RESEARCH ARTICLE

Genetic Analysis of 305-Day Milk Yield in Mehsana Buffaloes of Banaskantha and Mehsana Districts of Gujarat

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ABSTRACT

Buffaloes play a vital role in Indian dairy economy, contributing more than half of the nation's total milk production. Among indigenous breeds, the Mehsana buffalo is a high-performing dual-purpose breed predominantly found in Gujarat. The present study was aimed to estimate the genetic parameters and evaluate the 305-day milk yield (305DMY) of Mehsana buffaloes maintained under field conditions in Mehsana and Banaskantha districts. A total of 18,888 buffaloes (15,418 from Mehsana and 3,470 from Banaskantha) with 305DMY records were analyzed using data retrieved from the NDDB's INAPH–MIS (Information Network for Animal Productivity and Health - Management Information System) database. The mean 305DMY was 1962.75 ± 3.19 kg. Fixed effects, such as tehsil, year-season of calving, and age at calving significantly influenced milk yield, highlighting the role of environmental and management factors. Genetic variance was higher in Mehsana district (58,181) compared to Banaskantha (10,015), indicating greater genetic variability. Heritability of 305DMY was moderate in Mehsana (0.36) but appeared low in Banaskantha (0.051) mainly because of very high residual variation using BLUP model. Field data indicate that Banas animals show higher variability than Mehsana. This suggests that pedigree and phenotypic records alone are not sufficient to capture the true genetic variability, which results in underestimated heritability. Therefore, combining data from both Banaskantha and Mehsana for joint evaluation may improve genetic linkage and comparability between herds and lead to more accurate breeding value estimation. Using Random Regression Model (RRM), the overall heritability estimates were 0.2611 for Mehsana and 0.1436 for Banas buffaloes. The heritability estimate was observed as higher using random regression model than routine 305DMY BLUP model.

Key words: 305-day milk yield, Banaskantha, BLUP, Genetic evaluation, Heritability, Mehsana buffalo, Random Regression Model (RRM).

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INTRODUCTION

Livestock is a cornerstone of India's rural economy, contributing significantly to employment, household nutrition, and agricultural sustainability. Among livestock species, buffaloes form the backbone of the dairy industry, owing to their high fat content, superior adaptability, and ability to utilize low-quality feed resources (Sankhala *et al.*, 2015). As per DAHD (2025), the India's buffalo population stands at 111.04 million, marking a 1.09% increase from the previous census. The Mehsana buffalo is one of the 21 recognized indigenous breeds in India and is known for its high milk production, good temperament, and adaptability. Improving the genetic potential of dairy animals, especially buffaloes, in relation to milk energy value is crucial to addressing nutritional challenges in India. Selection and breeding play a significant role in enhancing genetics on dairy farms. Breeding bull selection involves methods like pedigree selection, full and half-sib family selection, and progeny testing, with progeny testing being the most precise. This method evaluates bulls based on their offspring's performance, generating a sire index that quantifies genetic merit and milk production potential. Accurate breeding value prediction enhances selection efficiency, ensuring genetic improvement in livestock. Gujarat is a prominent breeding tract for Mehsana buffaloes, supported by organized breeding programs such as the Mehsana Progeny Testing (PT) Project initiated by Dudhsagar Dairy in 1985 and the Banas PT Project launched in 1993 by Banas Dairy. These programs have substantially contributed to genetic improvement through systematic data recording and bull evaluation. The Mehsana Buffalo Progeny Testing Project has significantly

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improved the Mehsana buffalo breed, increasing milk yield to 1,976 kg and reducing the calving interval to 15.9 months. The program has tested 346 bulls, recorded 109,177 buffaloes, and conducted 517,603 artificial inseminations (AIs) (Anonymous, 2024).

Genetic evaluation plays a central role in improving dairy productivity. The NDDB uses a structured Test Day Milk Yield (TDMY) recording system first recording between 5-25 DIM, followed by monthly records and stores data through the INAPH–MIS platform. Given the large population and field-based recording system, assessing genetic parameters for economically important traits such as 305-day milk yield (305DMY) is crucial for accelerating genetic progress. The present study was aimed to estimate genetic parameters and evaluate the performance of Mehsana buffaloes in Banaskantha and Mehsana districts of Gujarat using the BLUP methodology.

MATERIALS AND METHODS

Data Source

The performance data of Mehsana buffalo for the present study were collected from the National Dairy Development Board (NDDB), Anand (Gujarat, India). The data on 305-day milk yield (kg) (305DMY) related to Mehsana buffalo bulls were retrieved from the INAPH-MIS database maintained by NDDB. The dataset included historical records of the Progeny Testing (PT) project covering 18,888 daughters of Mehsana buffalo, including 15,418 from Mehsana district and 3,470 from Banaskantha district.

Standardization of Records

Animals with first lactation records were included in the study. The dataset was classified across various levels, with the minimum number of observations required for each classification effect as follows: 3 for individual animals, 1 for the herd effect, 1 for the year of calving × season of calving (YSC) effect, and 1 for the age effect. Based on the least squares analysis, animals were distributed across 24 tehsils, which were considered as herd effects. The age at calving was classified at 6-month intervals (age) and considered as a fixed effect. Year-season combination was treated as a single fixed effect. For herd, age and YSC as fixed effects, the number of levels were 24, 12 and 94, and the average number of animals in these classes as 787, 1574 and 201, respectively.

Method of Calculation of 305DMY

The primary trait analyzed was 305-day milk yield (305DMY). Total milk yield was computed according to International Committee for Animal Recording (ICAR, 2020) standards using:

$$305\text{DMY} = I_0 M_0 + I_1 * \frac{M_1 + M_2}{2} + I_2 * \frac{M_2 + M_3}{2} + \ldots$$

$$+ I_n - 1 * \frac{M_n - 1 + M_n}{2} + I_n M_n$$

Where,

$M_1 M_2 ..., M_n$ are the weights in kgs of milk produced in 24 hours of the recording day.

$I_1, I_2 \ldots, I_{n-1}$ are the intervals, in days, between recording dates.

I_0 is the interval, in days, between the lactation period start date and the first recording date.

I_n is the interval, in days, between the last recording date and the end of the lactation period.

Random Regression Model (Mrode and Thompson, 2005)

A single trait linear mixed random regression test day model was applied to monthly test day records (19,409) of Mehsana buffalo for FLMY (first lactation milk yield). The FLMY data was modeled Legendre polynomials (LP) or order 3 for the additive genetic effect and the permanent environmental effect. The herd (village)-year-month of the test day was considered as a random effect.

The random regression model used in the analysis was represented as:

$$Y_{tijkl} = T_i + YS_j + AG_l + \sum_{k=0}^{n_f} \varnothing_{tk} \beta_k + \sum_{k=0}^{n_a} \varnothing_{tk} a_{jk} + \sum_{k=0}^{n_p} \varnothing_{tk} p_{jk} + e_{tijkl}$$

Where,

Y_{tijkl} = Vector of FLMY of cattle

T_i = Fixed effect of the i^{th} *tehsil*

YS_j = Fixed effect of the j^{th} year–season of calving

AG_l = Fixed effect of the l^{th} age at first calving grouped into 6-month intervals

$\varnothing_{tk}$ = Legendre polynomial for the test-day record of the j^{th} animal made on the t^{th} day in milk.

β_k = Fixed regression coefficients describing the average lactation curve

K^{th} = additive genetic random regression coefficient for animal *j*

P_{jk} = permanent environmental random regression coefficient for animal *j*

e_{tijkl} = Random residual associated with the test-day record of the j^{th} animal

n_f = Order of polynomial for fixed regression

n_a, n_p = Orders of polynomials for additive genetic and permanent environmental effects, respectively

The assumption of this model is

$$\begin{matrix} a \\ [p] \sim N(0,V) e \\ e \end{matrix} \qquad \text{With} \qquad V = \begin{bmatrix} G \otimes A & 0 & 0 \\ 0 & I \otimes P & 0 \\ 0 & 0 & R \end{bmatrix}$$

Where,

G = Variance-covariance matrix of additive genetic random regression coefficients

A = Additive genetic relationship matrix among the animals

$\otimes$ = Kronecker product function (Searle, 1982)

P = Variance-covariance matrix of permanent environment random regression coefficient

I = Identity matrix and

R = Diagonal matrix of homogenous residual variances

Statistical Analysis

Variance components were estimated using the AIREML algorithm, and breeding values were computed using the BLUP animal model using genetic evaluation by Putty software.

Average Information Restricted Maximum Likelihood (AIREML) Model (Meyer, 2007, Sahoo and Gupta, 2021)

$$\sqrt{\sum_{i=1}^{p}(\hat{\theta}_i^t - \hat{\theta}_i^{t-1}) / \sum_{i=1}^{p}\left(\hat{\theta}_i^t\right)^2}$$

here, $\hat{\theta}_i^t$ denotes the estimate of the *i*th parameter from iterate *t*, and *p* is the number of parameters.

Best Linear Unbiased Prediction Model (BLUP) (Henderson, 1975) Model:

y = Xb + Za + e

Where, y = Vector of observations;

b= Vector of observation of fixed effect;

a = Vector of additive genetic effect (Random animal effect);

X = Incidence matrix of fixed effect;

Z= Incidence matrix of random effect;

e = Vector of residual errors

RESULTS AND DISCUSSION

The data of 305DMY and TDMY followed a normal distribution, where most values clustered around the mean, with equal likelihood for values above and below the center (Fig. 1). The overall performance analysis of Mehsana buffaloes revealed a mean 305-day milk yield of 1962.75 ± 3.19 kg based on 18,888 observations, with a standard deviation of 438.99 kg, reflecting better performance under field progeny testing programs compared to earlier reports, including 1901.68 kg by Chaudhari *et al.* (2021) and 1714.75 kg by Dhakad *et al.* (2024). Similarly, Joshi *et al.* (2016), Prajapati *et al.* (2018), and Sathwara *et al.* (2020) documented consistent production performance of Mehsana buffaloes under field progeny testing programs in Gujarat. They reported a mean first lactation milk yield (FLMY) of 1900.68 ± 7.65 liters. The observed improvement may be attributed to enhanced management, selective breeding, and effective progeny testing systems implemented in both districts.

The least squares analysis of fixed effects demonstrated that the intercept was highly significant, establishing the baseline level of the trait under study. Among the factors, Tehsil was the most influential factor, with 21 out of 24 levels showing significant variation, indicating strong regional differences in production. Year-season effects also contributed meaningfully, with 15 significant levels out of 94, demonstrating temporal and seasonal impact on 305DMY (Table 1). Age effects were moderate but significant, suggesting physiological maturity affects milk production. Overall, the analysis underscores that environmental and management-related factors, particularly location and season, exert substantial influence on the trait, while age provides an additional but more moderate effect.

Table 1: Fixed effects of various factors on 305DMY in Mehsana buffalo

Fixed Effect	No. of levels	Range of estimates	No. of significant levels ($p < 0.05$)
Intercept	1	2560.92	1
Tehsil	24	– 652.97 to 37.09	21
Year-season of calving	94	– 262.28 to 133.13	15
Age	12	– 217.45 to –4.01	7

Variance Components, Heritability, and Breeding Values

The variance component analysis revealed clear differences between the Mehsana and Banaskantha buffalo populations (Table 2). Genetic variance was higher in Mehsana district (58,181) compared to Banaskantha (10,015), showing greater scope for selection in Mehsana. Heritability of 305DMY was moderate in Mehsana (0.36) but low in Banaskantha (0.051), largely due to higher residual variation in Banaskantha.

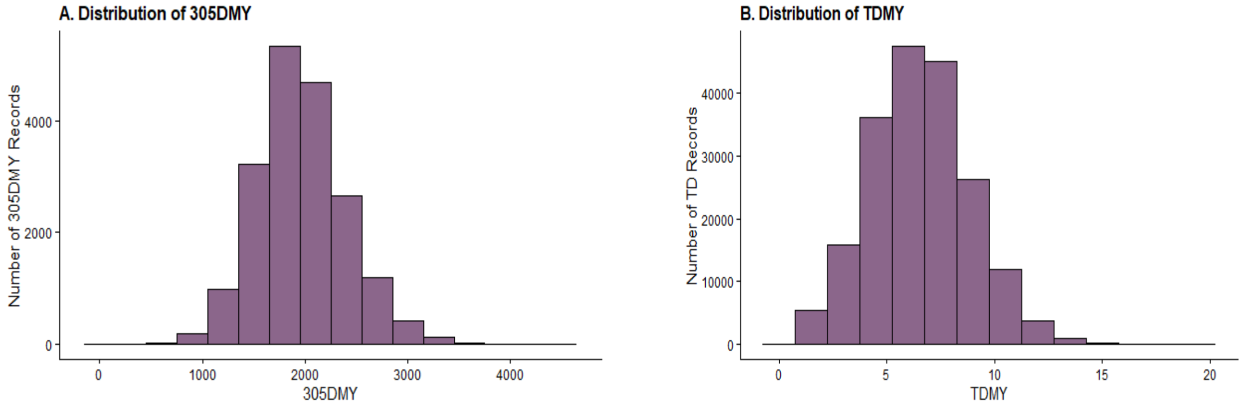

Fig. 1: Distribution of various 305DMY and TDMY records in Mehsana buffalo

This suggests that the available pedigree and field records may not be fully capturing the existing genetic differences in Banaskantha. Overall, the study highlights the need to strengthen data quality and evaluation procedures in Banaskantha to better utilize the true genetic potential for improving milk yield.

The estimated breeding values (EBVs) further supported these findings: The highest EBV observed in Mehsana was 888.92 kg, whereas Banaskantha showed lower EBV of 125.10 kg due to mainly reflecting its smaller population size and weaker data structure rather than true genetic inferiority. These patterns agree with earlier reports by Singh *et al.* (2008) and Rana *et al.* (2021). These results aligned with previous studies, supporting the effectiveness of structured progeny testing in improving genetic merit. Similarly, Joshi *et al.* (2016) reported heritability estimates of 0.25 ± 0.03 for 305DMY in Mehsana buffaloes.

The random regression model was convergence based on the norm of the gradient vector criterion. In the RRM model, the overall heritability estimates were 0.2611 for Mehsana and 0.1436 for Banas buffaloes. The heritability estimate was observed as higher using random regression model than routine 305DMY BLUP model.

Table 2: Variance components of the BLUP model for the different Mehsana populations

Components of Variances	For the Mehsana buffalo population in Banaskantha District	For the Mehsana buffalo population in Mehsana District
Genetic variance	10015	58181
Residual variance	40094	105480
Phenotypic variance	155710	9008.9
Heritability	0.051	0.36
Standard error	0.009	0.006

Table 3: Variance components of the RRM model for the Mehsana buffalo

Particulars	Value
Genetic variance	0.74898 $-0.70428E^{-01}$ −0.18148 $-0.70428E^{-01}$ 0.44349 0.18329 −0.18148 0.118329 0.18878
Pre variance (In Matrix Form)	2.0198 0.14507 −0.16725 −0.14507 0.77277 $0.94571E^{-01}$ −0.16725 $0.94571E^{-01}$ 0.29924
Residual variance	0.71562
Phenotypic variance(hymr)	$0.90293E^{-01}$
Phenotypic variance(village)	0.24357
Heritability	0.2083
Standard error	0.008

CONCLUSION

The present study evaluated the genetic parameters and 305-day milk yield of Mehsana buffaloes in Mehsana and Banaskantha districts of Gujarat. Results showed higher genetic variance and moderate heritability (0.36) for 305DMY in Mehsana, indicating substantial potential for genetic improvement through selection. In contrast, the Banaskantha population exhibited low heritability (0.051), largely due to high residual effects and limitations in pedigree and phenotypic data, rather than a lack of genetic variability. Field observations suggest that genetic variability in Banaskantha may even be higher than in Mehsana, but limitations in data structure constrain the estimated heritability. The estimated breeding values further supported these observations, highlighting the superior EBVs recorded in Mehsana under current data limitations. These results emphasize the importance of strategic selection, careful data management, and consideration of joint evaluation of both populations to fully exploit genetic variability and enhance milk production, alongside ongoing progeny testing and genetic evaluation programs.

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Conflict of Interest: None

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