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Estimating Genetic Parameters to Enhance Brahman Cattle Performance in Indonesia

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ABSTRACT

Brahman cattle represent a critical resource for beef production in Indonesia, necessitating a comprehensive genetic improvement program to meet commercial demand and customer preferences. This study aimed to estimate genetic parameters and predict breeding values for body weight measured at different ages in the Indonesian Nucleus Breeding Centre located in Sembawa, Sumatra. The dataset comprised 1,082 records from 32 sires and 552 dams. Body weight measurements were obtained at birth, weaning, yearling, and 18 months of age. The fixed effects of sex and parity were analyzed by using a general linear model to determine levels of significance. Genetic parameters—including heritability and breeding values—were estimated using restricted maximum likelihood and best linear unbiased prediction. Two models were fitted: one incorporating only the additive genetic effect and another integrating both additive and maternal genetic effects. The results showed heritability estimates from the additive-only model ranged from 0.571 to 0.674, while estimates from the model that included additive and maternal genetic effects ranged between 0.426 and 0.501. There was substantial maternal influence on offspring performance across all ages, resulting in upwardly biased heritability estimates when only additive genetic effects were considered. For accurate genetic evaluation and reliable prediction of breeding values, the inclusion of maternal genetic effects in the analytical model is strongly recommended to optimize genetic gain in breeding programs.

Keywords: Brahman cattle; genetic parameters; heritability; body weight; estimated breeding value

INTRODUCTION

Indonesia's national beef demand currently outpaces its domestic supply. This production deficit, driven by population growth and economic progress, has created a heavy reliance on imports. To achieve self-sufficiency, improving cattle productivity through genetic improvement has become a primary national priority. Breeding programs and reproductive technologies, such as advanced artificial insemination (AI), consequently play an important role in speeding up genetic improvement and increasing population. The Brahman breed is well known worldwide for its adaptability under tropical conditions, and it serves as a primary breed for national genetic improvement initiatives, including crossbreeding programs. However, its genetic potential is often underused. Therefore, the development of systematic breeding programs is crucial to improving the genetic potential to meet a standard quality of Brahman cattle, as outlined in the Indonesian National Standard (BSN, 2020). Genetic improvement of Brahman cattle in the Nucleus Breeding Centre (NBC) is an essential strategy, as superior animals are disseminated to many areas in Indonesia, including to smallholder farmers.

Body weight is an important trait in genetic selection programs for Brahman cattle. However, there have been limited studies on genetic parameters such as heritability, in relation to estimates of additive and maternal genetic effects measured at different ages from birth to 18 months (Javier *et al*., 2024). Several studies showed that there were positive genetic correlations among body weights at different ages of measurement, which indicates that selection at earlier ages may improve slaughter weight (Bessa *et al*., 2021).

To accelerate the national genetic improvement of Brahman cattle in Indonesia and optimize breeding strategies, it is necessary to develop more productive and resilient Brahman herds that can perform well under harsh environmental conditions in Indonesia. An effective breeding program is dependent on the accuracy of genetic parameters, such as heritability, derived from specific populations and environments. Previous studies on Indonesian local beef cattle have primarily focused on non-genetic factors to provide the phenotypic basis of populations (Zulkarnaen *et al*., 2025). The present study is the first multi-trait genetic evaluation of Brahman cattle in Indonesia using long-term nucleus herd data. A robust genetic model and strong scientific foundation are required to establish appropriate breeding designs and selection strategies that support better genetic progress. The objective of this study was to examine genetic parameters, including heritability and breeding values for body weight at different ages from birth to 18 months, using models that incorporate additive and maternal genetic effects in the Nucleus Breeding Center of Brahman cattle in Indonesia.

MATERIALS AND METHODS

Study Site and Management System

Brahman performance records were obtained from the Nucleus Breeding Centre (NBC) in Sembawa, Sumatra. The NBC is a central development site for Zebu cattle, as previously reported by Zulkarnaen *et al*. (2022), and is located in a hot climate with an average daily temperature of 29.5 °C and an average relative humidity of 77.5%. The cattle were reared under a semi-intensive management system, as described by Zulkarnaen *et al*. (2025), where they grazed during the day and were sheltered at night. The cattle were fed a diet of tropical grasses supplemented with 14% crude protein concentrate, and they had free access to water and mineral blocks. Furthermore, feeding management protocols were carefully monitored during the study to minimize variability.

Animals and Traits Recorded

A total of 1,082 records were analyzed, originating from 32 sires and 552 dams. The traits observed included birth weight (BW), weaning weight (WW), yearling weight (YW), and weight at 18 months of age (18MW). All traits were considered as selection criteria in the genetic selection program.

Information used in the analyses included animal ID, birth date, sex, dam ID, dam parity, and body weight records. Comprehensive data screening was conducted before the analysis to identify outliers and inconsistencies. Missing data were retained in the analysis as relationship matrices in the animal model have the capacity to predict incomplete information (Mrode & Pocrnic, 2023).

Statistical Analyses

To understand the influence of fixed effects on observed traits, significance was analyzed using the general linear model (GLM) in SAS 9.0. Duncan's multiple range test (DMRT) was then applied to identify significant differences among fixed effects, including sex and dam parity (Zulkarnaen *et al*., 2025). The statistical model is described below:

$$Y_{ij} = \mu + S_i + P_j + \varepsilon_{ij}$$

Where Y_{ij} is the observed trait (body weight at different measurement of age), μ is the mean population, S_i is the sex effect, P_j is the parity effect, and ε_{ij} is the error.

Genetic Parameter Estimation

Genetic parameters were estimated using a univariate animal model with restricted maximum likelihood (REML), and breeding values were predicted using best linear unbiased prediction (BLUP). The estimation of parameters was performed using ASReml (Gilmour *et al*., 2015). The model fitted for the additive genetic effect (Model 1) is described as follows:

$$y = Xb + Zu + e$$

Where y is a vector of the observations (body weight), b is a vector of the fixed effects (calf sex and dam parity), u is a vector of random additive genetic effects, e is a vector of residual effects, X is a matrix related to fixed effects, and Z is a matrix related to additive genetic effects.

The solution matrices for the model with an additive genetic effect are described as follows:

$$\begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + A^{-1}\alpha \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{u} \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \end{bmatrix}$$

Where: $\alpha = \frac{\sigma_e^2}{\sigma_a^2}$; σ_a^2 = additive genetic variance; σ_e^2 = residual variance; A= relationship matrix; $\hat{b}$= solution of fixed effects; and $\hat{u}$= estimates of breeding values (Mrode & Pocrnic, 2023).

The model with additive and maternal genetic effects (Model 2) is described as follows:

$$y = Xb + Zu + Wm + e$$

Where m is a vector of random maternal genetic effects, and W is a matrix related to maternal genetic effects.

The associated solution matrices for the above model are described as follows:

$$\begin{bmatrix} X'X & X'Z & X'W \\ Z'X & Z'Z + A^{-1}\alpha_1 & Z'W + A^{-1}\alpha_2 \\ W'X & W'Z + A^{-1}\alpha_2 & W'W + A^{-1}\alpha_3 \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{u} \\ \hat{m} \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \\ W'y \end{bmatrix}$$

Where: $\hat{b}$= solutions for fixed effects; $\hat{u}$= estimates of breeding values, $\hat{m}$= solution of maternal genetic effect, respectively (Mrode & Pocrnic, 2023).

RESULTS

Body Weight Trends

Figure 1 displays the development of growth from birth weight (BW), weaning weight (WW), yearling weight (YY), and 18-month weight (18-MW). Each measurement showed distinct patterns, which interpreted performance, genetic progress, and the influence of the environment over time from 2013 to 2020. Birth weight ranged from 30.32 to 35.16 kg and remained relatively stable across years. The low variability in birth weight indicates consistent maternal and prenatal management, which has led to good uniformity.

Weaning weight (WW) indicated moderate fluctuation, ranging from 85.72 to 106.40 kg, which may suggest variability in environmental conditions.

Yearling weight (YY) displayed wider variation, ranging from 153 to 219 kg, likely influenced by weaning weight and greater sensitivity to feed availability, pasture quality, and management factors. Samples with 18-month weight showed the largest fluctuation among the traits, reaching the peak in 2019, which may reflect exceptional performance during the period.

Figure 1 revealed generally positive progress in body weight over the eight-year period despite some variability. The improvement between 2018 and 2019 suggests better management practices and highlights strong potential for evaluating breeding programs and future selection strategies.

Effects of Sex and Parity on Body Weight

Analysis of herd dynamics revealed a carefully managed and stable population structure (Figures 2 and 3). Figure 2 illustrates annual fluctuations in calf sex ratios compared to the expected natural proportion. In 2016, a deviation toward male predominance (57.89%) represented a stochastic fluctuation typical of breeding populations and did not compromise the availability of selection candidates. With regard to the dam structure, Figure 3 reflects the replacement. The low proportion of cows in advanced parities (7-8) and the substantially higher proportion in early parities (1-4) demonstrate an intensive culling policy. This population structure is critical for accelerating genetic gain through the minimization of generation intervals.

The GLM analysis revealed statistically significant sources of variation across all growth stages ($p<0.05$). As shown in Table 1, male calves exhibited higher body weight than females, with this superiority being significant at birth (35.03 kg vs. 32.29 kg), and at 18 months (253.59 kg vs 236.66 kg). This sexual dimorphism likely reflects the anabolic effects of androgens, which stimulate muscle protein synthesis and promote skeletal growth. Given the progressive divergence in growth performance between male and female calves, it is essential to include calf sex as a fixed effect in genetic evaluation models to ensure unbiased comparisons among selection candidates.

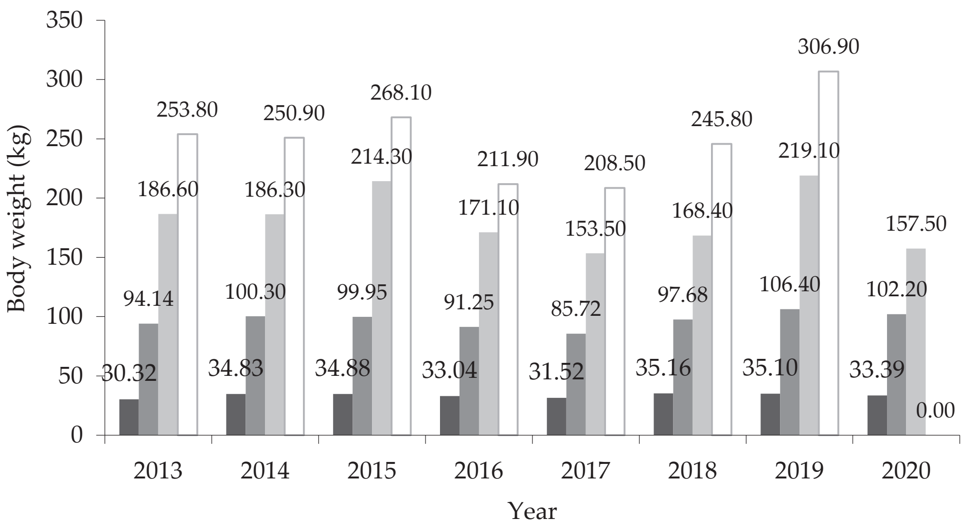


Figure 1. Mean body weight of Brahman cattle at the Nucleus Breeding Centre from 2013 to 2020. Note: ■ Birth Weight; ■ Weaning Weight; ■ Yearling Weight; □ 18-month Weight.

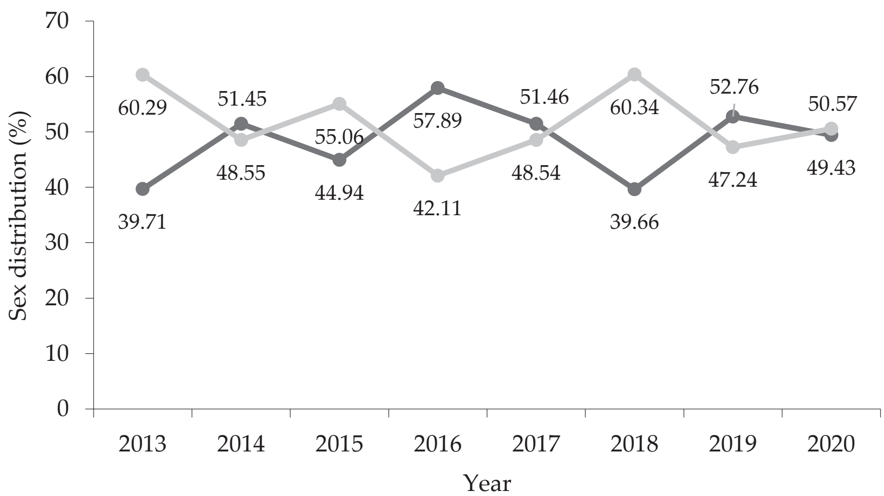
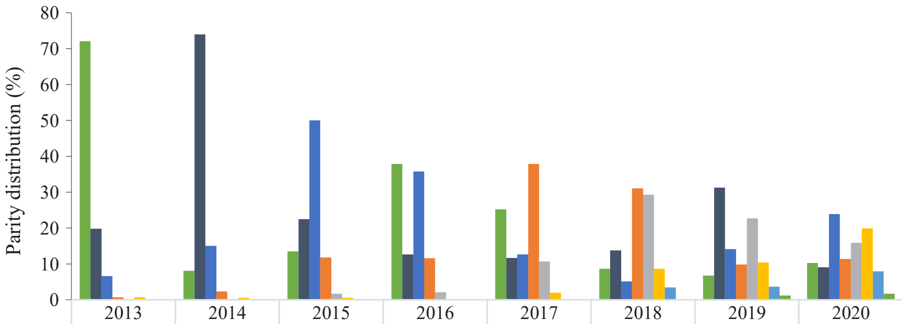


Figure 2. Sex distribution percentage of Brahman calves at the Nucleus Breeding Centre from 2013 to 2020. Note: Male; Famale.



	2013	2014	2015	2016	2017	2018	2019	2020
1st	72.06	8.09	13.48	37.89	25.24	8.62	6.75	10.23
2nd	19.85	73.99	22.47	12.63	11.65	13.79	31.29	9.09
3rd	6.62	15.03	50.00	35.79	12.62	5.17	14.11	23.86
4th	0.74	2.31	11.80	11.58	37.86	31.03	9.82	11.36
5th	0.00	0.00	1.69	2.11	10.68	29.31	22.70	15.91
6th	0.74	0.58	0.56	0.00	1.94	8.62	10.43	19.89
7th	0.00	0.00	0.00	0.00	0.00	3.45	3.68	7.95
8th	0.00	0.00	0.00	0.00	0.00	0.00	1.23	1.70

Year

Figure 3. Parity distribution percentage of Brahman dams at the Nucleus Breeding Centre from 2013 to 2020.

Table 1. Influence of sex on Brahman cattle body weight at Sembawa's Nucleus Breeding Centre

Sex	Body weight (kg)			
	Birth weight	Weaning weight	Yearling weight	18-month weight
Male	5.03 ± 0.25[a]	100.48 ± 1.52[a]	192.86 ± 2.48[a]	253.59 ± 3.67[a]
Female	2.29 ± 0.21[b]	95.89 ± 1.28[b]	184.93 ± 2.45[b]	236.66 ± 3.12[b]
Average	33.63 ± 0.17	98.16 ± 0.98	188.64 ± 1.85	244.72 ± 2.39

Note: Different superscripts within the same column indicate a significant difference ($p<0.05$).

The influence of dam parity on birth weight was statistically significant, with the most pronounced effect observed at birth (Table 2). In contrast, subsequent growth phases exhibited minimal impact. A significant performance disadvantage was observed among calves at the first parity, as demonstrated by Duncan's test. Calves of primiparous dams weighed 31.06 kg, significantly lighter than those born to mature dams (parity 2-5). This disparity is attributed to physiological nutrient portioning in primiparous dams, where nutrients are allocated to maternal somatic growth and fetal development, thereby limiting in utero nutrient availability for the fetus.

During peak reproductive performance, especially at parities 2 to 5, cows exhibit optimal uterine capacity and physiological development, resulting in higher birth weights in their offspring. Cows at advanced parities demonstrated declining birth weights due to reduced biological reproductive efficiency. In addition, post-weaning weights, including weaning weight, yearling weight, and 18-month weight, did not differ significantly across parity groups, as the calves had been maternally separated, allowing the genetic potential for growth to perform.

Genetic Parameter Estimation

The estimates of genetic parameters are presented in Table 3. Two models were employed for the evaluation. Model 1 incorporated the direct additive genetic effect solely, resulting in estimates of heritability (h^2), ranging from 0.571 to 0.674. By incorporating maternal genetic effects, the heritability estimates decreased to between 0.426 and 0.501, which were lower than the estimates produced by Model 1. Maternal genetic effects (m^2) were remarkably consistent across growth stages, ranging from 0.253 to 0.265, which indicates that maternal influences contributed approximately 25% of the phenotypic variance throughout the growth trajectory.

Estimates of heritability obtained under Model 1 were inflated due to the omission of maternal genetic effects. This overestimation resulted from confounding between direct additive and maternal genetic effects, which led to higher estimates of variance components. Model 2 revealed that maternal genetic effects represent a significant source of phenotypic variation for growth in the Brahman population. These findings emphasize the necessity of considering maternal genetic effects in genetic evaluations to have an accurate estimate of breeding value.

Genetic Evaluation and Ranking Based on Estimated Breeding Values

Genetic evaluation was conducted to establish the ranking of animals based on estimated breeding values (EBVs) to identify superior animals for breeding purposes. EBVs for BW, WW, YW, and 18-MW for proven bulls, dams, and young animals are presented in Tables 4 to 7. Table 4 presents the genetic potential of the top 10 sires ranked by EBVs. The results showed that sire S-80903 exhibited the highest EBVs for BW, WW, and YW, thereby representing the superior sire, while sire S-877.888 recorded the highest EBV for the 18MW trait. Table 5 indicates a significant variation in the growth trajectory of the dams. The highest EBVs for the dams were observed in individual D-8258 for BW, D-0921 for WW, D-4738 for YW, and D-3072/048 for 18MW. Interestingly, the presence of negative values both for sires and dams in several high-ranking sires and dams indicates the possibility of choosing the bulls and dams at an early stage without sacrificing market weight.

The evaluation of candidate animals is summarized in Tables 6 and 7. Table 6 presents the performance metrics of the top 10 male calves. Individual 1-15.04.138 exhibited the highest EBV for BW, while the highest values for WW, YW, and 18MW among male calves were observed in 1-1458, 1-15.04.191, and 1-15.04.087, respectively. Notably, the EBV of the top-ranking young sire exceeded the previous proven sire, which indicates the genetic superiority of the young sire over older sires. The increased EBV across cohorts indicates a favorable genetic trend, which leads to enhanced genetic potential in the herd. The superiority of young sires is expected to accelerate genetic progress in subsequent generations and keep the breeding program sustainable.

Table 7 shows the rank of female calves based on EBV across four key growth stages. Individual 2-15.04.012 exhibited the highest EBV for BW, while individual 2-15.04.140 outperformed others in both WW and YW, and individual 2-15.04.118 showed the highest EBV for 18MW within the female calves' population.

Table 2. Influence of parity on Brahman cattle body weight at Sembawa's Nucleus Breeding Centre

Parity	Body weight (kg)			
	Birth weight	Weaning weight	Yearling weight	18-month weight
1st	31.06 ± 0.25[b]	89.55 ± 1.47[a]	179.03 ± 2.61[a]	236.29 ± 3.64[a]
2nd	34.51 ± 0.44[a]	102.79 ± 2.53[a]	189.85 ± 5.03[a]	255.33 ± 5.71[a]
3rd	34.30 ± 0.49[a]	102.02 ± 3.01[a]	200.15 ± 4.97[a]	244.04 ± 6.16[a]
4th	34.22 ± 0.74[a]	97.42 ± 4.27[a]	184.76 ± 8.46[a]	239.14 ± 11.15[a]
5th	34.95 ± 0.92[a]	103.22 ± 4.70[a]	183.56 ± 8.48[a]	242.06 ± 10.22[a]
6th	33.44 ± 1.36[ab]	96.16 ± 6.89[a]	191.38 ± 11.51[a]	244.97 ± 12.45[a]
7th	33.23 ± 1.73[ab]	95.85 ± 4.35[a]	186.22 ± 7.12[a]	243.54 ± 1.66[a]
8th	31.20 ± 1.31[b]	98.15 ± 2.14[a]	186.00 ± 9.35[a]	-
Average	33.63 ± 0.17	98.16 ± 0.98	188.64 ± 1.85	244.72 ± 2.39

Note: Different superscripts within the same column indicate a significant difference ($p<0.05$).

Table 3. Estimates of genetic parameters for body weight traits in Brahman cattle

Model	Trait	Genetic parameters	
		$h^2 \pm se$	$m^2 \pm se$
A Model 1	Birth weight	0.674 ± 0.10	-
	Weaning weight	0.638 ± 0.11	-
	Yearling weight	0.594 ± 0.09	-
	18-month weight	0.571 ± 0.12	-
A + M Model 2	Birth weight	0.501 ± 0.08	0.256 ± 0.02
	Weaning weight	0.477 ± 0.08	0.253 ± 0.02
	Yearling weight	0.436 ± 0.07	0.265 ± 0.02
	18-month Weight	0.426 ± 0.09	0.253 ± 0.02

Note: A=fitting only additive genetic effect, A+M = fitting additive and maternal genetic effects, h^2 = heritability; m^2 = maternal genetic effects; se = standard error.

Table 4. Top 10 sires based on total estimated breeding values

Rank	ID-S	Body weight (kg)			
		BW	WW	YW	18MW
1	S-80903*	3.52	22.42	68.14	34.94
2	S-877.888*	0.71	11.94	52.27	56.26
3	S-40002*	3.57	20.78	16.03	24.61
4	S-1157*	0.63	(8.84)	42.05	27.96
5	S-1477*	0.07	10.51	22.31	25.54
6	S-PM Ausi*	(3.29)	3.89	23.04	31.86
7	S-40990*	1.73	0.00	49.05	0.00
8	S-PM KA*	(2.21)	10.44	12.85	22.72
9	S-848532*	(3.10)	(10.50)	6.31	46.72
10	S-14BR0040*	(1.38)	2.37	16.69	21.59

Note: ID-S = Identification number of sire; BW = Birth weight; WW = Weaning weight; YW = Yearling weight; 18MW = 18-month weight.

Table 5. Top 10 dams based on total estimated breeding values

Rank	ID-D	Body weight (kg)			
		BW	WW	YW	18MW
1	D-4738*	1.93	7.90	33.88	40.18
2	D-3072/048*	2.85	4.98	28.79	46.44
3	D-1398*	2.10	15.51	23.79	34.64
4	D-2082*	0.33	20.92	29.46	24.45
5	D-8258*	5.31	10.74	16.17	35.61
6	D-0921*	3.66	27.57	17.60	17.06
7	D-1067*	(0.35)	13.38	29.17	19.23
8	D-3001/172*	2.15	8.09	14.01	36.40
9	D-1352*	0.55	14.31	14.97	29.35
10	D-1272*	1.40	7.72	29.93	20.05

Note: ID-D = Identification number of dam; BW = Birth weight; WW = Weaning weight; YW = Yearling weight; 18MW = 18-month weight.

Table 6. Top 10 male calves based on total estimated breeding values

Rank	ID-1	Body weight (kg)			
		BW	WW	YW	18MW
1	1-1458	(1.61)	52.53	70.83	58.84
2	1-15.04.138	6.26	23.46	72.32	70.84
3	1-15.04.117	5.41	13.73	71.12	77.19
4	1-15.04.087	2.20	16.06	61.82	80.10
5	1-15.04.103	(0.19)	12.59	72.48	70.83
6	1-15.04.191	1.97	15.75	77.26	53.24
7	1-19.04.081	4.39	29.38	74.83	24.47
8	1-15.04.034	1.93	18.48	37.68	69.99
9	1-15.04.011	6.22	10.04	36.12	72.73
10	1-15.04.017	0.38	2.83	41.83	77.29

Note: ID-1 = Identification number of male calves; BW = Birth weight; WW = Weaning weight; YW = Yearling weight; 18MW = 18-month weight.

Table 7. Top 10 female calves based on total estimated breeding values

Rank	ID-2	Body weight (kg)			
		BW	WW	YW	18MW
1	2-15.04.118	1.67	11.78	48.98	79.20
2	2-15.04.140	1.80	26.91	65.17	44.38
3	2-15.04.145	1.16	10.97	65.11	59.45
4	2-1499	(0.25)	18.44	47.29	67.36
5	2-15.04.121	2.65	4.94	60.22	62.41
6	2-15.04.012	5.94	6.54	45.29	71.29
7	2-15.04.059	4.94	12.77	44.48	66.78
8	2-1258	2.03	18.60	58.09	47.80
9	2-15.04.083	(0.79)	6.09	45.63	72.74
10	2-1500	0.93	15.60	38.63	67.69

Note: ID-2 = Identification number of female calves; BW = Birth weight; WW = Weaning weight; YW = Yearling weight; 18MW = 18-month weight.

This suggests different physiological growth curves among the top-tier calves.

DISCUSSION

The findings revealed that the Nucleus Breeding Centre (NBC) Sembawa serves as a benchmark for the genetic evaluation of improvement of Brahman cattle in Indonesia. The mean birth weight of 33.63 kg observed in this facility exceeds the mean birth weight reported by Farhani *et al*. (2021) (30.04 kg) under smallholder farming conditions in Lampung, Indonesia, with a difference of 11.9%. The findings revealed that the genetic and environmental conditions at the NBC are better than those in smallholder systems. This phenotypic gap highlights a critical reality: while the national herd possesses superior growth potential, its expression is constrained by environmental factors in the field (Santana *et al*., 2023; Londoño-Gil *et al*., 2025). Therefore, the role of the nucleus center is multifaceted, serving as a hub for genetic improvement technologies (Van Eenennaam, 2025) and maintaining superior genetic stock (Sharma *et al*., 2025). By providing optimal conditions, the center can identify genetic merit and contribute to improving the commercial sector by disseminating highly productive genetics (Tesema, 2023).

The fixed-effects analysis confirmed the necessity of fitting sex and parity to prevent bias or to obtain a robust model for genetic evaluation (Nascimento *et al*., 2022), as male calves exhibited greater body weight than females across all ages. Such dimorphism is commonly affected by hormonal mechanisms, and it is recommended that for predictable biological inherent, the body weight be standardized (Tahira *et al*. 2022). Moreover, dam parity is a maternal disadvantage and is limited solely to birth weight, and consistently declines as the animals get older (Santana *et al*., 2023). The absence of parity effects on weaning and post-weaning weights indicates that the management system—particularly nutritional supplement protocols—is effective in altering maternal milk production (Javier *et al*. 2024). The finding suggests that selection can be effectively implemented after weaning.

The most remarkable finding of this study is that the magnitude of direct heritabilities was consistently high across all growth traits, exceeding those documented in Brazil (Bessa *et al*., 2021), Colombia (Bedoya *et al*., 2019), and Thailand (Kamprasert *et al*., 2019). This phenomenon might be due to lower variability of environmental conditions, such as nutritional variability and managerial system in the Indonesian NBC, which led to high genetic variability being expressed (Sharma *et al*., 2025). Further analysis is required to investigate the reason behind the inflated estimates of heritability. Londoño-Gil *et al*. (2025) note that the possible reason may be due to internal environmental conditions related to dams. Including maternal effects in the model revealed that dams have a substantial influence on inflated estimates resulting from additive-only models (Santana *et al*., 2023). Maternal heritability estimates (m^2) were approximately 0.25 across all ages, which confirms that maternal genetics has a crucial influence on growth. Consequently, maternal genetic effects must be considered in predicting breeding values to prevent overestimation of direct genetic merit (Javier *et al*., 2024).

Estimated breeding value (EBV) is the prediction of an animal's genetic for a particular trait, such as growth rate, expressed as the difference from the individual average of the population. EBVs are fundamental to modern beef cattle breeding, as they accelerate genetic progress and enable comparisons across herds. Ranking candidates for selection (Tables 6 and 7) determines selection strategies; for instance, yearling weight EBVs can identify the top 10% of young bulls for replacement stock or artificial insemination programs to disseminate superior genetics across the population (Tesema, 2023; Sharma *et al*., 2025) and support national beef cattle improvement. Notably, several young candidates exhibited high EBVs compared to proven sires, indicating favorable genetic trends and providing evidence of an effective breeding program (Van Eenennaam, 2025).

The limitation of this study includes the high environmental variability across populations and generations. The estimates of parameters are precise and satisfactory for selection decisions under the NBC, but they may not capture genotype by environment interaction across Indonesian regions (Silveira *et al*., 2021). Future breeding strategies should incorporate multi-location genetic evaluation by integrating NBC and commercial production partners (Van Eenennaam, 2025). Such an approach has proven successful in the United States and Brazil (Londoño-Gil *et al*., 2025) and may increase the accuracy of the national estimate breeding value.

Changing from phenotypic selection to EBV-based selection in Indonesia represents a significant technological advancement (Van Eenennaam, 2025). This study confirms the genetic potential of local Brahman cattle, which can support the reduction of dependency on imported genetic resources (Tesema, 2023). In addition, integrating local improved Brahman genetics into NBC programs will enhance productivity among smallholder farmers and improve income generation.

CONCLUSION

This study demonstrated that Brahman cattle exhibit considerable genetic potential for body weight improvement, as indicated by high estimates of heritability for additive genetic effects. Maternal genetic effects were also found to have a strong impact on body weight, which indicates the need to integrate maternal genetic effects into genetic evaluation models to ensure unbiased prediction for breeding values and to optimize selection accuracy. Selection based on EBVs has proven effective for identifying superior animals within nucleus herds; however, to reduce genetic by environment interaction, incorporating information from multiple locations is necessary.

CONFLICT OF INTEREST

The authors certify that there is no conflict of interest with any financial, personal, or other relationships with individuals or organizations related to the material presented in this manuscript.

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DECLARATION OF GENERATIVE AI AND AI-ASSISTED WRITING

During the preparation of this work, the authors used Gemini to assist with data analysis and to provide supplementary insights to enhance the quality of the content. After using this tool, the authors reviewed and edited the content as needed and take full responsibility for the final publication.

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