04	0.98 ± 0.02	0.99 ± 0.01	0.47 ± 0.15	0.95 ± 0.02	0.90 ± 0.06	0.85 ± 0.04	0.81 ± 0.06	0.63±0.11
TD ₆	0.69±0.11	0.84 ± 0.07	0.93±0.04	0.96 ± 0.02	0.97 ± 0.02	0.45 ± 0.14	0.94 ± 0.04	0.87 ± 0.05	0.83 ± 0.08	0.64±0.13
TD7	0.59 ± 0.14	0.78 ± 0.09	0.87 ± 0.06	0.88 ± 0.05	0.88 ± 0.06	0.92 ± 0.04	0.47 ± 0.15	0.86 ± 0.07	0.82 ± 0.09	0.66±0.12
TD ₈	0.58 ± 0.14	0.77 ± 0.09	0.89 ± 0.06	0.89 ± 0.05	0.93 ± 0.04	0.88 ± 0.05	0.82 ± 0.07	0.32 ± 0.17	0.93 ± 0.02	0.74±0.10
TD9	0.56 ± 0.14	$0.74{\pm}0.10$	0.83 ± 0.08	0.82 ± 0.07	0.88 ± 0.06	0.82 ± 0.08	0.79 ± 0.09	0.96 ± 0.02	0.35±0.16	0.79±0.09
TD10	0.68 ± 0.12	0.78 ± 0.10	0.77 ± 0.11	0.75 ± 0.11	0.79 ± 0.11	0.70±0.13	0.71±0.12	0.76 ± 0.10	0.77 ± 0.09	0.33±0.15

All phenotypic correlation significant at (** *P*<0.01)

3.3 Between production performance and test day milk records

Genetic correlations between test day milk records with production performance traits were positive and low to high ranged from 0.01 to 0.99, except negative association ship of AFC with all test day milk records ranged from -0.38 to -0.16. Estimates of phenotypic correlations of test day milk records with all production performance traits (LMY, LMY-305, LL, PY, AMY, MCI and MSC) were significant (p<0.01), high and positive barring few exceptions. However, TD_1 to TD_3 had negative and low phenotypic association with AFC but the association of AFC with subsequent test days were low and positive. Phenotypic associations of various test day milk records with production performance traits viz. SP and CI were significantly (p<0.01) moderate to high ranged from 0.36 to 0.50. Low to moderate, negative associations of all test day milk records with DP ranged from -0.26 to -0.14. (Table 3). Dalal et al. (1999)^[5] observed that the test-day milk yield records had positive and high genetic and phenotypic correlations among themselves in Hariana cattle and also reported high genetic and phenotypic correlation between test day milk records (TD₂, TD₃ and TD₄) and FLMY

which revealed that either of these three test day milk records could successfully be utilized for genetic evaluation of sires for FLMY. Machado also reported that genetic correlation between milk yield on an individual's test days and 305 day milk yield ranged from 0.78 to 1.00. Similarly, Kokate et al. (2013) ^[16] also reported that estimates of phenotypic and genetic correlations of monthly test day yields with 305-day milk yield ranged from 0.42 to 0.78 and 0.80 to 0.99, respectively, and the phenotypic correlations among monthly test day milk yields with 305 day milk yield were highly significant and the estimates was generally higher in the middle segment of lactation. Likewise, Santos also reported genetic correlations were high and positive, ranging from 0.51 to 0.99 among TDMY records, from 0.81 to 0.98 between each TDMY and MY305, and from 0.71 to 0.94 between each TDMY and LL. Kumar (2015)^[18] also reported high positive genetic and phenotypic correlations of test day milk records with FLMY suggested that we may predict the FLMY on the basis of early test day records (TD₂, TD₃ and TD₄). The high correlation among proximate test day milk records suggested that for prediction of FLMY on the basis of test day milk records, number of test day could be reduced, with a small

loss of accuracy of prediction. The use of TDMY can also be used as selection criteria that would result in indirect gains in production performance traits. Although results indicate that selection on basis of production performance traits viz. LMY, LMY-305 would be more efficient as a selection criterion to the improvement of milk production, it can be argued that the use of test-day milk yields brings the possibility of selecting for milk production before the end of lactation (mainly in the first third), allowing the inclusion of animals with unfinished lactations in the genetic evaluations which, in turn, could affect the genetic progress because the evaluation of bulls would include more daughters, improving accuracy, and more young animals, males and females, would be available for selection, which could improve both selection intensity and generation interval.

Table 3: Estimates of genetic correlations between various production performance and test day milk records

Trait	TD ₁	TD ₂	TD ₃	TD ₄	TD5	TD ₆	TD ₇	TD ₈	TD9	TD ₁₀
LMY	0.62 ± 0.13	0.71 ± 0.11	0.75 ± 0.10	0.73 ± 0.11	$0.74{\pm}0.11$	0.70 ± 0.12	$0.74{\pm}0.11$	0.63 ± 0.14	0.58 ± 0.15	0.57 ± 0.16
LMY-305	0.55 ± 0.15	$0.61 \pm .14$	0.66 ± 0.13	0.64 ± 0.14	$0.63 \pm .14$	0.56 ± 0.16	0.60 ± 0.15	$0.54{\pm}0.16$	0.50 ± 0.17	0.42 ± 0.19
LL	0.19±0.23	0.30 ± 0.22	0.34 ± 0.22	0.39 ± 0.21	0.43 ± 0.21	0.46 ± 0.20	0.64 ± 0.15	0.32 ± 0.22	0.38 ± 0.21	0.49 ± 0.19
PY	0.85 ± 0.06	$0.94{\pm}0.03$	0.99 ± 0.01	0.98 ± 0.01	0.96 ± 0.02	0.90 ± 0.04	$0.83 {\pm} 0.07$	0.86 ± 0.06	$0.81 {\pm} 0.09$	0.77 ± 0.11
AMY	0.64±0.13	0.68 ± 0.12	0.72 ± 0.11	0.68 ± 0.13	0.65 ± 0.14	0.56±0.16	0.52 ± 0.17	0.58 ± 0.15	0.49 ± 0.17	0.38±0.19
MCI	0.49±0.16	0.59 ± 0.14	0.66 ± 0.14	0.65 ± 0.14	0.61±0.15	0.58±0.16	0.58 ± 0.16	0.50 ± 0.17	0.45 ± 0.19	0.31±0.21
MSC	0.70 ± 0.11	0.75 ± 0.09	0.77 ± 0.09	0.76 ± 0.10	0.76 ± 0.10	0.69±0.12	0.71 ± 0.12	0.60 ± 0.14	0.59 ± 0.15	0.61±0.15
Persistency	0.09 ± 0.22	0.13 ± 0.22	0.15±0.23	0.13 ± 0.24	0.15 ± 0.24	$0.14{\pm}0.25$	0.30 ± 0.23	0.07 ± 0.23	0.04 ± 0.24	0.06 ± 0.24
AFC	-	-	-	-	-	-	-	-	-	-
AFC	0.38 ± 0.18	0.30 ± 0.19	0.25 ± 0.20	0.24 ± 0.20	0.27 ± 0.21	0.19 ± 0.22	0.16 ± 0.22	0.16 ± 0.21	0.23 ± 0.21	0.36 ± 0.20
SP	0.32 ± 0.21	0.38 ± 0.21	0.37 ± 0.22	0.39 ± 0.22	0.48 ± 0.21	0.46 ± 0.21	0.60 ± 0.18	0.55 ± 0.18	0.61±0.17	0.84±0.12
CI	0.37±0.21	0.42 ± 0.20	0.40 ± 0.21	0.39 ± 0.22	0.51±0.21	0.50 ± 0.21	0.63 ± 0.18	0.53±0.19	0.53±0.19	0.79±0.14
DP	0.18 ± 0.23	0.11 ± 0.24	0.02 ± 0.25	0.01 ± 0.25	0.09 ± 0.27	0.07 ± 0.27	$0.01 {\pm} 0.26$	0.26 ± 0.25	0.21 ± 0.26	0.33±0.25

4. Conclusion

The study revealed performance evaluation of crossbred cattle for production performance traits is important in judging their relative merits in adaptation, health and productivity in given agro-climatic conditions. The production performance traits considering both the production and reproduction aspect of an animal are important parameters for ensuring profitability of dairy animal over longer period. The milk yield expressed as average daily milk yield (LMY/LL), milk yield per day of calving interval (MCI= first lactation milk yield/first calving interval) and milk yield per day of age at second calving (MSC= first lactation milk yield/age at first calving + first calving interval) are good measures of both the reproduction and production performance of an animal. These results also suggested that selection of relatives on the basis of production performance traits would lead to positive genetic responses and high genetic gain. Critical appraisal among genetic and phenotypic correlations between production performance traits, it may be inferred that selection based on milk yield per day of age at second calving that had high estimates of heritability (0.50) and appreciably high genetic and phenotypic correlations with production performance traits, would not only improve production performance but also take care of reproductive performance.

Table 4: Estimates of phenotypic correlations among various production performance and test day milk records

Trait	LMY	LMY-305	LL	PY	AMY	MCI	MSC	Persistency	AFC	SP	CI	DP
TD_1	0.63**±0.13	0.59**±0.15	$0.41^{**\pm 0.23}$	$0.88^{*\pm0.06}$	0.55**±0.13	$0.50^{**\pm0.16}$	0.63**±0.11	0.11±0.22	-0.06 ± 0.18	0.37**±0.21	$0.36^{*}\pm 0.21$	-0.18 ± 0.22
				0.94**±0.03							$0.38^{*\pm}0.20$	
TD_3	$0.71^{*\pm}0.10$	0.64**±0.13	$0.52^{*}\pm 0.22$	0.99**±0.01	0.59**±0.11	$0.57^{*\pm}0.14$	0.68**±0.09	0.12±0.23	-0.01 ± 0.20	0.41**±0.22	$0.41^{**\pm 0.21}$	-0.14 ± 0.25
TD_4	0.75**±0.11	0.68**±0.14	0.60**±0.21	0.96**±0.01	0.58**±0.13	$0.61^{**\pm}0.14$	0.72**±0.10	$0.21*\pm0.24$	0.03 ± 0.20	0.43**±0.22	$0.42^{**\pm}0.22$	$-0.22*\pm0.25$
TD ₅	$0.76^{**\pm}0.11$	0.72**±0.14	$0.63^{*}\pm 0.21$	0.93**±0.02	0.57**±0.14	$0.62^{**\pm}0.15$	0.72**±0.10	$0.25*\pm0.24$	$0.03{\pm}0.21$	0.43**±0.21	$0.41^{**\pm}0.21$	$-0.24*\pm0.27$
TD_6	0.76**±0.12	0.70**±0.16	0.67**±0.20	0.89**±0.04	0.52**±0.16	0.59**±0.16	0.70**±0.12	0.27**±0.25	0.06 ± 0.22	0.48**±0.21	$0.47^{**\pm}0.21$	$-0.23*\pm0.27$
TD_7	$0.75^{*\pm}0.11$	0.70**±0.15	0.70**±0.15	0.82**±0.07	0.49**±0.17	0.59**±0.16	0.70**±0.12	0.33**±0.23	0.06 ± 0.22	$0.49^{**\pm}0.18$	$0.49^{**\pm}0.18$	$-0.26*\pm0.27$
TD_8	$0.66^{*}\pm 0.14$	0.61**±0.16	$0.62^{*}\pm 0.22$	0.77**±0.06	$0.42^{**\pm 0.15}$	$0.49^{**\pm}0.17$	0.61**±0.14	$0.23*\pm0.23$	0.05 ± 0.21	$0.47^{**\pm}0.18$	0.46**±0.19	-0.19 ± 0.25
TD ₉	0.67**±0.15	0.61**±0.17	$0.63^{*}\pm 0.21$	0.74**±0.09	$0.41^{**\pm 0.17}$	0.47**±0.19	0.61**±0.15	$0.26^{*}\pm 0.24$	0.05 ± 0.21	0.50**±0.17	0.49**±0.19	-0.17 ± 0.26
TD_{10}	0.55**±0.16	0.49**±0.20	0.58**±0.20	0.58**±0.11	0.29**±0.20	0.35**±0.21	0.51**±0.15	0.23**±0.24	0.01 ± 0.20	$0.48^{**\pm}0.12$	0.47**±0.14	-0.14 ± 0.25

Where, (** *P*<0.01)

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