

Estimates of Genetic and Phenotypic Parameters for Milk Yield and Milk Composition Traits in Karan-Fries Cattle

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ABSTRACT : The records of 1481 Karan-Fries cows on first lactation data of production, progenies of 82 sires and the records of 934 Karan-Fries cows on milk composition traits, progenies of 64 sires were utilized to estimate the heritability, genetic and phenotypic correlations among these traits. The genetic and phenotypic parameters of milk yield along with milk composition traits is required to plan the profitable dairying. The data for milk yield and milk composition traits was gathered from records of various registers for each animal under study. The heritabilities for FL305MY, PY305MY, 180DMY, fat yield, fat (%), SNF yield and SNF (%) traits were 0.346 ± 0.10 , 0.271 ± 0.09 , 0.343 ± 0.10 , 0.636 ± 0.15 , 0.181 ± 0.11 , 0.485 ± 0.14 and 0.360 ± 0.13 , respectively. The moderate to high heritability estimates of milk yield and milk composition traits indicated ample scope of their genetic improvement through selection and breeding. The phenotypic (r_p) and genetic (r_g) correlations among FL305MY, PY305MY and 180DMY traits were of high magnitude, positive and highly significant. It had indicated that predicted and part lactation milk yield traits can be used for animal evaluation in field condition based on close association among them. The phenotypic (r_p) and genetic correlations (r_g) of milk yield traits with fat yield and SNF yield traits were positive and non-significant. The phenotypic correlations (r_p) of milk yield traits with fat percent and SNF percent were negative and non-significant. The genetic (r_g) correlations of milk yield traits with fat percent were positive, moderate and non-significant except between FL305MY and fat percent. The genetic (r_g) correlations of milk yield traits with SNF percent were negative except between FL305MY and fat percent, low and non-significant. The phenotypic (r_p) and genetic correlations (r_g) of fat yield with fat% and SNF yield was positive and significant and with SNF% was negative and significant. The phenotypic (r_p) and genetic correlations (r_g) of fat% with SNF yield and SNF% were positive and significant. The phenotypic (r_p) and genetic correlations (r_g) of SNF yield with SNF% were positive and non-significant and negative and non-significant, respectively. Selection of animals for increased milk yield alone would lead to improvement in fat content and SNF yield traits, deterioration in performance of SNF% and overall reduction in quality of milk. The increase in fat yield was associated with simultaneous increase in fat% and SNF yield traits and decrease in SNF%. The increase in fat% was also associated with simultaneous increase in SNF%. The study indicates that milk yield and composition traits were liable to be optimally improved with selection and breeding. Thus, milk composition traits should also be given appropriate considerations in animal breeding besides the milk yield traits.

Keywords: Parameters, Milk yield, Milk Composition, Karan-Fries cattle.

INTRODUCTION

Increased milk yield with optimum level of milk constituents (fat and SNF content) in routinely initiated lactations is a desirable objective of genetic improvement programme for dairy animals. The breeding policy adopted to improve the Karan Fries (KF) cattle was mainly directed to enhance the milk production so far and the milk composition traits were not given due consideration in genetic improvement programmes. The first lactation 305-day or less milk yield (FL305MY) is the most important economic trait

of the dairy animal productivity which determines profitability, culling and genetic progress of animals in the herd. Sire evaluation based on part lactation yield has been reported to be useful in early evaluation, reducing the generation interval and increasing the rate of genetic improvement (Van Vleck, 1962; Iype and Nagarcenkar, 1992). Further, the use of part lactation records and test day records for predicting the total lactation milk yield has great advantage in the field conditions as well as on the organized herds. Rashia (2010) reported high and positive genetic and

phenotypic correlation of 180-day cumulative milk yields with first lactation 305-day or less milk yield and predicted 305-day milk yield based on 180 days cumulative milk yield with an accuracy of 75% in Karan Fries cattle. Therefore, the predicted 305-day milk yield (PY305MY) based on first lactation 180 days cumulative milk yield fitting best regression model and part lactation record viz. first lactation 180 days cumulative milk yield (180DMY) may be used for animal evaluation. Fat and SNF are important constituents of milk. Wide variation in fat and SNF content of milk of bovines provides scope for altering this constituent genetically in the milk. The existing variation in milk composition (Mishra and Joshi, 2004) confirms the possibility of their improvement in Karan-Fries cattle. The genetic parameter for milk and constituent yield traits of Sahiwal cattle was reported and indicated to consider constituent traits along milk yield traits for genetic improvement (Verma, R. K. *et al.*, 2017). The accurate and precise estimates of heritability, genetic and phenotypic correlations of lactation milk yield, part-lactation milk yield and composition traits are reported scantily in literature for Karan-Fries cattle which is required for development, formulation, execution and evaluations of genetic improvement programme. Therefore, the present investigation was aimed to examine the genetic parameters (heritability, genetic and phenotypic correlation estimates) for milk yield and milk composition traits of first lactation in Karan-Fries cattle.

MATERIALS AND METHODS

The records of 1481 Karan-Fries cows on first lactation data of production (305-day or less milk yield and daily milk yield), progenies of 82 sires spread over a period of 26 years from 1984 to 2009 and the records of 934 Karan-Fries cows on milk composition traits (Fat% and SNF%), progenies of 64 sires from 1990 to 2009 (20 years) were collected from the history-cum pedigree sheet, daily milk yield registers and milk composition registers maintained at National Dairy Research Institute (NDRI), Karnal. The first lactation predicted 305-day milk yield (PY305MY) was predicted using regression equation $PY305MY = 463.16 + 1.297 (X_1)$ based on first lactation 180-days cumulative milk yield (180DMY). 180-day cumulative milk yield (180DMY) was calculated by summing up the daily milk yield after calving till 180th days (excluding first five days of colostrum). The first lactational percent of fat and SNF was generated by averaging monthly test day milk composition records over 10 months of first lactation. The first lactational yield of Fat and SNF was estimated by averaging monthly yield of Fat and SNF over 10 months of first lactation. The monthly yield of fat and SNF were estimated using following formula given formula.

$$\text{Monthly Fat or SNF yield} = \sum M_i \frac{X_i}{100}$$

where M_i is the monthly milk yield of i^{th} month ($i = 1-10$ for 305-day milk yield) and X_i is the fat or SNF percentage of the i^{th} month ($i = 1-10$ for 305-day milk

Rathore *et al.*, *Biological Forum – An International Journal* 13(4): 278-282(2021)

yield). Culling in the middle of lactation, abortion, still-birth or any other pathological causes which affected the lactation yield were considered as abnormalities and thus, such records (9%) were not taken for the study. The records of progenies of only those sires were included in present study which had minimum five or more progenies in data records. The outliers beyond two-standard deviation on both the tail ends of normal distribution were excluded from the data. The cows that had produced milk for at least 100 days and maximum 305 days in the first lactation were considered for the study. A total of 15% records were discarded on account of these restrictions. The cows were maintained under uniform condition of feeding, housing, breeding milking, health cover and other managerial condition. Paternal half sib correlation method (Becker, 1975) under least-squares mixed model (LSML) using Harvey, (1990) was used to estimate the heritability of different traits. The standard error of heritability of different traits was estimated using the formula given by Swiger *et al.* (1964). The genetic correlations among traits were estimated from the analysis of variance and covariance among sire groups as given by Becker, (1975). The standard error of genetic correlation was derived by using the formula of Robertson, (1959). The phenotypic correlations among different traits were computed as per Snedecor and Cochran (1964).

RESULTS AND DISCUSSION

The results of heritability, phenotypic and genetic correlation estimates for various traits are presented in Table 1. The heritability of FL305MY was 0.346 ± 0.10 (Table 1). The estimate of heritability of FL305MY was close to the estimate (0.30 ± 0.02) reported by Saha (2001) and (0.39 ± 0.09) by Kokate (2009) in Karan Fries cattle. However, higher heritability estimates of FL305MY have been reported as 0.44 ± 0.13 by Sivakumar (1998); 0.41 ± 0.13 by Sahana and Gurnani (2000); 0.45 ± 0.18 by Singh *et al.* (2006); 0.48 ± 0.01 by Nehra (2011) and 0.48 ± 0.01 by Tripathy *et al.* (2017) and lower heritability estimates of FL305MY have been reported as 0.20 ± 0.06 by Rashia (2010) and 0.21 ± 0.14 by Divya, (2012) in Karan Fries cattle. The heritability of PY305MY was 0.271 ± 0.09 (Table 1). However, lower heritability estimate (0.138 ± 0.115) of PY305MY has been reported by Jain (1996) in Murrah buffaloes. The heritability of 180DMY was 0.343 ± 0.11 (Table 1). The estimate of heritability of 180DMY was close to the estimate range (0.41-0.44) of mid part lactation reported by Kumar *et al.*, (1992) in Sahiwal and Singh (2006) in Karan Fries cows. However, higher estimate of heritability (0.43 ± 0.09) of 180DMY was reported by Rashia (2010) and lower estimate of heritability (0.27 ± 0.15) of 180DMY was reported by Singh (2006) in Karan Fries cattle. The heritability estimates of fat yield and fat percent was 0.636 ± 0.15 and 0.181 ± 0.110 , respectively (Table 1). However, lower estimate of heritability (0.20 ± 0.72) of fat yield and higher estimate of heritability (0.29 ± 0.05) of fat percent were reported by Misra and Joshi (2004) in Karan Fries cattle.

The heritability estimate of SNF yield and SNF percent were 0.485 ± 0.14 and 0.360 ± 0.13 , respectively (Table 1). However, Lower heritability estimates of SNF yield (0.13 ± 0.07 ; 0.34 ± 0.08) and SNF percent (0.17 ± 0.04 ; 0.291 ± 0.08) were reported by Misra and Joshi (2004); Tripathy *et al.* (2017), respectively in Karan Fries cattle. The heritability estimates of FL305MY, PY305MY, 180DMY, fat yield, fat percent(%), solids-not-fat (SNF) yield and solids-not-fat percent (SNF%) was moderate in magnitude which indicates traits is more influenced by additive genetic variability and hence there is more scope of improvement by selection.

Phenotypic and Genetic (r_g) correlations. The estimates of phenotypic (r_p) and genetic (r_g) correlations among FL305MY, PY305MY, 180DMY, fat yield, fat%, SNF yield and SNF% were given Table 1. The estimates of phenotypic (r_p) and genetic (r_g) correlations between FL305MY and PY305MY were positive, high (0.804 ± 0.01 and 0.897 ± 0.07 , respectively) and significant ($p < 0.01$). The estimates of phenotypic and genetic correlations between FL305MY and 180DMY were positive, high (0.804 ± 0.02 and 0.897 ± 0.07 , respectively) and significant ($p < 0.01$). The estimates of phenotypic and genetic correlations between PY305MY and 180DMY were positive, high (0.804 ± 0.01 and 0.996 ± 0.06 , respectively) and significant ($p < 0.01$). Similar estimates of phenotypic (r_p) and genetic (r_g) correlations between FL305MY and 180DMY (0.88 ± 0.01 and 0.95 ± 0.02 , respectively) were also reported by Rashia (2010) in KF cattle. Hence, the results of phenotypic (r_p) and genetic (r_g) correlations among FL305MY, PY305MY and 180DMY traits were of high magnitude, positive and highly significant which indicated close association among them. Hence, the predicted and part lactation milk yield traits can be used for animal evaluation in field condition.

The estimates of phenotypic correlations (r_p) of FL305MY with fat yield and fat percent were 0.874 ± 0.01 and -0.044 ± 0.05 , respectively (Table 1). The estimates of phenotypic correlations (r_p) of PY305MY with fat yield and fat percent were 0.807 ± 0.02 and -0.016 ± 0.04 , respectively (Table 1). The estimates of phenotypic correlations (r_p) of 180DMY with fat yield and fat percent were 0.807 ± 0.02 and -0.016 ± 0.04 , respectively (Table 1). The r_p between milk yield traits and fat yield trait were positive and high and significant. Similar estimates of phenotypic (r_p) correlation between FL305MY and fat yield were reported to be 0.91 ± 0.01 and 0.82 ± 0.02 by Misra (2001); Tripathy *et al.*, (2017) respectively in KF cattle. The r_p between milk yield and fat yield traits indicated that increase in milk production result in increase in milk fat yield which may be due to environmental influence. The r_p between FL305MY and fat percent traits were negative, small and non-significant which was in consonance with Misra (2001) in KF cattle. The r_p between milk yield traits and fat percent trait indicated that increase in milk production result into decline in milk fat percent which may be due to environmental influence.

The estimates of genetic correlations (r_g) of FL305MY with fat yield and fat percent were 0.957 ± 0.04 and

0.865 ± 0.09 , respectively (Table 1). The estimates of genetic correlations (r_g) of PY305MY with fat yield and fat percent were 0.874 ± 0.07 and 0.668 ± 0.39 , respectively (Table 1). The estimates of genetic correlations (r_g) of PY305MY with fat yield and fat percent were 0.874 ± 0.07 and 0.669 ± 0.39 , respectively (Table 1). The r_g between milk yield and fat yield traits were observed to be positive, high and significant. However, slightly higher estimate of genetic correlation between milk yield and fat yield traits were reported to be 0.98 ± 0.01 and 0.97 ± 0.02 by Misra (2001); Tripathy *et al.*, (2017) respectively in Karan Fries cattle. The results indicated that these traits are governed by similar set of genes and selection of animals on the basis of milk yield traits would lead to desirable improvement in milk fat yield trait. The r_g between FL305MY and fat percent traits were observed to be positive, high and significant. However, Misra and Joshi (2004) in Karan Fries (KF) cattle had reported similar positive (0.30 ± 0.18) genetic correlation between FL305MY and fat percent traits but lower in magnitude than the present result.

The estimates of phenotypic correlations (r_p) of FL305MY with SNF yield and SNF percent were 0.898 ± 0.02 and -0.042 ± 0.03 , respectively (Table 1). The estimates of phenotypic correlations (r_p) of PY305MY with SNF yield and SNF percent were 0.825 ± 0.04 and -0.029 ± 0.02 , respectively (Table 1). The estimates of phenotypic correlations (r_p) of 180DMY with SNF yield and SNF percent were 0.825 ± 0.05 and -0.019 ± 0.04 , respectively (Table 1). However, slightly higher estimates of phenotypic correlations (r_p) of FL305MY with SNF yield have been reported as 0.92 ± 0.009 by Misra and Joshi (2004) in Karan Fries cattle. The r_p between milk yield traits and SNF yield trait were positive, high and significant. The r_p between milk yield and SNF yield traits indicated that increase in milk production result into increase in milk SNF yield which may be due to environmental influence. The r_p between FL305MY and SNF percent was negative, small in magnitude and non-significant with high standard error. However, estimate of phenotypic (r_p) correlation between milk yield and SNF percent traits was reported to be positive 0.06 ± 0.02 by Misra (2001) in KF cattle. The r_p between FL305MY and SNF percent indicated that increase in milk production result into decline in milk SNF percent which may be due to environmental influence.

The estimates of genetic correlations (r_g) of FL305MY with SNF yield and SNF percent were 0.956 ± 0.03 and 0.049 ± 0.29 , respectively (Table 1). The estimates of genetic correlations (r_g) of PY305MY with SNF yield and SNF percent were 0.893 ± 0.06 and -0.291 ± 0.31 , respectively (Table 1). The estimates of genetic correlations (r_g) of FL305MY with SNF yield and SNF percent were 0.894 ± 0.06 and -0.291 ± 0.31 , respectively (Table 1). However, higher estimates of genetic correlations (r_p) of FL305MY with SNF yield have been reported as 0.98 ± 0.007 by Misra and Joshi (2004) in Karan Fries cattle. The r_g between milk yield and SNF yield traits were observed to be positive, high and significant. The results indicated that these traits

are governed by similar set of genes and selection of animals on the basis of milk yield traits would lead to desirable improvement in milk SNF yield trait. The positive genetic correlations (r_g) between FL305MY and SNF percent was in agreement with the estimates of genetic correlations 0.38 ± 0.18 by Misra and Joshi (2004) in KF cattle. The obtained estimates of genetic correlations between FL305MY and SNF percent traits were positive, low in magnitude with very high standard error. However, the obtained estimates of genetic correlations between PY305MY and SNF percent and between 180DMY and SNF percent traits were negative in direction and low in magnitude with very high standard error. The results indicated that these traits are governed by similar set of genes and selection of animals on the basis of milk yield traits would lead to desirable improvement in milk SNF percent trait.

The estimates of phenotypic correlations (r_p) of fat yield with SNF yield and SNF percent were 0.954 ± 0.01 and -0.017 ± 0.04 , respectively (Table 1). The estimates of phenotypic correlations (r_p) of fat percent with SNF yield and SNF percent were 0.032 ± 0.04 and

0.197 ± 0.06 , respectively (Table 1). The positive phenotypic correlations (r_p) between fat yield and SNF yield was in agreement with the estimates of genetic correlations 0.99 ± 0.003 by Misra and Joshi, (2004) in KF cattle. The positive phenotypic correlations (r_p) between fat yield and SNF percent was in agreement with the estimates of genetic correlations 0.06 ± 0.024 by Misra and Joshi (2004) in KF cattle. The estimates of genetic correlations (r_p) of fat percent with SNF yield and SNF percent were 0.993 ± 0.01 and 0.989 ± 0.09 , respectively (Table 1). The estimates of genetic correlations (r_p) of fat percent with SNF yield and SNF percent were -0.114 ± 0.24 and 0.505 ± 0.32 , respectively (Table 1). The positive genetic correlations (r_g) between fat percent and SNF yield was in agreement with the estimates of genetic correlations 0.21 ± 0.20 by Misra and Joshi, (2004) in KF cattle. The positive genetic correlations (r_g) between fat percent and SNF percent was in agreement with the estimates of genetic correlations 0.79 ± 0.101 by Misra and Joshi (2004) in KF cattle.

Table 1: Genetic and phenotypic correlations among milk yield and milk composition traits of Karan-Fries cattle.

TRAITS	FL305MY	PY305MY	180DMY	Fat yield	FAT%	SNF yield	SNF (%)
FL305MY	0.346 ± 0.10	0.804 ^{***} ± 0.01	0.804 ^{**} ± 0.02	0.874 ^{**} ± 0.01	-0.044 ± 0.05	0.898 ^{**} ± 0.02	-0.042 ± 0.03
PY305MY	0.897 ^{**} ± 0.07	0.271 ± 0.09	0.998 ^{**} ± 0.04	0.807 ^{**} ± 0.02	-0.016 ± 0.04	0.825 ^{**} ± 0.04	-0.029 ± 0.02
180DMY	0.897 ^{**} ± 0.07	0.996 ^{**} ± 0.06	0.343 ± 0.11	0.807 ^{**} ± 0.02	-0.016 ± 0.04	0.825 ^{**} ± 0.05	-0.019 ± 0.04
Fat yield	0.957 ^{**} ± 0.04	0.874 ^{**} ± 0.07	0.874 ^{**} ± 0.07	0.636 ± 0.15	0.204 ^{**} ± 0.03	0.954 ^{**} ± 0.01	-0.017 ± 0.04
FAT (%)	0.865 ^{**} ± 0.09	0.668 ± 0.39	0.669 ± 0.39	0.996 ^{**} ± 0.08	0.181 ± 0.11	0.032 ± 0.04	0.197 ^{**} ± 0.06
SNF yield	0.956 ^{**} ± 0.03	0.893 ^{**} ± 0.06	0.894 ^{**} ± 0.06	0.993 ^{**} ± 0.01	0.989 ^{**} ± 0.09	0.485 ± 0.14	0.038 ± 0.04
SNF (%)	0.049 ± 0.29	-0.291 ± 0.31	-0.29 ± 0.31	-0.114 ± 0.24	0.505 ± 0.32	-0.036 ± 0.25	0.360 ± 0.13

The principle diagonal values are the estimates of heritability, the estimates above the diagonal are the phenotypic correlations and those below diagonal are the genetic correlations

* P 0.05 and ** P 0.01 level of significance

High, positive and significant phenotypic correlations (r_p) were estimated among milk yield traits. Selection of animals for any of milk yield traits results in simultaneous improvement in other traits. Milk yield traits had positive and significant phenotypic correlations (r_p) with fat and SNF yield traits and had low negative and significant phenotypic correlations (r_p) with fat% and SNF% traits. The estimated phenotypic correlations (r_p) indicated favorable association of Milk yield traits with fat and SNF yield traits and indicate unfavorable association with fat% and SNF%. The low to high positive and significant phenotypic correlations (r_p) were estimated among milk composition traits except between fat yield and SNF%. Selection of animals for any of positively associated traits results in desirable improvement among themselves and undesirable improvement in SNF% trait.

The high positive and significant genetic correlations (r_g) was estimated among milk yield traits and thus indicate selection of animals for any of milk yield traits results in simultaneous improvement in other milk yield traits. Milk yield traits had high positive and significant genetic correlations (r_g) with milk composition traits except SNF% trait which had low positive to negative and non-significant genetic correlations (r_p) with milk yield traits. Selection of animals for milk yield traits

result in simultaneous improvement of fat content, SNF yield traits and reduction performance of SNF% trait. The high positive and significant genetic correlations (r_p) were estimated among milk composition traits except between fat yield and SNF% traits. Improvements in fat content traits indicate overall reduction in performance of SNF content traits.

CONCLUSION

The moderate to high heritability estimates of milk yield and milk composition traits indicated ample scope of their genetic improvement through selection and breeding. Selection of animals based on milk yield trait alone lead to improvement in fat content traits and deterioration in performance of SNF content and overall reduction in quality of milk. The milk composition traits should also be given appropriate considerations in animal breeding besides the milk yield traits.

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REFERENCES

- Becker, W. A. (1975). *Manual of Quantitative Genetics*. 3rd Edition. Pub. Program in Genetics, Washington State University, Washington, USA.
- Divya, P. (2012). *Single versus multi-trait models for genetic evaluation of fertility traits in karan fries cattle*. M.V.Sc. Thesis. NDRI (Deemed University), Karnal, India.
- Harvey, W. R. (1990). *Guide for LSMLMW, PC-Iversion, mixed model least squares and maximum likelihood computer programme, January 1990*. Mimeograph Ohio State., university, USA.
- Iype & Nagarcenkar (1992). Influence of non-genetic factors influencing on part and 300 days first lactation milk yield in Murrah buffaloes. *J. Dairy, Food and Home. Sci., 11*: 50.
- Jain, A. (1996). *Sire evaluation under multiple trait models in Murrah buffaloes*. Ph.D. Thesis, NDRI (Deemed University) Karnal, India.
- Kokate, (2009). *Genetic evaluation of Karan Fries sires based on Test day milk records*. (Deemed University) Karnal, India.
- Kumar, V., Chauhan, V. P. S. , & Singh, B.P. (1992). Genetic parameters of 300 days and part lactation milk yields of Haryana cattle. *Indian J. Anim. Sci., 62*(7): 655.
- Misra, S.S. (2001). *Genetic studies on certain milk constituents of Karan Fries cattle*. M.Sc. Thesis, NDRI (Deemed University), Karnal, India.
- Misra & Joshi (2004). Estimates of genetic parameters for lactational milk constituents and yield traits in Karan-Fries cattle. *Indian Vet. J., 81*: 776-779.
- Nehra, M. (2011). *Genetic analysis of performance trends in Karan Fries cattle*. M.V.Sc. Thesis. NDRI (Deemed University), Karnal, India.
- Rashia (2010). *Genetic evaluation of the lactation curve in Karan Fries cattle*. Ph. D. Thesis, NDRI (Deemed University) Karnal, India.
- Robertson, A. (1959a). The sampling variance of the genetic correlation coefficient. *Biometrics, 15*: 469-485.
- Saha, S. (2001). *Generation wise genetic evaluation of Karan Swiss and Karan Fries cattle*. Ph.D. Thesis, NDRI (Deemed University) Karnal, India.
- Sahana, G., & Gurnani, M. (2000). Performance of crossbred cattle and comparison of sire evaluation methods under organized farm condition. *Indian J. Anim. Sci., 70*(4): 409-414.
- Singh, S. (2006). Genetic evaluation of Karan Fries sires on the basis of part lactation milk yield. NDRI (Deemed University) Karnal, India.
- Sivakumar, R. (1998). *Reproductive performance at different levels of production in Karan Fries cattle*. M.Sc. Thesis, National Dairy Research Institute, Karnal, Haryana.
- Snedecor, G. W., & Cochran, W. G. (1964) *Statistical Methods*. 8th edn. Affiliated East-West Press New Delhi.
- Swiger, L.A., Harvey, W. R., Everson, D. O., & Gregory, K. E. (1964). The variance of intraclass correlation involving groups with one observation. *Biometrics, 20*: 818-826.
- Tripathy, S. S., Atish Kumar Chakravarty, Mohsin Ayoub Mir, Arun Pratap Singh, Valsalan Jamuna & Sreela Lathika (2017). Genetic and Non-Genetic Parameters of First Lactation Milk Yield, Composition and Energy Traits in Karan-Fries Cattle. *Journal of Animal Research, 7*(1) 49-57.
- Van Vleck, L. D. (1962). Sire Evaluation from Five-Month Daughter Records. *Journal of Animal Science, 21*: 633-638.
- Verma, R. K., Gupta, A. K., Kumar, M., & Ratwan, P. (2017). Estimates of genetic parameters for milk and milk constituent's yield traits in Sahiwal cattle. *Indian J. Dairy Sci., 70*(6): 751-754.

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