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RESEARCH ARTICLE

Precision sire evaluation in Murrah buffaloes via BLUP model optimization

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Abstract: Evaluation of buffalo bulls under progeny testing program to estimate their breeding value is a cornerstone of genetic improvement programs. For Murrah buffalo such an effort was initiated in 1993 under the Network Project for Buffalo Improvement (NPBI). The objective of this study was to outline the best suited model to evaluate the test Murrah bulls under associated herd progeny testing program. Breeding value was estimated based on the daughter's 1st lactation milk yield. Four different Best Linear Unbiased Prediction; Sire Model (BLUP-SM) with varying fixed effects were evaluated via the software Wombat using AIREML approach. The Sire families and the data from 14th set of Progeny Testing (PT) Bulls generated under ICAR-NPBI was used for precision breeding of Murrah buffaloes. The study revealed BLUP-SM with age at first calving, season and year of calving as a fixed factor in the model is best suited for sire evaluation in the Murrah buffalo associated herd progeny testing program.

Keywords: AIREML, BLUP-SM, Murrah buffalo, Precision Breeding

Introduction

Buffalo is the major milch species in India, and it also provides meat, draught power, dung, and hides. Presently buffalo contributes around ~44% of the total milk production in India (BAHS, 2025). The buffalo production thrusts on the propagation and multiplication of superior germplasm from a nucleus herd to the livestock breeders in the field. Murrah buffalo is the dominant buffalo germplasm with superior milk-producing ability found throughout India with native tract present mostly in the Haryana. Availability of high genetic merit bulls can be only achieved through their genetic evaluation on regular basis, which is vital to the success of any genetic improvement and breeding program in dairy buffaloes. Considering the significance and contribution of buffaloes, systematic research on breeding in buffaloes was undertaken by the Indian Council of Agricultural Research (ICAR) through All India Coordinated Research Project (AICRP) on buffaloes in the year 1970-71. Four centers namely, Punjab Agriculture University (PAU), Ludhiana and National Dairy Research Institute (NDRI), Karnal were established for the improvement of Murrah buffalo, and Sukhadia University, Vallabhnagar (Rajasthan) and University of Agricultural Sciences (UAS), Karnataka for Surti / Mehsana breeds, respectively. This programme remained in operation till April 1993 when the AICRP was later continued into Network Mode and is presently known as Network Project on Buffalo Improvement. The mandate of the Network Project was to undertake genetic improvement and conservation of important breeds of buffaloes. The concept of Network Project was discussed in first scientist meet held on 28-29 April, 1994 at PAU, Ludhiana and a common technical programme was developed for improvement of Murrah buffalo. Key decisions made during the meeting were: PAU, Ludhiana center to work with Murrah buffalo, also a new centre at Haryana Agricultural University (HAU), Hisar was proposed and included in the network project and decision was taken for Nabha campus of CIRB to concentrate on Nili-Ravi buffalo. The four centres i.e., CIRB Hisar campus, NDRI Karnal, PAU Ludhiana, and HAU Hisar are currently involved in the associated herd progeny testing program by maintaining institutional herds and incorporating field progeny testing data. The Restricted Maximum Likelihood (REML) method, introduced by Patterson and Thompson (1971), has become the preferred approach for estimating variance and covariance components in animal breeding due to its favourable statistical properties (Rönnegård et al. 2010). When applied under an animal model, REML facilitates the separation of genetic effects from random environmental and other nuisance effects. Additionally, it can be extended to estimate a range of other variance components. However, the precision of variance component esti-

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mates largely depends on the population's data structure and the chosen statistical model (Meyer, 2007). Multivariate animal models are now widely employed in the genetic evaluation of livestock. These models account for additive genetic effects for each individual, utilize the complete pedigree information, consider correlations between traits, and can accommodate other random effects. Despite their popularity, the optimal model for estimating variance components is often not well-defined. Furthermore, it remains uncertain whether simpler models that include only direct genetic effects can provide estimates as accurate as those derived from more complex models. The objective of this study is to optimize a suitable model to estimate precise breeding value for Murrah bulls in a progeny testing data set.

Materials and Methods

Performance testing and trait recording

The technical program entails the development and management of an elite herd of 500 Murrah buffaloes, including 300 breedable females at a centre. A key focus is the selection and testing of at least 15 Murrah bulls every 18 months, aiming to produce a minimum of 10,000 frozen semen doses per bull. To enable accurate progeny-based evaluation, at least 8,000 doses per bull are preserved until the assessment is complete. Bulls are evaluated based on the performance of their daughters, particularly first-lactation traits, and the top 20–25% are identified and retained as proven bulls in each evaluation cycle.

The data was collected from the records maintained at the main coordinating unit ICAR-CIRB, Hisar. The season of calving were classified into four different classes i.e., April-June, July-Aug, Sep-Nov, and Dec-March and the periods were assigned as per different year of calving. Age at 1st calving (AFC) in months was deduced and the bins for the classes were decided based on the Sturges rule. Extreme age at first calving records with values <36 & >70 months were removed from the data assuming recording error. The AFC, season, and periods were treated as fixed effects in multiple combinations to optimize the model.

Models and statistical analyses

For estimation of the breeding value for the Sires and model optimization, 14th set Murrah buffalo bulls were evaluated. Data adjustment, pre- and post-processing were done using a custom code generated in R 4.3.3 which included the normalization of data, descriptive statistics and least square analysis. A total of 4 different sire models were tested with the help of the software "WOMBAT" (Meyer, 2007). The models can be represented in matrix terms by;

$$y = Xb + Za + e$$

where ***y*** = vector of observations; ***X*** = incidence matrix of fixed effects; ***b*** = vector of fixed effects; ***Z*** = incidence matrix of random effects; ***a*** = vector of random effects; ***e*** = vector of residuals.

Akaike's Information Criterion (AIC), Bayesian information criteria (BIC) tests were used for comparison of the models and model optimization. In both tests, the most accurate model is the one which had the lowest AIC and BIC values. The values of the AIC and BIC are assessed as follows:

$$AIC = -2\log(ML_k) + 2p_k$$

$$BIC = -2\log(ML_k) + p_k\log(n)$$

where, ML_k = Maximum Log Likelihood for model *k*; p_k = number parameter for model k; *n* = number of observations in model *k*.

The following models were compared;

M1: $y_{ijkm} = \mu + a_i + AFC_j + S_k + e_{ijkm}$

M2: $y_{ikm} = \mu + a_i + S_k + e_{ikm}$

M3: $y_{iklm} = \mu + a_i + S_k + P_l + e_{iklm}$

M4: $y_{ijklm} = \mu + a_i + AFC_j + S_k + P_l + e_{ijklm}$

Where,

y_{ijklm} is standard 305 days or less lactation milk yield of ith Murrah buffaloes in jth AFC class, kth season, and lth period

μ is the population mean

a_i is random Sire effect of ith sire

AFC_j is fixed effect of AFC with jth classes

S_k is fixed effect of kth season of calving

P_l is fixed effect of lth period of calving

e is the Random error associated with each observation

Results and Discussion

Bulls, once considered half the herd due to their genetic contribution, are now seen as more than half owing to widespread use of frozen semen in artificial insemination, making sire selection the key driver of genetic improvement in dairy populations. In the present study, 14th test set consisting a total of 10 bulls were evaluated on the basis of their daughter's 305-days standard lactation milk yield recorded both on farm and field. Bull-wise daughter average performance for Lactation Length (LL), First Lactation 305-days Milk yield (FLMY), and Age at First Calving (AFC) are summarized in Table 1. The least squares mean of first lactation milk yield (FLMY) varied across different levels of age at first calving (AFC), period of calving, and season of calving are presented in Table 2. The overall mean first lactation milk yield (FLMY) was 2416 kg with a standard deviation of 398 kg, and a coefficient of variation (CV) of 16.5%.

The selection of best fit model is a critical step in statistical modeling. In the present study, four different linear models (M1 to M4) were evaluated for the purpose of genetic evaluation of bulls based on their daughter's performance (Table 3). These models varied in their fixed effect structures, incorporating combinations of factors such as age at first calving, season of calving and period of calving. Incorporating fixed effects in sire evaluation studies is crucial for accurately assessing the genetic potential of different sires. Fixed effects help control for environmental factors that is essential to ensure that the differences in performance are attributed to genetic differences rather than environmental variations. In given study AFC, season and period of calving are taken as fixed effect, which are important factors that affect the production performance of daughters on the basis of bull's breeding value to be estimated (Tamboli et al. 2022; Pawar et al. 2012). Modelling with fixed factor such as herd has also been studied and considered significant for sire evaluation (Singh et al. 2022). Singh et al. (2022) used Herd-Year-Season as a fixed effect. In the

Table 1: Bull wise daughter average performance records

Bulls	Total no. of daughters recorded / bull	Daughter's average LL	Daughter's average FLMY	Daughter's average AFC (in months)
1	51	306	2472.8	44.0
2	130	307	2457.6	45.0
3	29	304	2382.2	45.0
4	26	291	2225	44.0
5	21	298	2505.16	45.0
6	39	306	2353.3	44.0
7	49	323	2343.5	42.0
8	34	313	2469.22	42.5
9	6	317	2441.1	43.4
10	54	313	2413.1	43.6

Lactation Length (LL), First Lactation 305-days Milk yield (FLMY), and Age at First Calving (AFC)

Table 2: Least Squares Means (LSM ± SE) of First Lactation Milk Yield (FLMY) Across Levels of Fixed Factors in Murrah Buffaloes

S.No.	Fixed factors	No. of observations	LSM ± SE of FLMY
1.	AFC (in months)		
	27-31	3	2260.55±237.32
	31-35	22	2140.69±99.99
	35-39	65	2203.56±76.00
	39-43	133	2274.05±64.50
	43-47	111	2301.95±64.74
	47-51	66	2287.79±69.76
	51-55	25	2387.28±89.87
	55-60	10	2250.14±126.52
	60-64	2	2387.38±263.64
	64-68	2	2164.49±261.37
2.	Period of calving		
	2016	2	1953.75±237.46
	2017	109	2396.96±85.42
	2018	279	2442.45±85.07
	2019	49	2269.99±101.54
3.	Season of calving		
	April-June	66	2276.65±41.00
	July-August	97	2204.21±35.76
	September-November	152	2290.18±32.59
	December-March	124	2292.09±34.51

Table 3: Comparison of different BLUP models used to estimate the breeding value of the Sire

Model No.	Fixed effects used in Model	Log L	AIC	BIC	Penalty factor
M1	AFC and season of calving as fixed effect	-2785.564	5575.128	5583.236	3.027
M2	Season of calving as fixed effect	-2833.286	5670.572	5678.724	3.038
M3	Season, period of calving as fixed effect	-2823.442	5650.884	5659.026	3.035
M4	AFC, season, period of calving as fixed effect	-2775.189	5554.378	5562.478	3.025

present study a non-significant effect of herd was observed. It might be possible because the bulls involved in the progeny testing program under the network project are used rotationally. Feeding standards and other management practices are maintained according to the standard guidelines of the NPBI. So, this factor was excluded from the model.

A total of 4 different sire models were tested by BLUP (Best Linear Unbiased Prediction) method. Estimates of BLUP based model were efficient for sire evaluation by various research workers (Dubey et al. 2006; Bajetha 2006; Moges et al. 2009; Tailor et al. 2000; Sahoo et al. 2019). This method was developed by Charles Roy Henderson (1973). BLUP can be modelled with various factors to predict breeding values of bulls and to account for non-genetic effects. The key properties of the BLUP are as follows: It minimizes the mean squared error of the prediction, predicted breeding values are a linear function of the observations, estimates of random effects are unbiased as BLUP correctly account for fixed effect and random effect simultaneously, estimation of breeding values for a random variable, such as sire's breeding values. Both fixed effects and random effects are fitted in the same model and estimated simultaneously in the same analysis. BLUP uses all available information to estimate an animal's EBV, i.e., information from all genetically related animals, and possibly from correlated traits in the case of multi-trait BLUP. Moreover, BLUP corrects for fixed effects, it accounts for unequal use of the best sires in different herds, for selection and non-random mating (van der Werf, 2009).

Performance of a model can be judged on its ability to accomplish specified objective, like how well a model explains observed data and makes predictions. The two most widely used model selection criteria are the AIC (Akaike, 1974) and the BIC (Schwarz, 1978). The AIC was one of the earliest model selection criteria. Classical methods like p-values and confidence intervals focus on parameter significance, AIC offers a more holistic view by directly linking model likelihood and parameter count. AIC is based on the Kullback-Leibler Divergence (Kullback and Leiber,1951) and essentially estimates the information lost by a given model. Consequently, a model is considered to be of higher quality when it results in minimal information loss. The BIC criterion is derived in the framework of Bayesian theory, which maximize the posterior probability of a model given the data. Therefore, these criteria provide an objective framework for comparing models by balancing the trade-off between model complexity and goodness-of-fit (Burnham & Anderson, 2002). In the present study, AIC and BIC were used to compare the models. The method of maximum likelihood was used to evaluate the AIC and BIC values. Among the four models assessed, Model 4 (M4) - which includes AFC, season, and period of calving as fixed effects - demonstrated the lowest AIC (5554.378) and BIC (5562.478). For other models AIC and BIC values indicates that model 4 offers the best trade-off between goodness-of-fit and parsimony. The penalty factor is the part of the AIC and BIC formulation that adds a penalty for the number of parameters and helps to control overfitting to enhance the model performance (Bozdogan, 1987). The practical implication is that a lower penalty factor, as seen in Model (M4), indicates that the model offers a more efficient parameterization, explains the data effectively while minimizing redundancy. Various studies across livestock utilized these criterions for genetic evaluation.

Lukaè et al. (2017) adopted a similar approach to study the comparison of models for genetic analysis of traits from the performance test of gilts using AIC and BIC information. Mäntysaari and Mäntysaari (2015) also examined the accuracy of the model based on AIC and BIC coefficients to predict BW of the cows based on daily BW measurements. The heritability coefficient of gestation length for the Polish Holstein-Friesian cow population was calculated according to the best-fitted linear model (Sobek et al. 2022). Similarly, on account of relatively low error variance, high R^2, higher CV, lower AIC and lower BIC Animal model was selected as the best fit model in Mehsana buffaloes for breeding value estimation (Sathwara et al. 2019). However, recent studies advocate other information criteria to select the appropriate or best-fit model. Hamadani et al. (2023) employed the Deviance Information Criterion (DIC) in Bayesian animal models to simultaneously evaluate heritability estimates and breeding values, reinforcing the need to assess both genetic parameter accuracy and predictive utility. Similarly, Passafaro et al. (2021) demonstrated that models with lower DIC values provided better insights into the genetic resistance of beef cattle to worm and tick infestations. The results suggest that proper modeling of fixed effects is crucial to avoid confounding genetic merit with environmental influence, which ultimately enhances the reliability of selection decisions in breeding programs.

Conclusion

The relevance of determining a suitable model structure for precise genetic assessment of bulls is well shown by the present study. To determine the best-fit model for sire evaluation based on the daughter's first lactation performance, a total of four different BLUP model was assessed for their accuracy. The model (M4) emerged as the most suitable model based on likelihood, Akaike, and Bayesian model metrics. The model (M4) had the lowest AIC and BIC values suggested superior goodness-of-fit while preserving parsimony. The results highlighted the manner in which the reliability of breeding value estimation is increased by incorporating pertinent fixed effects. We recommend to include 3 fixed effects (AFC, Season & Period of calving) in BLUP mixed model for systematic sire evaluation for identifying the proven bull(s) in a Network Project on Buffalo Improvement to strengthen the genetic improvement in Murrah buffaloes.

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