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Genetic parameter estimation for growth traits in males of Karan fries cattle

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ABSTRACT

The significance of sire selection in the herd is reflected by the total genetic gain through sire-to-sire and sire-to-dam pathways contributing greater than 50% contribution. The present investigation was carried out to estimate genetic parameters of males of Tharparkar (TP) and Karan-Fries (KF) cattle. Data on body weights of Tharparkar and Karan Fries males born during the period 1994–2012 at ICAR–National Dairy Research Institute (ICAR-NDRI), Karnal, India were utilized in the present study. The genetic and phenotypic correlations among different body weights were estimated from the analysis of variance and covariance among sire groups. Paternal half-sib correlation method was used to estimate heritability of growth traits. Heritability estimates in KF were found to be of moderate to high magnitude, as 0.23±0.06, 0.43±0.10, 0.28±0.10, 0.36±0.11, 0.39±0.12, 0.38±0.14, 0.27±0.19 for weight at birth and weight at monthly interval up to six months, respectively. Genetic and phenotypic correlations were found to vary from moderate to high among the traits. Our study revealed that the magnitude of heritability indicates a high scope of further improvement in Karan Fries. Selective breeding and positive genetic correlations should be considered while designing selection programs.

Keywords: Cattle, Correlation, Genetic parameters, Heritability

Cattle husbandry is an integral part of Indian civilization and the country possesses rich biodiversity of cattle genetic resources. Despite harbouring large livestock heads, the true genetic potential of the cattle genetic resources has not been fully exploited. This may be due to the lack of conservation of indigenous breeds and the dearth of systematic programmes of their genetic improvement through crossbreeding. Further, a serious bottleneck in sustainable cattle improvement programmes is the non-availability of genetically proven male germplasm. It is, therefore, necessary to have a nucleus herd of high genetic merit cattle for production and dissemination of quality germplasm to meet the requirement of pure as well as crossbred bulls. Keeping all this in view, the Tharparkar breed is being maintained at ICAR-NDRI Karnal. Further a composite breed, Karan Fries was developed in the 1970's at ICAR-NDRI, Karnal, using Tharparkar and Holstein Friesian breeds. This breed is currently being maintained at a level of Holstein inheritance of around 62.5%. In order to maintain these breeds at the farm, to assess their progress, and for the implementation of a sound breeding program, genetic parameter estimates are needed. This is especially important because the improvement of growth traits is an essential breeding goal in cattle and other livestock production systems. Heritabilities and genetic correlations are critical population parameters required in livestock breeding researches as well as in the design and application of practical animal breeding programmes. Genetic parameters are unique to each population in which these were estimated, and these may change over time due to various selection and management decisions. It is also advantageous to know the empirical relationships (genetic, phenotypic and environmental correlations) of these measures of growth rate in the population, eg. growth rates that are correlated with birth weights (Simm 1998). The genetic relationships among growth traits have been studied by multiple authors (Kumar 2011, Manoj 2010, Rehman *et al.* 2013, Mishra *et al.* 2017). However, there is a paucity of reported genetic parameter estimates of growth traits of crossbred Karan-Fries and for indigenous breeds of cattle. Therefore, it would be useful to investigate the effect of genetic and non-genetic factors on growth traits, so that appropriate breeding programmes can be made for bringing about genetic improvement in these herds.

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MATERIALS AND METHODS

Data collection and farm details: For the present investigation, data on body weights of male calves of KF (2,047) and TP (130) born during last 19 years (1994–2012), were utilized for the study. The geographical location of

ICAR-NDRI livestock farm is at an altitude of 250 meters above the MSL in the Indo-Gangetic alluvial plains on 29°42′ N latitude and 72°02′ E longitude. The climate of the farm is subtropical. Therefore, cattle maintained at ICAR-NDRI farm get exposed to extreme climatic conditions. The data of all traits were normalized using mean and standard deviation of the traits.

Both sexes were reared together up to 6 months of age and weaning was performed at birth. Calves were fed colostrum for first five days and then whole milk was provided up to 30 days. The calves were provided with a mixture of skimmed milk and whole milk up to four months of age and skimmed milk up to six months of age. Concentrates, mineral mixture and roughages were given to the calves from the first month. They were fed according to body weight as per accepted nutritional standards. Most of the males were disposed after 6 months, leaving only a few calves. These were selected from high yielding dams with good pedigree records for use as future bulls.

Standardization and classification of data: The data were suitably classified according to different periods, genetic groups, seasons, parity (Primiparous and Pleuriparous). The year was split into 12 classes based on the month of birth of calves. Due to limited data size for TP breed, the year was divided into four seasons (winter, summer, rainy and autumn). The periods were classified in such a way that there was no overlapping of sires between the periods thus minimizing sire-period confounding. Also, to examine the effect of periods, the data were classified approximately into 6 periods of 3 consecutive years duration except the last period which was of 4 years in KF.

Estimation of genetic parameters: Heritability, genetic and phenotypic correlations were estimated only from those progeny groups of sires that had a minimum of four daughters.

Estimation of heritability: Paternal half-sib correlation method (Becker 1975) was used for the estimation of heritability of growth traits. The following model was used:

$$Y_{ij} = \mu + s_i + e_{ij}$$

where, Y_{ij}, adjusted value of j^{th} progeny of i^{th} sire; μ, overall population mean; S_i, effect of i^{th} sire; e_{ijk}, random error assumed to be distributed normally and independently with mean zero and constant variance, i.e. NID (0, σ^2_e). The analysis of variance for half-sib data with unequal number of progeny under different sires was also conducted. The standard error of heritability was estimated as per the procedure given by Swiger *et al.* (1964).

Estimation of genetic and phenotypic correlations: The genetic and phenotypic correlations for different body weights were estimated from the analysis of variance and covariance among sire groups as given by Becker (1975). The model and procedure for the analysis used was the same as that used for heritability. The analysis of covariance for half-sib data with unequal number of male progeny under different sires was also performed.

RESULTS AND DISCUSSION

Heritability estimates of birth weight and other body weights: The heritability estimates for growth traits indicated that the traits under study were moderately affected by additive gene action. The heritability of birth weight was moderate and significant (0.23±0.06) for KF (Table 1). Similar estimates of heritability of birth weight were observed in different breeds of cattle globally (Khan *et al.* 1999 and Kumar 2011). However, higher estimates of heritability for birth weight were reported by Plasse *et al.* (2002a) and Plasse *et al.* (2002b). Lower estimates of heritability for birth weight were observed by Khan *et al.* (1999), Jain *et al.* (2000), Bakir *et al.* (2004) and Manoj (2010).

The heritability of body weights at 1M (0.43±0.10), 2M (0.28±0.10), 3M (0.36±0.11), 4M (0.39±0.12) and 5M (0.38±0.14) were moderate to high and significant for KF calves implying the presence of variability in the population

Table 1. Heritability (h^2) estimates of birth weight and body weights at different ages in KF males

Trait	N	S	K	$h^2 \pm SE$
Birth weight	1,800	87	19	0.23±0.06
1M	1,230	86	13	0.43±0.10
2M	1,000	86	11	0.28±0.10
3M	853	83	9	0.36±0.11
4M	715	81	8	0.39±0.12
5M	567	81	6	0.38±0.14
6M	370	77	4	0.27±0.19

N, progeny; S, sire; K, average number of progeny.

Table 2. Genetic and Phenotypic correlations among different body weights in KF males

Trait	Birth weight	1M	2M	3M	4M	5M	6M
Birth weight		0.83[a]±0.12	0.67[a] ±0.27	0.35±0.36	0.44±0.38	0.36±0.55	0.27±0.40
1M	0.79[b]±0.03		NE	0.73[a]±0.20	0.78[a]±0.24	0.64±0.44	0.34±0.37
2M	0.57[b]±0.04	0.83[b]±0.03		0.87[b]±0.11	0.90[b]±0.16	0.70±0.38	0.31±0.47
3M	0.45[b]±0.05	0.70[b]± 0.04	0.90[b]±0.02		0.97[b]±0.05	0.90[a]±0.21	0.51±0.34
4M	0.37[b]±0.05	0.60[b]± 0.04	0.80[b]±0.03	0.92[b]±0.02		0.99[b]±0.11	0.70[b] ±0.11
5M	0.30[b]±0.05	0.52[b]±0.05	0.71[b]±0.04	0.84[b]±0.03	0.94[b]±0.02		0.99[a]±0.24
6M	0.27[b]±0.05	0.47[b]±0.05	0.65[b]±0.04	0.78[b]±0.03	0.88[b]±0.03	0.95[b]±0.02	

Figures above the diagonal are the genetic correlations. Figures below the diagonal are the phenotypic correlation. NE, Not estimable; [a], Significant at 5% level; [b], Significant at 1% level.

which can be exploited for genetic improvement (Table 2). However, heritability of body weight at 6M (0.27±0.19) was not found to be significantly different from zero. This may be because the standard error was high (Table 2). However, lower estimates of heritability for 6 month body weight were observed by Khan *et al.* (1999), Plasse *et al.* (2002b), Bakir *et al.* (2004) and Manoj (2010). High estimates for heritability were reported by Freetly *et al.* (2020) and recommended for selection which is similar to our results. It is pertinent to mention that heritability can be affected by method of estimation, location and year (Gathura *et al.* 2020) when they were estimated and may therefore be used for selection at any given time.

While in TP, the heritabilities of birth weight and 1-month body weight were 0.67±0.36 and 0.28±0.33 respectively. These values were high, yet not significantly different from zero. The higher value of standard error may be attributed to limited data size in TP. The results of the present study indicated that the growth traits were moderate to highly heritable.

Phenotypic and genetic correlation among growth traits: The phenotypic and genetic correlation estimates obtained are presented in Table 2. The genetic (0.83±0.12), (0.67±0.27) and phenotypic correlations (0.79±0.03) (0.57±0.04) of birth weight with 1 month body weight, birth weight with 2M body weight were positive and significant in KF. However genetic correlation between birth weight and body weights at 3M (0.35±0.36), 4M (0.44±0.38), 5M (0.36±0.55) and 6M (0.27±0.40) were positive and not significantly different from zero although phenotypic correlations at the respective months (0.45±0.05, 0.37±0.05, 0.30±0.05, 0.27±0.05) were positive and significant. Genetic correlation of 1M body weight with 3M (0.73±0.20) and 4M (0.78±0.24) was positive and significant but at 5M (0.64±0.44) and 6M (0.34±0.37) it was found to be positive and non-significant. However phenotypic correlation of 1M body weight at respective months (0.70±0.04, 0.60±0.04, 0.52±0.05 and 0.47±0.05), between 3M body weight with 4M (0.92±0.02), 5M (0.84±0.03) and 6M (0.78±0.03), between 2M body weight with 3M (0.90±0.02), 4M (0.80±0.03), 5M (0.71±0.04) and 6M (0.65±0.04) were positive and significant. The genetic correlation of 2M body weight with 3M (0.87±0.11) and 4M (0.90±0.16) were positive and significant but at 5M (0.70±0.38) and 6M (0.31±0.47) they were not significant. The genetic correlation between 3M body weight with 4M (0.97±0.05) and 5M (0.90±0.21) were found to be positive and significant but non-significant for 6M (0.51±0.34. The genetic and phenotypic correlations of 4M body weight with 5M (0.99±0.11 and 0.70±0.11) and 6M (0.94±0.02 and 0.88±0.03) body weights respectively were positive and significant in KF calves. Similar positive and significant genetic and phenotypic correlation respectively was observed between 5M body weight and 6M (0.99±0.24; 0.95±0.02) body weight of KF calves. Kumar (2011) and Gathura *et al.* (2020) also observed high genetic (0.75±0.16) and phenotypic correlation (0.70±0.03) of birth weight with 6M body weight in KF calves and for economically important traits in beef cattle. However negative genetic correlations were reported by Dash *et al.* (2015) for the traits under their study in Karan Fries cattle. Contrarily Manoj (2010) observed lower genetic (0.10±0.40) and phenotypic correlation (0.06±0.04) between birth weight with 6M body weight in Sahiwal calves while moderate phenotypic correlation (0.40±0.11) was observed by Aduli *et al.* (1996) in Friesian × Bunaji crosses. Positive genetic correlations among traits may be useful during selection programs (Verma *et al.* 2019) in Red Sindhi and direct selection for one trait would consequently lead to the improvement in other traits in Gir (Prata *et al.* 2015).

Overall estimates of genetic parameters, i.e. heritabilities especially for 1-month body weight in KF and genetic correlations revealed a wide scope of selection for direct as well correlated response in growth traits. Growth traits could also be considered as selection criterion for selecting males for future breeding.

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