RESEARCH ARTICLE

Estimation of Genetic Parameters for Production Traits Using Test-Day Random Regression Model in Holstein Friesian Crossbred Cattle

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ABSTRACT

This study was aimed to estimate genetic parameters for milk production traits in Holstein Friesian (HF) crossbred cattle using test-day random regression models. A total of 1,59,950 first-lactation test-day milk yield records of 17,135 HF crossbred cows, sired by 259 bulls, maintained in four districts of Gujarat (Panchmahal, Sabarkantha, Surat, and Tapi) between 1997 and 2019 were obtained from the INAPH-MIS database of NDDB, Anand. Variance components, heritability, and repeatability were estimated using the Average Information Restricted Maximum Likelihood (AI-REML) algorithm fitted with a Legendre polynomial function of days in milk. The average values for test-day milk yield (TDMY), fat yield (TDFY), solid-not-fat yield (TDSNFY), and protein yield (TDPY) were 9.12, 0.38, 0.80, and 0.30 kg, respectively. Heritability was moderate (0.24 for TDMY, 0.16 for TDFY, 0.22 for TDSNFY, and 0.17 for TDPY), with repeatability estimates higher for TDMY (0.79) than other traits. Sire evaluation using univariate BLUP revealed average EBVs of 63.17 kg for 305-d milk yield, 1.69 kg for fat yield, 4.19 kg for SNF yield, and 1.39 kg for protein yield. The findings demonstrate the suitability of random regression test-day models for genetic evaluation and highlight their potential utility in structured breeding programmes of HF crossbred cattle in Gujarat.

Key words: Breeding value, Heritability, HF crossbred cattle, Random regression, Test-day model.

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INTRODUCTION

Genetic improvement in dairy cattle primarily relies on the accurate identification and selection of superior sires and dams. The efficiency of such programmes depends on reliable estimates of genetic parameters, as they determine selection response, optimize breeding plans, and predict breeding values of animals (Cobuci *et al.,* 2005). Traditionally, sire evaluation has been based on the 305-day lactation yield; however, this approach neglects variations across the lactation curve and delays early selection decisions. Test-day models (TDM) have gained importance as they consider individual test-day records rather than the total lactation yield, enabling more precise and timely genetic evaluation (Swalve, 1995). Monthly test-day yields capture the dynamics of lactation and provide multiple records per animal, which improves the accuracy and intensity of selection compared to a single lactation yield (Singh *et al.,* 2016). Moreover, TDM reduces the cost of recording, allows early evaluation, and accounts for environmental and managemental effects at the test-day level (Kokate *et al.,* 2013).

Random regression models (RRM) are widely recognized as robust tools for analyzing longitudinal traits such as milk yield, fat yield, protein yield, and solids-not-fat yield across lactation. Unlike multiple trait models, RRMs enable estimation of variances and breeding values at any day of lactation and can model the shape of the lactation curve using Legendre polynomials (Bignardi *et al.,* 2011). Recent advances in computational methods and statistical packages have further facilitated the application of RRMs in large-scale field data analysis (Gebreyohannes *et al.,* 2016).

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Holstein Friesian (HF) crossbred cattle form the backbone of India's dairy sector and play a significant role in augmenting milk productivity under diverse agro-climatic conditions. However, there is a scarcity of information on genetic parameters of test-day yields in crossbred populations under Indian field conditions. Estimating heritability, repeatability, and breeding values using RRMs is essential for designing efficient genetic improvement programmes in crossbred cattle herds. Therefore, the present study was undertaken to estimate genetic parameters for test-day milk yield (TDMY), test-day fat yield (TDFY), test-day solids-not-fat yield (TDSNFY), and test-day protein yield (TDPY) using random regression models in first lactation HF crossbred cows of Gujarat, and to evaluate the breeding values of sires for these traits.

MATERIALS AND METHODS

Data Source and Population

The data used in this study were retrieved from the INAPH-MIS database maintained by the National Dairy Development Board (NDDB), Anand, Gujarat. A total of 1,65,929 first-lactation test-day milk yield (TDMY) records from 18,543 Holstein Friesian (HF) crossbred cows sired by 301 bulls and distributed across four districts of Gujarat (Panchmahal, Sabarkantha, Surat, and Tapi) during 1997-2019 were initially available.

Data Editing and Standardization

To ensure quality and uniformity, the dataset was subjected to a series of restrictions. Only first-lactation records were retained, and cows without sire information were excluded. Test-day records were restricted to the range of 5 to 325 days in milk (DIM), while the age at first calving (AFC) was limited to 18-72 months. Test-day milk yield values outside the range of 1-25 kg were discarded, and biological limits were applied for milk composition, namely fat (1.5-6.5%), protein (1.5-4.5%), and solids-not-fat (7.0-11.0%). Further, animals with fewer than three test-day records and sires with fewer than ten daughters were removed to minimize bias. After applying these edits, the final dataset comprised 1,59,950 records from 17,135 cows, sired by 259 bulls.

Fixed and Random Effects Considered

In the model, herd, age at first calving, and season-year of calving were considered as fixed effects, while owner, herd-year-month of recording (HYMR), additive genetic effect of animal, and permanent environmental (PE) effect were taken as random effects.

Statistical Model

A Random Regression Test-Day Model (RRM) (Mrode and Thompson, 2005) fitted with Legendre polynomials (LP) of order 2 for DIM was applied. Variance components were estimated using the Average Information Restricted Maximum Likelihood (AI-REML) algorithm. The model equation was:

$$y_{thijkl} = Herd_j + Owner_h + HYMR_i + \Sigma\beta_l Z_{tl} + \Sigma a_{kl} Z_{tl} + \Sigma pe_{kl} Z_{tl} + e_{thijkl}$$

Where, y_{thijkl} = test-day record of kth animal at DIM t, β_l= fixed regression coefficients, a_{kl} = additive genetic effect of kth animal, pe_{kl} = permanent environmental effect, Z_{tl}= lth Legendre polynomial evaluated at DIM t, and e_{thijkl}= residual error.

The DIM was transformed using second order of Legendre polynomials in the present study. Here, standardized DIM was calculated after calculating the total milk yield from the known part of lactation length, the rest of the unknown lactation part up to 305 days lactation lengths was estimated by the prediction equations (Habib *et al*., 2019).

Estimation of Genetic Parameters

Heritability was estimated as: $h^2 = \frac{\sigma_a^2}{\sigma_p^2}$

Where, σ_a^2 = additive genetic variance, and σ_p^2 = total phenotypic variance.

Repeatability was estimated as: $r = \frac{\sigma_a^2 + \sigma_{pe}^2}{\sigma_p^2}$

Where, σ_{pe}^2 = permanent environmental variance.

Sire Evaluation

Estimated variance–covariance components were further utilized to predict Estimated Breeding Values (EBVs) of sires using a univariate Best Linear Unbiased Prediction (BLUP) animal model. EBVs were calculated for 305-day milk yield (MY), fat yield (FY), SNF yield (SNFY), and protein yield (PY) by multiplying Legendre polynomial solutions with animal-specific regression coefficients.

Reliability of EBVs

Reliability measures the precision of estimated breeding value (EBV) thus, it is important parameter in breeding value estimation. This measure of reliability is commonly used to reflect the extent to which EBV may change when more information becomes available (Gorjanc *et al*., 2015).

Reliability (R^2) of EBVs was computed as: $R^2 = 1 - \frac{PEV}{G}$

Where, PEV = predicted error variance (square of standard error of EBV), and G = genetic variance of sires.

RESULTS AND DISCUSSION

Descriptive Statistics

Descriptive statistics for the first lactation test-day records are presented in Table 1. The mean test-day milk yield (TDMY) was 9.12 kg, with a range of 1.0 to 24.93 kg. The mean test-day fat yield (TDFY), solids-not-fat yield (TDSNFY), and protein yield (TDPY) were 0.38, 0.80, and 0.30 kg, respectively. These averages are in close agreement with values reported in HF crossbreds under Indian conditions (Lakshmi *et al.*, 2010; Adsul, 2018). Sharma *et al.* (1983) estimated 305-day fat, SNF and milk yields for three zebu breeds (Tharparkar, Sahiwal and Red Sindhi) and for halfbred F1 and F2 (Brown Swiss x Sahiwal and ¾ Brown Swiss x Sahiwal cattle). The 305-day fat, SNF and milk yields differed significantly between different breeds (p<0.01). These yields were similar for the three zebu breeds but halfbreds showed significantly higher yields than the zebu breeds, the highest being for F1 halfbreds. They concluded that selection of animals based on milk production alone was also found to increase the yield of milk constitutes.

Effects of Non-Genetic Factors on Various Traits in HF Crossbred Cattle

The non-genetic effects, *viz.,* year of calving and season of calving showed significant (p<0.01) effects on all traits under study except that effect of season of calving on protein percent was non-significant. The highest TDMY was observed during winter followed by summer and monsoon. Hassan and Khan (2013) observed significant effect of herd and year of calving on milk yield and non-significant effect of season of calving on milk yield. Sharma *et al*. (1983) also observed non-significant effect of season of calving on fat percent whereas, Desyibelew and Wondifraw (2019) found significant effect of seasons on fat content in milk. Verma *et al*. (2016) also reported significant effect of season of calving on first lactation milk yield and first lactation peak yield. Singh *et al*. (2014) found non-significant effect of season on total lactation milk yield and milk yield per day of lactation length in Frieswal cows. Khunte *et al*. (2016) also observed non-significant effect of season on daily milk yield, total lactation milk yield and peak yield in crossbred and graded animals.

Genetic Parameters

Heritability and repeatability estimates derived from the random regression model (Table 1) revealed that the heritability was moderate for TDMY (0.24), indicating a reasonable potential for genetic improvement through selection. Heritability estimates for TDSNFY (0.22) and TDPY (0.17) were higher than for TDFY (0.16), suggesting that selection based on SNF and protein yields may also be effective. Repeatability estimates were highest for TDMY (0.79) compared to other traits (0.66-0.75), highlighting the consistency of milk yield across lactation and supporting the utility of test-day records for sire evaluation. Similar trends have been reported in Frieswal and Karan Fries cattle (Singh *et al.,* 2016). The current average heritability estimate for TDMY (0.24) was lower than values reported by Dhara (2016) but similar to findings of Chaudhari (2019). Heritability estimates for component traits in the present study also fell within the ranges observed in international studies on Holstein and crossbred populations (Koonawootrittriron *et al.,* 2002; Bignardi *et al.,* 2011).

Variance Components

Variance components transformed to 305-day equivalents (Table 2) showed that additive genetic effects explained approximately 24% of the total phenotypic variance for milk yield, while permanent environmental effects accounted for more than 50%. This indicates that non-genetic factors such as management and feeding strongly influence production performance under field conditions, consistent with observations of Kokate *et al.* (2013) in Karan Fries cattle.

Sire Evaluation

Estimated Breeding Values (EBVs) for sires (Table 3) revealed substantial variation, with the best sires showing EBVs up to 796.82 kg for 305-d MY, 29.66 kg for FY, 61.89 kg for SNFY, and 21.78 kg for PY. The average EBVs of sires were positive for all traits, with a large proportion achieving reliability levels ≥60%, particularly for milk yield (89.7% of sires). These results demonstrate the effectiveness of BLUP methodology

Table 1: Descriptive statistics, heritability and repeatability estimate for production traits in HF crossbred cattle

Traits	Descriptive statistics				Heritability	Repeatability
	No. of records	Mean	Min	Max		
TDMY (kg)	159950	9.12	1.00	24.93	0.24	0.79
TDFY (kg)	142400	0.38	0.03	1.59	0.16	0.66
TDSNFY (kg)	133377	0.80	0.07	2.36	0.22	0.75
TDPY (kg)	131465	0.30	0.02	1.03	0.17	0.66

Table 2: Variance components (305-d basis) for production traits

Variance components	305-d MY	305-d FY	305-d SNFY	305-d PY
Genetic	126020.06	166.05	915.75	110.74
Permanent Environment	292756.37	511.88	2170.67	325.82
HYMR	3107.11	47.27	47.27	47.27
Owner	50496.19	99.04	431.97	63.54
Residual	59860.82	206.91	532.85	109.85
Phenotypic	532240.54	1031.15	4098.51	657.22

Table 3: Estimated breeding values (EBVs) and reliability of sires

Traits	Min EBV (kg)	Max EBV (kg)	Average EBV (kg)	Average Reliability (%)	No. of sires ≥60% reliability
305-d MY	-639.41	796.82	63.17	78 (48-93)	233
305-d FY	-25.07	29.66	1.69	70 (21-92)	192
305-d SNFY	-57.36	61.89	4.19	68 (15-93)	175
305-d PY	-20.85	21.78	1.39	67 (20-92)	175

in identifying superior sires and its potential for improving milk production traits in HF crossbreds.

Rank Correlations among Traits

Spearman's rank correlations (Sedgwick, 2014) of sire EBVs (Table 4) revealed significant negative associations between 305-d MY and component yields (SNFY, PY). This suggests that selection solely for higher milk yield may negatively impact milk composition traits. Such antagonistic relationships highlight the importance of balanced breeding objectives that incorporate both yield and composition traits, a finding consistent with studies in Frieswal and crossbred populations (Verma *et al.,* 2016; Chaudhari, 2019).

Table 4: Rank correlation of sires based on EBVs for production traits

Traits	305-d MY	305-d FY	305-d SNFY	305-d PY
305-d MY	1	0.041	-0.191**	-0.187**
305-d FY	-	1	0.635**	0.644**
305-d SNFY	-	-	1	0.948**
305-d PY	-	-	-	1

These results confirm that random regression test-day models are reliable tools for genetic evaluation under Indian field conditions, where data quality and heterogeneity are challenges.

CONCLUSION

The present study demonstrated the effectiveness of random regression test-day models in estimating genetic parameters and sire breeding values for production traits in Holstein Friesian crossbred cattle under field conditions in Gujarat. Moderate heritability estimates for milk yield (0.24) and associated traits, along with high repeatability for test-day milk yield (0.79), indicate considerable potential for genetic improvement through sire selection. The wide variability in estimated breeding values among sires, with a high proportion achieving reliable predictions, underscores the scope for identifying genetically superior animals. However, the observed negative rank correlations between milk yield and component traits highlight the need for balanced selection indices that simultaneously account for both yield and milk quality attributes. Overall, this study provides a baseline for implementing structured breeding programmes using test-day records and reinforces the importance of integrating advanced statistical models with large-scale field data for sustainable genetic improvement in crossbred dairy cattle populations.

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