The Haryana Veterinarian (September, 2023) **62(SI-2)**, 1-5 ISSN 0033-4359 (P) **Research Article**

GENETIC ANALYSIS OF REPRODUCTION TRAITS IN CROSSBRED CATTLE

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ABSTRACT

The current study examined data on first reproduction traits of crossbred cows kept at an organized herd of Govind Ballabh Pant University of Agriculture and Technology, Pantnagar (Uttarakhand) spread over a 30-year period (1990-2019). The effect of numerous genetic and non-genetic factors on first reproduction traits, as well as their genetic control, was evaluated using mixed model least-square analysis. The performance records with respect to first reproduction traits *viz.*, age at first calving (AFC), first dry period (FDP), first service period (FSP) and first calving interval (FCI) were collected during from 529 animals sired by 79 bulls. The least square means for AFC, FDP, FSP and FCI were 1170.62 ± 31.50 days, 115.90 ± 19.84 days, 263.94 ± 3.40 days and 513.00 ± 22.60 days, respectively. The results of the analysis of variance revealed that the period of birth significantly influenced AFC ($P<0.05$) and FSP ($P<0.01$). Differences were statistically significant for the random effect of sire on AFC ($P<0.05$). Genetic groups significantly influenced FSP ($P<0.05$). The magnitude of heritability estimates were low for AFC, FDP, FSP and FCI ranging from 0.11 ± 0.03 to 0.18 ± 0.04. The genetic correlations were positive between FDP and FSP, FCI and FDP and FSP and FCI while negative genetic correlation was observed between AFC with FDP, FSP and FCI. The significant and positive genetic correlation between FSP and FCI suggested that selection for improvement in FSP will also improve FCI. Low heritability estimates were indicative of the presence of less additive genetic variance showing a significant role of management and environment in enhancing performance of reproduction traits for better gains in herd improvement.

Keywords: Crossbred cattle, Correlation, Heritability, First reproduction traits

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In the 1980s and 1990s, India had witnessed a white revolution, owing largely to an increase in milk production ascribed primarily to crossbred cows. To improve the genetic potential of milk production, indigenous cows (*Bos indicus*) were crossed with exotic (*Bos taurus*) bulls. The overall goal was to combine the milk output potential of exotic breeds with the sustainability and disease resistance qualities of indigenous breeds in their crossbred progenies (Kaur *et al.*, 2023). Today, India is the world's leading producer of milk, with an annual output of 221.06 million tonnes and 29.91% milk is contributed by crossbred cows while only 10.35% milk is shared by indigenous cows to the total milk production (Anonymous, 2021-22), i.e., why the selection programs involving crossing of native animals with exotic breeds is considered as a viable option. The aim of selection programs in most nations has recently been shifted to increase fertility in lactating animals (Shetkar *et al.*, 2022). The ability of dairy cow to reproduce is influenced by both genetic and non-genetic factors. However, genetic variations are important for breed development (Birhanu *et al.*, 2015). Furthermore, an animal's performance records should be corrected for classifiable non-genetic sources of variance, which directly prevent genetic potential from being recognized, thereby impeding reliable estimation of genetic parameters. Production efficiency is essentially determined by three processes: female production, reproduction, and growth of offspring (Kumar *et al.*, 2018). Reproduction is economically significant because it induces lactation in dairy cattle, decreases reproductive diseases and maximizes profitability through prompt calf crop (Valsalan *et al.*, 2022). Under Indian conditions, impaired fertility in crossbred cows is a serious problem, as it is the primary reason for involuntary culling of crossbreds. Female fertility is characterized by a variety of traits, and it can be challenging to identify the trait that best identifies the reproduction trait. However, it is more cost-effective to use heifer traits, such as age at first service and age at first calving, as an early indicator of evaluating reproductive performance (Kumar *et al.*, 2017). Maintaining a high level of production and enhancing genetic gain in dairy herds require accurate genetic evaluation of the animals (Vinothraj *et al.*, 2016). The development of appropriate selection criteria for dairy cattle is also predicated on knowledge of genetic factors. Heritability and correlations are the major genetic factors needed for animal breeding studies as well as for designing and implementing actual animal breeding programs (Dev and Dahiya, 2018). Heritability estimation is fundamental to evaluating breeding values and response to selection and to ascertaining management strategies (Ali *et al.*, 2019). Important reproduction traits must be improved in

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*Corresponding author: sudansimran321@gmail.com order to overcome the decline in fertility. Therefore, the goal of the current study was to determine how different genetic and non-genetic factors affect reproduction traits, as well as to estimate the genetic parameters in crossbreds maintained at the university farm.

MATERIALS AND METHODS

Data: The data on first reproduction traits of 529 crossbred cows that were sired by 79 bulls were gathered from the history sheets of the dairy farm at Govind Ballabh Pant University of Agriculture and Technology (GBPUA&T), Pantnagar, Uttarakhand spread over a period of 30 years (1990-2019). There were animals with varying amounts of Jersey, Holstein-Friesian and Red- Dane inheritance.

Management practices: The crossbred cows at the dairy farm of the GBPUA&T were kept utilizing a loose housing, zero grazing approach, this enabled free movement and enough exercise. The cows' nutritional needs were addressed with a uniform composition of concentrate feed and ad libitum access to green forage. Dry and green fodder were fed in a 2:1 ratio, respectively. Winter fodders included berseem, oats and maize while summer and rainy season fodders included maize, wheat bran, cowpea, rice bran and sorghum. The concentrate mixture used to feed various sorts of animals was specifically designed to satisfy their nutritional requirements. The animals were housed under hygienic conditions. All animals were vaccinated as a prophylactic measure on a regular basis and the sick animals received veterinary attention and were housed separately.

Data classification and statistical analysis: The data on the first reproductive performance records of heifers born between 1990 and 2019 were employed for analysis. Animals having records of abortion, stillbirth, or premature birth were excluded from the study. The data collection was purged of missing sire and dam identity record numbers. Outliers were eliminated, and only data within the range of mean+3SD were taken into consideration in order to ensure a normal distribution. Age at first calving was determined by taking the difference between date of birth and the first calving date; first dry period was calculated as the number of days from the date of first dry to date of first calving; age at first service was determined by counting the days between the date of birth and the first successful conception and first calving interval is the time interval between first two successive parturition. For the genetic studies, sires having more than five daughters were only considered. The technique outlined by Harvey (1990) was used to do a least square analysis of variance to examine the effects of genetic and non-genetic variables on first reproductive traits. The model used was as follows:

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

where,

Y_{ijklm} : observation of m^{th} animal

μ: overall mean

S_i: the random effect of i^{th} sire

L_j: fixed effect of j^{th} genetic group (1-8)

G_k: fixed effect of k^{th} season of birth (1-3)

P_l: fixed effect of l^{th} period of birth (1-6)

e_{ijklm}: random error associated with each trait was assumed to be NID (0, $\sigma^2 e$).

The means among different sub-classes were compared by using Duncan's multiple range test (Kramer, 1957). The following fixed effects were fitted using the model: eight genetic groups viz. G_1 (HF × RD × S), G_2 (HF × J × RD × S), G_3 (J × HF × S), G_4 (H × S), G_5 (J × S), G_6 (HF × J × R × S), G_7 (HF × R × S) and G_8 (HF × S) where, HF=Holstein Friesian, RD=Red Dane, S= Sahiwal, J= Jersey, H= Hariana and R= Rathi; three seasons of birth: summer (March-June), rainy (July-October) and winter (November-February) and six periods of birth viz. P_1: 1990-1995, P_2: 1996-2000, P_3: 2001-2005, P_4: 2006-2010, P_5: 2011-2015 and P_6: 2016-2019. The model also took the sire's random effect into account. The mixed model Least Squares and Maximum Likelihood Computer Program PC-1 (Harvey, 1990) were used to statistically analyse the data for estimation of genetic parameters.

RESULTS AND DISCUSSION

The overall least square means and coefficient of variation of reproductive traits are depicted in table 1.

Effect of sire, genetic group, season of birth and period of birth on reproduction traits: Sire had a statistically significant ($P < 0.01$) effect on AFC (table 2). Significant sire effect on AFC was also reported by Jadhav *et al.* (2019) in HF×Gir, Girimal *et al.* (2020) and Arya *et al.* (2020) in crossbred dairy cattle which suggested that by choosing superior sires, it is possible to genetically improve age at first calving while a non-significant effect on sire was reported by Kumar (2016) in crossbred cattle. The non-significant effect of sire on FDP, FSP and FCI demonstrated that these traits were unaffected by the sires utilized in selection and for genetic improvement. The genetic group had a significant effect on FSP ($P < 0.05$), which was analogous to the findings of Lodhi *et al.* (2016) in crossbred dairy cattle. The FSP for Holstein Friesian × Rathi × Sahiwal was 241.89±20.44 days, whereas FSP for

Table 1. Least squares mean (±SE) and coefficient of variation (% CV) for first reproduction traits in crossbred cows

Factor	Traits								
	No. of daughters	AFC (days)	%CV	FDP (days)	%CV	FSP (days)	%CV	FCI (days)	%CV
				Genetic groups					
HF×RD×S	66	1152.77± 51.16	23.4	122.70± 33.14	36.2	267.69 ± 4.24^{ab}	10.82	529.33± 61.61	28.9
HF×J×RD×S	251	1142.73± 39.29	23.6	127.59± 24.75	36.2	266.23 ± 13.99^{b}	10.88	533.44 ±28.19	28.7
J×HF×S	85	1165.61± 52.61	23.2	114.54± 30.02	40.4	268.07 ± 9.26^{ab}	10.81	553.38 ±58.50	27.7
H×S	18	1116.78± 85.86	24.2	140.06± 54.09	33.0	262.93± 5.68^{b}	11.02	519.40 ± 34.19	29.5
J×S	9	1549.66± 189.42	17.4	68.87± 81.65	67.2	276.67 ± 8.80^{bc}	10.4	524.14 ± 37.75	29.2
HF×J×R×S	66	1073.15 ± 47.65	25.1	127.83± 32.23	36.2	263.34 ± 5.52^{b}	11.0	527.55 ±36.71	29.0
HF×R×S	18	1024.84± 81.52	26.3	156.69± 51.36	29.5	241.89 ± 20.44^{ab}	11.9	461.57 ±93.00	33.2
HF×S	16	1139.45± 129.61	23.7	68.92± 119.34	67.1	264.71 ± 5.14^{b}	10.95	455.19±135.92	33.7
				Season of birth					
Summer	189	1178.73 ± 39.05	22.94	128.50 ±22.39	36.0	265.55 ± 3.83	10.97	520.27 ±25.51	29.5
Rainy	113	1186.55 ± 35.55	22.79	114.02± 23.64	40.6	260.49 ± 4.21	11.18	495.41± 28.02	30.9
Winter	227	1146.59 ± 37.53	23.5	105.18±24.60	44.0	265.78 ± 4.05	10.96	523.32± 26.93	29.3
				Period of birth					
Period 1 (1990-1995)	55	946.26 ± 83.92^{cd}	28.5	144.05± 52.87	32.1	248.37 ± 11.69^{a}	11.7	507.30± 45.11	30.2
Period 2 (1996-2000)	136	1027.07 ± 75.52^{d}	26.3	160.97± 68.25	28.7	261.07 ± 7.16^{ab}	11.16	536.56 ±60.22	28.6
Period 3 (2001-2005)	124	1095.53 ± 62.86^{a}	24.6	105.39 ±45.63	43.9	263.70 ± 6.78^{b}	11.05	490.76± 51.97	31.2
Period 4 (2006-2010)	102	1107.49 ± 72.42^{cd}	24.4	101.04 ±39.60	45.8	266.38 ± 9.06^{ab}	10.93	522.51 ±77.74	29.3
Period 5 (2011-2015)	59	1523.51±108.34^{b}	17.7	109.98 ±47.58	42.0	272.75 ± 8.15^{b}	10.6	533.38± 54.19	28.7
Period 6 (2016-2019)	53	1323.89 ± 66.34^{bc}	20.4	73.97 ±41.79	62.5	271.36 ± 7.81^{b}	10.7	487.47 ±47.60	31.4
Overall mean	529	1170.62 ± 31.50	23.1	115.90 ± 19.84	39.9	263.94 ± 3.40	11.0	513.00 ± 22.60	29.9

Least square means within subclasses with different superscripts (a, b and c) are significantly (P< 0.05) different from each other. The number of observations is indicated by figures in parenthesis. where, HF=Holstein Friesian, RD=Red Dane, S= Sahiwal, J= Jersey, H= Hariana and R= Rathi; AFC= Age at first calving, FDP= first dry period, FSP= first service period and FCI= first calving interval.

Jersey×Sahiwal was 276.67±8.80 days. The non-significant disparities across genetic groups for AFC, FDP and FCI suggested that animals were able to express their full genetic potential regardless of their genetic groups. Season of birth had a non-significant effect on AFC, FSP, FDP and FCI. This corroborates with the findings of Lodhi *et al.* (2016) in crossbred cattle and Ambhore *et al.* (2017) in Phule Triveni, while a significant effect was discerned by Arya *et al.* (2020) in AFC, FSP, FDP and Mote *et al.* (2019) in Gir × Holstein-Friesian × Jersey. The non-significant effect of the season of birth on AFC, FSP, FDP and FCI concluded that animals were able to express their full genetic potential for the respective traits irrespective of fluctuations in environmental conditions during different seasons of birth (table 1).

Period of birth had statistically significant effect on AFC and FSP. Significant effect of period (P< 0.01) on AFC (table 1) was also reported by Lodhi *et al.* (2016) and Girimal *et al.* (2020) in various crosses of cattle, while non-significant effect of period of birth on AFC was discerned by Singh *et al.* (2015) in crossbred cattle. Cows that calved during first period i.e. Period 1 (1990-1995) had the shortest AFC (946.26±83.92 days) while the cows that calved during Period 5 (2011-2015) had the longest AFC (1523.51±108.34 days). The significant differences due to the period of birth on AFC might be due to the variations in fodder availability at different time periods that affect the growth rate of heifers and AFC of crossbreds. The period of birth had a significant (P< 0.05) influence on FSP. Cows that calved during 1990-1995 had the shortest FSP (248.37±11.69 days) while the cows that gave births during 2011-2015 had the longest FSP (272.75±8.15 days). A similar finding was observed by Lodhi *et al.* (2016) in crossbred cows while a non-significant effect of the period was reported by Verma (2016) in Frieswal bulls. The non-significant influence of period of birth on FDP and FCI revealed that the animals were well acclimated to the changes in period of their birth, which may allow animals to demonstrate their greatest genetic potential for the relevant trait regardless of their period of birth.

Estimates of genetic parameters

Heritability: Heritability estimates for AFC, FSP, FDP and FCI are presented in table 3. The heritability estimate

Table 2. Analysis of variance of AFC, FSP, FDP and FCI of crossbreds influenced by sire, genetic group, season and period of birth

Source of variation	Mean sum of squares				
	d.f	AFC	FSP	FDP	FCI
Sire	78	141414.264**	1087.71	20167.69	25419.87
Genetic group	7	109163.31	575.40*	6378.14	7194.71
Season of birth	2	70968.53	914.794	18118.81	24051.44
Period of birth	5	256047.87**	495.09*	16488.25	17508.56
Error	436	77677.924	905.21	30832.27	39995.65

*Significant at 5% level (P<0.05), **Significant at 1% level (P<0.01), d.f= degree of freedom

Table 3. Overall estimates of heritability (diagonal), genetic correlation (above diagonal) and phenotypic correlation (below diagonal) for reproductive traits.

Traits	AFC	FDP	FSP	FCI
AFC	0.18 ± 0.04	-0.10±0.85	-0.11±0.23	-0.10±0.08
FDP	-0.07±0.43	0.12± 0.02	0.31±0.27	0.46±0.12
FSP	0.08 ± 0.32	0.36±0.12*	0.14±0.01	0.58±0.17*
FCI	0.05±0.42	0.56±0.25	0.81±0.03**	0.11 ± 0.03

* P≤ 0.05 and ** P≤ 0.01 level of significance.

for AFC (0.18±0.04) in the present study was in line with the finding of Lodhi *et al.* (2016) in different breeds of cattle (0.20±0.12). Kumar (2015) and Jadhav *et al.* (2019) estimated a lower heritability of 0.16±0.14 in Frieswal and HF×Gir while higher estimates of heritability (0.43±0.13 to 0.48±0.19) were divulged by Chaudhari *et al.* (2013) in Frieswal, Ambhore *et al.* (2017) in Phule Triveni and Arya *et al.* (2020) in various crosses of cattle.

Heritability estimates in the present study confirm the results of Lodhi *et al.* (2016) as 0.10±0.03 and Jadhav *et al.* (2019) as 0.12±0.12. Lower estimate than the present study was reported by Arya *et al.* (2020) as 0.05±0.08 while higher (0.32±012 to 0.42±0.23) values were obtained by Kumar (2015) and Sawant *et al.* (2016) in Gir. The estimate of heritability for FSP in the present finding (0.14±0.01) conform the result of Dash *et al.* (2016) in Karan Fries. Lower estimates were discerned by Kumar (2015) as 0.02±0.17 in Frieswal and Divya *et al.* (2014) as 0.05 ± 0.13 in Karan Fries while higher estimate was found by Chaudhari *et al.* (2013) as 0.40±0.14 in in Frieswal. The heritability estimates for FCI (0.11 ± 0.03) conform the reports of Dash *et al.* (2016) as 0.15±0.07. Lower estimate was reported by Arya *et al.* (2020) as 0.09±0.08 while higher value was reported by Saha *et al.* (2010) as 0.35± 0.10 in Karan Fries.

Genetic and phenotypic correlations among reproduction traits: Low and negative genetic correlation between AFC and FDP (-0.10±0.85), AFC and FSP (-0.11±0.23) and AFC and FCI (-0.10±0.08) presented in table 3 conform the reports of Lodhi *et al.* (2016) and Arya *et al.* (2020) in various crossbred cattle while positive association between these traits was reported by Jadhav *et al.* (2019) in HF×Gir. Positive genetic correlation was found for FDP with FSP (0.31±0.27) and FCI (0.46±0.12). Significant and positive rg (0.58±0.17*) was obtained between FSP and FCI. The results in the present study conform the reports of Arya *et al.* (2020) and Jadhav *et al.* (2019). Negative rp (-0.07±0.43) between AFC and FDP agree with the reports of Lodhi *et al.* (2016) and Arya *et al.* (2020) while positive rp was calculated by Jadhav *et al.* (2019). Positive rp between AFC and FSP (0.08 ± 0.32) was in conformity with the results obtained by Jadhav *et al.* (2019) and Arya *et al.* (2020). Significant and positive rp between AFC and FDP (0.36±0.12*) was also divulged by Lodhi *et al.* (2016) and Jadhav *et al.* (2019) while negative rp between AFC and FDP was obtained by Arya *et al.* (2020). Positive rp of AFC with FCI (0.05±0.42), FDP with FCI (0.56±0.25) and FSP with FCI (0.81±0.03**) agree with the reports of Lodhi *et al.* (2016), Jadhav *et al.* (2019) and Arya *et al.* (2020). Positive and significant rp of AFC with FDP indicated that increase in age also tend to increase first dry period. Likewise, significant and positive association between FSP with FCI stipulated that increase in first service period favour increase in first calving interval. However, at genetic scale negative association was found between AFC and FDP specifying that cows with longer age at first calving tended to have shorter first dry period. The results in the present investigation correspond with the results obtained by Lodhi *et al.* (2016), Jadhav *et al.* (2019) and Arya *et al.* (2020) in different studies.

CONCLUSION

The sire and period of birth had a significant effect on age at first calving (AFC) while genetic group and period of birth affected first service period (FSP) of crossbred heifers. The low heritability measures indicated a limited role of additive genetic variance and major influence of environmental variance. Thus, better management strategies can help in ameliorating the performance of animals as the selection has a limited role to bring improvement in the herd. The significant and positive genetic correlation between FSP and FCI suggested that selection for improvement in FSP will also improve FCI. It can be concluded that for optimal genetic improvement and their correlated response, all economic traits that lead to greater accuracy must be included in selection programs.

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