Estimation of Genetic Parameters of First Lactation 305 Days or Less Milk Yield, Milk Composition and Reproduction Traits using Sire and Animal Models in Karan Fries Cattle

Aakanksha Rathore[1] , Ramesh Kumar Singh[2] and Avtar Singh[3]*
[1]Part Time Teacher, College of Veterinary Science and Animal Husbandry,
Anjora, Durg, (Chhattisgarh), India.
[2]Department of Animal Genetics and Breeding, BVC, Patna, (Bihar), India.
[3]Dairy Cattle Breeding Division,
ICAR-National Dairy Research Institute, Karnal-132001, (Haryana), India.

ABSTRACT: The records of 1481 Karan-Fries cows on first lactation 305 days or less milk yield and reproduction (AFC and FSP) traits, 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 utilized to compare between single trait sire model (ST-SM) and single trait animal model (ST-AM). Variance components and genetic parameters for different traits were estimated by single trait sire model (ST-SM) and single trait animal model (ST-AM), applying average information algorithm (AI-REML) using the WOMBAT software. The averages of FL305MY, fat yield, fat (%), SNF yield, SNF (%), AFC and FSP were 3189 ± 22 Kg, 130.81 ± 1.29 Kg, 4.16 ± 0.01%, 273.28 ± 2.54 Kg, 8.72 ± 0.01%, 984 ± 4 days and 141 ± 3 days, respectively. The obtained CV% of different traits was moderate to high in magnitude and revealed high variation in traits for better differentiation among animals. The heritability estimate of traits from single-trait sire model (ST-SM) was considerably lower than corresponding single-trait animal model (ST-AM). The improvement in h^2 of FL305MY, PY305MY, 180DMY, fat yield, fat (%), SNF yield, SNF (%), AFC and FSP traits by ST-AM were 349.10%, 349.05%, 316%, 32.75%, 53.55%, 30.76% and 233.33%, respectively compared to the estimate of ST-SM analysis. The estimates of genetic (r_g) and phenotypic (r_p) correlations of FL305MY with fat yield, SNF yield, AFC and FSP traits from single-trait sire model were observed not only changed in magnitude but also in sign than the corresponding estimates of single-trait animal model for different traits. The estimates of genetic (r_g) and phenotypic (r_p) correlations of FL305MY with fat yield, SNF yield, AFC and FSP traits from single-trait animal model were observed improved in their estimates than the corresponding estimates of single-trait sire model for different traits. The estimates of genetic parameters from single-trait animal model may be considered more accurate and unbiased than those of single-trait sire model based on their improved estimate and lower residual variance of model.

Keywords: Genetic parameters, milk yield, Sire model, Animal model, Karan Fries cattle.

INTRODUCTION

The primary aim in dairy cattle selection is to produce more efficient and economically viable animals within short span of time. The estimates of genetic parameters are helpful in determining the method of selection to predict direct and correlated response to selection, choosing a breeding system to be adopted for future improvement as well as in the estimation of genetic response. In general, more efficient and economic viable dairy cattle come in milk in early age and produce large quantities of milk in routinely initiated lactations with remaining functionally sound. Selection on milk yield traits alone result in deterioration of genetic production potential of milk composition and reproduction traits. Genetic response in selected traits

results not only from use of sires having high genetic merit but also from use of mates having high genetic merit. Thus, animal model has replaced other methods of evaluation in dairy cattle. Because animal model predict breeding values of both sires and dams simultaneously utilizing all relationships between animals with or without records. Animal model is considered superior to sire model in the estimation of variances and other genetic parameters (Hudson and Schaeffer, 1984). The genetic parameters required for best linear unbiased prediction (BLUP) of breeding values using sire and animal models are usually estimated using residual maximum likelihood (REML; Patterson and Thompson, 1971) with the same model as used to estimate breeding values. Sire model analyses take account of relationship between sires only ignore

the relationship of sire mates and between the mates. Further, sire model assume that mates of sires are non-related, non-inbred, non-selected and that each dam has one recorded progeny only. If selection intensity for males were greater than for females, the male genetic variance would be smaller subsequently, sire model might underestimate genetic variability and thus lead to poor estimates of genetic parameters. Genetic parameters estimates of animal model were often higher than the corresponding estimates of sire model for different traits (Dong and Van Vleck, 1988.) The précise and accurate estimates of genetic parameters were required to form selection indices besides the breeding values prediction. The objective of this study was to estimate the variance components and heritability of first lactation 305 days or less milk yield (FL305MY), milk composition viz. fat yield and SNF yield and reproduction traits viz. AFC and FSP traits and genetic and phenotypic correlations of first lactation 305 days or less milk yield (FL305MY) with fat yield, SNF yield, AFC and FSP traits of Karan Fries cattle using single trait sire model (ST-SM) and single trait animal model (ST-AM) and to test the superiority of animal model over sire model.

MATERIALS AND METHODS

The records of 1481 Karan-Fries cows on first lactation 305 days or less milk yield and reproduction (AFC and FSP) traits, 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 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 as lactational yield 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

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

where M_i is the monthly milk yield of ith month (i = 1-10 for 305-day milk yield) and X_i is the fat or SNF percentage of the ith month (i = 1-10 for 305-day milk yield). Age at first calving (AFC) trait of reproduction trait group was calculated as the difference between date of birth and date of first calving. First service period (FSP) of reproduction trait group was estimated as the difference between date of first calving and date of next successful service. 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 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 managemental condition. The same data of traits was used to estimate genetic parameters from both sire model and animal model using WOMBAT (Meyer, 2007).

Models. The following two single trait linear models were used to estimate the genetic parameters of FL305MY, milk composition and reproduction traits.

Sire Model (SM): $Y = Xb + Z_1 u_S + e$

Animal Model (AM): $Y = Xb + Z_2 u + e$

Where Y was the vector of observations of a particular considered trait; b was the vector of fixed effects, including season of calving, period of calving and age groups for all traits except AFC; For AFC, season of birth and period of birth was considered as the vector of fixed effects; u_S was the vector of sire genetic effects; u was the vector of animal additive genetic effects and the X, Z_1 and Z_2 were incidence matrices pertaining to b, u_S and u. The distributions for the random effects were assumed as follows:

$a \sim N(0, A_s\, \sigma_s^2), \quad e \sim N(0, I\, \sigma_{e_s}^2)$

$a \sim N(0, A\, \sigma_a^2), \quad e \sim N(0, I\, \sigma_e^2)$

where, A_s and A were the matrices of the genetic relationship between individuals in the pedigree for sires and animals, respectively; σ_s^2 and σ_a^2 were sire genetic variance and animal additive genetic variance, respectively; and $\sigma_{e_s}^2$ and σ_e^2 were residual variances for SM and AM, respectively. Variance components and genetic parameters for different traits were estimated by single trait sire model (ST-SM) and single trait animal model (ST-AM), applying average information algorithm (AI-REML) using the WOMBAT software (Meyer, 2007).

RESULTS AND DISCUSSION

The simple arithmetic averages of various economic traits viz. first lactation 305 days or less milk yield (FL305MY), fat percent, milk fat yield, Solids-not-fat (SNF) percent, Solids-not-fat (SNF) yield, age at first calving (AFC) and first service period (FSP) along with standard error (S.E.) and coefficient of variation (C.V.) are presented in Table 1.

Averages of various traits. FL305MY: The simple mean for first lactation 305-day or less milk yield (FL305MY) was 3189 ± 22 Kg (Table 1) which was in close to the reports of Singh, (2006); Kokate, (2009); Rashia, (2010); Divya, (2012); Tripathy et al. (2017) in Karan Fries cattle.

The coefficient of variation (CV) of FL305MY was estimated as 20.13% (Table 1). Kokate (2009), Rashia (2010); Manju, (2011); Divya, (2012); Tripathy et al. (2017) also reported the average 305-day milk yield was 3068 ± 22 Kg, 3076 Kg, 3243.59 ± 47.33 Kg, 3110 ± 25 Kg and 3121 ± 26.8 Kg with coefficient of variation 24.98%, 24.4%, 25%. 24.43% and 31.05% respectively for first lactation in Karan Fries cattle.

Singh, (2006) also observed that, the average 305-day milk yield was 3197 ± 43 Kg with coefficient of variation 24.98% for first lactation in Karan Fries. The reasonably high estimate of CV for FL305MY trait indicated that FL305MY can be used for evaluation of genetic merit of animals as it may provide an opportunity for better differentiation among animals.

Table 1: Averages of various economic traits.

Traits	No. of records	Mean ± S E	CV (%)
FL305MY (Kg)	1481	3189 ± 22	20.13
Fat yield (Kg)	934	130.81 ± 1.29	23.96
Fat (%)	934	4.16 ± 0.01	5.23
SNF yield (Kg)	934	273.28 ± 2.54	22.16
SNF (%)	934	8.72 ± 0.01	1.99
AFC (days)	1481	984 ± 4	12.50
FSP (days)	1481	143 ± 3	59.60

Fat content: The simple mean for fat yield and fat percent in the present study were 130.81 ± 1.29 Kg and 4.16 ± 0.01% (Table 1), respectively. The higher estimate of mean for fat yield and fat percent of Karan-Fries was reported by 446.74 ± 3.62 Kg and 4.2 ± 0.01% respectively by Tripathy *et al.* (2017). However, higher estimate of milk fat yield was reported as 192.8 Kg by Boujenane, (2002) in Moroccan Holstein-Friesian; 203.58 Kg by Yaeghoobi *et al.*, (2009) in Iranian Holstein-Friesian cattle; 361.95 Kg by Pantelic *et al.* (2012) in Holstein-Friesian cattle and 198.79 Kg by Toghiani, (2012) in Iranian Holstein-Friesian and lower estimate of milk fat yield was reported 60 Kg by Freitas *et al.* (1995) in ½ Holstein-Friesian × Gir cross bred cattle. However, slightly higher estimate of milk fat percent was reported 4.58 ± 0.04% and 4.5 ± 0.08% by Haile *et al.,* (2008) in Holstein-Friesian × Boran crossbred cattle and Barbosa *et al.* (2008) in ½ Holstein-Friesian × Gir cross bred cattle, respectively and slightly lower estimate of milk fat percent was reported 3.55% by Freitas *et al.,* (1995) in ½ Holstein-Friesian × Gir crossbred cattle; 3.63% by Boujenane, (2002) in Moroccan HF; 3.53% by Pantelic *et al.* (2012) in Holstein-Friesian cattle and 3.07% by Toghiani, (2012) in Iranian HF.

The coefficients of variation (CV) of milk composition traits viz. fat yield and fat%, were estimated as 23.96% and 5.23% (Table 1), respectively. However, higher estimates of coefficient of variation (CV) of milk fat yield and Fat Percent were reported as 29.27% and 8.18% respectively by Tripathy *et al.* (2017) Karan Fries cattle. The obtained CV estimates of milk fat yield was in close to the estimates 26.5%, 26.24% and 26.5% as reported by Boujenane, (2002) in Moroccan HF, Yaeghoobi *et al.*, in Iranian Holstein-Friesian cattle (2009); Toghiani (2012) in Iranian Holstein-Friesian, respectively. However, slightly higher CV estimates of milk fat yield was reported as 42% by Freitas *et al.,* (1995) in ½ Holstein-Friesian × Gir crossbred cattle and slightly lower CV estimate of milk fat yield was reported 15.68% by Pantelic *et al.* (2012) in Holstein-Friesian cattle. The obtained CV estimate of milk fat percent was in close to the estimates 7.16% and 5.27% as reported by Boujenane, (2002) in Moroccan Holstein-Friesian and Pantelic *et al.* (2012) in Holstein-Friesian cattle, respectively. However, higher CV estimate of milk fat percent was reported as 32%,

18.4% and 19.24% by Freitas *et al.,* (1995) in ½ Holstein-Friesian × Gir crossbred cattle, Haile *et al.,* (2008) in Holstein-Friesian × Boran crossbred cattle and Toghiani, (2012) in Iranian Holstein-Friesian, respectively.

The coefficient of variation (CV) for fat yield revealed that fat yield was moderately variable traits and could be used in combination with milk production traits for better evaluation of dairy animals. The obtained CV for fat% was low in estimates and so may not aid significantly in evaluation and differentiation of animals based on their genetic merit.

Solids-not-fat (SNF) content: The simple mean for SNF yield and SNF percent in the present study were 273.28 ± 2.54 Kg and 8.72 ± 0.01% (Table 1), respectively. Slightly lower estimate (8.35 ± 0.04%) of SNF% was reported by Haile *et al.,* (2008) in Holstein-Friesian × Boran crossbred cattle. The coefficients of variation (CV) of milk composition traits viz. SNF yield and SNF% traits were estimated as 22.16% and 1.99% (Table 1), respectively. However, higher estimate of CV (11.9%) of SNF% was reported by Haile *et al.* (2008) in Holstein-Friesian × Boran crossbred cattle. The coefficient of variation (CV) for SNF yield revealed that SNF yield were moderately variable traits and could be used in combination with milk production traits for better evaluation of dairy animals. The obtained CV for SNF% was low in estimates and so may not aid significantly in evaluation and differentiation of animals based on their genetic merit.

AFC: The phenotypic mean of AFC was 984 ± 4 days with a coefficient of variation (CV) 12.5% (Table 1). Singh, (1995); Panja (1997); Sivakumar (1998); Sinha (1999); Nehra (2011); Divya (2012) reported close estimates of age at first calving as 978 ± 10 days, 940 ± 18 days, 985 ± 5 days, 985 ± 16 days, 1006 ± 8 days and 984 ± 4 days, respectively in Karan Fries cattle. The CV 12.5% was in agreement with the reports of C.V estimate 15% by Nehra (2011) and 14.62% by Divya (2012). The moderate CV estimate of AFC indicated that AFC trait had potentiality to differentiate animals based on their genetic merit.

FSP: The phenotypic mean of FSP was 143 ± 3 days with a CV 59.6% (Table 1). Similar estimates were reported by Sahana (1996); Saha (2001); Divya (2012) in Karan Fries cattle as 128 ± 6 days, 128 ±11 days and 130 ± 3 days, respectively. The CV 60% was in close to

with the reports of CV estimate 54.25% by Divya (2012). The high CV estimate of FSP indicated that FSP trait had potentiality to differentiate animals based on their genetic merit.

(a) Comparison between heritability estimates of sire and animal models for different traits. The heritability estimates of FL305MY along with variance and covariance components from single-trait sire model (ST-SM) and single-trait animal model (ST-AM) are presented in Table 2.

Table 2: REML estimates of (co) variance components and heritability under single trait sire model and single trait animal model.

Traits	Sire Model			Animal Model		
	Genetic variance	Residual variance	Heritabilities	Genetic variance	Residual variance	Heritabilities
FL305MY	20573	370981	0.053 ± 0.024	94089	301725	0.238 ± 0.087
Fat yield	132	730	0.154 ± 0.043	297	555	0.349 ± 0.091
SNF yield	391	3143	0.111 ± 0.038	1196	2333	0.339 ± 0.094
AFC	1455	12048	0.108 ± 0.031	2082	11274	0.156 ± 0.058
FSP	24	7126	0.003 ± 0.015	72	7078	0.010 ± 0.047

The sire component of variance for different traits under single-trait sire model (ST-SM) was lower than the corresponding estimates of different traits under single-trait animal model (ST-AM). It was expected because where selection intensity for sires selection is very high in comparison to no selection pressure or very less selection pressure on the mates (dams) of sires. The residual variance for different traits under single-trait sire model (ST-SM) was considerably higher than the corresponding estimates of different traits under single-trait animal model (ST-AM). It indicated that single-trait animal model (ST-AM) is more accurate method than single-trait sire model (ST-SM).

The heritabilities of FL305MY, fat yield, SNF yield, AFC and FSP were obtained as 0.053 ± 0.024, 0.050 ± 0.023, 0.111 ± 0.038, 0.108 ± 0.031 and 0.003 ± 0.015, respectively from single trait-sire model (ST-SM). The corresponding heritability estimates of these traits from single-trait animal model were estimated as 0.238 ± 0.087, 0.349 ± 0.091, 0.339 ± 0.094, 0.156 ± 0.058 and 0.010 ± 0.047, respectively. The heritability estimates of traits from single-trait sire model (ST-SM) were considerably lower than corresponding single-trait animal model (ST-AM). The improvement in h^2 of FL305MY, PY305MY, 180DMY, fat yield, fat (%), SNF yield, SNF (%), AFC and FSP traits by ST-AM were 349.10%, 349.05%, 316%, 32.75%, 53.55%, 30.76% and 233.33%, respectively compared to the estimate of ST-SM analysis. The lower heritability estimate of traits from single-trait sire model (ST-SM) in comparison to single-trait animal model (ST-AM) was in agreement with the literatures of Sun *et al.,* (2009); Meszaros *et al.* (2013). Sire model take account of only genetic relationship between of sires only existing in the pedigree of animal population under estimation and ignore genetic relationship existing between the sire and dam and between dams. It also does not account for the selection effects on mates of sires and assume mating is random. The result of sire model is further biased for the animal population of genetic improvement where selection intensity for sires selection is very high in comparison to no selection pressure or very less selection pressure on the mates

(dams) of sires. It result into reduction in sire component of variance and produce lower estimate of heritability. Therefore, heritability of FL305MY from single-trait animal model (ST-AM) appeared better in accuracy then that of sire model.

Comparison of phenotypic and genetic correlation estimates of FL305MY with fat yield, SNF yield, AFC and FSP traits between single trait sire and animal models. The results of phenotypic (r_p) and genetic (r_g) correlations of FL305MY with fat yield, SNF yield, AFC and FSP traits estimated from single-trait sire model and single-trait animal model were presented in Table 3. The results of phenotypic (r_p) and genetic (r_g) correlations from single-trait sire model were compared with corresponding estimates from single-trait animal model. The estimates of genetic (r_g) and phenotypic (r_p) correlations of FL305MY with fat yield, SNF yield, AFC and FSP traits from single-trait sire model were observed changed in magnitude than the corresponding estimates of single-trait animal model for different traits. The estimate of genetic (r_g) correlation of FL305MY with AFC traits from single-trait sire model was not only changed in magnitude but also in sign from the corresponding estimate of single-trait animal model. The estimates of phenotypic (r_p) and genetic (r_g) correlations of FL305MY with fat yield, SNF yield, AFC and FSP traits from single-trait animal model were observed improved in their estimates than the corresponding estimates of single-trait sire model for different traits. The estimates of phenotypic (r_p) and genetic (r_g) correlations of FL305MY with fat yield, SNF yield, AFC and FSP traits from single-trait animal model were observed changed in magnitude than those of single-trait sire model. The phenotypic (r_p) and genetic (r_g) correlations estimates from single-trait animal model were considered more accurate and unbiased than those of single-trait sire model. Because, animal model take account of all kind of relationship among animals existing in pedigree whereas sire model takes into account of between sires relationships of pedigree only. The difference in magnitude and sign between genetic (r_g) and phenotypic (r_p) correlation estimates from sire and animal models analysis exerts the need of traits to be included in animal model evaluation of animals.

Table 3: Comparison of genetic and phenotypic correlation estimates of FL305MY with fat yield, SNF yield, AFC and FSP traits between single trait sire and animal models.

Traits included in model analysis	Phenotypic correlation	Genetic correlation
FL305MY and Fat yield traits		
Sire model	0.485 ± 0.031	0.499 ± 0.085
Animal model	0.508 ± 0.025	0.547 ± 0.042
FL305MY and SNF yield traits		
Sire model	0.478 ± 0.033	0.392 ± 0.020
Animal model	0.513 ± 0.025	0.526 ± 0.037
FL305MY and AFC traits		
Sire model	0.048 ± 0.048	0.114 ± 0.024
Animal model	0.051 ± 0.047	-0.221 ± 0.056
FL305MY and FSP traits		
Sire model	0.143 ± 0.029	-0.934 ± 0.036
Animal model	0.139 ± 0.034	-0.926 ± 0.032

Hence, the estimates of genetic parameters from single-trait animal model were considered more accurate and unbiased than those of single-trait sire model based on their improved estimate and lower residual variance of model. The single-trait animal model should be used to estimate genetic parameters instead of single-trait sire model.

Conflict of Interest. None.

REFERENCES

Barbosa, S. B. P., Ramalho, R. P., Monardes, H. G., Dias, F. M., Santos & Batista, A. M. V. (2008). Milk and fat production of crossbred Holstein-Gir cows (Bos Taurus taurus-Bos taurus indicus) in the Agreste region of the Brazilian state of Pernambuco. *Genetics and Molecular Biology*, *31*(3): 468-474.

Boujenane, I. (2002) Estimates of genetic and phenotypic parameters for milk production in Moroccan Holstein-Friesian cows. *Revue Elev. Med. Vet. Pays Trop*, *55*, 63-67.

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.

Dong, M. C., & Van Vleck, L. D. (1988). Effect of Relationships on Estimation of Variance Components with an Animal Model and Restricted Maximum Likelihood. *J Dairy Sci., 7: 3047-3052.*

Freitas, A. F., Wilcox, C. J., & Roman, R. M. (1995). Genetic parameters for milk yield and composition of cross-bred dairy cattle in Brazil. *J. Dairy Sci. 81*: 2306-2311.

Haile, A., Joshi, B. K., Ayalew, W., Tegegne, A., Singh, A., & Yilma, Z. (2008). Genetic evaluation of Ethiopian Boran cattle and their crosses with Holstein Friesian for milk constituent traits in central Ethiopia. *J. Cell Anim. Biol.*, *2*(10), 171-176.

Hudson, G. F. S., & Schaeffer, L. R. (1984). Monte Carlo comparison of sire evaluation models in populations subject to selection and nonrandom mating. *J. Dairy Sci., 67*: 1264-1272.

Kokate (2009). *Genetic evaluation of Karan Fries sires based on Test day milk records.* (Deemed University) Karnal, India.

Meszaros, G., Kadlecik, O., Kasarda, R., & Solkner, J. (2013). Analysis of longevity in the Slovak Pinzgau population extension to the animal model. *Czech J. Anim. Sci., 58*(7): 289-295.

Meyer, K. (2007). WOMBAT – A tool for mixed model analyses in quantitative genetics by REML, *J.* Zhejiang Uni. Science B *8*: 815–821.

Nehra, M. (2011). *Genetic analysis of performance trends in Karan Fries cattle.* M.V.Sc. Thesis. NDRI (Deemed University), Karnal, India.

Panja, P. (1997). *Optimization of economic-traits in Karan Fries cattle.* M.Sc. Thesis, National Dairy Research Institute, Karnal Haryana, India.

Rashia, (2010). *Genetic evaluation of the lactation curve in Karan Fries cattle.* Ph.D. Thesis, NDRI (Deemed University) Karnal, India.

Saha, S. (2001). *Generation wise genetic evaluation of Karan Swiss and Karan Fries cattle*. Ph.D. Thesis, NDRI (Deemed University) Karnal, India.

Sahana, G. (1996). *Effectiveness of sire evaluation methods for milk production alongwith auxiliary traits vis-à-vis other methods in crossbred cattle.* Ph.D Thesis, NDRI (Deemed University) Karnal, India.

Singh, M. K. (1995). *Factors affecting trend in performance of Karan Swiss and Karan Fries cattle.* Ph.D Thesis, NDRI (Deemed University) Karnal, India.

Singh, S. (2006). Genetic evaluation of Karan Fries sires on the basis of part lactation milk yield.NDRI (Deemed University) Karnal, India.

Sinha, S. (1999). *Studies on level of heterozygosity of Karan Fries animals.* M.Sc. Thesis, NDRI (Deemed University), Karnal.

Sivakumar, R. (1998). *Reproductive performance at different levels of production in Karan Fries cattle.* M.Sc. Thesis, National Dairy Research Institute, Karnal, Haryana.

Sun, C., Madsen, P., Lund, M., Zhang, S.Y., Nielsen, U.S. and Su, G. (2010). Improvement in genetic evaluation of female fertility in dairy cattle using multiple-trait models including milk production traits. *J. Anim Sci*. 88:871-878.

Toghiani, S. (2012). Genetic relationships between production traits and reproductive performance in Holstein dairy cows. *Archiv Tierzucht, 55*(5) 458-468.

Tripathy, S. S., Chakravarty, A. K., Mir, M. A., Singh, A. P., Jamuna, V., & Lathika, S. (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.

Yaeghoobi, R., Roshanfekr, H., Mamooee, M., Fayazi, J., Ashayerizadeh, A., Bojarpour, M., & Nasiri, M. T. B. (2009). Genotype by environmental interactions for milk and fat production across western provinces of Iran. *Journal of Animal and Veterinary Advances*, *8*(11): 2110-2114.