

Genetic evaluation of Sahiwal and crossbred cattle for some economic traits

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ABSTRACT : The standard data available on 166 Sahiwal cattle, distributed over a period of 30 years from 1987 to 2016, and on crossbred cattle distributed over a period of 40 years from 1977 to 2016, were utilized to know the inheritance pattern of the traits viz. Age at first calving (AFC), First lactation milk yield (FL305DMY), First lactation length (FLL) and First lactation peak yield (FLPY). The heritability estimates for AFC, FL305DMY, FLL and FLPY were observed as 0.452 ± 0.152 , 0.378 ± 0.128 , 0.277 ± 0.101 and 0.447 ± 0.146 , respectively in case of Sahiwal cattle. The corresponding values in case of crossbreds were estimated as 0.209 ± 0.061 , 0.346 ± 0.082 , 0.225 ± 0.063 and 0.262 ± 0.069 . The AFC trait was positively correlated with the FLL and FLPY traits at genetic level (r_g) and negatively correlated with FL305DMY trait in Sahiwal cattle. The phenotypic correlation (r_p) of AFC with FL305DMY, FLL and FLPY were positive in magnitude in case of Sahiwal and crossbred cattle. The r_g and r_p values for FL305DMY trait with FLL and FLPY were positively correlated in Sahiwal and crossbred cattle. The FLL trait was found to be positively correlated at genetic and phenotypic levels with FLPY traits in both the Sahiwal and crossbred cattle.

Key words: Age at first calving, lactation period, lactation yield, peak yield

The genetic and economic success in any breeding programme depends on many factors. The genetic progress could be assessed by knowing the inheritance pattern of different traits like age at first calving, lactation milk yield, lactation period, peak yield etc. The magnitude of heritability values and correlation among different traits under study suggest the ways and methods of selecting dairy cattle for exploring the possibilities of making future genetic improvement. The level of genetic variation may be different among different dairy herds. Therefore, it is of utmost importance to study the herd specific variation for making proper decision for selecting the dairy cattle for milk production. The heritability values for all the economic traits and correlations among these traits should be computed for adopting the proper selection strategy and knowing the actual genetic progress made over time (Kumar *et al.*, 2010). This study was carried out in Sahiwal and crossbred cattle herd to know the inheritance pattern for different traits and correlations too among these traits. The traits under study were age at first calving, first lactation milk yield, first lactation length and first lactation peak yield.

MATERIALS AND METHODS

The data on production traits pertaining to 799 crossbred cattle and 166 Sahiwal cattle, maintained at Instructional Dairy Farm, Nagla of G. B. Pant University of Agriculture and Technology, Pantnagar (Uttarakhand) were utilized. The incomplete records were not considered in this study. The loose housing system, proper health measures, standard feeding conditions and standard management practices were followed at the farm. The crossbred cattle

belonged to different level of exotic inheritance (Holstein Friesian, Jersey, and Red Dane as the exotic cattle) less than 50% and more than 50% reaching to the level of 75%. The cows were crossed in later years with the semen having 50% Holstein Friesian (HF) and 50% Sahiwal characters to maintain exotic inheritance level below 75% and F_1 were inter-se mated. The cows having exotic inheritance level near about 75% were inseminated using the semen from Sahiwal sire. The data were corrected for non-orthogonality of data due to unequal subclass frequency applying the mixed model likelihood programme (Harvey, 1990). The traits studied were age at first calving (AFC), first lactation milk yield (FL305DMY), first lactation length (FLL) and first lactation peak yield (FLPY) traits in case of Sahiwal and crossbred cattle. The genetic and phenotypic correlations were also computed among these traits.

Estimates of Genetic Parameters

The estimates of variance and covariance components were utilized for estimating the genetic and phenotypic correlations among different economic traits and for estimating the heritability for different traits as detailed below:

Estimation of Heritability

Paternal half-sib correlation (intra sire correlation among the daughters) method as described by Becker (1975) was used to estimate the heritability of different traits. The following models may be used.

Where,

$$\text{Heritability } (h^2) = \frac{\frac{1}{NR1} \cdot \hat{s}_s^2}{\frac{(1-NW)}{NR1} \cdot \hat{s}_s^2 + \hat{s}_e^2}$$

\hat{s}_e^2 = error variance component,
 \hat{s}_s^2 = Sire component of variance.
 NR1 is the decimal percentage of additive genetic variance in \hat{s}_s^2 and
 NW is the decimal percentage of additive genetic variance in \hat{s}_w^2
 NR1 is between variance components and equal to 0.25 and NW is within variance component and equal to 0.75.

Estimation of genetic and phenotypic correlation

The genetic and phenotypic correlation among different traits is estimated from the analysis of variance /covariance Becker (1975) as per following,

$$r_g(hh') = \frac{\text{Covs}(hh')}{\sqrt{\hat{s}_{S(h)}^2 \cdot \hat{s}_{S(h')}^2}}$$

Phenotypic correlation (r_p)

The phenotypic correlation coefficient between different traits has been calculated by using sire and error component of variance and covariance as follows,

$$r_p(XY) = \frac{\hat{s}_e^2(hh') + \left[\left(\frac{1-NW}{NR1} \right) \hat{s}_s^2(hh') \right]}{\sqrt{\left\{ \hat{s}_e^2(h) + \left(\left(1 - \frac{NW}{NR1} \right) \hat{s}_s^2(h) \right) \right\} \left\{ \hat{s}_e^2(h') + \left(\left(1 - \frac{NW}{NR1} \right) \hat{s}_s^2(h') \right) \right\}}}$$

Where,

Cov_s = The sire or family covariance,
 h = h^2 traits, h'^2 = another trait,
 \hat{s}_e^2 = is among variance or covariance components, and
 \hat{s}_s^2 = is within variance or covariance components.

Estimation of Standard error

The standard error of heritability has been calculated as suggested by Swiger *et al.* (1964),

$$\text{S.E. } (h^2) = 4 \sqrt{\frac{2(N-1)(1-t)^2(1+(k-1)t)^2}{k^2(N-s)(s-1)}}$$

Where, N= total no. of observations, s= no. of sires, t= intra class correlation between paternal half sib = $\frac{\hat{s}_s^2}{\hat{s}_s^2 + \hat{s}_e^2}$, and k= average no. of progenies per sire. The standard errors of genetic correlation coefficients were estimated according to the formula suggested by Robertson (1959)

$$(\text{S.E.}) r_g(hh') = \frac{1 - r_g^2(hh')}{\sqrt{2}} \sqrt{\frac{(\text{S.E.}) \cdot h_{(h)}^2 \cdot (\text{S.E.}) \cdot h_{(h')}^2}{h_{(h)}^2 \cdot h_{(h')}^2}}$$

Where, (S.E.) $r_{g(hh')}$ = standard error of genetic correlation of subscripted characters, (S.E.) $h_{(h)}^2$ and (S.E.) $h_{(h')}^2$ = standard errors of h^2 of the subscripted characters, & $h_{(h)}^2$ and $h_{(h')}^2$ = heritability of subscripted characters. The standard errors of the phenotypic correlation

coefficient have been determined as per the method described by Panse and Sukhatme (1967),

$$\text{S.E.}(r_p)(hh') = \frac{\sqrt{1 - r_{p(hh')}^2}}{\sqrt{(N-2)}}$$

Where, $r_{p(hh')}$ = phenotypic correlation between h and h' traits based on the sire, and N= total number of observations.

The significance of phenotypic correlation is tested from the table of Snedecor and Cochran (1967) at (N-2) degrees of freedom.

RESULTS AND DISCUSSION

Heritability

The heritability estimate along with their standard errors of first lactation milk yield traits in Sahiwal and crossbred cattle are given in Table 1.

Age at first calving (AFC)

The heritability estimate of AFC was found to be 0.452 ± 0.152 in Sahiwal, which was in accordance with the report of Chander *et al.* (2008) and Singh *et al.* (2005). However, Gopal and Bhatnagar (1972) and Rehman *et al.* (2008) reported lower heritability of AFC in Sahiwal cattle. The differences among the heritability values for these traits may be due to different number observations under study (herd size), the genetic makeup of differences for the genetic makeup among the animals in the herd and different management practices followed on various herds over different locations.

The heritability estimate of AFC was found to be 0.209 ± 0.061 in crossbred cattle. Moges *et al.* (2009) reported still lower heritability then the present findings for AFC trait in crossbred cattle. The lower heritability indicates that there is little genetic variability present in AFC. There is little scope by selecting the animals for lower AFC as the trait is highly influenced by environmental factors.

First lactation milk yield 305-day milk yield (FL305DMY)

The heritability estimates of FL305DMY were observed

Table 1: Heritability estimates along with standard errors of first lactation trait in Sahiwal and crossbred cattle

| Traits | Heritability(Sahiwal) | Heritability(Crossbred) |
|----------|-----------------------|-------------------------|
| AFC | 0.452 ± 0.152 | 0.209 ± 0.061 |
| FL305DMY | 0.378 ± 0.128 | 0.346 ± 0.082 |
| FLL | 0.277 ± 0.101 | 0.225 ± 0.063 |
| FLPY | 0.447 ± 0.146 | 0.262 ± 0.069 |

AFC- Age at First Calving, FL305DMY- First Lactation 305 Day Milk Yield, FLL- First Lactation Length, FLPY-First Lactation Peak Yield

as 0.378 ± 0.128 in case of Sahiwal cattle, which was in conformity with the reports by Gopal and Bhatnagar (1972), Yadav *et al.* (1992) and Gandhi and Gurnani (1991). However, Chopra *et al.* (1973) and Tamar *et al.* (1996) reported high heritability estimate for FL305DMY in Sahiwal cattle. Dahlin *et al.* (1998) reported low value of heritability than the present estimate of heritability.

The heritability estimates of FL305DMY in case of crossbred cattle were found to be 0.346 ± 0.082 . This agreed with the findings of Koley *et al.* (1981), Panda and Sandhu (1983), and Ambhore *et al.* (2017). However, Kumar and Bhatnagar (1989) reported higher range of heritability than the value found in this study. The differences in heritability values could be different level of variation for FL305DMY trait and number of animals in the herd.

First lactation length (FLL)

The heritability estimates of FLL was observed to be 0.277 ± 0.101 in Sahiwal, which showed higher value than the report by Ilatsia *et al.* (2007). However, Chander *et al.* (2008), and Thore and Kothekar (2001) found heritability value to be more than present estimate. The heritability estimates of FLL were observed to be 0.225 ± 0.063 in crossbred. However, Ambhore *et al.* (2017) reported higher range of heritability than the result of present study. The results of this study indicated that the FLL trait had low genetic base. The trait can be improved by adopting the better feeding, health measures, and good management practices.

First lactation peak yield (FLPY)

The heritability estimates of FLPY were observed to be 0.447 ± 0.146 in Sahiwal cattle. Similar observations were made by Chander *et al.* (2008). The heritability estimate of FLPY was found to be 0.262 ± 0.069 in crossbred cattle. The heritability estimate of FLPY was similar as reported by SubhaLaxmi *et al.* (2009) in crossbred cattle. However, Roy and Katpatal (1987) reported higher value of

heritability in Jersey cattle.

Genetic and phenotypic correlations

An animal breeder computes the genetic correlation coefficient to develop selection strategies for getting better individuals. The genetic correlation is the correlation between the animal's genetic values for the other trait. A phenotypic correlation is a correlation between records of two traits on same animal and is estimated by the product moment correlation statistics.

Correlations among first lactation traits

The association at genetic and phenotypic levels among age at first calving (AFC), first lactation 305day milk yield (FL305DMY), first lactation length (FLL) and first lactation peak yield (FLPY) are presented in the Table 2 and Table 3 for Sahiwal and crossbred cattle, respectively.

The critical appraisal of Table 2 revealed that the AFC trait was positively correlated with the FLL and FLPY traits at genetic level, whereas AFC was negatively correlated with FL305DMY trait Sahiwal cattle. The positive magnitude of genetic correlation of AFC trait with FLL and FLPY traits were also reported by Kannan and Gandhi (2004) in Sahiwal.

The phenotypic correlation of AFC trait with FL305DMY, FLL and FLPY were positive in magnitude in Sahiwal cattle, which was in accordance with the report of Kannan and Gandhi (2004) and Raja (2010).

The FL305DMY trait was positively correlated with FLL and FLPY at the genetic level in Sahiwal cattle. This was in accordance with Rehman *et al.* (2008). While Kathivaran (2009) reported the negative correlation in between FL305DMY and FLL in Sahiwal cattle.

The phenotypic correlation of FL305DMY with FLL and FLPY was positive in Sahiwal cattle. The report by Rehman *et al.* (2008), Kathiravan (2009) and Raja (2010)

Table 2: Genetic and phenotypic correlations among first lactation milk yield traits in Sahiwal cattle

| TRAITS | AFC | LM305DMY | FLL | FLPY |
|----------|--------------|--------------|--------------|-------------|
| AFC | | -0.013±0.255 | 0.435±0.215 | 0.118±0.249 |
| LM305DMY | 0.163±0.077 | | 0.618±0.167 | 0.877±0.061 |
| FLL | 0.191±0.0766 | 0.632±0.0605 | | 0.526±0.195 |
| FLPY | 0.152±0.0772 | 0.851±0.041 | 0.461±0.0693 | |

Table 3: Genetic and phenotypic correlations among first lactation milk yield traits in crossbred cattle

| TRAITS | AFC | LM305DMY | FLL | FLPY |
|----------|--------------|--------------|--------------|--------------|
| AFC | | -0.195±0.193 | -0.048±0.212 | -0.211±0.202 |
| LM305DMY | 0.021±0.0378 | | 0.864±0.053 | 0.672±0.099 |
| FLL | 0.019±0.0378 | 0.82±0.0216 | | 0.57±0.134 |
| FLPY | 0.018±0.0378 | 0.801±0.0226 | 0.659±0.0284 | |

in Sahiwal agreed with the present results. The genetic correlations as indicated that the cows having lower AFC showed higher FLPY, and higher FLL and lower FL305DMY. Kumar and Kumar (2003) and Shahi and Kumar (2010) also suggested almost similar results.

In case of crossbred cattle, the AFC trait was negatively correlated with FL305DMY, FLL, and FLPY at the genetic level. This was in confirmatory with the report by Butte and Deshpande (1987) and Ambhore *et al.* (2017) in crossbred cattle. The values of genetic correlations of AFC trait with FL305DMY, FLL and FLPY were positive in direction, low in magnitude and non-significant in nature.

The phenotypic correlation of AFC trait with the other traits FL305DMY, FLL and FLPY were positive in crossbred cattle. The FL305DMY trait was positively correlated with FLL and FLPY at genetic level in crossbred cattle. Similar findings were reported by Dhumal *et al.* (2000), SubhaLaxmi *et al.* (2009), Kathiravan (2009) and Ambhore *et al.* (2017).

The phenotypic correlation of FL305DMY with FLL and FLPY was positive in direction crossbred cattle. The reports by Dhumal *et al.* (2000) and Subha Lakshmi (2009) in crossbred cattle agreed with the present results. The FLL trait was found to be positively correlated with FLPY at genetic level. Similar findings were found by Dhaka and Raheja (2002) in indigenous and crossbred cattle.

The phenotypic correlation of FLL with FLPY found positive in direction. The genetic correlations among various traits revealed that crossbred cows having lower AFC were having FL305DMY, higher FLL and FLPY. The higher producers can be selected by selecting the cows having lower AFC. The similar reports were given by Shahi and Kumar (2010).

CONCLUSION

The heritability estimates of AFC, FL305DMY, FLL and FLPY were found to be moderate in magnitude in Sahiwal cattle. The estimates of AFC, FL305DMY, FLL and FLPY in crossbred cattle were estimated lower in magnitude than the Sahiwal cattle. The cows having lower AFC were having higher FL305DMY, higher FLL and FLPY. The higher producers can be selected by selecting the cows having lower AFC.

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