



Assessment of Genetic Parameters for First Lactation Production Traits in Crossbred Cattle in India

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ABSTRACT

The present study was undertaken to assess the genetic parameters for first lactation production traits in crossbred cattle. Data on 529 crossbred cattle spread over a span of 30 years (1990-2019) were collected from pedigree sheets of organised herd maintained at dairy farm of Govind Ballabh Pant University of Agriculture and Technology, Pantnagar. Various production traits studied were 305 days milk yield (305DMY), total milk yield (TMY), lactation length (LL), peak yield (PY) and days to attain peak yield (DAPY). Heritability, phenotypic and genetic correlations were estimated using least-squares analysis. Heritability estimates obtained were low to medium (0.04±0.02 to 0.30±0.09). The phenotypic and genetic correlations between TMY with LL were 0.72±0.08 and 0.77±0.37, 305DMY with LL were 0.42±0.12 and 0.30±0.95, LL with PY were 0.16±0.45 and 0.14±0.00, LL with DAPY were 0.09±0.77 and 0.10±0.05, 305DMY with TMY were 0.79±0.66 and 0.76±0.46, PY with TMY were 0.41±0.17 and 0.25±0.28, TMY with DAPY were 0.14±0.67 and 0.10±0.58, 305DMY with PY were 0.70±0.26 and 0.74±0.29, 305DMY with DAPY were 0.14±0.15 and 0.07±0.23 and DAPY with PY were 0.13±0.08 and 0.15±0.61. Positive and high genetic correlation between TMY with LL, 305DMY with TMY and 305DMY with PY suggested that tandem selection can improve both the traits simultaneously. Positive and high phenotypic as well as genetic correlation of 305DMY with other traits advocated that selection for 305DMY would be beneficial for enhancing the production in crossbred animals.

HIGHLIGHTS

- Genetic parameters like heritability and correlation affect first lactation production as well as reproduction traits in cattle.
- This study was conducted to know about the genetic parameters affecting first lactation traits and the results are summarised in this paper.

Keywords: Correlation, Crossbred cattle, Heritability, Genetic, Phenotypic

The total cattle population of India is estimated to be 192.49 million. Out of this population, about 142.11 million are indigenous/non-descript while crossbred/exotic breeds account for about 50.42 million. From the total milk production in India 51% came from cattle, whereas; 45% and 3% come from buffalo and goats, respectively (20th Livestock Census All India Report, 2019). Of the total milk produced from cattle 20% of the milk is produced by the indigenous stock while the remaining 28% and 3% from improved crosses

and pure grade (exotic) cattle, respectively. Genetic analysis of animal genetic resources most often aims at segregating genetic and environmental effects. The genetic factors are due to a random sample of genes received from the two parental gametes whereas the

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environmental factors include influences of climate, nutrition, health and management. Precise information on genetic parameter estimates is essential for accurate evaluation of genetic worth of animals, implementation of breeding programs and assessment of progress of ongoing programs where accuracy of their estimation is of paramount importance (Wasike, 2016). The observed relationship between the phenotypic performances of different traits is measured through phenotypic correlation while the genetic correlation is an expression of degree of association between genes responsible for the additive variance of different traits.

In a broader research context, genetic correlations furnish to understand the co-occurrences of traits, population level flow of genes and pathways of traits (Via and Hawthorne, 2015). The genetic improvement of trait(s) under selection is reliable on heritability of the trait. Heritability estimation is significant for selection of polygenic traits. When selection is made for trait(s), heritability determines extent of expected genetic improvement in the trait(s) while genetic correlation between selected traits selected and other correlated trait (s) resolves expected response to selection for unselected traits besides the response for the selected traits (Rao and Bhatia, 2012). Thus, this study was initiated with the objective to obtain the estimates of heritability, genetic and phenotypic correlations among the first lactation traits in various crossbred dairy cattle using LSML (Least Squares Mean Analysis).

MATERIALS AND METHODS

Description of study area

The present study was conducted on crossbred dairy cattle maintained at an organized herd of Govind Ballabh Pant University of Agriculture and Technology (GBPUAT), Pantnagar spread over a period of 30 years (1990-2019). The farm is located in subtropical region on 28° 52' N to 28° 25' N latitude and 78° 58' to 79° 42' E longitude and has a moderate climate. The summer holds a temperature maximum of around 42-45°C while it falls heavily to 2-4°C during winter. The maximum humidity is 97% and minimum humidity is 48%. The annual rainfall is on an average 1450 mm. Thus, it is obvious that cattle maintained here get exposed to wide range of variations in temperature and humidity.

Data

Information on 529 records of crossbred cattle sired by 79 sires pertaining to different first lactation traits viz. 305 days milk yield (305DMY), total milk yield (TMY), lactation length (LL), peak yield (PY) and days to attain peak yield (DAPY) spread over a period of 30 years (1990-2019) were utilised for the study. Only first lactation traits were considered in the study because number of observations in subsequent lactation was meagre. The abnormal records like dystocia, still birth, culling due to chronic illness were omitted from the present study. Further, animals having less than 305 days lactation length were also not considered.

Statistical analysis

The influence of important genetic and non-genetic factors on various was discerned by using least-squares analysis in order to overcome the non-orthogonality of data due to unequal and disproportionate sub-class frequencies (Harvey, 1990). The data were adjusted for significant non-genetic factors and effect of sire, genetic groups of animals, season of calving and period of calving was studied using following model.

$$\text{Model: } Y_{ijklm} = \mu + S_i + L_j + G_k + P_l + e_{ijklm}$$

Where, Y_{ijklm} is m^{th} observation of crossbred cattle that is progeny of i^{th} sire, j^{th} genetic group calved in k^{th} season and l^{th} period; μ is overall population mean; S_i is random effect of i^{th} sire (1-79); L_j is fixed effect of j^{th} genetic group (1-8); G_k is fixed effect of k^{th} season of calving (1-3) three seasons: summer (March-June), rainy (July-October) and winter (November-February) and P_l is fixed effect of l^{th} period of calving (1-6) and e_{ijklm} is random error that was assumed to be normally and independently distributed with mean zero and constant variance i.e., NID (0, σ_s^2).

Phenotypic variances and covariance were estimated from the sum of sire and error variance and covariance components.

$$r_{p(hh')} = \frac{\hat{\sigma}_{e(hh')}^2 + \left[\left(\frac{1-NW}{NR1} \right) \hat{\sigma}_{S(hh')}^2 \right]}{\sqrt{\left\{ \hat{\sigma}_{e(h')}^2 + \left(\frac{1-NW}{NR1} \right) \hat{\sigma}_{S(h)}^2 \right\} \left\{ \hat{\sigma}_{e(h')}^2 + \left(\frac{1-NW}{NR1} \right) \hat{\sigma}_{S(h)}^2 \right\}}}$$

Where, cov_s is sire or family covariance, h is heritability of trait, h' is heritability of trait another trait; $\hat{\sigma}_s^2$ is among

variance or covariance component; $\hat{\sigma}_e^2$ is within variance or covariance component; NR1 is between variance component and is equal to 0.25 and NW is within variance component and is equal to 0.75.

Phenotypic and genetic correlations were estimated from ratios of sire covariance to the square root of the product of corresponding sire variance components (Becker, 1975).

$$r_{g(hh')} = \frac{cov_s(hh')}{\sqrt{[\hat{\sigma}_{S(h)}^2 \cdot \hat{\sigma}_{S(h')}^2]}}$$

RESULTS AND DISCUSSION

The least-squares means of first lactation traits viz., 305 days milk yield (305DMY), total milk yield (TMY), lactation length (LL), peak yield (PY) and days to attain peak yield (DAPY) were 2854.26±59.61 kg, 3584.92±118.42 kg, 397.25±9.19 days, 14.18±0.27 kg and 48.42±0.87 days, respectively. Analysis of variance for different first lactation traits is summarised in Table 1. Sire had highly significant (P<0.01) influence on TMY, 305DMY and PY. The significant effect of

genetic group was found on 305DMY (P<0.01) and DAPY (P<0.05). Season of calving significantly (P<0.05) affected 305DMY and DAPY in the present study. Period of calving had significant influence on the LL (P<0.01), TMY (P<0.01), 305DMY (P<0.01) and DAPY (P<0.01).

The heritability estimates of all lactation traits under study were low to medium in magnitude, ranged from 0.04±0.02 to 0.30±0.09. The heritability, phenotypic and genetic correlations among different lactation traits are presented in Table 2. In the present study, the heritability for LL was estimated as 0.04±0.02. Heritability estimates for LL in the range of 0.07±0.08 to 0.28±0.19 were substantiated by Kumar *et al.* (2014) in H.F crossbreed as 0.28±0.19, Dash *et al.* (2016) in Karan-Fries as 0.11±0.05, Kokati *et al.* (2017) as 0.17±0.10, Jadhav *et al.* (2019) in HF×Gir as 0.11±0.10 and Arya *et al.* (2020) in crossbred dairy cattle as 0.07±0.08; heritability for TMY was estimated as 0.24±0.10. Heritability estimates for TMY that ranged from 0.17±0.19 to 0.32±0.17 were found by Kumar *et al.* (2014) in H.F crossbreed as 0.17±0.19, Verma *et al.* (2016) in Hardhenu as 0.32±0.17, Jadhav *et al.* (2019) in HF×Gir as 0.18±0.10 and Arya *et al.* (2020) in crossbred dairy cattle as 0.26±0.11; heritability

Table 1: Least square analysis of variance for first lactation traits

Source of variation	Mean sum of squares					
	d.f.	LL	TMY	305DMY	PY	DAPY
Sire	78	8546.13	1799937.37**	534817.85**	13.82**	94.17
Genetic Group	7	733.61	510614.95	246054.99**	3.76	33.73*
Season	2	17460.54	281363.52	496208.78*	0.54	226.87*
Period	5	18103.24**	3937106.60**	1358442.49**	2.19	234.64**

Table 2: Heritability (diagonal), Phenotypic (above diagonal) and genetic (below diagonal) correlations of different first lactation traits in crossbred cattle

TRAITS	LL	TMY	305DMY	PY	DAPY
LL	0.04±0.02	0.72±0.08	0.42±0.12**	0.16±0.45	0.09±0.77
TMY	0.77±0.37*	0.24±0.10	0.79±0.66*	0.41±0.17*	0.14±0.67
305DMY	0.30±0.95	0.76±0.46	0.30±0.09	0.70±0.26	0.14±0.15
PY	0.14±0.00	0.37±0.20	0.74±0.29	0.19±0.04	0.13±0.08*
DAPY	0.10±0.05	0.10±0.58	0.07±0.23	0.15±0.61	0.11±0.02

LL: lactation length, TMY: total milk yield, 305DMY: 305 days milk yield, PY: peak yield and DAPY: days to attain peak yield. ** and * represent significant difference at 1% and 5% level of significance, respectively.

estimates for 305DMY was found as 0.30 ± 0.09 in the present study. Heritability values ranged from 0.12 ± 0.10 to 0.51 ± 0.14 were estimated by Dash *et al.* (2016) in Karan Fries as 0.39 ± 0.09 , Kokati *et al.* (2017) in Frieswal as 0.51 ± 0.14 , Jadhav *et al.* (2019) in HF \times Gir as 0.19 ± 0.14 , Bhoite *et al.* (2020) in HF \times Gir as 0.12 ± 0.10 and Arya *et al.* (2020) in crossbred dairy cattle as 0.27 ± 0.11 ; heritability estimates for PY was obtained as 0.19 ± 0.04 . Heritability values (0.25 ± 0.14 to 0.28 ± 0.17) were reported by Kumar (2015) in Frieswal as 0.26 ± 0.22 , Verma *et al.* (2016) in Hardhenu as 0.28 ± 0.17 and Jadhav *et al.* (2019) in HF \times Gir as 0.25 ± 0.14 and heritability estimate for DAPY was 0.11 ± 0.02 in the present finding. Heritability estimates ranged from 0.12 ± 0.00 to 0.13 ± 0.12 were estimated by Patond *et al.* (2013) in Jersey cattle and Thorat *et al.* (2017) in HF \times Deoni. Perusal of Table 2 depicted phenotypic and genetic correlation between various first lactation traits.

TMY with LL

The positive and high phenotypic correlation between TMY and LL were found to be 0.72 ± 0.08 . Positive and lower phenotypic correlation between TMY and LL (0.11 ± 0.16 to 0.69 ± 0.27) were reported by Lodhi *et al.* (2016) in crossbred dairy cattle, Jadhav *et al.* (2019) in HF \times Gir and Arya *et al.* (2020) in crossbred dairy cattle. The positive and significant ($P < 0.05$) genetic correlation between TMY and LL was estimated to be 0.77 ± 0.37 . Similar results (0.79 ± 0.01) were reported by Arya *et al.* (2020) in crossbred dairy cattle. Lower (0.63 ± 0.17) and positive genetic correlation between TMY and LL were reported by Lodhi *et al.* (2016) in crossbred dairy cattle. The positive and high genetic correlation indicated that the high values occur together and almost the same genes had an influence on TMY and LL. Period wise trend of lactation length and total milk yield for last 30 years in crossbred cattle as observed is presented in Fig. 1 which illustrates the tandem relationship between two variables. During the period 1996–2000, as total milk yield increased, lactation length also increased. A similar trend of TMY and LL was observed during 2001–2005. Hence, the trend of TMY and LL over the period of calving represented agonistic relationship between two production traits. In other words, selection for improvement in total milk

yield will result in higher lactation length which is desirable for economical livestock production.

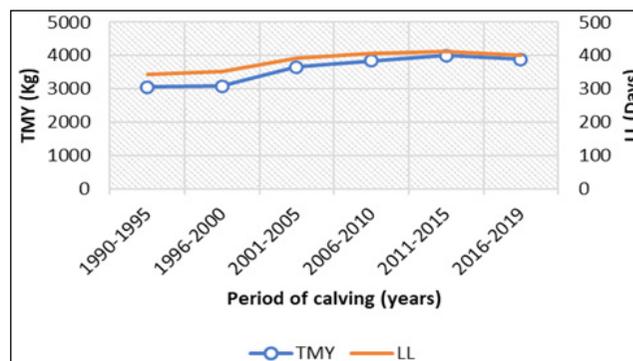


Fig. 1: Positive correlation between total milk yield (TMY) and lactation length (LL) in crossbred cattle. During the period 1996–2000, as TMY increased, LL also increased. A similar trend of TMY and LL was observed during 2001–2005

305DMY with LL

The phenotypic correlation between 305DMY with LL was observed as positive 0.42 ± 0.12 and significant ($P < 0.01$) which is presented in Table 2. Similar findings (0.44 ± 0.03 to 0.48 ± 0.71) were published by Dash *et al.* (2014) in Holstein Friesian crossbred and Jadhav *et al.* (2019) in HF \times Gir while negative and low (0.11 ± 0.04) estimates of association was reported by Arya *et al.* (2020) in crossbred dairy cattle. Lower correlation (0.22 ± 0.10 to 0.25 ± 0.05) between 305DMY with LL was reported by Ambhore *et al.* (2017) in Phule Triveni. Higher estimates (0.63 ± 0.00 to 0.82 ± 0.02) than the present finding was obtained by Girimal *et al.* (2020) in crossbred dairy cattle. Table 2 discerned that the positive genetic correlation between 305DMY with LL was 0.30 ± 0.95 which was in close agreement with the results (0.35 ± 0.28) reported by Bajetha (2015) in crossbred dairy cattle while negative genetic correlation (-0.11 ± 0.00 to -0.78 ± 0.00) was reported by Pol *et al.* (2013) in Phule Triveni and Ambhore *et al.* (2017) in Phule Triveni. Higher values (0.48 ± 0.09 to 0.96 ± 0.00) than the present estimates were reported by Girimal *et al.* (2017) in crossbred dairy cattle, Jadhav *et al.* (2019) in HF \times Gir and Arya *et al.* (2020) in crossbred dairy cattle. During 1996–2000 a rise in 305DMY was followed by moderate increase in LL

(Fig. 2) suggesting moderate relationship between the two traits.

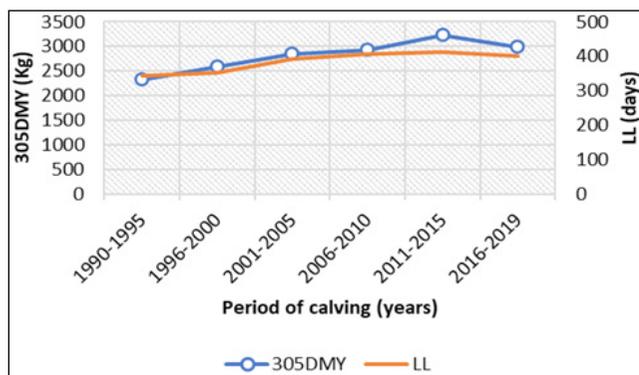


Fig. 2: Positive correlation between 305 days milk yield (305DMY) and lactation length (LL) in crossbred cattle. During 1996-2000 a rise in 305DMY was followed by moderate increase in LL suggesting moderate relationship between the two traits

LL with PY

The positive phenotypic correlation between LL and PY was found as positive (0.16 ± 0.45) in the present study. Similar results (0.17 ± 0.00) were reported by Anarase *et al.* (2015) in HF×Deoni while negative (0.10 ± 0.00) correlation between the two traits were reported by Patond and Bhoite (2014) in Gir triple cross cows.

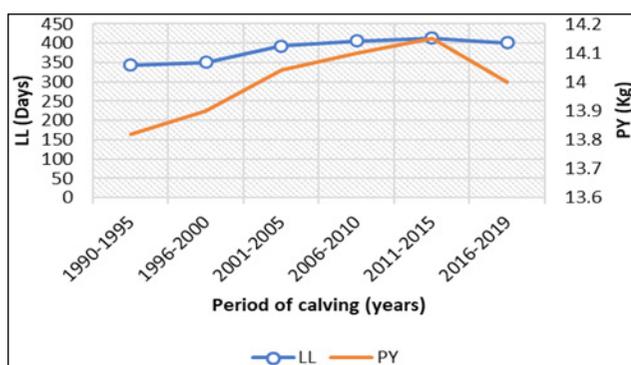


Fig. 3: Positive and low magnitude of correlation between lactation length (LL) and peak yield (PY) in crossbred cattle

The genetic correlation (Fig. 3) between LL and PY was found as positive (0.14 ± 0.00) in the present study while negative correlation estimate (-0.69 ± 0.00) was reported by Patond and Bhoite (2014) in Gir triple cross cows. Higher estimate of correlation (0.62 ± 0.20)

was substantiated by Pundir *et al.* (2016) in Kankrej cattle.

LL with DAPY

The phenotypic correlation as obtained in the present study between LL and DAPY was low and positive 0.09 ± 0.77 as presented in Table 2. The genetic correlation between LL and DAPY as obtained in the present study was 0.10 ± 0.05 (Fig. 4).

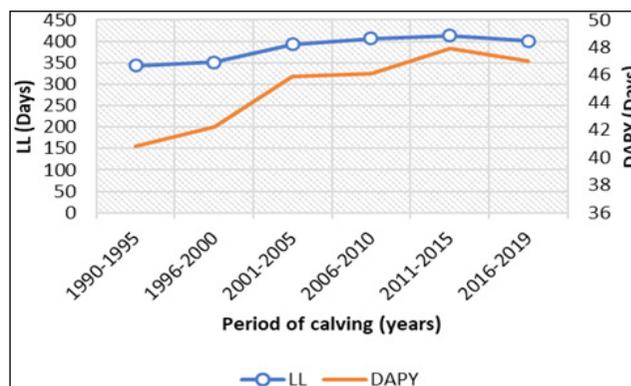


Fig. 4: Positive and low magnitude of correlation between lactation length (LL) and days to attain peak yield (DAPY) in crossbred cattle

However, the negative phenotypic correlation (-0.41 ± 0.00) was reported by Anarase *et al.* (2015) in HF×Deoni. During the period 1996–2000, as lactation length increased, days to attain peak yield also increased. A similar trend of LL and DAPY was observed during 2001-2005. Fig. 4 represented the antagonistic relationship between the two traits, i.e., longer lactation length would result in more time to reach peak yield which is undesirable.

305DMY with TMY

The positive and significant ($P < 0.05$) phenotypic correlation between 305DMY and TMY under the present finding was calculated as (0.79 ± 0.66). Lower estimate was (0.467 ± 0.00) analysed on HF×Deoni by Thorat *et al.* (2017) while higher values (0.90 ± 0.00 to $>1 \pm 0.00$) of association between the two traits was reported by Jadhav *et al.* (2019) in HF×Gir. The genetic correlation between 305DMY and TMY was obtained as high and positive (0.76 ± 0.46) which was in

close agreement with the result (0.76 ± 0.00) analysed by Thorat *et al.* (2017) in HF×Deoni. Higher estimates (0.93 ± 0.95 to 1.00 ± 0.00) were substantiated by Jadhav *et al.* (2019) in HF×Gir and Singh *et al.* (2011) in Vindavani. The positive and high genetic correlation (Fig. 5) indicated that higher 305 days milk yields were associated with higher total lactation milk yields. Therefore, sires could be evaluated for either of the trait due to the reason that selection for 305DMY trait could bring concomitant improvement on the TMY and vice-versa.

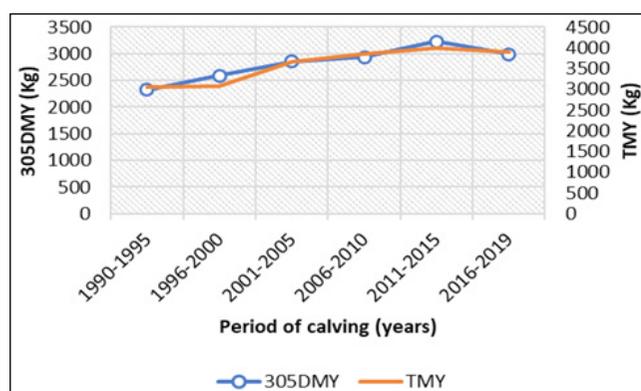


Fig. 5: Positive correlation between 305 days milk yield (305DMY) and total milk yield (TMY) in crossbred cattle. Higher 305DMY was associated with higher TMY (period 2005-2010 clearly depicts the increasing trend between two traits in crossbred cattle

PY with TMY

Perusal of Table 2 revealed that the phenotypic correlation between PY and TMY was positive (0.41 ± 0.17) and significant ($P<0.05$) which was in close agreement with the results (0.430 to 0.49 ± 0.00) analysed by Patond and Bhoite (2014) in Gir triple cross and Anarase *et al.* (2015) in HF×Deoni. Higher estimate (0.85 ± 0.28) than the present study was reported by Verma *et al.* (2016) in Hardhenu crossbred. The genetic correlation between PY and TMY was estimated as 0.37 ± 0.20 . Higher estimates (0.70 ± 0.04 to 0.94 ± 0.03) of genetic correlation between PY and TMY were analysed by Dash *et al.* (2014) in HF crossbred and Verma *et al.* (2016) in Hardhenu crossbred. It is evident from Fig. 6 that the increase in peak yield upto fifth period (1990-2015) is associated

with corresponding rise in total milk yield and slight decline of peak yield from fifth period to sixth period (2015-2019) is correlated with comparable decrease in total milk yield suggesting that improvement in either of the two traits will increase the performance of another trait.

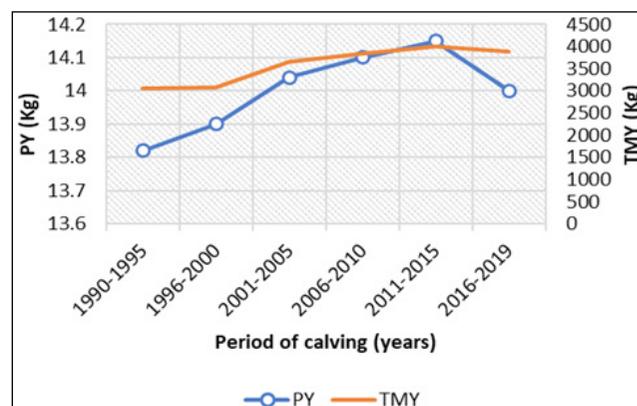


Fig. 6: Increase in peak yield (PY) upto fifth period (1990-2015) is associated with corresponding rise in total milk yield (TMY) and slight decline 6th period (2015-2019) is correlated with comparable decrease in TMY in crossbred cattle

TMY with DAPY

The positive phenotypic correlation between TMY and DAPY was found as 0.14 ± 0.67 in the present investigation while negative phenotypic correlation (-0.05 ± 0.00) between TMY and DAPY was substantiated by Thorat *et al.* (2017) in HF×Deoni. The genetic correlation between TMY and DAPY in the present study was found as 0.10 ± 0.58 which was in close agreement with the result (0.10 ± 0.00) reported by Thorat *et al.* (2017) in HF×Deoni. During the period from 1996–2000, total milk yield increased, days to attain peak yield also increased. Hence, the trend of TMY and DAPY over the years represented antagonistic relationship between, i.e., as total milk yield increases, days to attain peak yield also shows a similar increase which is not desirable (Fig. 7).

305DMY with PY

The phenotypic correlation between 305DMY and PY was found as 0.70 ± 0.26 in present study which was in close agreement with the results (0.79 ± 0.00) reported by

Pundir *et al.* (2016) in Kankrej and Ratwan *et al.* (2016) in Jersey crossbred while lower values of association (0.26 ± 0.28 to 0.288) were analysed by Patond and Bhoite (2014) in Gir triple cross. The positive and high genetic correlation between 305DMY and PY was obtained as 0.74 ± 0.29 in present study. Positive and high genetic correlation (0.863 to 0.99 ± 0.02) between these two traits were also substantiated by Patond and Bhoite (2014) in Gir triple cross, Pundir *et al.* (2016) in Kankrej and Ratwan *et al.* (2016) in Jersey cross. Fig. 8 shows the increasing trend of 305 DMY and PY around 1990-1995, a similar trend appeared during the 1996-2015 while concurrent decline in 305DMY and PY were noticed during 2016-2019 and same trend was observed in successive years of calving.

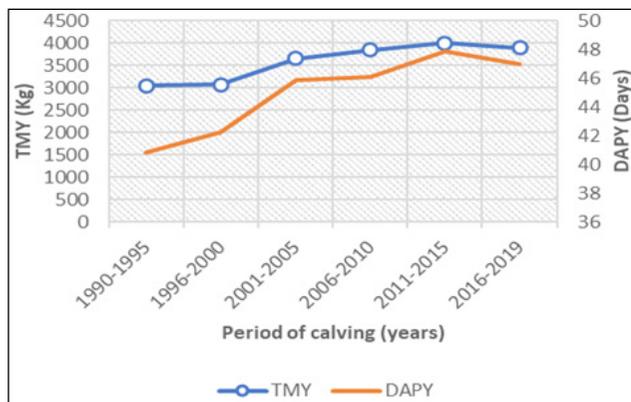


Fig. 7: From 1996–2000, total milk yield (TMY) increased, days to attain peak yield (DAPY) also increased. Hence, the trend of TMY and DAPY over the years represented antagonistic relationship between two traits in crossbred cattle

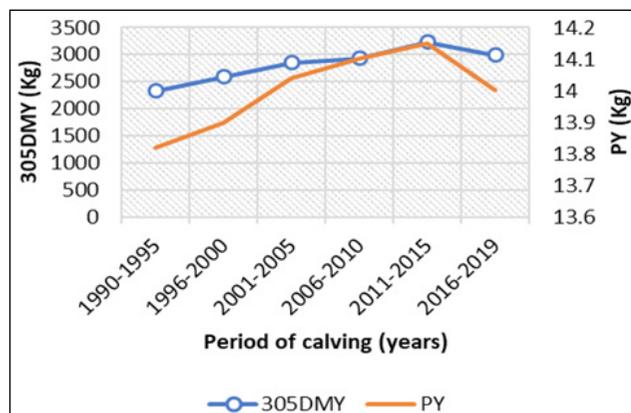


Fig 8: Increasing trend of 305 days milk yield (305DMY) and peak yield (PY) around 1990-1995, a similar trend appeared

during the 1996-2015 while concurrent decline in 305DMY and PY were noticed during 2016-2019 and same trend was observed in successive years of calving in crossbred cattle

305DMY with DAPY

The phenotypic correlation between 305DMY and DAPY was estimated as 0.14 ± 0.15 in the present study while negative (-0.04 ± 0.00) phenotypic correlation was reported by Thorat *et al.* (2017) in HF×Deoni. The genetic correlation between 305DMY and DAPY was estimated as 0.07 ± 0.23 while Thorat *et al.* (2017) reported genetic correlation as (0.45 ± 0.00) between these two traits in HF×Deoni. Low correlation (Fig. 9) between the characters suggested that there was minimal relationship between the traits.

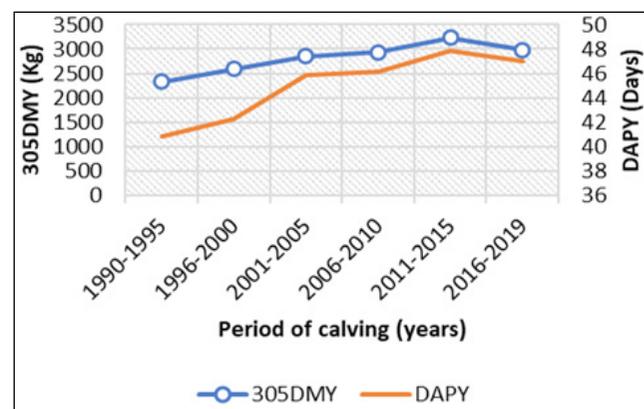


Fig. 9: Low correlation between the 305 days milk yield (305DMY) and days to attain peak yield (DAPY) shown in this figure suggested that there was minimal relationship between the traits in crossbred cattle

DAPY with PY

The phenotypic correlation between DAPY and PY was found as 0.13 ± 0.08 . The association between two traits that ranged from (0.003 ± 0.00 to 0.36 ± 0.00) were discerned by Anarase *et al.* (2015) in HF×Deoni and Thorat *et al.* (2017) in HF×Deoni cattle. The genetic correlation between PY and DAPY was obtained as 0.15 ± 0.61 in the present study while negative genetic correlation (-0.33 ± 0.00) between these two traits was reported by Thorat *et al.* (2017) in HF×Deoni cattle. The correlation between DAPY and PY is presented in

Fig. 10 which represents the low magnitude of positive correlation between the traits.

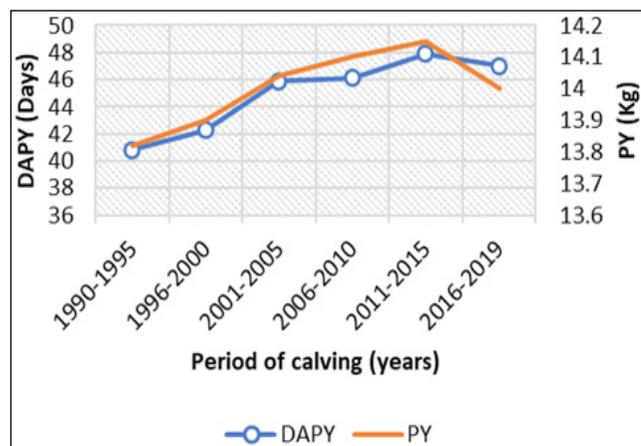


Fig. 10: Low magnitude of positive correlation between the traits days to attain peak yield (DAPY) and peak yield (PY) in crossbred cattle

CONCLUSION

The findings under present investigation confirmed that heritability estimates are low to medium indicated that faster genetic progress is possible through proper management and selection for the first lactation production traits. The sign and size of genetic correlation between the two traits would decide the amount and direction of change. Positive and high phenotypic and genetic correlation between some of the traits like total milk yield with lactation length (0.72 ± 0.08 and 0.77 ± 0.37), 305 days milk yield with total milk yield (0.79 ± 0.66 and 0.76 ± 0.46) and 305 days milk yield with peak yield (0.70 ± 0.26 and 0.74 ± 0.29) advocated that traits are favourably correlated and tandem selection can improve both the traits simultaneously, i.e. selection for lactation length (LL) and 305 days milk yield (305DMY) increase the selection response to total milk yield (TMY) and peak yield (PY). The low correlation between the traits is likely due to environmental variations. Due to positive and high phenotypic as well as genetic correlation of 305 days milk yield (305DMY) with total milk yield (TMY) and peak yield (PY), selection for 305DMY would be beneficial for enhancing the production in crossbred dairy cattle.

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