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Genetic evaluation of Tharparkar cattle based on first lactation reproduction traits of economic importance

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Abstract

This research was aimed to investigate the reproduction traits and their genetic parameters of Tharparkar cattle under local agroclimatic conditions of northwestern region of India. Heritability, phenotypic, and genetic parameters were estimated for reproductive traits of first parity. This study revealed the averages AFC, FSP and FCI were 1510.88±22.29 days, 149.66±5.15 days and 423.60±6.23 days respectively. The heritability estimates for reproductive traits of the first lactation were 0.52±0.070, 0.12±0.166 and 0.18±0.232, respectively. Age at first calving had positive genetic correlation with first service period. The genetic correlation of AFC with FCI was very high (0.74), Negative and significant. The genetic correlations of FSP with FCI was positive, high and significant. Phenotypic correlation of all reproductive traits was positive. The heritability estimates of AFC was medium which revealed that this trait had more additive genetic variance which might be utilized by individual selection and it could be achieved owing to sire selection. First service period and first calving interval largely controlled by factors other than additive gene action, which might be non-additive gene action and environmental factors. Hence, better feeding and management practices seem conductive for ameliorating this trait.

Keywords: Heritability, phenotypic correlation, Tharparkar, reproduction traits

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) [2]. Tharparkar cattle is a *Bos indicus* lyre-horned breed, derives its name from the Thar Desert (Lall, 1994) [7]. Tharparkar is a milch breed of India (Singh, 2006) [15]. 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 reproduction performance of tharparkar cattle that are of financial consequence to the dairy farming.

Materials and Methods

The data for the current investigation were collected from the records of Tharparkar cattle, located at the Livestock Research Station, Beechwal, Bikaner. Records of the 91 cows which calved during the year 2006 to 2016 were included in the study. Some animals were shifted from Livestock Research Station, Chandan, Jaisalmer to Livestock Research Station, Beechwal, Bikaner in the year 2011 along with their records. Records of these animals were also included in the study. The collected productive traits were age at first calving (AFC), first service period (FSP) and first calving interval (FCI).

Statistical analysis
Estimation of heritability

Paternal half sib correlation method given by Becker (1968) was used to estimate the heritability of different traits. The sires with less than three progeny were excluded for the estimation of heritability. The data adjusted for significant effects of non - genetic factors were 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 jth progeny of the ith sire

μ = Overall mean

s_i = Random effect of the ith sire NID $(0, \sigma e^2)$

e_{ij} = Random error NID $(0, \sigma e^2)$

σs^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,

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

Genetic and Phenotypic Correlations
The genetic correlations calculated from the analysis of variance and covariance among sire groups is as follows:

Genetic Correlations
Genetic correlations was estimated as

$$r_{g(XY)} = Cov_{S(XY)} / \sqrt{[(\sigma^2_{S(X)})(\sigma^2_{S(Y)})]}$$

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 (1954):

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

Where, h^2_x and h^2_y are the heritability estimates of the two traits X and Y, respectively.
The statistical significance of genetic correlation was determined using 't-test'.

Phenotypic correlations
Phenotypic correlation was estimated by using the following formula:

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

Where, $Cov_{S(XY)}$ = Sire component of covariance between traits X and Y.
$\sigma^2_{e(X)}$ and $\sigma^2_{e(Y)}$ = Error components of variance for traits X and Y.
The standard error of phenotypic correlations can be calculated by formula given by Panse and Sukhatme (1967) [10].

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

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 was determined by using the 't-test'.

Results

Table 1: Reproductive traits of Tharparkar (means, standard deviations (SD) and heritability estimates (h^2) and standard errors (SE) for these traits

Traits	Mean ± SD	$h^2 \pm SE$
AFC	1510.88±22.29	0.52±0.070
FSP	149.66±5.15	0.12±0.166
FCI	423.60±6.23	0.18±0.232

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

Traits	AFC	FSP	FCI
AFC	0.52±0.070	0.21±0.298	-0.74±0.132**
FSP	0.19±0.109	0.12±0.166	0.63±0.581**
FCI	0.12±0.110	0.29±0.106**	0.18±0.232

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

Discussions
The estimate of heritability of AFC was found to be 0.52±0.070 in the present study. Wide range of heritability estimates for AFC have been reported which ranged from 0.18±0.09 in Hariana cattle (Kaushik, 2000) [5] to 0.74±0.22 in Tharparkar cattle (Chand, 2011) [2]. Kumar (2012) [6] estimated heritability for age at first calving in Rathi as 0.44±0.28. Gahlot (1999) [4] in Tharparkar (0.52±0.129), Singh et al. (1999) [14] in Sahiwal (0.69±0.215) and Singh (2012) in Rathi (0.625±0.37) also reported higher estimates of heritability.

The higher estimates of heritability of AFC in present study suggested that fairly good possibility exist for improving this trait in desirable direction using individual selection.

Heritability estimate of first service period in this study was estimated 0.12±0.166, which was in the range of estimates reported by various workers i.e. 0.09±0.09 Gahlot (1999) [4] to 0.23±0.27 Pirzada (2012) [11] in Tharparkar cattle. Nehra (2004) [9] in Rathi cattle reported a higher estimate of heritability for first service period.

Heritability estimates of first calving interval in this study were estimated as 0.18±0.232. The literature reflects the range of this estimate reported by various workers in Tharparkar cattle from 0.04±0.08 (Gahlot, 1999) [4] to 0.23±0.27 (Pirzada, 2012) [11]. Nehra (2004) [9] reported heritability of first calving interval in Rathi cows as (0.21±0.108), Dahiya (2002) [3] in Hariana cows (0.079±0.07).

The genetic correlation of AFC with FCI was very high (0.74), negetive and significant. The genetic correlations of FSP with FCI was positive, high and significant. Pirzada (2012) [11] reported the genetic correlation of age at first calving with all first lactation reproduction traits to be positive in Tharparkar cattle. Raja (2004) [12] observed that genetic correlation between age at first calving and first calving interval was -0.12±0.46 in Sahiwal cattle.

Phenotypic correlation of all reproductive traits were positive. Pirzada (2012) [11] reported phenotypic correlation of AFC with FCI, FSP as 0.45, 0.01 respectively in Tharparkar cattle.

Conclusion
Moderate heritable estimates for age at first calving indicated that the possibility of genetic improvement of this trait could be achieved through individual selection, while low heritability estimates (first service period and first calving interval) indicated that the most variation in these traits may be due to non–genetic factors and this could be improved through better feeding and managemental practices. Selection for first service period will be associated with genetic improvement in first calving interval, these parameters might be enhanced concurrently via selection for any of the trait.

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