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Genetic Analysis of Herd Life Traits and its Relationship with Production and Reproduction Traits in Jersey Crossbred Cattle

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ABSTRACT

Background: Herd life is a crucial economic trait, since it affects both total milk yield over a lifetime and the expenses associated with herd replacement. The genetic improvement of longevity traits is frequently challenging due to their typically poor heritability. Consequently, employing indirect selection based on production and reproductive attributes genetically related to longevity may yield a more efficacious breeding strategy. Assessing genetic parameters and interrelations among these traits is crucial for developing effective breeding strategies in jersey crossbred cattle.

Methods: This research examined the performance records of 357 Jersey crossbred cows over a span of 39 years (1980-2018). Genetic parameters were assessed for various longevity-related traits, including herd life (HL), productive herd life (PHL), total milk production (TMP), number of days in lactation (NDL) and number of lactations completed (NLC). Their correlations with production traits, including first lactation 305-day milk yield (FL305MY) and first lactation total milk yield (FLTMY), alongside reproductive traits. [Age at first calving, service period and calving interval] were examined. Heritability estimations were derived *via* the paternal half-sib approach and a restricted maximum likelihood (REML)-based animal model. Covariance component analysis was employed to determine genetic and phenotypic associations among characteristics.

Result: Estimates of heritability obtained from paternal half-sib analysis were 0.08±0.15 for HL, 0.06±0.14 for PHL, 0.23±0.17 for TMP, 0.26±0.17 for NDL and 0.38±0.18 for NLC. Estimates derived from the animal model varied between 0.05 and 0.18, signifying a modest to moderate additive genetic impact on longevity traits. The genetic correlations observed among longevity and productivity traits varied from 0.37 to 0.71, indicating positive correlations, although the phenotypic correlations were somewhat less. Most reproductive traits demonstrated low to moderate positive genetic associations with longevity traits, with the exception of the association between NLC and AFC. The identified correlation structure indicates that the selection for increased longevity may concurrently boost milk production without adversely impacting reproductive efficiency.

Key words: Genetic correlations, Genetic parameters, Herd life, Heritability, Jersey crossbred cattle, Longevity traits.

INTRODUCTION

Longevity is a crucial functional trait since it directly influences lifetime milk yield, replacement expenses and agricultural profitability. Cows with longer productive lifespans enhance herd performance, while inadequate reproductive efficiency frequently results in premature culling and diminished economic returns (Joshi *et al*., 2023). The genetic enhancement of herd longevity is difficult owing to its low heritability, which constrains the efficacy of direct selection (Mukherjee *et al*., 1999). Consequently, indirect selection predicated on genetically linked productivity and reproductive traits may offer a viable alternative. The efficacy of these breeding procedures relies on precise estimate of genetic parameters and the interrelations among economically significant traits (Dangi *et al*., 2021). Prior research has indicated positive correlations between first-lactation production traits and herd longevity, suggesting that early performance metrics may serve as effective predictors of productive lifespan (Ram and Goswami, 2005; Kumar *et al*., 2014). Moreover, comprehending the intricate relationships between genetic factors and phenotypic expressions in the realm of production, reproduction and lifetime traits is crucial for formulating effective breeding programs. The current research focused on evaluating the genetic characteristics associated with herd life traits in Jersey crossbred cattle and to analyse their correlations with specific production and reproductive traits.

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MATERIALS AND METHODS

Study area, animals and data collection

The research was conducted at the ICAR-National Dairy Research Institute (NDRI), Eastern Regional Station, Kalyani, West Bengal, India, during 2019-20. The farm is home to a population of Jersey crossbred cattle were

developed by crossing Jersey bulls with tharparkar and red sindhi cows. Animals were raised in a loosely structured housing system and fed balanced rations according to farm management practices.

Data from 357 Jersey crossbred cattle spanning 39 years (1980-2018) were utilized. A total of 1,710 lactation records were analyzed. Information collected from farm records included animal identification, pedigree details, birth date, calving and drying dates, lactation yield, days in milk, service records and other relevant reproductive information. The detailed descriptions of the herd have been described elsewhere by Kumar and Mandal (2021).

The herd life traits studied were HL, PHL, TMP, NDL and NLC. Productive traits such as FL305MY and FLTMY, along with reproductive traits including AFC, SP and CI were also considered. Records lacking complete pedigree information or involving twin births, stillbirths and abortions were excluded from the analysis.

Estimation of genetic parameters

Heritability estimates for herd life traits were acquired utilising a simple animal model and the paternal half-sib (PHS) technique. Prior to genetic analysis, the data underwent adjustments to account for notable non-genetic influences, including the timing of calving, season of calving and parity using least-squares procedures.

For the PHS method, the model employed was:

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

Y_{ij}= The observation for the j^{th} progeny of the i^{th} sire.
μ = The overall mean.
S_i= The sire effect.
e_{ij}= The random error associated with mean 0 and unknown variance.

Genetic variables were determined through the application of a simple animal model implemented through DFREML (Meyer, 2000).

$$Y = Xb + Za + e$$

Table 1: Estimates of heritability of calving traits from paternal half sib method.

Trait	Heritability
Herd life (HL)	0.08±0.15 (357)
Productive herd life (PHL)	0.06±0.14 (357)
Total milk production (TMP)	0.23±0.17 (357)
No. of days in lactation (NDL)	0.26±0.17 (357)
No. of lactations (NLC)	0.38±0.18 (357)

Figures in parenthesis represent number of observations.

Where,
Y= The vector of observations.
b= Fixed effects
a= Constitutes the vector of additive genetic effects.
e= The residual error vector.
X and Z= The corresponding incidence matrices.

Convergence was assumed when changes in variance estimates became negligible.

Phenotypic relationships among herd life traits and productive FL305MY, FLTMY as well as reproductive traits AFC, SP, CI were assessed using simple correlation analysis.

RESULTS AND DISCUSSION

Estimated heritability of herd life traits

Heritability estimates for herd life originating from the PHS technique and animal model are displayed in Table 1 and 2. Estimates derived from the PHS method exhibited a range from 0.06±0.14 to 0.38±0.18, while the estimates derived from the animal model fluctuated between 0.05 and 0.18. The animal model yielded lower yet more consistent estimates compared to the paternal half-sib technique. The observed low to moderate heritability values in this study align with findings from many cattle breeds (Saha *et al*., 2010; Dinesh *et al*., 2014; Vinothraj *et al*., 2016; Tefera *et al*., 2021; Hu *et al*., 2023). The data suggest that longevity traits are predominantly affected by environmental and managerial factors, with a lesser impact from additive genetic influences. Consequently, direct selection for herd life traits may provide restricted genetic advancement, although enhancements in management methods could significantly influence herd longevity and lifetime output.

Association of herd life traits with production traits

Table 3 presents the estimated values of the genetic and phenotypic associations between herd life and productivity traits in Jersey crossbred cattle. The genetic correlations among herd life as well as FL305MY varied from 0.65 to 0.71, but the phenotypic correlations originated from 0.29 to 0.42. Likewise, FLTMY exhibited beneficial genetic correlations (0.37-0.56) and low to moderate phenotypic correlations (0.09-0.33) with longevity characteristics. The results correspond with previous research (Dalal *et al*., 2002; Saha *et al*., 2010; Jenko *et al*., 2015; Dash *et al*., 2018) and indicate that cows yielding higher milk in their initial lactation are likely to maintain productivity for extended durations. Stronger genetic correlations relative to phenotypic associations suggest that selection for early

Table 2: Estimates of variance components and genetic parameters by animal model.

Traits	HL	PHL	TMP	NDL	NLC
o^2_a	7965.81	8990.76	117760536.0	2070.78	0.124
o^2_e	126411.41	125116.12	855528121.4	35982.92	0.576
o^2_p	134377.22	134106.88	973288657.4	38053.71	0.700
h^2	0.06(0.15)	0.07(0.15)	0.12 (0.11)	0.05 (0.09)	0.18(0.12)

o^2_a: Direct additive genetic variance; o^2_e: Environmental variance; o^2_p: Phenotypic variance; h^2: Direct heritability.

Table 3: Estimates of genetic and phenotypic correlations of herd life traits with production traits of jersey crossbred cattle.

Herd life traits		Production traits	
		First lactation 305-days milk yield (FL305DMY)	First lactation total milk yield (TMY)
Herd life traits	Herd life (HL)	0.66±0.19 (r_p =0.29)	0.49±0.21 (r_p=0.21)
	Productive herd life (PHL)	0.66±0.19 (r_p =0.29)	0.50±0.21 (r_p=0.21)
	Total milk production (TMP)	0.67±0.19 (r_p =0.29)	0.56±0.20 (r_p=0.33)
	No. of days in lactation (NDL)	0.71±0.17 (r_p =0.42)	0.49±0.21 (r_p=0.26)
	No. of lactations (NLC)	0.65±0.19 (r_p =0.32)	0.37±0.23 (r_p=0.09)

(Figures in the parenthesis indicate phenotypic correlations).

Table 4: Estimates of genetic and phenotypic correlations of herd life traits with reproductive traits in Jersey crossbred cattle.

		Reproductive traits		
		Age at first calving (AFC)	Service period (SP)	Calving interval (CI)
Herd life traits	Herd life (HL)	0.21±0.21	0.41±0.23	0.49±0.26
		(r_p = 0.17)	(r_p = 0.13)	(r_p = 0.15)
	Productive herd life (PHL)	0.06±0.23	0.38±0.23	0.46±0.26
		(r_p = 0.03)	(r_p = 0.13)	(r_p = 0.14)
	Total milk production (TMP)	0.04±0.24	0.48±0.23	0.55±0.26
		(r_p = -0.02)	(r_p = 0.11)	(r_p = 0.15)
	No. of days in lactation (NDL)	0.04±0.23	0.34±0.24	0.38±0.27
		(r_p = -0.03)	(r_p = 0.12)	(r_p = 0.12)
	No. of lactations (NLC)	-0.03±0.2	0.29±0.25	0.28±0.28
		(r_p = -0.10)	(r_p = -0.04)	(r_p = -0.04)

Figures in the parenthesis indicate phenotypic correlations.

lactation performance may indirectly enhance herd longevity and overall lifetime output.

Association of herd life traits with reproductive traits

Table 4 presents estimations of the genetic and phenotypic relationships between reproductive traits and herd life in Jersey cross-bred cattle. The genetic associations between herd life traits and reproductive traits were predominantly low to moderate. There were weakly favourable genetic associations with the age of first calving (0.04-0.21) with the majority of longevity traits, while the number of completed lactations displayed a marginal negative correlation (-0.03). Positive genetic relationships were identified between herd life and service period (0.29-0.48) and calving interval (0.28-0.55). Phenotypic associations were rather minimal. The results align closely with earlier studies (Ajili *et al*., 2007; Chander *et al*., 2004; Abbas and Sachdeva, 2008; Ambhore *et al*., 2017). The favourable correlations indicate that animals exhibiting adequate production levels may persist in the herd despite extended reproductive intervals. In general, reproductive characteristics had less robust correlations with herd longevity compared to production traits.

CONCLUSION

Sustainable livestock production necessitates the optimisation of raising expenses and enhancement of operational efficiency, reliant on precise measurement of genetic characteristics. This study's heritability values estimated for longevity traits ranged from weak to high (0.06 ±0.14 to 0.38±0.18), whereas the simple animal model yielded more exact estimates (0.05-0.18). The results reveal that a significant part of phenotypic diversity in herd life is affected by non-additive genetic influences, implying restricted potential for direct genetic enhancement through selection. Consequently, enhancements in herd lifetime may predominantly rely on superior management and environmental conditions. Aside from the number of completed lactations, the genetic and phenotypic associations among herd life and production traits were predominantly favourable, varying from 0.37 to 0.71 and 0.09 to 0.42, respectively. The genetic connections related to herd longevity and reproductive factors varied from 0.04 to 0.55. The genetic relationship between the age at which a cow first calves and the total number of lactations she experiences is negative, suggesting that cows calving at a younger age tend to achieve a higher number of lactations. The moderate genetic correlation between herd life and production traits indicates that selecting for first lactation production performance may indirectly enhance herd life and lifetime productivity in Jersey crossbred cattle.

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Disclaimers

The opinions, findings, conclusions used in this manuscript represent exclusively the authors' own views and do not invariably reflect the opinions of their affiliated institutions. Despite our best efforts to verify the correctness and completeness of this data, the authors assume no liability for errors or omissions.

Ethics approval

All investigative the procedures underwent a thorough examination and authorized by the Committee of Experimental Animal care and handling techniques were authorized by the Academic Research Council of the ICAR-NDRI in Karnal, India.

Conflict of interest

The authors state that they have no competing interests in relation to this publication.

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