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# Genetic parameters of first lactation production traits of Tharparkar cattle

# Garima Choudhary, U Pannu and GC Gahlot

# Abstract

This research was aimed to investigate the production traits and their genetic parameters in Tharparkar cattle of northwestern India. Heritability, phenotypic, and genetic parameters were estimated for productive traits of first parity. This study revealed the average First lactation milk yield (FLMY), First lactation Length (FLL), First Dry period (FDP) and lactation milk yield per day of first lactation length (LMY/FLL) were 1832.99 kg, 283.65 days, 148.14 days and 6.18 kg/day respectively. The heritability estimates for productive traits of the first lactation were 0.401, 0.33, 0.04 and 0.19 for FLMY, FLL, FDP and LMY/FLL, respectively. First lactation milk yield had significant, high and positive genetic correlation with all traits. The genetic correlation of FLMY with FLL was very high (0.77), positive and Significant. The genetic correlations of FLL with FDP and lactation milk yield per day of first lactation length (LMY/FLL) were negative. Phenotypic correlation of FLMY were positive with all traits, with an exception of FDP. FDP had negative phenotypic correlation with all traits. The heritability estimates of FLMY and FLL were medium which revealed that these traits had more additive genetic variance which might be utilized by individual selection and it could be achieved owing to sire selection. Selection for high milk yield will be associated with genetic improvement in lactation length also.

Keywords: FDP, parameters, lactation, traits, phenotypic correlation

# 1. Introduction

India is a rural based country. The agriculture and livestock are the main source of employment in rural areas. Due to tremendous contribution of cattle to the Indian agriculture, livelihood and food security, the cow has occupied a prime position in rural life of India. Various indigenous breeds of cattle in the country are the result of thousands of years of selection, evolution and development of the wild species in the process of domestication to the local agro climatic conditions. These breeds are now losing ground due to intense competition from other breeds and risk of economic viability under the present system of management. (Chand, 2011)<sup>[3]</sup>. Tharparkar cattle is a *Bos indicus* lyre-horned breed, derives its name from the Thar Desert (Lall, 1994)<sup>[7]</sup>. Tharparkar is a milch breed of India (Singh, 2006)<sup>[14]</sup>. Average animals of the Tharparkar breed are strongly built, medium sized with straight limbs with an alert and springy carriage and the usual colour of this cattle breed is white or gray. This investigation aimed to evaluate heritability, phenotypic, genetic correlations of some production performance of tharparkar cattle that are of financial consequence to the dairy farming.

# 2. Materials and Methods

The data for the current investigation is collected from the records of Tharparkar cattle, located at the Livestock Research Station, Beechwal, Bikaner, Rajasthan. Records of the 91 cows which calved during the year 2006 to 2016 are included in the study. The collected productive traits are total first lactation milk yield (FLMY), first lactation length (FLL), first dry period (FDP) and lactation milk yield per day of first lactation length (LMY/FLL).

# 3. Statistical analysis

# 3.1 Estimation of heritability

Heritability of different traits is estimated by paternal half sib correlation method given by Becker (1968)<sup>[1]</sup>. The sires with less than three progeny are excluded for the estimation of

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heritability. The data adjusted for significant effects of nongenetic factors is used for estimation of heritability. The model for estimating the heritability is-

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

Where,  $Y_{ij}$  = Observation of the j<sup>th</sup> progeny of the i<sup>th</sup> sire  $\mu$  = Overall mean  $s_i$  = Random effect of the i<sup>th</sup> sire NID (0,  $\sigma e^2$ )  $e_{ij}$  = Random error NID (0,  $\sigma e^2$ )  $\sigma s^2$  = Sire component of variance = (MSS – MSW) / K  $t = \sigma^2 s / (\sigma^2 s + \sigma^2 w)$  $h^2 = 4t$ 

Where, t = intra - class correlation among half sibs,

# 3.2 Standard error of heritability

The standard error of heritability is estimated using the formula given by Swiger *et al.* (1971)<sup>[15]</sup>, as follows:

S.E.  $(h^2) = 4 \text{ S}\sqrt{\{[2(N-1) (1-t^2) (1 + (K-1) t)^2] / [K^2(N-S)(S-1)]\}}$ 

Where, N = number of observations,

t = intra-class correlation,

S = number of sires and

K = average number of progenies per sire.

 $K = \{ [1/(S - 1)] [N - (\Sigma n_i^2) / N] \}$ 

Where, N and S are defined above, and  $n_i$  is the number of progeny for the  $i^{\text{th}}$  sire.

The heritability is obtained from the Animal model WOMBAT programme (Meyer, 2007)<sup>[8]</sup>, which takes into consideration all the genetic relationships of the individual.

#### **3.3 Genetic and Phenotypic Correlations**

The genetic correlations calculated from the analysis of variance and covariance among sire groups are as follows:

# **3.4 Genetic Correlations**

Genetic correlations was estimated as

 $\mathbf{r}_{g(XY)} = \operatorname{Cov}_{S(XY)} / \sqrt{\left[ (\sigma^2_{S(X)}) (\sigma^2_{S(Y)}) \right]}$ 

Where, X and Y are traits of the same individual,

Cov  $_{S(XY)}$  = Sire component of covariance between traits X and Y.

 $\sigma^2_{S(X)}$  and  $\sigma^2_{S(Y)}$  = Sire components of variance for traits X and Y.

The standard error of genetic correlations can be calculated by formula given by Robertson (1959)<sup>[12]</sup>:

S.E.  $(r_g)$  = [(1-r^2\_g) /  $\sqrt{2}$ ] \* { $\sqrt{2}$  [SE  $(h^2_x)$  SE  $(h^2_y)$ ] /  $\sqrt{2}$  [( $h^2_x)(h^2_y)$ ]}

Where,  $h_x^2$  and  $h_y^2$  are the heritability estimates of the two traits X and Y, respectively.

The statistical significance of genetic correlation is determined using the 't-test'.

#### **3.5** Phenotypic correlations

Phenotypic correlation is estimated by using the following formula:

$$r_{p(XY)} = \frac{Cov_{s(XY)} + Cov_{e(XY)}}{\sqrt{\left\{ \left[ \sigma^2_{s(X)} + \sigma^2_{e(X)} \right] \left[ \sigma^2_{s(Y)} + \sigma^2_{e(Y)} \right] \right\}}}$$

Where,  $Cov_{S (XY)}$  = Sire component of covariance between traitsX and Y.

 $\sigma^2_{e\ (X)}$  and  $\sigma^2_{e(Y)}$  = Error components of variance for traits X and Y.

Following formula given by Panse and Sukhatme (1967)<sup>[10]</sup> is used to calculate standard error of phenotypic correlations:

SE (
$$r_p$$
) =  $\sqrt{[1 - r_{P(XY)}^2]} / \sqrt{[N - 2]}$ 

Where,  $r_{p (XY)}$  = Phenotypic correlation between the traits X and Y of the same individual.

N - 2 = Degree of freedom

The statistical significance of correlations is determined by using 't-test'.

#### 4. Results

**Table 1:** Productive traits of Tharparkar (means, standard deviations(SD) and heritability estimates  $(h^2)$  and standard errors (SE) for thesetraits

Traits	Mean ± SD	$h^2 \pm SE$
FDP	$148.14 \pm 6.05$	0.04±0.030
FLL	283.65±7.65	0.33±0.288
FLMY	1832.99±42.43	0.40±0.394
LMY/FLL	6.18±0.14	0.19±0.142

 
 Table 2: Heritability, genotypic and phenotypic correlation with their standard error of different production traits

	FDP	FLL	FLMY	LMY/FLL
FDP	$0.04 \pm 0.030$	-0.32±0.523**	0.56±0.425**	0.01±0.539
FLL	$-0.08 \pm 0.110$	$0.33 \pm 0.288$	0.77±0.266**	-0.39±0.480**
FLMY	-0.27±0.107*	0.58±0.086**	$0.40 \pm 0.394$	$0.30 \pm 0.550 **$
LMY/FLL	-0.11±0.110	-0.54±0.088**	0.22±0.102*	0.19±0.142

(Values at the diagonal are heritability estimates, and values above and below the diagonal are genotypic and phenotypic correlations, respectively). \*\* - Highly significant ( $p \le 0.01$ ); \* - Significant ( $p \le 0.05$ )

# **4.1 Productive traits**

The current investigation revealed the averages FLMY, FLL, FDP and LMY/FLL were 1832.99 kg, 283.65 days, 148.14 days and 6.18 kg/day respectively (Table 1).

# 4.2 Heritability estimates

There were strong  $h^2$  values for first lactation milk yield (0.40) and first lactation length (0.33) (Table 1), while it was moderate for lactation milk yield per day of first lactation length (0.19). The heritability estimates were very weak for first dry period (0.04) (Table1).

# 4.3 Genetic and phenotypic correlation

Table 2 presents the genetic and phenotypic correlation for production performance of Tharparkar cattle. First lactation milk yield had significant, high and positive genetic correlation with all traits. The genetic correlation of FLMY with FLL was very high (0.77) (Table2), positive and significant. The genetic correlations of FLL with FDP and LMY/FLL were negative. Phenotypic correlation of FLMY were positive with all traits, with an exception of FDP. FDP had negative phenotypic correlation with all traits.

# 5. Discussion

In the present investigation, the estimate of heritability of first lactation milk yield was 0.401±0.394. It lies well in the range reported by Bhatnagar et al. (1982)<sup>[2]</sup> in Tharparkar and Doharey (2012) <sup>[5]</sup> in Hariana cattle. In the present investigation the estimate of heritability of first lactation length was 0.33±0.288 and it lies well in the range reported by Sengar et al. (1987)<sup>[13]</sup> and Gahlot (1999)<sup>[6]</sup> in Tharparkar. Whereas, Pirzada (2012)<sup>[11]</sup> reported higher magnitude of heritability for first lactation length in Tharparkar cattle. Heritability of first dry period in this study was estimated as  $0.04\pm0.030$ , which was in the range of estimates reported by various workers. Gahlot (1999)<sup>[6]</sup> in Tharparkar, Dahiya (2002)<sup>[4]</sup> in Hariana, Nehra (2004)<sup>[9]</sup> in Rathi Heritability of lactation milk yield per day of first lactation length was estimated as  $0.19\pm0.142$ . It lies well in the range reported by Gahlot (1999)<sup>[6]</sup> in Tharparkar. It was lower than the reported by Nehra (2004)<sup>[9]</sup> in Rathi cattle and Pirzada (2012)<sup>[11]</sup> in Tharparkar cattle.

The genetic correlation of FLMY with FLL was very high  $(0.77 \pm 0.266)$ , positive and significant. Pirzada (2012) <sup>[11]</sup> reported high and positive genetic correlations of FLMY with all first lactation traits in Tharparkar cattle.The genetic correlations of FLL with FDP and LMY/FLL were negative and with rest of the trait was positive and significant. Pirzada (2012) <sup>[11]</sup> reported positive genetic correlations of FLL with all first lactation traits in Tharparkar cattle. Doharey (2012) <sup>[5]</sup> reported negative genetic correlations of FLL with FDP in Hariana cattle.

First lactation milk yield had positive phenotypic correlations with all first lactation traits except FDP. Pirzada (2012)<sup>[11]</sup> reported positive phenotypic correlations of FLMY with all first lactation traits in Tharparkar cattle. Doharey (2012)<sup>[5]</sup> reported negative genetic correlations of FLMY with FDP in Hariana cattle. The phenotypic correlations of FLL with FDP and LMY/FLL were negative and with rest of the traits were positive. Pirzada (2012)<sup>[11]</sup> reported positive phenotypic correlations of FLL with all first lactation traits in Tharparkar cattle. Doharey (2012)<sup>[5]</sup> reported negative phenotypic correlations of FLL with all first lactation traits in Tharparkar cattle. Doharey (2012)<sup>[5]</sup> reported negative phenotypic correlation of FLL with FDP in Hariana cattle

# 6. Conclusion

High and moderate heritable estimates for first lactation milk production and first lactation length indicated that the possibility of genetic improvement of these traits could be achieved through individual selection, while low heritability estimates (first dry period) indicated that the most variation in this trait may be due to non–genetic factors and this could be improved through better feeding and manage mental practices. Selection for high milk yield will be associated with genetic improvement in lactation period. Moreover, high genetic correlation among first lactation milk yield and first lactation length elucidated that these parameters might be regulated by similar genes so that these parameters might be enhanced concurrently via selection for any of the trait.

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