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Genotype×Environment Interactions in Growth Performance of Brahman Crossbred Cattle in Bangladesh

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ABSTRACT

The objective was to evaluate the effects of genotype×environment interaction on growth traits of Brahman crossbred cattle. The animals were reared in two environments viz., Central Cattle Breeding Station (on-station) and farmer's herd (on-farm) where management system was respectively intensive and semi-intensive in nature. Birth weight was very similar across environments. Average body weight at different ages was greater in on-station herd than in on-farm herd ($p < 0.01$). Body weight was 23.0, 25.4, 41.5 and 27.5 kg greater at 6, 9, 12 and 18 month in on-station herd than in the on-farm herd, respectively. Significant interaction between sire×environment in most of the growth traits ($p < 0.001$) was observed. Heritability estimates for growth traits were greater in on-station herd (ranged from 0.29-0.47) than in on-farm herd (ranged from 0.48-0.50). Genetic correlations of the same growth trait between two environments showed a decreasing tendency with the increase in age of animal (from 0.74 ± 0.05 at 3 months to 0.57 ± 0.05 at 24 months). These results demonstrate that effects of G×E in Brahman crossbred cattle are large between two types of management system indicating that breeding bull selection and use should be carried out within environment basis.

Key words: Brahman crossbred, heritability, genetic correlation, body weight, herd, sire

INTRODUCTION

In the animal breeding field, one of the main objectives is to develop and identify genotypes that present consistent economic performance in different production systems. To achieve this objective, different effects have been tested and one of them, which has become the focus of lots of discussion until now a days is the genotype by environment interaction (G×E), which has already been defined as important in different breeds (De Paula *et al.*, 2009). Identification of genotype-environment interaction in beef cattle may help the artificial selection process and increase the efficiency of genetic evaluation on sires submitted to different environments (Guidolin *et al.*, 2012). Identification of environmental factors important in G×E and identification of animals best suited for given environment will help producers in making optimal decisions given their management setting (Williams *et al.*, 2012). The G×E means simply that the effect of the environment on different breeds or genotypes is not the same; this implies that there is no universally "Best" genotype; the best genotype will vary from one environment to another and will depend on the prevailing environment conditions. The G×E interactions must be understood if they are to be

exploited to improve animal production, particularly in production systems associated with large environments (Vercoe and Frisch, 1992).

Earlier studies have reported the existence of significant G×E in growth traits between production systems (Bradfield *et al.*, 1997; Amelie, 2007; Assenza *et al.*, 2010; Raidan *et al.*, 2015), among regions (Van Niekerk *et al.*, 2004; Guidolin *et al.*, 2012; Bresolin *et al.*, 2015), between countries (Espasandin *et al.*, 2011) and between seasons of birth (De Alencar *et al.*, 2005; Williams *et al.*, 2012). For example, Assenza *et al.* (2010) found that the genetic correlations between each trait expressed in an intensive fattening system and the same trait expressed in a pasture spanned from 0.31-0.93 while Raidan *et al.* (2015) reported genetic correlation to be 0.75 for final weight between nellore cattle reared in feedlot and on pasture.

Differences between sires in the genetic ability of their daughters to perform in different environments may result from interactions between genotype and environment (Cienfuegos-Rivas *et al.*, 1999). As proposed by Falconer (1952), the definition of the environment in which the analyzed trait is considered to be different is relevant for the study of G×E. The method used to estimate the existence as well as the magnitude of G×E was suggested by Falconer (1952). Mathur (2002) advocated the multivariate approach to estimate the genetic correlation for each pair of environments to evaluate the significance of the interactions on breeding programs. The magnitude of G×E interaction was increased when the difference in environmental conditions became larger (Pegolo *et al.*, 2006).

In Bangladesh, a crossbreeding program has been undertaken using local zebu cows and American Brahman sire to boost up meat production. The F₁ Brahman-Local crossbred calves are reared at two different management systems. One factor that could cause G×E in these Brahman crossbred cattle, however, is differences in feeding and management systems in particular between nucleus herd reared in Central Cattle Breeding Station (intensive system) that confine cattle for the entire year versus cattle reared at farmers house (semi-intensive system) with moderately grazing round the year in different districts. Confinement feeding with similar management in Central Cattle Breeding Station (CCBS) and confinement feeding with grazing under different management condition in individual farmer's house are different environments and genetic evaluations of sires with daughters primarily in one environment may not be adequate predictors of progeny performance in another environment. In intensive system, the ideal animals are those that give most production with maximal energy inputs, while under semi-intensive system the optimal genotypes are those that give moderately high levels of production given somewhat limited energy inputs (Boettcher *et al.*, 2003). Van Niekerk *et al.* (2004) suggested that it will be of economic importance to identify the presence of a genotype by environment interaction, as this will influence the genetic progress in a breeding program. Thus, the objective of this study was to evaluate effects of genotype environment interaction on growth traits of Brahman crossbred cattle raised under intensive versus semi-intensive system in Bangladesh.

MATERIALS AND METHODS

Breeding and management in two environments: A total of 150 local cows, reared in Central Cattle Breeding Station, Savar, Dhaka were inseminated by the semen of five Brahman sires. Artificial insemination and calf birth information were recorded in the register of CCBS. From 150 local cows, 254 Brahman-Local crossbred F₁ calves were born in the year 2010, 2011, 2012 and 2013.

A total of 384 local cows reared at individual farmer's house of 7 districts (namely Thagurgaon, Dinajpur, Rangpur, Bogra, Rajshahi, Sirajgonj and Jessore) were inseminated by the semen of

same five Brahman sires. Artificial insemination and calf birth information were recorded in the register of Upazila Livestock Office. From 384 local cows, 384 Brahman-Local crossbred F₁ calves were born in the year 2010, 2011, 2012 and 2013.

Body weight at birth (BW) and body weight at 3 month (3W), 6 month (6W), 9 month (9W), 12 month (12W), 18 month (18W) and 24 month (24W) of these F₁ Brahman-Local crossbred calves born at CCBS as well as farmer's house were taken until December, 2014. Birth weight and body weight at 3, 6, 9 and 12 month of each animal was measured with a digital platform weighing balance and body weight at 18 and 24 month was measured with a manual platform weighing balance at CCBS, whereas, digital platform weighing balance was used for all traits at farmer's level.

According to feeding and management systems, CCBS that confine cattle for the entire year is considered as herd-1 and farmer's house at seven districts that confine cattle for the entire year with moderately grazing round the year is considered as herd-2. The data on growth traits (BW, 3W, 6W, 9W, 12W, 18W and 24W) of Brahman-Local F₁ crossbred cattle raised at CCBS (intensive system) and at individual farmer's house of 7 districts (semi-intensive system) born between 2010 and 2013 from five Brahman sires were used for this study.

Statistical analysis

Estimation of heritability (h²): For genetic analyses, (co) variance components and heritability (h²) of each trait of two herds were estimated applying Residual Maximum Likelihoods (REML) approach by VCE 4.2.5 computer package (Groeneveld, 1998). For REML analysis, animal model was used considering year of birth, season of birth, sex and sire as fixed effects. The general animal model was of the form:

$$Y = Xb + Za + Wc + e$$

where, Y is vector of observations, X, Z and W are known incidence matrices associated with the level of b, a and c with Y, b is Unknown vector of fixed effects (i.e., year, season, sex and sire), a is unknown vector of breeding value, c is unknown vector of permanent environmental effects and e is vector of residual effects.

Estimation of breeding value: The PEST-13.4.10 (Groeneveld *et al.*, 1998) program was used to estimate breeding value of growth traits using co-variance matrices found from VCE-4.2.5 (Groeneveld, 1998) analyses. All analyses were done using a single trait animal model where animal's additive genetic effect was the only random factor and sex of calf, season of birth, year of birth and sire as fixed factor for growth traits.

Estimation of G×E (Method 1): The G×E for growth traits of Brahman crossbred cattle were measured taking two environments (Herd-1 and herd-2) into consideration described above. In this study, factorial analysis of variance (Mathur and Horst, 1994) using a linear model with an environmental factor (herd), a genetic factor (sire) and interaction effect between the two factors was fitted with genetic and interaction effects as random effects. Animals were arranged based on sex, season, year, sire and environment. Data were analyzed using General Linear Model (GLM) procedure of SAS (2003) to estimate sire×environment interaction and Duncan's multiple range test was used for mean comparisons (Steel and Torrie, 1980).

The following model was used:

$$Y_{ijklm} = \mu + S_i + N_j + T_k + B_l + e_{ijklm}$$

where, Y_{ijklm} is Dependent variables (BW, 3W, 6W, 9W, 12W and 18W), μ is overall population mean for any of the said trait, S_i is effect of i^{th} sex (where i = male and female), N_j is effect of j^{th} season of birth (where j = winter, summer and rainy), T_k is effect of k^{th} year of birth (where k = 2010, 2011, 2012 and 2013), B_l is effect of l^{th} sire of calf (where l = 10, 40, 41, 522 and 525) and e_{ijklm} is random residual error associated with Y_{ijklm} observation.

Estimation of G×E (Method 2): The scale of G×E was also calculated by estimating correlations (genetic) of breeding values between animals of two herds. The requirement was that the animals in the two herds should be genetically related (Ojango and Pollott, 2002), which in this case was established through the use of common sires in both environments. SAS (2003) computer package program was used to estimate correlations (genetic) of breeding value between animals of two herds.

Estimation of genetic correlation: In method 2, heritability (h^2) value of the traits was estimated. Breeding values of the animals for a certain trait were predicted and then correlations (r_g) between the breeding values of the animals (genetic correlations) for a trait in two herds (X and Y) were regarded as the scale of G×E.

RESULTS AND DISCUSSION

Growth traits: Table 1 shows the least squares means and standard error of means for growth traits for both environments and estimates of sire×environment interaction. Not surprisingly,

Table 1: Effect of sire of calves and environments on body weight (kg) of Brahman crossbred cattle

Factors	Body weight at different ages (Least Squares Mean±SE)					
	BW	3W	6W	9W	12W	18W
Sire of calf						
10	21.0±0.41 ^{ab}	56.8±1.42 ^{abc}	93.2±2.45	128±3.41	159±4.35 ^{bc}	218±8.06
	-136	-116	-111	-105	-102	-68
40	19.5±0.69 ^b	57.4±2.53 ^c	94.6±4.73	133±7.00	168±9.93 ^c	265±21.7
	-39	-37	-37	-36	-33	-21
41	22.6±0.37 ^a	55.9±1.30 ^{ab}	91.8±2.65	128±3.93	167±5.56 ^{ab}	221±7.33
	-138	-124	-122	-121	-119	-99
522	21.2±0.33 ^{ab}	58.9 ±1.31 ^a	99.2±2.52	137±3.70	172±4.88 ^a	232±8.39
	-117	-103	-103	-102	-102	-73
525	20.0±0.21 ^b	53.1±0.84 ^{bc}	90.1±1.87	124 ±2.75	153±3.42 ^{bc}	199±4.97
	-210	-188	-181	-179	-175	-157
p-value	<0.0001	0.018	0.96	0.064	0.004	<0.0001
Environment						
Environment-1	20.9±0.24	60.1±0.78 ^a	105±1.47 ^a	147±2.07 ^a	185±2.89 ^a	241±4.68 ^a
	-254	-217	-206	-200	-196	-149
Environment-2	20.8±0.21	52.7±0.77 ^b	82.3 ±1.42 ^b	122±2.10 ^b	143±2.80 ^b	213±4.53 ^b
	-386	-351	-348	-343	-335	-269
p-value	0.91	<0.0001	<0.0001	<0.0001	<0.0001	0.0004
Sire×Environment						
p-value	<0.0001	0.074	0.007	0.0005	<0.0001	<0.0001

BW: Birth weight, 3W: 3 month weight, 6W: 6 month weight, 9W: 9 month weight, 12W: 12 month weight, 18W: 18 month weight, Means within a column without a common superscript differed significantly, Figures in the parenthesis indicate the number of observation, SE: Standard error of means

Table 2: Heritability of growth traits of Brahman crossbred cattle in environments

Trait	Herd-1		Herd-2	
	Number of animals	Heritability±SE	Number of animals	Heritability±SE
BW	270	0.49±0.031	385	0.47±0.028
3W	227	0.48±0.037	350	0.47±0.029
6W	214	0.49±0.033	347	0.45±0.034
9W	207	0.48±0.038	341	0.44±0.038
12W	203	0.48±0.046	334	0.42±0.044
18W	148	0.50±0.055	267	0.29±0.081
24W	131	0.49±0.061	197	0.42±0.053

BW: Birth weight, 3W: 3 month weight, 6W: 6 month weight, 9W: 9 month weight, 12W: 12 month weight, 18W: 18 month weight, 24W: 24 month weight, SE: Standard error

average body weight in different ages of crossbred cattle was greater in herd-1 than in herd-2 ($p < 0.01$). Birth weight was very similar across environments. Sire had significant influence in all traits except 6W and 9W. Significant effect of sire×environment interaction on BW, 6W, 9W, 12W and 18W ($p < 0.001$) was found.

In this study, the significant differences in weight at 6, 9, 12, and 18 month between two environments were 23.0, 25.4, 41.5 and 27.5 kg, respectively. In a similar study, Rahman (2013) observed that the differences in weight at birth and 9 month in Red Chittagong cattle were 2.29 and 7.53 kg, respectively between nucleus and farmer's herd, although differences were not significant. Evaluating growth traits of Maxican Nellore cattle, Martinez-Gonzalez *et al.* (2010) revealed that the phenotypic means were 31.4, 175.0 and 333.0 kg, respectively for birth weight, weaning weight and yearling weight, which are higher compared to present results. In dairy cattle, Boettcher *et al.* (2003) found that per cow production was greater in the conventionally managed herds than in the grazing herds.

Heritability for growth traits: Estimates of heritability within each environment are presented in Table 2 for all traits evaluated. Heritability estimates were generally lower in herd-2. For the growth traits, heritability estimates fell in the range of 0.48-0.50 for the herd-1 versus 0.29-0.47 for the herd-2.

The increased estimates of heritability in the herd-1 suggested that genetic differences among animals were expressed to a greater degree in the herd-1. The lowest heritability for the weight was associated to the animals raised at herd-2. This proved a better expression of the genetic potential in intensive feeding regime where animals were raised in more homogenous and controlled conditions than at herd-2. A decrease in the heritability for the weight in herd-2 (0.47 at 3W vs. 0.29 at 18W) could be explained by a higher effect of the environment on the phenotypic variance with the age. However, this tendency was not observed at herd-1 where the heritability only varied from 0.48-0.50 along the whole period. This would mean that the proportion between genetic variance and phenotypic variance stayed equal during the whole rearing period at herd-1.

In a study to analyse the G×E interaction in tropical conditions, Amelie (2007) observed a decrease in the heritability for the weight of Creole beef cattle in intensive feeding regime (0.45 at 270 days of age vs. 0.23 at 540 days) and on the other hand, this tendency was not observed at pasture where the heritability only varied from 0.18-0.23 along the whole fattening period. These results are fairly consistent with the present findings. In comparison to present results, relatively less interaction effects were reported by Raidan *et al.* (2015) for final weight with heritability values of 0.44 and 0.50, respectively for feedlot-raised and pasture-raised Nellore bulls while Espasandin *et al.* (2011) reported similar direct heritability (0.35 and 0.34) for weaning weight in

Table 3: Correlation (genetic) of breeding values for growth traits between two herds

Growth trait	Genetic correlation (r_g) \pm SE
3W	0.74 \pm 0.049
6W	0.74 \pm 0.049
9W	0.72 \pm 0.050
12W	0.64 \pm 0.045
18W	0.53 \pm 0.044
24W	0.57 \pm 0.050

BW: Birth weight, 3W: 3 month weight, 6W: 6 month weight, 9W: 9 month weight, 12W: 12 month weight, 18W: 18 month weight, 24W: 24 month weight, SE: Standard error

Angus cattle from Brazil and Uruguay. In dairy cattle, Boettcher *et al.* (2003) found greater heritability for milk yield in conventional herds (0.37) compared to pasture herds (0.31). Martinez-Gonzalez *et al.* (2010) showed that the direct heritability increased with the increase of age for Nellore cattle, which are 0.59, 0.29 and 0.24, respectively for birth weight, weaning weight and yearling weight. However, different heritability values (0.23, 0.45 and 0.25) were detected by Van Niekerk *et al.* (2004) in the Nguni cattle for weaning weight in three different ecological regions, which indicated a higher effect of the environment.

Estimates of G×E for growth traits: The scale of G×E for growth traits was also calculated by estimating correlations (genetic) of breeding value between animals of two environments for each trait and presented in Table 3. It was found that correlations (genetic) of 3W, 6W, 9W, 12W, 18W and 24W between animals of two environments were 0.74, 0.74, 0.72, 0.64, 0.53 and 0.57, respectively indicating existence of significant G×E in two environments and the weights at all ages were positively correlated ($p < 0.001$) between animals of two herds.

Effects of G×E on growth traits, as indicated by genetic correlations were medium to high. Robertson (1959) suggests that if the genetic correlation between environments is less than 0.80, the genotype×environment interaction is of biological importance. Vercoe and Frisch (1992) concluded that a G×E of small magnitude can only occur when genotypes with similar configurations of production potential and resistance to stress are compared, no matter how different the environments may be. In this study, genetic correlations between the weights in the two herds tended to decrease with the age (from 0.74 at 3 months of age to 0.57 at 24 months). It indicated a higher divergence in environmental impact on animal's performances between the herds and therefore an increase in the G×E interaction. It also indicated that the G×E interaction could only be appreciated when the difference in environmental conditions were enough contrasting. In partial agreement with this study, Amelie (2007) reported that genetic correlations between the weights in the two fattening systems tended to decrease with the age (from 0.97 at 300 days of age to 0.59 at 540 days), which demonstrates an increase in the G×E interaction. Similarly, Assenza *et al.* (2010) reported the existence of significant G×E interaction for yearling weight and growth during the post weaning period in Creole cattle, fattened in two contrasted environments and showed reduced correlation values between weights measured in both systems as age increases. These authors also found that the genetic correlations between each trait expressed in an intensive fattening system and the same trait expressed in a pasture spanned from 0.31-0.93. Raidan *et al.* (2015) reported genetic correlation to be 0.75 for final weight between Nellore cattle reared in feedlot and on pasture. On the contrary, Beffa *et al.* (2009) found high genetic correlation estimates (0.96-1.00) for different weight traits across different management environments and Boettcher *et al.* (2003) reported minor effects of G×E in dairy cattle with genetic correlations of 0.93 for milk yield trait. However, analyzing weaning weight data from three different region Van Niekerk *et al.* (2004) reported that the genetic correlations of region-2 and region-3 with region-1

were 1.00 and 0.71, respectively and this was 0.60 between region-2 and region-3. Similarly, Bresolin *et al.* (2015) reported that the genetic correlation for adjusted 205 days weight of Nellore bulls varied from 0.52-0.84 among three regions and Bradfield *et al.* (1997) reported that the genetic correlation was 0.63 for weaning weight in Santa Gertrudis cattle between two production environments. Moreover, Espasandin *et al.* (2011) found that the estimated genetic correlation for the direct additive genetic effect for weaning weight between two countries, Brazil and Uruguay, was 0.77. These results suggested that the best breeding bulls in one region or production system are not the same as in another region or production system.

In general, effects of G×E in Brahman crossbred cattle are large between two management systems. A number of factors could explain this existence of observed G×E. First, the two systems of management were extremely different. In herd-1, the feeding and management would be expected to be similar. In herd-2, each farmer had one Brahman crossbred cattle reared along with few other local cattle or Friesian crossbred cattle. Therefore, farmer to farmer variations in respect to management and feeding were immense in on-farm condition. The heritability values for weights were greater in herd-1. Other effects of G×E were large with genetic correlations of near 0.75 or lower for all traits between two environments.

CONCLUSION

The results demonstrate that effects of G×E are large on growth traits for F₁ Brahman-Local crossbred cattle between two management systems in tropical conditions and point out the importance to take into account the environmental conditions when the purpose is to make genetic improvement in both situations using a single genotype. Furthermore, these results indicate that breeding bull selection and use should be done within environment basis.

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