International Journal of Bio-resource and Stress Management https://ojs.pphouse.org/index.php/IJBSM

IJBSM September 2025, 16(9): 01-08

Article AR5871

Research Article

Natural Resource Management

DOI: HTTPS://DOI.ORG/10.23910/1.2025.5871

Estimation of Breeding Values by Various Sire Evaluation Methods for Selection of Sires in Crossbred Cattle

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ABSTRACT

The study was conducted from January to November, 2022 at G.B. Pant University of Agriculture and Technology, Pantnagar, with the objective of ranking sires based on first lactation traits. The breeding values of 66 crossbred sires were evaluated for age at first calving, first lactation length, and first lactation milk yield using Best Linear Unbiased Prediction, Least Squares Method, and Restricted Maximum Likelihood methods. The average breeding values for age at first calving were 1153.41 days (Best Linear Unbiased Prediction), 1152.25 days (Least Squares Method), and 1153.93 days (Restricted Maximum Likelihood); for first lactation length, 340.51 days (Best Linear Unbiased Prediction), 353.24 days (Least Squares Method), and 354.04 days (Restricted Maximum Likelihood); and for first lactation milk yield, 3348.81 kg (Best Linear Unbiased Prediction), 3602.34 kg (Least Squares Method), and 3612.37 kg (Restricted Maximum Likelihood). Significant and highest Spearman's rank and Pearson correlation coefficients were observed between LSM and REML for the first lactation length and milk yield, indicating that these methods were highly correlated and equally accurate for ranking sires. Sire no. 15 showed consistently high breeding values for age at first calving across all methods, securing the top rank for this trait. For the first lactation length, sire no. 23 ranked first with BLUP, while sire no. 59 led in LSM and REML. Different sires topped the rankings for first lactation milk yield in each method. Overall, 4–5% of top-ranked sires maintained similar ranks across evaluation methods, providing insights into sire performance.

KEYWORDS: Breeding value, BLUP, LSM, REML, rank correlation

Citation* (VANCOUVER)*: Shashikant et al., Estimation of Breeding Values by Various Sire Evaluation Methods for Selection of Sires in Crossbred Cattle. *International Journal of Bio-resource and Stress Management,* 2025; 16(9), 01-08. HTTPS://DOI.ORG/10.23910/1.2025.5871.

Data Availability Statement: Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

Conflict of interests: The authors have declared that no conflict of interest exists.

RECEIVED on 14th October 2024 RECEIVED in revised form on 13th August 2025 ACCEPTED in final form on 07th September 2025 PUBLISHED on 19th September 2025

1. INTRODUCTION

The genetic evaluation of livestock, particularly cattle, has seen significant advancements in recent decades, primarily due to the development of various sire evaluation methods. These methods are crucial for assessing and selecting sires that possess desirable genetic traits, ultimately improving herd performance and productivity. In crossbred cattle, where genetic diversity and performance variability are substantial, the estimation of breeding values is a key factor in enhancing traits such as milk yield, growth rates, and reproductive efficiency (Smith and Hodges, 1990; Henderson, 1975). Traditional methods for sire evaluation include the Least Squares Method (LSM) and Best Linear Unbiased Prediction (BLUP), which have been extensively used due to their robustness in handling data variations. The LSM approach has been widely recognized for its efficiency in eliminating non-genetic variations and for providing unbiased estimates of genetic parameters (Henderson, 1984). Despite its advantages, LSM is less efficient in scenarios where random factors significantly affect trait variance, making BLUP a preferred choice in many cases (Harris and Johnson, 1998; Van Vleck, 1986). BLUP is a linear model that estimates breeding values by incorporating both fixed and random effects, making it suitable for complex trait evaluation in crossbred cattle (Thompson, 1977; Van der Werf and De Boer, 1990). Restricted Maximum Likelihood (REML), another widely used method, has gained popularity in recent years for its accuracy in estimating variance components. Unlike the conventional maximum likelihood approach, REML corrects for fixed effects, resulting in more precise estimates of genetic parameters (Patterson and Thompson, 1971; Meyer, 1989). Studies have shown that REML is highly effective for evaluating traits with substantial environmental influence, such as milk production and reproductive traits in cattle (Kirkpatrick and Lofsvold, 1992; Sorensen and Kennedy, 1984). The accuracy of breeding value estimation methods directly influences the genetic progress achievable through selective breeding. Therefore, comparative studies are essential to evaluate the effectiveness of these methods in different populations and environmental conditions (Henderson, 1988). In crossbred cattle, several factors, such as genotype-environment interaction, necessitate a tailored approach to sire evaluation. Studies by Powell and Freeman (1974) and Rendel and Robertson (1950) highlight that crossbreeding in cattle can introduce complexities that require advanced statistical models to achieve accurate breeding value estimates. A considerable amount of research has compared these sire evaluation methods, examining their strengths and limitations in the context of different cattle populations. For example, Yamada (1990) and Falconer and Mackay (1996) have demonstrated that BLUP is particularly effective for traits with moderate heritability, while REML has proven advantageous for traits influenced by non-additive genetic variance. Furthermore, empirical studies conducted by Koch and Pollak (1979) and Searle (1965) support the use of REML over LSM for more accurate parameter estimation in mixed model analyses.

Therefore, considering the diverse genetic backgrounds and varying management conditions in crossbred cattle, it is imperative to evaluate the effectiveness of these methods in accurately estimating breeding values. This study aimed to compare the efficiency of BLUP, LSM and REML methods in estimating breeding values for sire selection in crossbred cattle. By analyzing various traits associated with milk yield, growth, and reproduction, this research seeks to identify the optimal sire evaluation method, thereby contributing to the advancement of selective breeding programs for crossbred cattle.

2. MATERIALS AND METHODS

2.1. Source of data and data editing

The records of; first lactation traits of 976 crossbred cattle, progeny of 66 sires, spread over a period of 32 years (1988-2019) were analysed. The above cows were maintained at instructional dairy farm of G. B. Pant University of Agriculture and Technology, Pantnagar. The Instructional Dairy Farm of the university is situated in the Udham Singh Nagar district of Uttarakhand. The study was conducted during January to November, 2022 at G.B. Pant University of Agriculture and Technology, Pantnagar. Its geographical coordinates lie between 28°52' and 29°.25' north latitudes and 78°.58' and 79°.42' east longitudes. The region experiences an annual rainfall of approximately 1300 to 1400 mm, with 80 to 90% of the total rainfall occurring between June and September. The temperature in the area ranges from a minimum of 25°C to a maximum of 40°C. The data has been collected Cows with abnormal and incomplete records were excluded from the study. Only the sires having records on at least 5 daughters with known pedigree and normal lactation were considered. The lactation records of less than 150 days were considered as abnormal and were not included in the analysis.The total duration of the present study was divided into 6 periods, the first period being 7 years and the rest five periods were of five years each. The first lactation group was divided into 6 groups. Each year was divided into three seasons namely winter (November–February), Summer (March–June), and Rainy (July–October). In order to classify the data for first lactation milk yield group, periods and seasons of calving were considered for all the traits. The traits considered were abnormal births, sex ratio (percent male birth), mortality and culling of female calves up to the age of first calving (AFC), and replacement rate (based on female calf and total calf).

2.2. Statistical analysis

As the data in the present study were non-orthogonal in nature with unequal subclass numbers, were subjected to least squares analysis of variance without interactions using different models to examine the effect of non-genetic factors on various first lactation traits as per standard procedures of Harvey (1990). The model was based on the assumption that different components fitting in the model were linear, independent and additive. While sire was treated as random effect, the other non-genetic factors (season and period) were taken as fixed effects in the model. Breeding value of sires for first lactation traits were estimated by LSM as described by Harvey (1990), BLUP by Henderson (1975) and REML programme of Meyer and Smith (1996) taking single trait model. As described by Graser et al. (1987), for single trait method, quadratic approximation method was used which requires one-dimensional search. The convergence criteria were taken as the variance among the function values; convergence was assumed when this variance was less than 10^{-8}. The breeding value of sires was determined by adjusting the additive genetic value of sires from the overall population mean. After estimation of breeding value of sires, the sires were given ranks as per their genetic merit. Spearman's rank correlations as per Steel and Torrie (1960) and product moment correlations as per Snedecor and Cochran (1967) between breeding values of sires derived by various methods were also used to judge the effectiveness of different methods.

3. RESULTS AND DISCUSSION

In the present study, the breeding values of sires were estimated, evaluated and ranked on the basis of breeding value of their progeny by three different sire evaluation methods and presented in Table 1.

3.1. Breeding values

The average breeding value based on age at first calving of 66 crossbred sires was observed as 1153.41 days using BLUP, with a range from 1131.40 to 1170.48 days. Of these, 32 sires (48.59%) were above the average, while 34 (51.51%) were below. Using LSM, the average breeding value was 1152.25 days, with values ranging from 1102.87 to 1187.64 days. Here, 42 sires (63.64%) were above the average, and 24 (36.36%) were below. For REML, the average breeding was estimated as 1153.93 days, with a range from 137.57 to 1167.10 days. In this case, 34 sires (51.51%) were above, and 32 (48.49%) were below the average. Sahana et. al. (2004) and Singh et al. (20011) also reported similar results in their studies while estimating breeding value for dairy sires bull and stated that BLUP provided more reliable sire evaluation. The wider range of breeding value by LSM for this trait could result this method ignores the relationship matrix and therefore less accurate. Bhatnagar et al. (2004) and Chaudhary et al. (2011), however, reported lower estimates than the present findings using REML.

The average breeding value on the basis of first lactation length of 66 crossbred sires was 340.51 days using the BLUP method, with minimum and maximum values as 318.25 and 368.04 days, respectively. Half (33 sires) were above this average, and half were below. Using the Least Squares Method (LSM), the average breeding value was as 353.24 days, with minimum and maximum as 296.94 to 445.03 days, respectively. Here, 30 sires (45.45%) were above the average, and 36 (54.54%) were below. For the Univariate-REML method, the average breeding value of sires estimated as 354.04 days, with minimum and maximum values as 334.75 and 375.21 days, respectively. In this case, 34 sires (51.51%) were above the average, and 32 (48.49%) were below. Lodhi et al. (2015, 2016) also

Table 1: Average breeding values of crossbred sires based on first lactation traits by different sire evaluation method

Traits	Sire evaluation method	Average Breeding value (B.V.)	Minimum B.V.	Maximum B.V.	Number of sires above average B.V. (% of sires)	Number of sires below average B.V. (% of sires)
AFC	BLUP	1153.41	1131.40	1170.84	32 (48.59)	34 (51.51)
	LSM	1152.25	1102.87	1187.64	42 (63.64)	24 (36.36)
	REML	1153.93	1137.57	1167.10	34 (51.51)	32 (48.49)
FLL	BLUP	340.51	318.25	368.04	33 (50)	33 (50)
	LSM	353.24	296.94	445.03	30 (45.45)	36 (54.54)
	REML	354.04	334.75	375.21	34 (51.51)	32 (48.49)
FLMY	BLUP	3348.81	3061.02	3784.54	31 (46.97)	35 (53.03)
	LSM	3602.34	3236.19	3956.75	36 (54.55)	30 (45.45)
	REML	3612.37	3584.54	3639.23	33 (50)	33 (50)

LSM: Least squares method; BLUP: Best linear unbiased prediction method; REML: Restricted maximum likelihood method estimated breeding values with a comparatively low range with lowest error variance for dairy sires by BLUP methods which appeared to be aligned with the present findings for lactation length with a balanced distribution around the mean.

The average breeding value based on first lactation milk yield (FLMY) in 66 crossbred sires was found to be 3348.81 kg using the BLUP method, with a range from 3061.02 to 3784.54 kg. Of these, 31 sires (46.97%) had values above the average, while 35 (53.03%) were below. Using the Least Squares Method (LSM), the average FLMY was 3602.34 kg, ranging from 3236.19 to 3956.75 kg. Here, 36 sires (54.55%) were above the average, and 30 (45.45%) were below. For the REML method, the average was 3612.37 kg, with values from 3584.54 to 3639.23 kg. In this case, 33 sires (50%) were above the average, and 33 (50%) were below. Lodhi et al. (2015) reported the estimated breeding values of sires for all the production and reproduction traits studied exhibited considerable variation, indicating greater genetic diversity within the herd. This variation was observed across different evaluation methods, including BLUP, DFREML, LSM and the simple daughter average index and Jakhar et al. (2017), however, estimated superior estimates for this trait than the present ones. Similar results were reported by Banik and Gandhi (2006), who observed that LSM often inflated sire evaluations and resulted in lower accuracy compared to BLUP and REML.

3.2. Pearson and Spearman's rank correlation

Pearson correlation coefficients were computed by analysing the breeding values of the crossbred sires, and the findings are presented in table 2. Furthermore, Spearman's rank correlations were determined by considering the ranks of all 66 crossbred sires based on their estimated breeding values for first lactation traits, viz. age at first calving, first lactation length, and first lactation milk yield.

In conclusion, the study conducted a comprehensive analysis to assess the relationships and correlations between the breeding values of the sires, utilizing both Pearson and Spearman's Rank Correlations. These correlation coefficients provided valuable insights into the associations between the different first lactation traits which could aid in identifying potential relationships between these traits and the performance of crossbred sires.

Table 2: Pearson correlation (above diagonal) and Spearman's Rank correlations (below diagonal) among breeding values of sires for first lactation traits estimated by different sire evaluation

Methods	BLUP	LSM	REML
AFC			
BLUP	-	0.881**	0.978**
LSM	0.917**	-	0.881**
REML	0.988**	0.906**	-
Methods	BLUP	LSM	REML (Uni)
FLL			
BLUP	-	0.689**	0.765**
LSM	0.635**	-	0.869**
REML	0.748**	0.863**	-
Methods	BLUP	LSM	REML (Uni)
FLMY			
BLUP	-	0.316**	0.362**
LSM	0.256*	-	0.855**
REML	0.283*	0.771**	-

$^{*}p<0.05$

The evaluation of sires showed that for age at first calving, the BLUP and REML methods had a very high Pearson correlation and Spearman's rank correlation as 0.978 and 0.988, respectively. For first lactation length, the highest Pearson correlation of 0.869 and Spearman's rank correlation of 0.863 were observed between LSM and REML methods. For total lactation milk yield, the LSM and REML methods had the highest Pearson correlation of 0.855 and Spearman's rank correlation of 0.771. A similar statement regarding the high correlation and comparability between the BLUP and REML methods for sire evaluation in the context of first lactation traits was also reported by various researchers in different studies. Jain and Sadana (2000) reported comparable findings in Murrah buffaloes, stating that the BLUP method incorporating first lactation milk yield, first service period, and age at first calving proved to be more efficient and accurate for sire evaluation, Mukherjee et al. (2007) reported similar findings in Frieswal sires, suggesting that the DFREML method could be effectively used to estimate breeding values for 300-day first lactation performance with comparatively higher accuracy and reliability and Banik and Gandhi (2010) reported similar findings in Sahiwal sires, observing that the estimated breeding values did not differ significantly between the single-trait (305-day milk yield) and multiple-trait models (305-day milk yield, age at first calving, first service period, and first calving interval) using the DFREML method. Likewise, Dubey et al. (2006) reported that rank correlations among sires' EBVs indicated differing rankings for first lactation and lifetime performance traits in crossbred cattle. They suggested that to enhance lifetime productivity, major culling of bulls should be based on their daughters' first lactation milk yield, Singh and Singh (2011) and Singh et al. (2014) found very high and significant correlations by LSM, BLUP and DFREML in crossbred cattle, moreover, Dubey et al. (2014) reported that sire rankings varied between first lactation and lifetime performance traits, suggesting that sires should be evaluated based on the early performance of their daughters to achieve genetic improvement in lifetime productivity of crossbred cattle. Bajetha and Singh, (2015), Bajetha et al. (2015), Lodhi et al. (2015), Singh and Singh, (2016), Lodhi et al. (2016) and Lodhi and Singh (2018) found high correlations by BLUP and REML methods in crossbred sires which aligns with the present findings.

3.3. Top 10 sires

The top 10 sires ranked on the basis of estimated breeding values of sires for first lactation traits by all three methods have been presented in table 3.

The top 10 sires ranked on the basis of age at first calving revealed that sire no.2 ranked first by BLUP, LSM, and REML methods. Sire no.24 ranked 10th by the BLUP method while sire no.57 ranked 10th by LSM and REML methods. The top 10 sires ranked on the basis of first lactation length revealed that sire no.23rd ranked first by BLUP, sire no.59 by LSM, and REML methods. Sire no.30 ranked 10th by the BLUP method while sire no.46 ranked 10th by LSM and sire no.45 ranked 10th by the REML method

The top 10 sires ranked on the basis of first lactation milk yield revealed that sire no. 22nd ranked first by BLUP, sire no. 30 by LSM, and sire no. 45 by REML method. Sire no. 30 ranked 10th by the BLUP method while sire no. 12 ranked 10th by LSM and sire no. 60 ranked 10th by the REML method. Jakhar et al. (2017) and Singh et al. (2011), also supported the present findings who observed high correlations among BLUP, LSM, and REML in top-ranking sires, especially for traits with moderate heritability and lower environmental influence. Chaudhary et al. (2016), observed that REML and BLUP often produce closer estimates for traits like lactation length, whereas LSM tends to deviate due to its methodological limitations. Lodhi et al. (2015) and Sharma et al. (2002), reported that rankings by various methods were generally similar for top sires but deviated more at lower ranks which possibly explained how each method handles error variance, data completeness, and relationships among sires.

These rankings allow for the identification of top-performing sires for each of the first lactation traits, facilitating decision-making in breeding programmes and genetic selection to improve specific aspects of milk production in crossbreeding programmes. In the present study, a significant and high Spearman's rank correlation, as well as Pearson correlation coefficient of 0.988 and 0.978, respectively, were observed between the REML and BLUP methods for sire evaluation. These findings indicated that either of these two methods (BLUP and REML) could be utilized effectively for evaluating crossbred sires. Both methods demonstrated similar efficiency in accurately ranking the sires based on their first lactation traits.

The high correlations between these two methods suggested that they provided consistent and reliable results in estimating the breeding values of sires for first lactation traits. Therefore, breeders and researchers can confidently choose either the BLUP or REML method based on their preference or ease of implementation, knowing that both methods offered reasonable accuracy in evaluating and ranking crossbred sires, contributing to enhanced breeding programmes and genetic selection in the context of milk production and crossbreeding practices.

Table 3: Rankings of top ten sires based on estimated breeding values for AFC (minimum), FLL (maximum) and FLMY (maximum) by different sire evaluation methods

Rank	AFC			FLL			FLMY		
	BLUP	LSM	REML	BLUP	LSM	REML	BLUP	LSM	REML
1.	2	2	2	23	59	59	22	30	45
2.	7	39	44	59	57	9	42	45	23
3.	6	7	6	22	63	23	54	18	35
4.	40	44	7	63	45	12	23	23	16
5.	1	6	40	57	43	55	52	35	30
6.	39	3	1	43	55	57	28	16	18
7.	66	1	66	42	42	11	45	17	42
8.	57	46	39	12	23	63	35	33	54
9.	3	40	24	45	60	15	63	22	6
10.	24	57	57	30	46	45	30	12	60

4. CONCLUSION

Sire evaluation methods were crucial for accurately ranking sires based on specific traits, aiding breeders and researchers in selecting sires to enhance desired traits in crossbred cattle, thereby improving herd productivity. The findings emphasized the importance of selecting the appropriate evaluation method for traits like FLMY, as 4–5% of top sires consistently ranked similarly across methods.

5. ACKNOWLEDGEMENT

We are grateful to the Dean, College of Veterinary and Animal Sciences, Joint Director, IDF, Head, Animal Genetics and Breeding and all technical staff of IDF for their contribution to this work.

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