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Simulation model for the heritability estimation of milk yield in crossbred dairy cattle under field conditions

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Abstract
The successful selection of superior animals requires a combination of accurate data collection, rigorous evaluation methods, and a clear understanding of breeding objectives. The absence of performance records poses a significant challenge to conducting meaningful research and developing analytical models for field animals. The simulation study was conducted in ten replicates of 500, 1000, and 3000 first lactation records with different levels of input heritability (0.15, 0.20, and 0.25) from the field performance records of crossbred dairy cattle. The datasets were examined to assess the heritability of lactation milk yield and determine the optimal simulation model for analysis. Two distinct models, incorporating varied combinations of fixed effects such as village, year, and month of calving, were tested, each including the sire effect. Between the models considered, the heritability was generally higher for model 2 and the trend was similar for data sets with different sizes. The trend in the variation of R^2–values and heritability among models and replicates exhibited a decrease with an increase in progeny size. The magnitude of R^2–values explained by various models across different datasets was greater for a heritability of 0.25 compared to values of 0.15 and 0.20.

Keywords: Simulation model, heritability, milk yield, genetic parameters, crossbred

Introduction

India, primarily an agricultural nation, relies significantly on the livestock sector, which holds a pivotal position in the country's economy. This sector plays a crucial role in supplying nutritious food abundant in animal protein to the general public, contributing to supplementary family incomes, and creating productive employment opportunities in rural areas. About 70 percent of the rural farmers are dependent on agriculture and rearing of livestock for their livelihood, with 82 percent of farmers being small and marginal (Economic Survey, 20). The compound annual growth rate of the livestock sector has grown nearly 8 percent over the last five years, it assumes an important role in income, employment, and nutritional security.

Out of 192.49 million cattle in India (20th Livestock Census), the growth of zebu cattle breeds accounts for only 10% (142.11 million) and the crossbred cattle population has grown to 26.9% (50.42 million). Crossbred cows, constituting only 10% of the total breedable cow population, demonstrate superior productivity by contributing to 40% of the country's cow milk production. This highlights their efficiency compared to indigenous cows and represents a significant share of the overall national milk output, amounting to 26% (Jamuna *et al*., 2022) [6]. Despite India is being the leading global producer of milk, the productivity per animal remains notably low at 987 kg per lactation, significantly below the world average of 2038 kg per lactation (Thompkinson and Latha, 2012) [15]. This reduced productivity in Indian dairy animals is attributed to their low genetic potential for milk production, compounded by suboptimal input conditions. Enhancing the genetic potential is critical for elevating animal profitability and ensuring the sustainability of dairy development in India. To achieve this, it is essential to systematically evaluate and select genetically superior animals, employing them extensively for breeding purposes.

The principal obstacle in executing large-scale breeding programs for field animals in India is the absence of essential infrastructure for recording the performance of dairy animals under field conditions. Consequently, the assessment of breeding value for milk production relies on data from limited locations. The planning and execution of effective dairy cattle breeding programs aimed at enhancing milk production in India face significant challenges due to the lack of performance records for dairy animals under field conditions (Policy Paper, 82). As a consequence, the estimation of genetic parameters, such as heritability, for dairy performance traits primarily relies on small datasets derived from records of animals maintained in

institutional or organized herds over extended periods. This data structure, combined with varying combinations of environmental factors in analytical models, has resulted in substantial discrepancies in the estimation of heritability and other genetic parameters across different studies on production traits of dairy cattle in India. This variance has generated confusion regarding the extent of genetic variation in milk production in cattle and buffaloes in the country, as well as the significance of various non-genetic factors that should be incorporated into analytical models when assessing the performance of dairy animals. Moreover, attempts to evaluate breeding bulls for milk production based on progeny performance are constrained to organized farms, limiting the assessment to a small number of progeny per sire. Reports from different researchers comparing various methods of sire evaluation also indicate significant variations in the efficiency of these methods, adding further complexity to the evaluation process.

The dairy production landscape in India diverges significantly from that of developed countries, characterized by very small herd sizes spread across numerous farmers and substantial variations in feeding and management practices. Such heterogeneity necessitates the identification of appropriate models and methods for effectively analyzing data recorded on animals reared under these diverse conditions. Consequently, this study takes a critical approach to address this issue by employing a simulation technique to generate data. The simulation incorporates different parameters gleaned from prior studies on the performance of crossbred cattle in the Southern region, where the animals are managed under field conditions. The primary objectives are to estimate the heritability of lactation milk yield and to determine the most suitable analytical model and method for evaluating dairy bulls based on their progeny records. This approach aims to provide insights into the unique challenges and intricacies of dairy production in India, offering a foundation for more effective and tailored management strategies in a context characterized by diverse farming practices and herd sizes.

Materials and Methods: Simulated first lactation milk production records of crossbred dairy cows were generated by employing various genetic parameters (Table 1) sourced from previous studies conducted in the Southern region. This was accomplished using the following mixed linear model:
Model:

$$Y_{ijklm} = \mu + V_i + P_j + M_k + S_l\sigma_s + W_{ijklm}\sigma_w$$

Where,

Y_{ijklm}=first LMY of mth daughter of the lth sire calving in k^{th} month and j^{th} year of calving in i^{th} village, μ= mean 305 days milk yield, V_i= Effect of ith village (i= 1…30/ 60/ 90), Y_j= Effect of jth year of calving (j = 1, …5), M_k= Effect of kth month of calving (k = 1, …12), S_l = Effect of lth sire NID (0, σ^2_s) (m=1,25/ 50/ 75), W_{ijklm}= Random error NID (0, σ^2_w), σ_s= variance of sire component, and σ_w= error variance

σ_p, σ_s and σ_w were calculated as follows;

σ^2_p= (Coefficient of variation x Mean)^2; σ^2_s = ¼. h^2. σ^2_p; σ^2_w = σ^2_p - σ^2_s

S_m and W_{ijklmn} are standardized normal random numbers generated by using the computer package (MS Excel). The h^2 is the heritability of first lactation milk yield and σ^2_p, σ^2_s and

σ^2_w are phenotypic, sire and error components of variances, respectively. The values taken from the published reports of earlier studies were used as input values for simulating the first lactation milk yields. In the model, the effects due to village, year of calving, month of calving and sex of the calf were treated as fixed and the values for different fixed effects influencing first lactation milk yield were chosen from earlier reports. Sire effect and error were treated as random while simulating the first lactation 305 days milk yield for each animal. Number of progeny per sire was varied at random (each sire contributing unequal number of progeny to the population). Finally the population mean value along with fixed and random variable values were summed together to get the phenotypic value (first lactation 305 days milk yield) of each animal.

Two different models comprising of different combinations of fixed effects such as village, year and month of calving and sire as random effect were used to identify appropriate mathematical model to analyze the data on crossbred dairy animals managed under field conditions, to estimate reliable genetic parameter (heritability) for first lactation 305 days milk yield and also for evaluating the breeding bulls using different methods. The sex of the calf is not considered in this study, because of very less contribution of this effect to the total variation in the milk yield.

The following models were employed to analyse the data,
Model 1: $Y_{ijkm} = \mu + S_i + V_j + Y_k + e_{ijkm}$
Model 2: $Y_{ijklm} = \mu + S_i + V_j + Y_k + M_l + e_{ijklm}$
where, Y_{ijklm}= first LMY of mth daughter of the ith sire calving in j^{th} village in k^{th} year and l^{th} month of calving, μ= Overall mean, S_i = Effect of ith sire (i = 1,25), V_j = Effect of jth village (i = 1,…30), Y_k= Effect of kth year of calving (k = 1, …5), M_l=Effect of lth month of calving (l = 1, …12), e_{ijklm}=Random error with mean zero and constant variance σ^2_e

Various datasets were simulated by combining 30 villages and 25 sires at three different levels of input heritability (0.15, 0.20, and 0.25), encompassing 500, 1500, and 3000 records. Ten replicates of each dataset were then generated and subjected to analysis using the previously described models. This analysis aimed to estimate heritability and compare different models and methods, ultimately identifying the most appropriate models and suitable methods for the evaluation of breeding bulls.

Table 1: Summery of parameters considered for generation of data on first lactation 305 day milk yield

Parameters	Values
Average first lactation 305 day milk yield (kg)	2450
Coefficient of variation (%)	35
Number of villages	30, 60 & 90
Effect due to village (% of μ)	-15 to +15
Number of years of calving	5
Effect due to year of calving (% of μ)	-5 to +5
Number of months of calving	12
Effect due to month of calving (% of μ)	-3 to +3
Heritability of first lactation milk yield	0.15, 0.20 and 0.25

Results and Discussion: Utilizing a simulation technique, first lactation milk production records were generated by adopting various parameters derived from earlier studies on the performance of crossbred cattle under field conditions in the Southern region. The resulting data were then analyzed to estimate the heritability of lactation milk yield and to identify the most appropriate analytical model and suitable method for evaluating dairy sires based on their progeny records.

Ten replicates of datasets, each containing 500, 1000, and 3000 records on the first lactation yield of progeny sired by 25 bulls distributed across 30 villages, were generated. These datasets encompassed three levels of heritability (0.15, 0.20, and 0.25). Subsequently, these datasets were analyzed by fitting two different models that included various combinations of fixed effects, such as village, year, and month of calving, with the sire included as a random effect in all models.

For each replicated dataset, the model's explained sum of squares (R^2 value) and heritability were computed. In Table 2, the R^2 values and heritability estimates obtained for various replicates with an input heritability value of 0.15 are presented for datasets comprising 500, 1000, and 3000 records, respectively. The progeny group size per sire ranged from 9 to 36, 20 to 57, and 93 to 147 for datasets with 500, 1000, and 3000 records. The table illustrates that the R^2 values explained by different models in distinct replicates varied from 4.55 to 28.12 percent, 10.27 to 21.26 percent, and 8.35 to 15.41 percent for datasets with 500, 1000, and 3000 records, respectively. Additionally, the tables indicate that model 2, encompassing fixed effects such as village, year, and month of calving, along with the random effect of sire, elucidated the maximum variation in the data. The variation explained by model 2 in different replicates ranged from 13.65 to 28.12 percent, 11.60 to 21.26 percent, and 9.04 to 15.41 percent for sets of 500, 1000, and 3000 records, respectively. Furthermore, a reduction in R^2 values by 1.33 to 5.09 percent was observed in different replicates for datasets containing 1000 and 3000 records (Table 2).

The degree of variation explained by the two fitted models exhibited variability from one replicate to another. In the case of replicates for datasets with 500 records, the R^2 values ranged from 13.65 to 28.12 percent for model 2 and from 11.55 to 26.54 percent for model 1 (Table 2). A comparable pattern was also noted in datasets with 1000 and 3000 records. The extent of variation elucidated by different models displayed a diminishing trend with an increase in data size. For model 2, the R^2 values ranged from 11.60 to 21.26 percent for 1000 records and 9.04 to 15.41 percent for 3000 records, in contrast to 13.65 to 28.12 percent for datasets with 500 records. Likewise, for model 1, the R^2 values among replicates varied from 10.27 to 19.78 percent for 1000 records and 8.35 to 14.76 percent for 3000 records.

The heritability estimates exhibited significant variation across replicates and the analytical models utilized for the analysis. Notably, the variability in heritability estimates was considerably lower when comparing different models within replicates as opposed to the variation observed across replicates within models. The estimated values derived from diverse analytical models and replicates spanned from 0.01 to 0.46, as given in Table 2.

An intriguing observation is that heritability estimates displayed minimal variance across models within replicates. Specifically, the variation was less than 0.08. Conversely, among replicates within models, the differences in estimates ranged from 0.37 to 0.46. In certain replicates, these differences were notably high (0.41 to 0.47), while in others, they were exceptionally low (less than 0.05), and in some instances, the sire components of variance were even negative. Comparing models, heritability values generally leaned towards higher estimates for model 2, which incorporated fixed effects such as village, year, and month of calving, along with sire as random effects. This trend

persisted in datasets with 1000 and 3000 records. However, the variation in the magnitude of heritability estimates decreased with increasing data size (progeny group size). The estimates ranged from 0.02 to 0.46 in replicates of 500 records, 0.02 to 0.26 in 1000 records, and 0.07 to 0.23 in 3000 records. As the progeny group size increased, the variation in the magnitude of heritability values estimated from different replicates within models decreased, along with a corresponding reduction in the variation across models within replicates.

The R^2 values and heritability estimates, derived from the analysis of data generated with an input heritability value of 0.20 using different models, are summarized in Table 3. Across replicates and models, the R^2 values ranged from 8.96 percent (for model 1) to 28.63 percent (for model 2), which incorporated all three fixed effects (Table 3). Generally, R^2 values were highest for model 2 (16.55 to 28.63 percent), followed by model 1, which included only village and year of calving among fixed effects (15.42 to 27.37 percent). The variability in the variation explained by the model, in terms of R^2 value, among the replicates in different models fluctuated by approximately 10-12 percent.

For datasets comprising 1000 and 3000 records, model 2 consistently exhibited the highest R^2 values. Model 2, incorporating all three fixed effects, explained 13.62 to 22.44 percent and 9.69 to 15.70 percent of the variation for datasets of 1000 and 3000 records, respectively (Table 3). Model 1, which included village and year of calving, closely followed this pattern. The heritability values, as outlined in Table 3, also displayed less variation across models within replicates compared to estimates across replicates within models. In datasets of 500 records, heritability estimates ranged from 0.02 to 0.53. Notably, in one replicate, heritability values estimated with two models were quite high (0.40 to 0.53), while in two other replicates, the values were very low, falling below 0.10 (Table 3).

The range of differences in heritability estimates across models within replicates was 0.01 to 0.13, contrasting with a notably higher range (0.37 to 0.51) across replicates within the models. As the progeny group size increased, the variation in heritability estimates across models and replicates diminished, ranging from 0.04 to 0.36 for datasets of 1000 records and 0.08 to 0.29 for datasets of 3000 records. Despite the reduction in the range of variation in heritability estimates with increasing progeny group size, the observed trend of lesser variation in estimates across models within replicates compared to the variation across replicates within models persisted in the case of datasets comprising 1000 and 3000 records.

The range of differences in heritability estimates across models within replicates was 0.01 to 0.13, contrasting with a notably higher range (0.37 to 0.51) across replicates within the models. As the progeny group size increased, the variation in heritability estimates across models and replicates diminished, ranging from 0.04 to 0.36 for datasets of 1000 records and 0.08 to 0.29 for datasets of 3000 records. Despite the reduction in the range of variation in heritability estimates with increasing progeny group size, the observed trend of lesser variation in estimates across models within replicates compared to the variation across replicates within models persisted in the case of datasets comprising 1000 and 3000 records.

The outcomes pertaining to R^2 values and heritability estimates derived from the analysis of data generated with an input heritability value of 0.25 are detailed in Table 4,

encompassing datasets of 500, 1000, and 3000 records. Generally, the R^2 values were higher for the model incorporating all fixed effects except the sire. Specifically, for this model (model-2), the R^2 values ranged from 16.29 to 30.54 percent, 15.85 to 21.74 percent, and 12.20 to 15.52 percent for datasets with 500, 1000, and 3000 records, respectively. Typically, the village factor accounted for approximately 5 to 12 percent of the variation, while the other two effects explained only a marginal proportion of the variation. Even in datasets with 1000 and 3000 records, the village effect explained around 4 to 10 percent of the variation. Examining the presented results, it is evident that the variation in R^2 values explained by different models exhibited a decreasing trend with the increase in progeny group size.

The variability in R^2 values explained by different models within replicates also diminished with an increase in progeny group size. The distinctions in R^2 values across models within replicates ranged from 9.33 to 12.93 percent in datasets of 500 records, 8.12 to 13.30 percent for datasets of 1000 records, and 5.69 to 10.09 percent in datasets with 3000 records.

The pattern in the variation of heritability values estimated from these datasets mirrored the values derived from datasets with input heritability values of 0.15 and 0.20 (Tables 2 & 3). Beyond the reduction in the variability of heritability estimates, the values converged toward the input values as the progeny group size increased. This aligns with findings from another study where heritability estimates from the best-fitted models ranged from 0.08 to 0.15 for milk according to days in milk of the first lactation (Cho et al., 2016) [3].

Sevaral research workers have examined performance records of dairy animals, comparing diverse models with various effects and endorsing models with the highest R2 values as optimal for breeding animal evaluation. For instance, Rao and Dommerholt (1980) [14] scrutinized 14 different models encompassing sires, years, seasons, age-linear, age-quadratic, lactation length-linear, and lactation length-quadratic effects. In their study, model 1, comprising all effects, yielded the highest R2 value (79.36 percent). Notably, they observed a substantial increase in R2 value (16 to 28.45 percent) when transitioning from models excluding sires to models incorporating sires, indicating potential confounding between sire and year of calving. Similarly, Nagarcenkar et al. (1985) [11] evaluated 25 different models involving sire as a random effect, calf sex, managerial factors, year and month of calving as fixed effects, along with age at first calving and lactation length as covariates. Meanwhile, Hamadani et al. (2023) [5] emphasized the significant impact of fixed and random factors on genetic factors and breeding-value accuracies in birth weight estimation models. Their findings highlighted that

model 1, encompassing all effects, exhibited the highest R2 value (28.45 percent) compared to other models. Furthermore, Mai et al. (2021) [10] highlighted the superiority of fixed-effect models over conventional methods in heritability estimation, emphasizing their increased effectiveness in such assessments.

In the evaluation of sire performance, Chauhan et al. (1987) [2] employed three distinct models and determined that the model encompassing all three fixed effects (AI center-year-month) was more suitable and exhibited less bias than models incorporating AI center-year as fixed effects or AI center-year-month as random effects. In contrast, Kumar (1987) [8] incorporated herd, calving period, age at calving, and the level of exotic inheritance of crossbred progeny in the model. Surprisingly, he found that when all effects were considered, the accuracy was at its lowest. Consequently, he concluded that the optimal linear model should exclusively incorporate herd and sire effects.

In a study by Kishore (1993) [7], three diverse models incorporating AI center, breed of the dam, sex of the calf, month and year of calving, and age at first calving as effects were compared. Kishore observed that Model C, achieved through the grouping of AI centers based on their production levels and locations, yielded the highest R^2 value (23.10 percent) compared to Model A (utilizing adjusted data for AI centers and breed of the dam) and Model B (formed by grouping AI centers into progeny testing units).

In a separate investigation, Parekh et al. (1994) [12] employed two models, one within genetic groups (Model 1) and the other across genetic groups (Model 2), incorporating herd-year-season subclasses for evaluating Friesian sires. Model 2 demonstrated greater efficiency with a 72.10 percent R^2 value, in contrast to Model 1, which achieved 60 percent. Notably, the R^2 values obtained in this study were relatively larger than those reported in the present study.

Lin and McAllister (1984) [9] conducted a simulation study to estimate heritability in the univariate case. Their findings revealed that estimates of heritability obtained through four methods (Henderson's method 3, maximum likelihood, restricted maximum likelihood, and minimum norm quadratic unbiased estimation) were similar in magnitude and closely approximated the heritability value used for generating milk production records. This alignment could be attributed to the utilization of very large datasets in their study, a contrast to the present study where the largest datasets comprised only 3000 records across 50 sire groups. Given the consistent superiority of model 2 in terms of R^2 values, this model was employed for the evaluation of sires using various sire evaluation methods based on progeny records.

Table 2: The sum of squares (R^2 – value in percent) and Heritability values estimated for different models in replicated data sets of records

R	N=500(h_i^2= 0.15)		N=1000(h_i^2= 0.15)		N=3000(h_i^2= 0.15)	
Model	M – 1(S, V, Y)	M – 2(S, V, Y, M)	M – 1(S, V, Y)	M – 2(S, V, Y, M)	M – 1(S, V, Y)	M – 2(S, V, Y, M)
1	11.55 (- ve)	13.65 (- ve)	12.62(0.15)	14.40(0.16)	11.86(0.17)	12.43(0.17)
2	18.37 (0.29)	19.26 (0.28)	12.47(0.10)	13.28(0.10)	14.44(0.23)	14.84(0.19)
3	19.34 (0.09)	19.64 (0.06)	11.92(0.05)	13.70(0.05)	11.65(0.21)	12.61(0.21)
4	15.30 (0.07)	16.93 (0.08)	14.03(0.20)	14.74(0.21)	12.23(0.09)	12.80(0.10)
5	18.87 (0.02)	21.98 (0.02)	12.48(0.02)	15.45(0.02)	14.76(0.19)	15.41(0.23)
6	21.79 (0.20)	23.91 (0.20)	19.78(0.25)	21.26(0.26)	10.66(0.12)	11.00(0.12)
7	26.54 (0.32)	28.12 (0.34)	12.22(- ve)	13.48(- ve)	10.23(0.10)	10.51(0.10)
8	18.31 (0.20)	20.91 (0.18)	11.66(0.09)	12.21(0.09)	10.93(0.08)	11.40(0.08)
9	23.29 (0.44)	25.41 (0.46)	15.10(0.06)	16.95(0.06)	12.36(0.12)	13.19(0.12)
10	13.51 (- ve)	16.15 (- ve)	10.27(0.04)	11.60(0.04)	8.35(0.09)	9.04(0.09)

R = Replicates; h_i^2= Input heritability; S = Sire; V = Village; Y = Year of calving and M = Month of calving. The figures in parentheses indicate heritability values. The number of progeny varied from 9 to 36 for different sires in different replicates.

Table 3: The sum of squares (R^2 – value in percent) and Heritability values estimated for different models in replicated data sets ($h_i^2 = 0.20$)

R	N=500(h_i^2= 0.20)		N=1000(h_i^2= 0.20)		N=3000(h_i^2= 0.20)	
	M – 1(S, V, Y)	M – 2(S, V, Y, M)	M – 1(S, V, Y)	M – 2(S, V, Y, M)	M – 1(S, V, Y)	M – 2(S, V, Y, M)
1	27.37(0.53)	28.63(0.48)	17.70 (0.33)	19.03 (0.33)	12.44 (0.22)	13.35 (0.22)
2	23.83(0.06)	26.94(0.05)	15.62 (0.06)	17.22 (0.06)	11.45 (0.09)	11.86 (0.09)
3	18.84(0.15)	19.01(0.15)	12.54 (0.12)	13.62 (0.12)	8.96 (0.13)	9.69 (0.13)
4	18.51(0.28)	22.83(0.30)	17.97 (0.34)	19.72 (0.35)	11.09 (0.19)	11.34 (0.19)
5	27.21(0.31)	28.27(0.32)	14.05 (0.15)	15.99 (0.14)	11.53 (0.22)	12.13 (0.22)
6	23.27(0.15)	24.75(0.15)	22.25 (0.27)	22.44 (0.27)	10.46 (0.13)	10.86 (0.13)
7	25.41(0.28)	26.58(0.26)	15.63 (0.17)	16.05 (0.16)	10.52 (0.18)	10.99 (0.18)
8	23.80(0.34)	27.09(0.35)	18.72 (0.17)	19.04 (0.16)	14.25 (0.23)	14.59 (0.23)
9	18.30(0.10)	23.03(0.10)	14.13 (0.15)	15.71 (0.14)	14.56 (0.27)	14.71 (0.27)
10	15.42(0.02)	16.55(0.02)	16.99 (0.34)	19.20 (0.36)	15.55 (0.28)	15.70 (0.29)

R = Replicates; h_i^2 = Input heritability; S = Sire; V = Village; Y = Year of calving and M = Month of calving. The figures in parentheses indicate heritability values. The number of progeny varied from 9 to 36 for different sires in different replicates.

Table 4: The sum of squares (R^2 – value in percent) and Heritability values estimated for models in replicated data sets ($h_i^2 = 0.25$)

R	N=500(h_i^2= 0.25)		N=1000(h_i^2= 0.25)		N=3000(h_i^2= 0.25)	
	M – 1(S, V, Y)	M – 2(S, V, Y, M)	M – 1(S, V, Y)	M – 2(S, V, Y, M)	M – 1(S, V, Y)	M – 2(S, V, Y, M)
1	25.57 (0.42)	26.64 (0.37)	15.02 (0.26)	16.29 (0.26)	11.41 (0.25)	12.20 (0.25)
2	18.90 (0.17)	20.67 (0.18)	18.85 (0.29)	19.15 (0.28)	13.47 (0.23)	14.05 (0.22)
3	17.03 (0.17)	19.39 (0.19)	14.49 (0.23)	16.31 (0.22)	13.82 (0.15)	14.23 (0.15)
4	24.75 (0.33)	27.25 (0.32)	18.10 (0.29)	19.19 (0.29)	14.81 (0.31)	15.24 (0.31)
5	19.44 (0.14)	22.36 (0.14)	19.05 (0.20)	19.94 (0.22)	11.75 (0.26)	12.38 (0.26)
6	28.45 (0.60)	30.54 (0.63)	21.21 (0.48)	21.74 (0.48)	13.10 (0.21)	13.78 (0.21)
7	14.67 (0.06)	16.29 (0.05)	16.72 (0.20)	17.11 (0.19)	14.62 (0.28)	15.30 (0.28)
8	26.67 (0.57)	27.05 (0.56)	15.51 (0.24)	16.19 (0.24	12.61 (0.18)	12.82 (0.18)
9	14.69 (0.09)	16.90 (0.11)	15.02 (0.26)	16.29 (0.26)	14.99 (0.28)	15.52 (0.28)
10	15.71 (0.14)	18.84 (0.13)	13.80 (0.23)	15.85 (0.25)	13.25 (0.22)	13.79 (0.22)

R = Replicates; h_i^2 = Input heritability; S = Sire; V = Village; Y = Year of calving and M = Month of calving. The figures in parentheses indicate heritability values. The number of progeny varied from 9 to 36 for different sires in different replicates.

Conclusion
The heritability estimates derived from diverse datasets, encompassing varying levels of input heritability, progeny group size, and number of sires, indicate that the inherent differences among sires play a more significant role in determining the estimated heritability magnitude compared to the environmental effects considered in the model. The trend in R^2 values and heritability variation across models and replicates diminishes with an increase in progeny group size. Additionally, the differences in R^2 values and heritability decrease within replicates and across replicates within models as progeny group size increases at all three heritability levels. The magnitude of R^2 values explained by different models in various datasets is higher for 0.25 heritability compared to 0.15 and 0.20.

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