



Estimation of genetic parameters for growth traits in Brahman crossbred cattle of Bangladesh

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ABSTRACT

The present study was conducted to estimate the genetic parameters (heritability and genetic correlation) and breeding value of Brahman crossbred cattle (50%) of Bangladesh. Data on 5662 Brahman graded calves (50%) were collected from the records maintained by Department of Livestock Services from the eight areas of the country. Basic statistical analyses were performed by using Statistical Analysis System (SAS) version 9.1.3. Heritability and genetic correlations were estimated with Variance Component Estimation (VCE) 5.1.2 software and finally breeding values were measured with PEST software. Heritability (h^2) estimates were 0.87, 0.59, 0.33, 0.33, 0.34, 0.34, 0.35 for birth weight (BW), Weight at 1-, 3-, 6-, 9-, 12- and 24-month (kg), respectively. Estimates of h^2 for ADG from BW to 3-month (g), ADG from 3- to 6-month (g), ADG from 6- to 9-month (g), and ADG from 9- to 12-month (g) were found to be 0.53, 0.71, 0.69 and 0.68, respectively. Genetic correlations between growth traits ranged from 0.15 to 0.92 and phenotypic correlations between these traits ranged from 0.17 to 0.88. Average daily gain showed positive phenotypic correlation with all of the growth traits considered whereas genetic correlation ranged from -0.10 to 0.72. On the basis of predicted breeding value sire ID 60003 had the highest breeding value for body weight at different ages and average daily gain at different ages. Strong genetic and phenotypic correlations will help to improve growth traits simultaneously and selection at early stage can be effective for the improvement of growth traits at later ages.

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Introduction

Most of the cattle population in Bangladesh is nondescript types, the productivity of these cattle is low due to poor genetic potentiality. Crossbreeding has been proposed as a means to improve production under different environmental conditions. Crossbreeding utilizes diverse breed resources and heterosis. One of the main reasons for estimating crossbreeding parameters is to predict the performance of untested genotypes, without actually producing the animals, in order to make a choice of breeding systems for the benefit of producers. Considering weather, agro-climatic condition, heat tolerance, disease and insect resistance, longevity, grazing ability, calving ease, mothering ability and management, Brahman breed is considered to be the most suitable and compatible beef breed in tropical and sub-tropical region (Antonio *et al.*, 2006). Growth rate remains the primary selection criterion for most beef cattle breeders around the world, thus the correct prediction of the genetic value of beef cattle is required for optimizing genetic gain. These traits are easy to

measure, have medium to high heritability, and respond well to selection, thereby resulting in genetic progress (Bertipaglia *et al.*, 2015, Boligon *et al.*, 2009).

Genetic parameters are unique to the population in which they were estimated and they may change over time due to selection and management decisions (Koots *et al.*, 1994; Lobo *et al.*, 2000). Genetic parameter estimates are needed to implement sound breeding programs and to assess the progress of ongoing programs. Heritabilities and genetic correlations are essential population parameters required in livestock breeding researches as well as in the design and application of practical animal breeding programs. The breeding worth of an individual judged by the mean value of its progeny is called the breeding value of the individual. The more accurate the estimate of the breeding value, the better results of the subsequent breeding can be expected. The genetic trend, which is the change in production per animal per unit of time due to change in mean breeding value of the animals would be an indicator to determine the direction of change

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brought about as a result of any kind of breeding program operated (Bhuiyan *et al.*, 2003). Brahman is a promising beef cattle breed getting popularity day by day in Bangladesh. The success of Brahman cattle breeding program depends on the identification of genetically superior sires and their utilization. There is no information on genetic parameter for growth performance in Brahman crossbred cattle population of Bangladesh. The objectives were to estimate genetic parameters (heritability and genetic correlation) of growth traits of Brahman crossbred population and estimate sire breeding value for growth traits.

Materials and Methods

Study period and area

The data used in this study were recorded from January 2014 to September 2018 under a project entitled “Beef breed development in Bangladesh” run by the Government of Peoples Republic of Bangladesh under the supervision of Department of Livestock Services (DLS) in 8 areas (Division) throughout the country namely Dhaka, Mymensingh, Rajshahi, Rangpur, Chattogram, Sylhet, Barishal and Khulna. The whole country were divided into four agro-ecological zones viz flood plains, southern coastal belts, north western ‘Barind’ steppe and the eastern hilly areas.

Management

Technical committee selected target farmers who were given 100% Brahman semen from six (6) 100% Brahman sire (ID 60001, 60002, 60003, 60004, 60005, 60006). Farmers had at least two native cows (having average body weight 180-250 kg) and interested to inseminate cows with pure beef breed were selected in this experiment. Heifers and cows in first and second parity were considered for insemination. The selected cows were inseminated with frozen semen from DLS field station with the help of Field Assistant for Artificial Insemination (FAAI). The data of 50% Brahman crossed population used in the experiment were collected from the record sheets maintained at the Central Cattle Breeding Station and Dairy Farm (CCBDF), Savar, Dhaka and the book maintained for recording of growth performance on individual animal at the Upazila Livestock Office of the respective selected areas. A training program was designed for the farmers to perform better animal husbandry practices. New borne calves were allowed to suckle colostrums and were left with dam upto 3 to 4 days. In some cases, calf milk replacer was fed to the calves and calves were separated from dam from day 4 and onward. The calf was fed 5-10 gm of grain (maize powder form) at the age of 4-5 days that influence to grow rumen bacteria. After about 3 weeks of eating grain, the calf rumen had enough bacteria fermenting enough feed to supply a substantial amount of energy. All calves were assisted to develop rumen by providing free-choice water and quality grain in the first few days after birth. With this feeding strategy by 3-4 weeks of age the calf rumen was well

develop and was ready for the change to a diet of solid feeds. The recorded data were weights at birth (BW), weight at 1-, 3-, 6-, 9-, 12- and 24-month (kg), ADG from BW to 3-month (g), ADG from 3- to 6-month (g), ADG from 6- to 9-month (g), and ADG from 9- to 12-month (g). Birth weight (kg) was recorded for all calves within 24 hours of their birth using the digital weighing balance. With the help of digital weighing balance weight at 1-, 3- and 6-month were recorded in the morning before feeding. The 9-, 12- and 24-month weight was calculated from hearth girth (smallest circumference of body immediately behind the shoulder) and the body length (distance between point of shoulder to the pin bone). Body length and hearth girth were measured in the inches using a measuring tape and the live weight of each calf was calculated according to Shaeffer’s formula as follows:

$$\text{Live weight (kg)} = \frac{[\text{Body wt.} \times (\text{Hearth girth})^2]}{(300 \times 2.2)}$$

The following formula was used to calculate the Average daily gain in gram (g).

$$\text{Average daily gain (g)} = \frac{(\text{Final wt.} - \text{Initial wt.})/\text{Interval (days) between final and initial wt.}}$$

Statistical analysis

The general linear model (GLM) procedures of the Statistical Analysis System (SAS) (SAS, Version 9.1.3, 2009) computer package, version 9.1.3 were used to test the significance of fixed effects according the following model:

$$Y_{ijklmn} = \mu + S_i + M_j + R_k + T_l + W_m + E_{ijklmn}$$

Where, Y_{ijklm} = dependent variable (individual animal record for the trait); μ = overall mean; S_i = fixed effect of i^{th} sex of calf; M_j = fixed effect of j^{th} season; R_k = fixed effect of k^{th} area; T_l = fixed effect of l^{th} AEZ; W_m = fixed effect of m^{th} sire, and E_{ijklmn} = residual error.

Heritability estimation

Genetic parameters were estimated with Residual Maximum Likelihood (REML) procedure fitting an animal model using VCE 5.1.2 software (Goreneveld Version 5.1.2, 2003). The methods used to estimate genetic parameters included random effects and all fixed effects that were found significant in least-squares analysis.

The model fitted for both uni-trait and two-trait analyses were as follows:

$$Y = Xb + Za + e$$

Where, Y = vector of observations; b = vector of fixed effects; a = vector of random animal effects (direct

genetic); X = incidence matrix for fixed effects; Z = incidence matrix for random effects; and e = vector of random residual effects.

It was assumed that all effects in the models are independent and normally distributed.

$$\text{Heritability } (h^2) = \frac{\sigma^2_A}{\sigma^2_P}$$

Where, σ^2_A = Additive genetic variance, and σ^2_P = Total phenotypic variance.

Genetic correlation estimation

The genetic and phenotypic correlation between traits was estimated using two-trait pair wise analyses. The fixed effects included in the multi-trait animal models were those in single-trait analyses. The genetic correlation between body weights at different age were estimated by using VCE 5.1.2 software. The phenotypic correlations were estimated by using Statistical Analysis System (SAS) computer package, version 9.1.3.

Breeding value

Breeding value of animals based on birth (BW), weight at 1-, 3-, 6-, 9-, 12- and 24-month (kg) and The ADG from BW to 3-month (g), ADG from 3- to 6-month (g), ADG from 6- to 9-month (g), and ADG from 9- to 12-month (g) were estimated using Best Linear Unbiased Prediction (BLUP) methodology. The BLUP in turn was carried out by computer program prediction and estimation (PEST) (Goreneveld Version 3.1. 1998). A single trait animal model was used for the PEST program considering the animal and genetic group as a random effect and year of birth and generation as fixed effects.

Results

Growth performance

The phenotypic means and standards deviations are presented in the Table 1. The growth performance estimates for basic statistics were 23.39 kg, 37.55 kg, 58.63 kg, 115.24 kg, 181.10 kg, 258.66 kg and 543.32 kg for birth (BW), weight at 1-, 3-, 6-, 9-, 12- and 24-month, respectively. The ADG from BW to 3-month ADG from 3- to 6-month, ADG from 6- to 9-month, and ADG from 9- to 12-month were 395.10 g, 629.05 g, 738.07 g, and 895.75 g, respectively.

Heritability

Estimated heritabilities for growth traits are presented in the Table 2. The highest heritability was found in case of birth weight (0.87±0.009) and lowest for weight at 3-month and weight at 6-month (0.33±0.005), followed by weight at 9-month and weight at 12-month (0.34±0.004).

Table 1. Mean values with standard errors for growth performance of Brahman crossbred cattle in Bangladesh

Parameter	Obs. number	Mean±SE
Birth weight (kg)	5662	23.39±0.07
Weight at 1-month (kg)	5634	37.55±0.12
Weight at 3-month (kg)	5601	58.63±0.21
Weight at 6-month (kg)	5584	115.24±0.56
Weight at 9-month (kg)	5548	181.10±0.94
Weight at 12-month (kg)	4704	258.66±1.22
Weight at 24-month (kg)	2370	543.32±3.68
ADG from BW to 3-month (g)	5563	395.10±2.33
ADG from 3- to 6-month (g)	5583	629.05±5.12
ADG from 6- to 9-month (g)	5485	738.07±5.75
ADG from 9- to 12-month (g)	4674	895.75±6.94

ADG, average daily gain

Table 2. Estimates of heritability with standard error of Brahman crossbred population of Bangladesh

Parameter	Obs. number	$h^2 \pm SE$
Birth weight (kg)	5662	0.87±0.009
Weight at 1-month (kg)	5634	0.59±0.016
Weight at 3-month (kg)	5601	0.33±0.005
Weight at 6-month (kg)	5584	0.33±0.005
Weight at 9-month (kg)	5548	0.34±0.004
Weight at 12-month (kg)	4704	0.34±0.004
Weight at 24-month (kg)	2370	0.35±0.005
ADG from BW to 3-month (g)	5563	0.53±0.005
ADG from 3- to 6-month (g)	5583	0.71±0.013
ADG from 6- to 9-month (g)	5485	0.69±0.015
ADG from 9- to 12-month (g)	4674	0.68±0.016

ADG, average daily gain

Genetic and phenotypic correlation

The genetic and phenotypic correlations between body weights at different ages are summarized in the Table 3. The genetic and phenotypic correlations between body weights at different ages were positive and moderate to high in magnitude. The highest phenotypic correlation (0.88) were found between weight at 6- and 9-month and lowest (0.17) were found between birth weight and weight at 9-month. Genetic correlation was highest (0.92) between weight at 9- and 6- month and lowest (0.15) between birth weight and weight at 9-month. Table 4 represents the phenotypic and genetic correlations among average daily gains at different ages. Phenotypic correlations for average daily gains at different stages of growth were positive and ranged very weak (0.02) to moderate (0.50). However, the genetic correlations between average daily gains at different stages of growth were low, except 3- to 6- month with 6- to 9-month, which was strong positive (0.72). The genetic correlations of average daily gain of birth to 3-month with 9- to 12-month was weak and negative (-0.10).

Genetic parameter estimation for growth traits in Brahman crossbred

Table 3: Phenotypic (above diagonal) and genetic (below diagonal) with standard error among body weight at different ages

Body weight (kg)	Birth weight	Weight at 1-month	Weight at 3-month	Weight at 6-month	Weight at 9-month	Weight at 12-month	Weight at 24-month
Birth weight (kg)		0.32	0.19	0.18	0.17	0.23	0.35
Weight at 1-month (kg)	0.17		0.65	0.48	0.43	0.41	0.55
Weight at 3-month (kg)	0.29	0.66		0.62	0.52	0.45	0.49
Weight at 6-month (kg)	0.16	0.48	0.63		0.88	0.76	0.69
Weight at 9-month (kg)	0.15	0.35	0.48	0.92		0.86	0.72
Weight at 12-month (kg)	0.21	0.31	0.37	0.79	0.87		0.75
Weight at 24-month (kg)	0.38	0.50	0.38	0.73	0.74	0.79	

Table 4: Phenotypic (above diagonal) and genetic (below diagonal) with standard error among average daily gain at different ages

Traits	ADG from BW to 3-month (g)	ADG from 3- to 6-month (g)	ADG from 6- to 9-month (g)	ADG from 9- to 12-month (g)
ADG from BW to 3-month (g)			0.24	0.23
ADG from 3- to 6-month (g)	0.29			0.50
ADG from 6- to 9-month (g)	0.16	0.72		0.02
ADG from 9- to 12-month (g)	-0.10	0.06	0.06	

Table 5: Estimated breeding values of sires based on body weight at different ages

Sire ID	Birth weight	Weight at 1-month	Weight at 3-month	Weight at 6-month	Weight at 9-month	Weight at 12-month	Weight at 24-month	Total score
60001	0.43965	0.2126	0.01496	-0.1841	-0.7123	0.424	-1.994	-1.79919
60002	0.03347	-0.0882	-0.11993	1.1232	3.0332	6.181	3.277	13.43974
60003	0.22205	1.0753	0.79901	4.2838	7.0819	14.283	38.407	66.15206
60004	0.56868	-0.6967	-0.45624	-5.011	-9.6308	-13.741	-39.132	-68.0991
60005	-0.87913	-0.1975	0.40274	-1.4657	-2.474	-1.795	-1.278	-7.68659
60006	-0.36083	-0.381	0.19654	0.9147	1.9346	-6.935	1.057	-3.57399

Table 6: Estimated breeding values of sires based on average daily gain at different ages

Sire ID	ADG from BW to 3-month (g)	ADG from 3- to 6-month (g)	ADG from 6- to 9-month (g)	ADG from 9- to 12-month (g)	Total score
60001	-2.559	-1.769	-1.812	-24.149	-30.289
60002	-2.526	13.771	24.307	11.717	47.269
60003	9.519	39.082	26.949	53.314	128.864
60004	-10.494	-49.958	-45.458	-8.135	-114.045
60005	0.784	-11.449	-17.019	25.497	-2.187
60006	5.709	8.42	10.802	-66.99	-42.059

Table 7: Ranking of sire based on their estimated breeding value

Sire ID	BV for body weight	BV for ADG	Index value	Ranking
60003	66.15206	128.864	194.794	1
60002	13.43974	47.269	60.67527	2
60005	-7.68659	-2.187	-8.99446	3
60001	-1.79919	-30.289	-32.5278	4
60006	-3.57399	-42.059	-45.2722	5
60004	-68.0991	-114.045	-182.713	6

BV, breeding value; ADG, average daily gain

Breeding value estimation

The estimated breeding values for different sires based on body weight are presented on Table 5, and based on average daily gain are presented in Table 6. Highest breeding value (66.15206) for body weight was found for bull no. 60003 and lowest breeding value (-68.0991) for body weight was found for bull no. 60004 (Table 5). For average daily gain bull no. 60003 had highest

breeding value (128.864) while bull no. 60004 had lowest breeding value (-114.045) for average daily gain (Table 6). Ranking of sire based on their estimated breeding values are presented in the Table 7. On the basis of breeding value for body weight and average daily gain bull no. 60003 stood first followed by 60002, 60005, 60001, 60006 and 60004.

Discussion

Growth performance

The mean body weights at different ages found in this study were higher compared to 21.40±0.24 kg birth weight (Hoque *et al.*, 2016) for 50% Brahman crossbred cattle, 52.72±1.31 kg 3-month weight (Haque *et al.*, 2015) for Brahman crossed calves, 261.1 kg 24-month weight (Johari and Jashmi, 2009) for Hereford-kk F1 crossbred cattle but lower weight were observed by Chen (2012) 194.49±18.42 kg for weight at 6-month in crossbred cattle of Piedmontese and Nanyang. The average daily gain results are consistent with the findings of 0.39 to 0.45 kg/d reported by Antonio *et al.* (2006) for pre-weaning average daily gain in crossbred calves and 390 g/day for 25% Brahman graded cattle for pre-weaning average daily gain reported by Hafiz *et al.* (2008) but disagreed with Toušva *et al.* (2014) who found 1313 g/d and 1192 g/d daily gain for 201 days and 365 days respectively in Charolais cattle. These variations may be due to environmental condition, feeding regime and management practices.

Heritability

Among all trait studied the highest heritability was for birth weight (0.87±0.009). The estimated value was higher than the range 0.42 to 0.75 reported by Bertipaglia (2015) for birth weight in Brazilian Brahman cattle, 0.75 (Khan *et al.*, 1995) for Brown Swiss, 0.54 (Kaygisiz, 1998) for Jersey, 0.36 (Norris *et al.*, 2004) for Nguni cattle. High estimates of heritability indicated that the additive genetic variance exists which can be exploited by mass selection for improving this trait. Heritability for three-month weight in this study was found 0.33±0.05, which value was lower than previously reported values of 0.46±0.08 (Rahman *et al.*, 2015) for local- Friesian crossbred, 0.49±0.06 (Afroz *et al.*, 2011) for Red Chittagong cattle, 0.47 (Rabeya *et al.*, 2009) for Red Chittagong cattle. Estimated heritability for six-month weight was found 0.33±0.05. These findings was more or less similar to 0.34±0.01 obtained by Chen *et al.* (2012) for Piedmontese and Nanyang crossbred cattle and 0.39±0.12 obtained by Rahman *et al.* (2015) for Red Chittagong cattle. The twelve-month heritability (0.34±0.04) was higher than 0.25 found by Norris *et al.* (2004) for Nguni cattle but lower than 0.40±0.02 found by Chen *et al.* (2012) crossbred cattle of Piedmontese and Nanyang. Twenty- four month heritability (0.035±0.05) was almost similar to Wang *et al.* (2004) for Chinese Simmental cattle but higher compared to Pico *et al.* (2004) who found 0.14 for South African Brahman cattle. Another cause of variation originated from differences in breed or genotype of calves rather than dams.

Genetic correlation

Estimates of genetic correlation and their approximate standard errors for body weight at different ages are presented below the diagonal in the Table 3. Genetic correlation among the body weights at different ages ranged from weak positive to strong positive. All the growth traits had favorable (positive) genetic correlation with each other. All of the positive genetic correlations are promising because they indicate that positive selection in animal for one body weight characteristics could improve all of the other body weight characteristics in the progeny. Highest genetic correlation (0.92) was observed between six-month and nine-month body weight and lowest (0.15) between birth weight and nine-month body weight. The magnitude of these correlations increased steadily with ages. Weak negative (-0.10) to strong positive (0.72) genetic correlation exists between average daily gain showed in the study. The high and positive genetic association between body weight traits indicate that indirect selection of one trait by another is possible. Genetic correlation between birth weight and 6-month weight (0.16), birth weight and 12-month weight (0.21), birth weight and 24-month weight (0.38) was higher than 0.20, 0.09, -0.12 and 0.20 respectively for Sahiwal cattle reported by Manoj *et al.* (2012). Manoj *et al.* (2012) also found comparatively lower (0.74 and 0.31) genetic correlation between 6-month and 12-month body weight and 6-month and 24-month body weight than the present findings (0.79 and 0.73). Genetic correlation between 12-month and 24-month weight was much higher (0.79) compared to Frizzas *et al.* (2009) findings (0.30) between 12-month and 18-month body weight for Nellore cattle.

Phenotypic correlation

The estimates of the phenotypic correlations between particular months of age for body weights and average daily gain at different ages were presented above the diagonal in Table 3 and Table 4, respectively. The phenotypic correlations between body weight at different ages ranges from moderate to strong positive (0.17 to 0.88). Phenotypic correlation for average daily gain ranged very weak positive (0.02) to moderate positive (0.50). Weak negative (-.10) to strong positive (0.72) for birth to three-month with nine to twelve-month and three to six-month with six to nine-month. Phenotypic correlation between birth weight and 6-month weight (0.18), birth weight and 12-month weight (0.23), birth weight and 24-month weight (0.35), 6-month and 12-month weight (0.76), 6-month and 24-month weight (0.79) were higher than 0.06, 0.10, 0.13, 0.64, 0.40, respectively reported by Manoj *et al.* (2012) for Sahiwal cattle. Phenotypic correlation (0.79) between weight at 12-month and weight at 24-month was very close to Frizzas *et al.* (2009) findings (0.80) for 12-month and 18-month phenotypic correlation in Nellore cattle. Gradual decreases in phenotypic

correlation for average daily gain with increase in ages were observed. Moderate to higher phenotypic correlations amongst most of the body weights indicated their effectiveness for formulating selection criteria on the basis of these traits.

Breeding value

Estimation of breeding value of sires is one of the most important aspects of genetic improvement program. This is particularly so because, only few sires are needed in a herd and more rigorous selection can be made in males. For birth weight highest breeding value was found 0.56868 for sire ID 60004 and lowest -0.87913 for sire ID 60005. Sire ID 60003 obtained highest breeding value of 1.0753, 0.79901, 4.2838, 7.0819, 14.283, 38.407 for weight at 1-, 3-, 6-, 9-, 12- and 24-month body weight, respectively. Lowest breeding value for weight at 1-, 3-, 6-, 9-, 12- and 24-month were -0.6967, -0.45624, -5.011, -9.6308, -13.741, -39.132, respectively obtained by sire ID 60004. For ADG from BW to 3-month, ADG from 3- to 6-month, ADG from 6- to 9-month and ADG from 9- to 12-month highest breeding value were 9.519, 39.082, 26.949 and 53.314, respectively which was obtained by sire 60003. Lowest breeding value for ADG from BW to 3-month, ADG from 3- to 6-month and ADG from 6- to 9-month were -10.494, -49.958 and -45.458, respectively were found for sire 60004. In case of ADG from 9- to 12-month lowest breeding value -66.99 was found for sire 60006. Sire ID 60003 obtained highest breeding value and sire ID 60004 obtained lowest breeding value.

Conclusion

The high magnitude of heritability estimates for growth traits derived from present study suggests selection can be highly effective in changing growth traits in Brahman crossbred cattle population in Bangladesh. Strong genetic and phenotypic correlation among most of growth traits also indicated that selection for one trait will improve simultaneously other trait. Top ranked animals should get top priority during selection and breeding while considering these growth traits for improving next generation.

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