



Genetic Evaluation of Reproductive Performance and Milk Production in Sahiwal Cows

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ABSTRACT

Background: Genetic parameter and covariance component estimation is an important aspect of animal breeding, as it helps to quantify additive and non-additive genetic variances. The precise estimation is also essential for reliable prediction of breeding values. The milk production for each animal in lactation has shown increasing trend over the last seven decades in the herd under study. The important fact is that more than 50% progress is associated with genetic progress and rest is credited to advances in management practices. However, on the other hand the picture is different while tracking for fertility over this period that showed a decline trend. The continuous selection for milk production traits leads to decline in reproduction traits. Thus, present study is planned to study the effect of continuous selection for milk yield on fertility traits and the probable measures to overcome these effects. The study was conducted on Sahiwal cattle herd maintained at ICAR-NDRI, Karnal.

Methods: The data was collected from records belonging to 1955-2024 on first lactation production and reproduction like FLTMY, FL305dMY, FSP, FCI, DPR and AFC traits. The effect of non-genetic factors was estimated using least-squares analysis by General Linear Model of SPSS. The variance and (co)variance components were estimated by using the BLUPF90 family of programs.

Result: The genetic variability measured by genetic parameters indicated that genetic and phenotypic correlation between production and reproduction traits was negative and between productions traits were high in the study. Overall, the genetic trend was positive in the present study for production traits whereas the reproduction traits exhibited unfavourable or inconsistent trends. The information generated in the present study will be useful in planning future breeding activities for further improvement of the breed.

Key words: Correlation, Genetic parameter, Genetic trend, Heritability, Sahiwal.

INTRODUCTION

Agriculture plays a vital role in national income and employment contributing about 16% in the country's GDP providing livelihood support to about 46.1% of the population. Among allied sectors livestock has emerged a key driver of growth with a representation of 5.5% of the total GVA and thus boosting the per capita availability of milk (Economic Survey 2024-25). India's bovine livestock resources consist of 53 breeds of different geographical regions. They contribute about 11.36% of total milk production in India (BAHS, 2024) and over years average milk production has been increased from 2.5 kg/day to 3.5 kg/day mainly due to selection of animals with higher production potential in the breeding programme. The precise estimation of genetic parameter and variance components are pre-requisite in estimating heritabilities, breeding values, genetic correlations between traits and can be improved over generations (Dass and Sadana, 2000; Chitra *et al.*, 2016; Van der Werf, 1990). There is a need to update the genetic parameters from time to time since different non genetic factors influence genetic parameters in a breeding program. The antagonistic genetic relationship exists between production and reproduction traits (Pryce *et al.*, 2004; Yamazaki *et al.*, 2014) and continuous selection for milk production traits leads to decline in reproduction traits. Despite the low heritabilities in reproduction traits, there exists sufficient additive genetic variation and improvement is possible along with

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production traits (Norman *et al.*, 2009). Moreover, Nordic countries (including Denmark, Finland and Sweden) since 1994 are pioneers in including reproduction traits in their selection programme. The Centre for Dairy Cattle Breeding (CDCB, 2025) in United States (US) reported that breeding programmes earlier focused solely on milk yield, leading to declining pregnancy rates and inclusion of traits like daughter pregnancy rate DPR made positive trends both in fertility and milk production (VanRaden *et al.*, 2004). The present study is aimed to investigate the genetic parameters, (co) variance components and genetic trends for production and reproduction traits in Sahiwal cattle to find out the favourable traits for giving due importance during selection of breeding animals for achieving higher genetic improvement in the herd. Sahiwal is one of the

milch breed having a population of 5.9 million in India (Livestock census, 2019) and is reared for its milk producing ability, climatic adaptation to tropics. The present study thus focussed to estimate the genetic parameters viz. heritability, genetic and phenotypic correlation and genetic trend.

MATERIALS AND METHODS

The data on first-lactation production and reproduction traits First lactation total milk yield (kg), First lactation 305 days milk yield (kg), First service period (days), First calving interval (days), First daughter pregnancy rate (%) and Age at first calving (days) (FLTM, FL305dMY, FSP, FCI, DPR and AFC) of Sahiwal cattle (1955–2024) at ICAR-NDRI, Karnal were collected. Least-squares analysis was performed using the General Linear Model in SPSS (v 26.0). The difference of means between subclasses of season, period and were tested for significance using DMRT as modified by Kramer (1957). Variance and (co)variance components and genetic correlations were estimated using single- and multi-trait animal models in the BLUPF90 program family (Misztal, 2002). Estimation was done by REML with the AI-REML algorithm (VCE option), with unknown parents coded as '0' and missing records as 999. A linear mixed model used:

$$y = X\beta + Z\alpha + r$$

Where,

y= Vector of phenotypic traits;

β = The vector of all fixed effects.

α = Vector of random additive genetic effect for each animal.

r= Vector of random residual.

X and Z= Incidence matrices for each corresponding effect.

Genetic trends were obtained by regressing yearly mean estimates of breeding values on year of birth. Phenotypic trends were estimated using the linear regression of average phenotypic values on the birth year.

RESULTS AND DISCUSSION

The least-squares means of FLTM 2060.94±55.06 kg, FL305dMY 1840.48±40.07 kg, FSP 132.34±3.70 days, FCI 484.98±6.53 days, FDPR 0.30±0.01% and AFC 1162.75±7.24 days were found in the present study (Table 1 and Table 2). The production and reproduction traits were significantly influenced by period of calving ($P<0.01$), while season and age at first calving had no effect, with only significant effect of season on FDPR with average as 0.34±0.008 and 69.5% variability that indicates scope for genetic improvement through the breeding programs. The main goal of animal breeding is to improve animal genetically through selection and breeding programs and which depend on the genetic variability that exists within the herd. The variability is measured by estimates of genetic parameters i.e. heritability and correlations of important traits that are used to estimate breeding values (EBV). Therefore, the estimation of genetic parameters is an essential component of animal breeding (Gandhi and

Kumar, 2014). The (co) variance and heritability estimates for production and reproduction traits were 0.22 for FLTM and FL305dMY, 0.04 for FSP, 0.09 for FCI, 0.06 for FDPR and 0.19 for AFC (Table 3). The Additive variance (σ^2_a) was higher in production traits having highest value for FLTM (190,150) and lowest for FDPR (0.0036). The moderate heritability estimates for production traits indicate sufficient additive genetic variability for improvement and can be effectively improved through selection (Parveen *et al.*, 2018). Higher heritability estimates for AFC than the present study was reported by Ayalew *et al.* (2017) and Ali *et al.* (2019), while Worku *et al.* (2021) and Roy *et al.* (2024) reported comparable values in Sahiwal cattle. The wide variation in heritability estimates for AFC might be due to differences in sire and management practices affecting the results. The estimate in present study indicated that genetic improvement in the trait is possible through selection. The heritability estimates for calving interval (0.01-0.14) and service period (0.04-0.09) and were also reported by VanRaden *et al.* (2004), whereas higher estimates reported by Ayalew *et al.* (2017), Ali *et al.* (2019), Worku *et al.* (2021) and Roy *et al.* (2024) reported lower values. The higher estimates of heritability as compared to current study of FSP were reported by Ali *et al.* (2019) and Roy *et al.* (2024). Thus, it can be concluded that most of the reproductive traits had low heritability that indicate low additive variance and can be modified by non-genetic factors. The genetic and phenotypic correlation between production traits (FLTM and FL305dMY) was positive and highly significant (0.99±0.04) and 0.92±0.004, respectively ($p<0.01$) (Table 4) and is comparable with the estimates reported by Ahmad *et al.* (2001) and Ayalew *et al.* (2017). This suggested that these production traits were affected by similar set of genes and environmental factors and were in agreement with Ahmad *et al.* (2001) and Roy *et al.* (2024). Both traits had positive and significant genetic correlation with FSP and FCI and it can be inferred that animals with higher milk yield generally had higher service period and calving interval and reconfirms that antagonistic association exists between production with reproduction traits, however contradicting findings were reported by Valsalan *et al.* (2022). The high positive genetic correlations between FL305dMY and CI revealed that increased milk yield might be due to prolong FCI and similar findings reported by Kgari *et al.* (2020). The present findings were in conformity with the findings of (0.51) Worku *et al.* (2021) and (0.57) Valsalan *et al.* (2022). The genetic correlation between FLTM and FDPR was low positive and significant, whereas in literature the correlation among them were reported as negative (Lucy, 2019). Thus, reproduction can be improved along with production by following stringent management practices. The production traits generally showed negative correlations with reproductive traits and both FLTM and FL305dMY were negatively correlated with AFC. It indicated that additive genes that helps to increase milk yield will lead to reduction in AFC and early onset of puberty eventually

Table 1: The least squares means (LSM±SE) for main effect on production and reproduction traits in sahiwal cattle.

Factor	No. of obs.	FLTM	No. of obs.	FL305dMY	No. of obs.	FSP	No. of obs.	FCI	No. of obs.	FDR
Overall mean	939	2060.94±55.06	1011	1840.48±40.07	832	132.34±3.70	836	484.98±6.53	832	0.30±0.01
SOC										**
Winter	448	2071.22±62.54	478	1876.54±45.55	428	133.25±5.97	392	474.41±7.46	428	0.34 ^{ab} ±0.01
Summer	306	2068.06±67.51	333	1846.85±48.51	232	132.24±6.81	240	492±8.41	232	0.32 ^b ±0.02
Rainy	128	2136.47±88.35	136	1915.74±64.39	113	157.31±8.17	131	484.9±10.11	113	0.31 ^a ±0.02
Autumn	57	1968.02±126.78	64	1722.8±88.51	59	120.01±5.45	73	488.62±13	59	0.23 ^a ±0.03
POC		**		**		**		**		**
1 (1958-63)	17	2849.86±226	17	2574.65±167.32	14	152.15 ^{cd} ±14.60	16	455.24 ^{ab} ±26.22	14	0.18 ^a ±0.06
2 (1964-68)	29	2744.66±170.75	29	2228.27±126.57	18	153.30 ^d ±12.68	26	518.85 ^c ±20.24	18	0.26 ^{ab} ±0.06
3 (1969-73)	121	2142.34 ^d ±93.62	121	1916.72 ^{cde} ±68.84	85	138.25 ^{bcd} ±6.51	97	492.85 ^{bc} ±11.53	85	0.29 ^{abcd} ±0.03
4 (1974-78)	27	1882.71 ^{bcd} ±179.15	30	1546.52 ^b ±126.37	19	105.40 ^a ±12.61	22	496.77 ^{bc} ±22.18	19	0.37 ^{bcd} ±0.06
5 (1979-83)	32	1976.65 ^{bcd} ±169.89	36	1617.78 ^b ±118.87	22	132.54 ^{abcd} ±11.85	21	489.28 ^{abc} ±23.10	22	0.31 ^{bcd} ±0.05
6 (1984-88)	55	2129.84 ^{cd} ±133.68	43	1962.44 ^{cde} ±109.46	42	111.56 ^{ab} ±8.90	33	458.87 ^{ab} ±18.95	42	0.39 ^{de} ±0.04
7 (1989-93)	60	2157.5 ^{cd} ±129.68	61	2070.4 ^d ±94.73	50	114.96 ^{ab} ±8.31	32	430.42 ^a ±19.08	50	0.42 ^a ±0.04
8 (1994-98)	59	2278.24 ^d ±128.88	60	2046.17 ^{de} ±94.46	53	136.86 ^{bcd} ±7.92	48	456.00 ^{ab} ±15.67	53	0.27 ^{abc} ±0.03
9 (1999-03)	72	1298.55 ^a ±117.95	93	1188.82 ^a ±78.43	93	132.81 ^{bcd} ±6.38	87	484.24 ^{abc} ±12.24	93	0.31 ^{bcd} ±0.03
10 (2004-08)	113	1830.67 ^{bc} ±99.09	119	1698.54 ^b ±70.89	126	126.47 ^{abc} ±5.82	116	489.36 ^{bc} ±11.07	126	0.36 ^{bcd} ±0.03
11 (2009-13)	93	1949.19 ^{bcd} ±102.09	103	1737.21 ^{bcd} ±72.44	124	126.63 ^{abcd} ±5.6	120	485.24 ^{abc} ±10.49	124	0.33 ^{bcd} ±0.02
12 (2014-18)	126	1947.41 ^{bcd} ±89.33	134	1785.92 ^{bcd} ±64.27	92	149.91 ^{cd} ±6.02	128	530.17 ^a ±9.85	92	0.24 ^{ab} ±0.03
13 (2019-24)	135	1604.66 ^{ab} ±88.96	165	1552.87 ^b ±60.20	94	139.62 ^{bcd} ±6.14	90	517.56 ^c ±11.52	94	0.27 ^{abcd} ±0.03
AFC										
1 (762-936)	62	2061.88±122.78	60	1772.38±91.57	55	130.68±7.6	56	496.32±14.22	55	0.31±0.03
2 (937-1110)	338	2059.54±64.14	341	1800.99±46.72	316	133.52±3.99	298	483.57±7.36	316	0.3±0.01
3 (1111-1284)	315	2139.88±62.38	359	1864.23±43.97	279	129.27±3.87	277	481.12±7.28	279	0.32±0.01
4 (1285-1458)	144	2165.48±85.98	162	1902.91±60.38	130	132.17±5.29	134	476.07±9.96	130	0.29±0.02
5 (1459-1632)	57	1889.53±126.02	65	1736.22±87.89	36	126.89±9.19	50	504.12±15.25	36	0.32±0.04
6 (1633-1806)	23	2049.33±194.95	24	1966.17±141.26	16	141.49±13.72	21	468.71±22.86	16	0.27±0.06

SOC (Season of calving) and POC (Period of calving); FLTM: First lactation total milk yield; FL305dMY: First lactation 305 days milk yield; FSP: First service period; FCI: First calving interval; FDP: First daughter pregnancy rate.

will lead to increase in milk yield in the herd (Ayalew *et al.*, 2017). In other words, animals with early AFC had more yields than the late calvers that are desirable for running the livestock farming as a profitable venture (Roy *et al.*, 2024). The negative genetic correlation between FL305dMY and AFC were also reported by Yosef (2006); Ayalew *et al.* (2017), however positive correlation was reported in Holstein Friesian dairy cattle (Ojango and Pollott, 2001). The negative phenotypic correlation between FLTMY, FL305dMY and AFC in the current study were also supported by study of (-0.02) Ahmad *et al.* (2001) and (-0.24) Roy *et al.* (2024) and conversely positive phenotypic correlation was reported by Yosef (2006) in Jersey cattle. The phenotypic correlation among reproductive traits association of FSP with FCI, FDPR and AFC respectively, were found to be positive. This indicates that improvement in one trait can positively influence others (Ayalew *et al.*, 2017 and Ayalew *et al.* (2017). These findings suggests that both FCI and FSP are controlled by similar genes i.e. they are pleiotropic in nature (Falconer and Mackay, 1996). The low to high phenotypic (0.15 to 0.51) correlations of FSP with FL305dMY and FLTMY reported in our study (Table 3) were well comparable with the study of Worku *et al.* (2021) and Roy *et al.* (2024). Positive phenotypic correlation between FCI and FSP were reported by Roy *et al.* (2024) which was in conformity with the findings of present study. In the present study FSP had negative genetic correlation with AFC and FDPR while FCI had negative genetic correlation with AFC only. In the recent report by Valsalan *et al.* (2022) positive genetic correlation of FDPR with SP and AFC was observed. In another study the pregnancy rate

Table 2: The least squares means (LSM±SE) for main effect on age at first calving in sahiwal cattle.

Factor	No. of obs.	Age at first calving
Overall mean	1514	1162.75±7.24
Season of birth		
Winter	642	1152.20±8.80
Summer	390	1156.22±10.82
Rainy	297	1169.64±11.59
Autumn	185	1172.93±14.31
Period of birth		
1 (1955-1964)	49	1167 ^{cde} ±60.59
2 (1965-1969)	127	1233.61 ^e ±14.07
3 (1970-1974)	73	1105.79 ^{abc} ±21.55
4 (1975-1979)	31	1222.54 ^{de} ±32.76
5 (1980-1984)	63	1069.81 ^a ±23.1
6 (1985-1989)	77	1068.01 ^a ±20.89
7 (1990-1994)	88	1078.91 ^{ab} ±19.41
8 (1995-1999)	125	1185.74 ^{de} ±16.33
9 (2000-2004)	198	1101.44 ^{abc} ±13.18
10(2005-2009)	203	1230.44 ^{de} ±13.06
11 (2010-2014)	220	1243.87 ^e ±12.49
12 (2015-2019)	192	1252.05 ^e ±13.20
13 (2020-2022)	68	1156.57 ^{bcd} ±22.25

Table 3: Estimates of variance components of production and fertility traits using multi trait animal model in sahiwal cattle.

	FL305dMY	FSP	FCI	FDPR	AFC
Additive genetic variance σ^2_a	115250±23092	281.59±188.87	1109.5±59.54	0.0035582±0.32716E-03	2780.2±725.25
Residual variance σ^2_c	381630±14402	6926.9± 281.12	10794±122.51	0.060388±0.28373E-02	12325± 649.88
Phenotypic variance σ^2_p	496880±22875	7208.4±281.59	11904±135.08	0.063946±0.28261E-02	15106±592.13
Heritability±SE (h^2 ±SE)	0.22±0.05	0.04±0.003	0.09±0.005	0.06±0.005	0.19±0.04

was found to be highly correlated with reproduction traits and suggested that pregnancy rate can be used to judge and improve reproduction in dairy animals (Jorjani, 2007).

Antagonistic relationship between the production and reproduction traits could probably be as a result of pleiotropic gene effect between these traits, whereby the genes that affect the production traits also influenced the reproduction traits. The negative relationship between production and reproduction traits shows that reproduction traits should be included in the selection criteria for dairy cattle. The study found negative genetic correlation between production and reproduction traits but sufficient additive variation to improve reproduction traits. However, progress in reproduction is possible only when selection targets both production and reproduction traits, supported by stringent management practices.

Genetic trends were estimated to assess progress in production traits achieved through selection and assist in breeding decisions for genetic improvement and higher economic return. The breeding value is used to find out the genetic trend when plotted against year of birth reflecting changes in performance per unit time due to changes in mean breeding value Harville and Henderson (1967) for the traits. The positive and significant ($p < 0.01$) genetic trend (Table 5) was found for FLTMY, FL305dMY, FCI although non-significant for AFC, whereas negative genetic trend was found for FSP and FDPR traits in the current study. The positive and significant genetic trend revealed that selection practices followed in the herd lead to genetic improvement. The coefficients of determination (R^2) were modest (0.143 and 0.132, respectively) such values are consistent with those reported by (VanRaden *et al.*, 2021), where residual R^2 often ranges between 3-18%. Thus, despite low R^2 , the positive slopes demonstrate meaningful long-term selection response. Positive genetic trends for

TMY and 305dMY were reported by Sahin *et al.* (2014); Dash *et al.* (2016) and Dash *et al.* (2023), while Sahin *et al.* (2012) found negative trends due to use of inferior sires. The declining genetic trend for FL305dMY in the present study indicated that new sires and cows were introduced for time to time in the present breeding scheme. The phenotypic trends were negative for FLTMY, FL305dMY, FSP and AFC, while positive trends were observed for FCI and FDR (Table 5). The similar trend for FSP was observed by (Solemani *et al.* 2014; Rahbar *et al.*, 2016). Whereas Van Vleck *et al.* (1986) suggested that production traits like milk yield have improved in Holstein cattle, reproductive traits have declined. Negative trend for FDPR was reported by Dash *et al.* (2016) in (Karan-Fries) cattle; Hansen (2008) in HF in contrast to an increasing trend in the milk production. VanRaden *et al.* (2004) reported breed-wise differences in DPR trends in the USA, with greater losses in Brown Swiss and Holstein than Jersey and Ayrshire. Introduction of DPR into genetic evaluation since 2003 led to decline in fertility due to improved reproductive management and selection (Norman *et al.*, 2009). The present study reported negative genetic trend for FSP and positive for FCI. In literature, both positive and negative genetic and phenotypic trends were reported. The main reason was different management and feeding practices followed in the herd. The shorter calving intervals require improved nutrition, disease control and reproductive management. Both negative Rahbar *et al.* (2016) and positive Dash *et al.* (2016); Choudhary *et al.* (2018) genetic trends for FSP were reported which is contrary to the current study where both phenotypic and genetic trend were negative. The results revealed that present management and breeding strategies were yielding positive results with regard to decrease in service period over the years. Negative genetic trend for FCI was reported Choudhary *et al.*

Table 4: Genetic and phenotypic correlation between production and reproduction traits.

Traits	305DMY	TMY	SP	CI	DPR	AFC
305 DMY	1	0.99±0.04**	0.71±0.34**	0.63±0.48**	-0.30±0.81**	-0.14±0.16**
TMY	0.92±0.004**	1	0.30±0.47**	0.50±1.04**	0.17±0.86**	-0.13±0.18**
SP	0.15±0.03**	0.51±0.02**	1	0.91±0.46**	-0.88±0.03**	-0.73±0.38**
CI	0.17±0.02**	0.26±0.03**	0.96±0.02**	1	0.79±0.03**	-0.53±0.41**
DPR	-0.12±0.04**	-0.28±0.04**	-0.80±0.01**	0.73±0.01**	1	0.32±0.76**
AFC	0.04±0.03	-0.01±0.03	-0.03±0.03	-0.55±0.03**	-0.01±0.03	1

** $P < 0.01$; * $P < 0.05$, Genetic correlation (above diagonal) and phenotypic (below diagonal) correlation.

Table 5: Genetic and phenotypic trend.

Traits	Genetic trend	R^2	Phenotypic trend	R^2
FLTMY (kg/year)	2.84±0.80**	0.143	-15.02±3.06**	0.26
FL305dMY (kg/year)	1.89±0.56 **	0.132	-11.06±2.31**	0.25
FSP (Days/year)	-0.02±0.04	0.005	-0.12±0.16	0.008
FCI (Days/year)	0.41±0.13**	0.107	0.73±0.44	0.04
FDPR (%)	-0.02±0.03	0.007	0.000676±0.000694	0.014
AFC (Days/year)	0.11±0.18	0.005	-0.16±0.63	0.00099

(2018) and Bene *et al.* (2024) and positive genetic trend for FCI reported by Parveen *et al.* (2018). The genetic trend for FCI was positive and significant which corresponds to a gain of 0.41 days/year. The positive genetic trend for calving interval indicates a tendency toward longer intervals, reflecting declining reproductive efficiency. This may result from selection prioritizing production over fertility traits (Bene *et al.*, 2024; Seno *et al.*, 2010). A longer FCI is undesirable for herds targeting one calf per year, shorter intervals require improved management, nutrition, disease control and AI. In the present study very low R^2 values (0.007-0.107) for FSP, FCI, FDPR and AFC indicated negligible genetic progress in reproductive traits, indicating historical selection emphasis on milk yield over reproduction. Thus, the selection pressure applied was directed towards the production traits and findings in the present study suggest that there is a need to inclusion of reproduction traits while selection of animals in the herd.

CONCLUSION

In the evaluation and success of Sahiwal cattle breeding program, the precise estimation of genetic parameter for production and reproduction traits is important for accurate prediction of genetic merit of individual in the next generation. These estimates serve as a guideline in implementation of genetic improvement in population using various approaches. The heritability estimates for all reproduction traits indicated that the major part of variation for those traits was due to environmental factors. Although the heritability estimates for total lactation milk yield and first lactation 305-dMY were relatively moderate, there is still room for genetic improvement in the herd. It may be stated that the present estimates of heritability and genetic correlation of different economically important traits are within the normal range reported by others in different cattle population. However, the variations so far observed may be due to sample sizes, analytical models and environmental and production management systems. The information of present study thus can be used in planning future breeding activities for further improvement of the breed.

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Conflict of interest

We certify that none of the authors of this manuscript have any conflict of interest for this research work.

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