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GENETIC EVALUATION OF BANGLADESH LIVESTOCK RESEARCH INSTITUTE CATTLE BREED-1 : Heritability and Genetic Correlation

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Abstract

Heritability and genetic correlation of economic traits of Bangladesh Livestock Research Institute (BLRI) Cattle Breed-1 (BCB-1) were estimated with Residual Maximum Likelihood (REML) principle. The BCB-1 is a native cattle breed developed by BLRI through selective breeding among indigenous cattle of Bangladesh. Data asserted from performance record sheets of 500 animals maintained during 1992 to 2005 were analyzed for estimation of genetic parameters. The heritabilities were estimated with single trait animal model for age at service and age at first calving and those of single trait repeatability model for other traits. However, two traits animal models were used for estimation of genetic correlations among different traits. The model includes sex, season and year of birth, parity, generation and additive genetic merit of each individual. The estimated heritabilities were higher for lactation milk yield (LMY, 0.404) and age at first calving (AFC, 0.404) followed by moderate estimates of daily milk yield (DMY, 0.257), lactation length (LL, 0.333), peak milk yield (PMY, 0.335), milk yield per day of calving interval (MYCI, 0.227), age at first service (AFS, 0.316), calving interval (CI, 0.273), and post partum heat period (PPHP, 0.276). The genetic correlations of lactation milk yield were high with DMY (+0.797), LL (+0.797) and MYCI (+0.876), moderate with CI (+0.399), PPHP (+0.205) and DP (-0.404) and low with AFS (-0.048) and AFC (-0.025). The moderate to high heritabilities for along with high genetic correlations among most of the milk yield traits emphasized continuation of selective breeding program for maximization of genetic improvement of this breed. The information generated in the present study may also be used in planning breeding program for other indigenous cattle germplasm of the country.

Key words : Cattle, Heritability, Correlation

Introduction

Bangladesh Livestock Research Institute Cattle Breed-1 (BCB-1) is a native cattle breed developed by Bangladesh Livestock Research Institute (BLRI), Savar, Dhaka. The BCB-1 is developed through selective breeding among indigenous cattle of Active Brahmaputra & Jamuna flood plain agro-ecological region (AEZ-14) of Bangladesh. In this region, an assorted type of cattle named 'Pabna' was evolved through admixture of Hariana, Tharparker and Sahiwal genetic materials. BLRI collected these cattle and conserved *Ex situ.* After that

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selective breeding program was undertaken with the goal of improvement of milk and meat production performance of the germplasm. Hence, the animals of the breeding herd were selected based on lactation yield and live weight over the last 14 years. Meanwhile, the physical appearance and production performance of the cattle is changed to a distinct feature than that of their progenitor. The weight of BCB-1 bulls ranged from 450 to 500kg and cows ranged from 250 to 350 kg at their mature age of 7 years. The cows of the breed produced 900-1000 liters milk in a lactation period of 240-260 days. The animals of the breed are red with a gradual shift to fawn or light brick at the ventral part of the body. The milk production level of the breed has yet to be maximized for profitable cattle farming.

The heritability and genetic correlation are two population parameters commonly used in planning genetic improvement program. These parameters are specific to breed or population and expressed the reliability of transferring genetic properties from parents to offspring. The genetic parameters are the measure of the individuals of a population and express the properties of that particular population (Aaron *et al*., 1987). In Bangladesh many researches have been carried out on phenotype of different cattle population but there are scanty in genetic information. Therefore, the present study was designed to estimate heritability and genetic correlation of economic traits of BCB-1 that will help in planning further genetic improvement program of the breed.

Materials and Methods

The present study was carried out at the BLRI Cattle Breed-1 Research Farm of BLRI to estimate variance components (additive genetic, common environment and residual) and half sib heritability of some economically important traits of the breed. Unknown parent groups represent the base population. Data recorded during 1992 to 2006 were included in this study. The seasons of the year were defined as the winter (October-January), the summer (February-May) and the monsoon (June-September). The recorded data were within 6 parities of cows belonging to five generations. The animals of this study were managed in semi-intensive system over the years and parities. The calves up to one year of age were fed and managed in groups conventionally under an open housing system. They were allowed to suck their dams for 15 to 20 minutes after hand milking both in the morning and afternoon with a little supplementation of concentrate feed. In addition to feeding green grass or silage, heifers and cows were allowed to pasture on naturally grown grasses for 4 to 5 hours a day and an amount of concentrate feed was supplied daily based on milk production. The urea and molasses impregnated rice straw were used as a basal feed in the absence of green grass or silage. The bulls were kept under stall-feeding system.

The variance and covariance components of each trait were estimated following residual maximum likelihood approach using variance component estimation program (Groeneveld, 1998). Heritability of age at first service and first calving were computed under following single trait animal model:

$$Y = X\beta + Zu + e$$

where, Y is the vector of observations, X and Z are known incidence matrices, β is a vector of fixed effects, u is a vector of random animal effects associated with the additive genetic merit of animal and e is random residual error term. The model includes season and year of birth, generation and additive genetic merit of each individual.

Estimates for daily milk yield (DMY), lactation milk yield (LMY), lactation length (LL), peak milk yield (PMY), days of peak milk yield (DPMY), milk yield per day of calving interval (MYCI), dry period (DP), service per conception (SPC), post partum heat period (PPHP) and calving interval (CI) were analyzed under a single trait repeatability model. The effect of season and year of birth, parity and generation were included in the analytical model as fixed effects and animal as random effect. The general model used to describe each trait was

$$Y = Xb + Za + Zp + e$$

where, Y is the vector of observations, X and Z are known incidence matrices, b is a vector of fixed effects, a is a vector of random animal effects associated with the additive genetic merit of animal, p is the vector of permanent environmental effect and e is the random residual error term. Co-variance components and genetic correlations among traits were estimated using two trait animal model having animals' additive genetic merit as only genetic term.

Results and Discussion

Heritability

The estimated variance components and heritability of different economic traits of BCB-1 are shown in Table 1.

Daily milk yield

The heritability estimate of DMY was low (0.257 ± 0.063). This estimate correspond to the heritability estimates reported by different researchers for different cattle population; 0.28 and 0.27 for Bangladeshi local and Red Sindhi, respectively (Hossain *et al.,* 2002), and 0.314 for Frisian × Sahiwal cows (Singh *et al*., 2003).

Lactation yield

Heritability estimate of LMY found in the present study are in agreement with the moderate to high estimates reported by others of different cattle population. The heritability estimates for LMY ranged from 0.28 to 0.49 in Holstein Friesian (Campos *et at.,* 1994), 0.26 to 0.83 in Jersey (Campos *et at.,* 1994; Deokar and Ulmek, 1988) or 0.27 to 0.40 in Sahiwal (Rege *et al.,* 1992). The high heritability estimate of the trait revealed that the continuation of selective breeding among high yielding animals of BCB-1 would lead to a higher LMY in subsequent generations.

Table 1. Variance components and heritabilities of production and reproduction traits of BCB-1

Traits	Variance components			Heritability
	Additive genetic	Common environmental	Residual	
Daily milk yield	0.16	0.1	0.36	0.257 ± 0.063
Lactation milk yield	31339	13066	33086	0.404 ± 0.087
Lactation le ngth	1299	168.38	2439	0.333 ± 0.059
Peak milk yield	0.58	0.34	0.80	0.335 ± 0.064
Days peak milk yield	33.65	3.06	174.96	0.159 ± 0.065
Dry period	613	31.91	11954	0.049 ± 0.054
Milk yield per day of calving interval	0.31	0.08	0.12	0.227 ± 0.065
Age at first service	17694	20542	17694	0.316 ± 0.074
Age at first calving	29587	13996	29587	0.404 ± 0.069
Post partum heat period	3105	341	1311	0.276 ± 0.070
Services per conception	0.06	0.06	0.06	0.073 ± 0.068
Calving interval	9312	293.46	3602	0.273 ± 0.071

Lactation length

Estimated moderate heritability (0.333) of LL of BCB-1 was within the range of reported estimates by other researchers. The reported values varied from 0.07 to 0.23 in Sahiwal (Yadev *et al.*, 1992; Hossain *et al.,* 2002;), 0.32 to 0.36 in Gir cows (Shaha and Khan, 1987; Bhadoria *et al*., 2004), 0.42 in Red Sindhi (Rao and Patro, 1984), 0.03 to 0.39 in Tharparkar (Sengar *et al.,* 1987) and 0.486 in Pabna cattle (Deb *et al*., 2004).

Peak milk yield and days to peak milk yield

Estimated heritability of PMY was 0.335 ± 0.065, which indicated that 33.5% of variation in peak milk yield was caused by heredity. Therefore, emphasis may be given in selection program for improvement of these traits. However, the heritability of DPMY was low in magnitude (0.159 ± 0.065). Therefore, emphasis should be given on proper management and nutritional status of the milking animals of the herd, because, the trait is linked with the LMY and LL of the animals.

Milk yield per day of calving interval

The MYCI is a function of total milk produced by a cow in lactation between two successive calving. The MYCI defines economic efficiency of milk yield of cows. The heritability of the trait was 0.227 ± 0.065, and it was found within the range of the estimate of Ageeb and Hayes (2000) in Sudanian Holstein-Friesian population (0.23 ± 0.23).

Dry period

The heritability estimate of dry period was very low (0.049 ± 0.054) in present study indicated that the trait was mostly governed by the management practices of the herd. Therefore, any improvement in the trait will depend on proper management of the individuals of the herd.

Age at first service

The heritability estimate of AFS was 0.316 ± 0.074, which was very close to the values of 0.11 to 0.42 reported by different researchers in different cattle population (Souza *et al.,* 1995; Lee *et al.,* 1995). Moderate heritability of present study implied that AFS may be shortening in subsequent generations following the selection of breeding animals based on their individual performances.

Age at first calving

The heritability of AFC of BCB-1 indicates that additive gene action was the major determinant of the trait. Therefore, the heifers delivered the first calf at an earlier age compared to others must be used as bull or dam mothers for the improvement of the trait. This is important because a shorter age of first calving results in a higher chance for harvesting of more calves and longer production lives.

Post partum heat period

The heritability of post partum heat period of BCB-1 was 0.276 ± 0.070, and this was in agreement with the value (0.29 ± 0.05) reported by Arai *et al. (*1976) in Japanese crossbred population. However, the present estimate was higher than that of Campos *et al* (1994) in US Friesian (0.05 ± 0.01) and Jersey (0.02 ± 0.02) population. The heritability of post partum heat period of BCB-1 found in the present study was lower than that reported by others (0.47 ± 0.10 in Bangladeshi Local, 0.40 ± 0.15 in Japanese Friesian crossbred, 0.55 ± 0.29 in Hariana-Sindhi crossbred in India and 0.56 ± 0.22 in Friesian-Jersey crossbred of tropical countries; Ghani and Rahman, 1954; Ito, 1966; Parmar *et al.,* 1997 and Tibbo *et al.,* 1994, respectively).

Services per conception

The heritability estimate of service per conception was very low (0.073 ± 0.068), and it was within the range of the estimates of Singh *et al.* (1997) in Indian Holstein population (0.06 ± 0.11), Menendez and Dempfle (1998) in Cuban Frisian crosses (0.03), Hayes *et al.* (1993) in Canadian Frisian crossbred population and Weller (1989) in Israelis Friesian population (0.03). However, some researchers reported higher estimates (0.18 ± 0.001 in

Frisian crosses by Al-Salman, 1985 and 0.18 ± 0.05 in Shahiwal crosses by Khan *et al.,* 1992) than that was found in the present study. The low estimate implied that genetics have negligible contribution to the expression of the trait, and the management practices followed in the herd dictated the trait. Therefore, care should be taken in estrus detection and timing of insemination, semen quality and nutritional status of the animal to improve the trait.

Calving interval

The heritability of calving interval found in the present estimate (0.273 ± 0.071) agreed with the value reported by Jain *et al.* (1995) in three-breed crossbred cows of India. The heritability of the trait in 3-breed crossbred population was 0.43 ± 0.32. However, it may vary from nearly zero (0.003 ± 0.07) to as high as 0.77 ± 0.03 (Sethi *et al.,* 1997; Iqbal, 2005 and Singh *et al*., 2003). Therefore, the cows with a shorter calving interval should be selected to produce replacement stocks to have more productive future generations.

Genetic correlations

Genetic correlations between and among the studied traits are shown in Table 2. The LMY was correlated at a higher magnitude with DMY (0.797), LL (0.797) and MYCI (0.876), in moderate with CI (0.399), PPHP (0.205) and DP (-0.404), and low with AFS (-0.048) and AFC (-0.025). The genetic correlation between LMY and LL found in the present study was within the range reported by different authors in different cattle population. The genetic correlation between LMY and LL varied from 0.126 ± 0.06 (Katoch and Yadav, 1990) to 0.89 ± 0.07 (Roy and Katpatal, 1988) in Jersey cattle population. The genetic correlation between LMY and CI varied from 0.06 ± 0.29 in Holstein to 0.33 ± 0.30 in Karan Swiss cows (Lara *et al*., 1989; Roy and Katpatal, 1988).

Table 2. Additive genetic correlation among different quantitative traits of BCB-1

Parameters	DMY	LMY	LL	DP	AFS	PPHP
LMY	0.797	-	-	-	-	-
LL	0.067	0.797	-	-	-	-
DP	-	-0.404	-0.580	-	-	-
AFS	-	-0.048	-	-	-	-
AFC	-	-0.025	-	-	0.867	-
MYCI	-	0.876	0.316	-0.480	-	-
CI	-	0.399	0.560	0.356	-	0.250
PPHP	-	0.205	0.321	0.149	-	-

DMY: daily milk yield; LMY: lactation milk yield; LL: lactation length; DP: dry period; AFS: age at first service; AFC: age at first calving; MYCI: milk yield per day of calving interval; CI: calving interval and PPHP: postpartum heat period

The genetic correlations of DMY and DP with LL were 0.067 and -0.580, respectively. However, MYCI, PPHP and CI were genetically positively correlated with LL (0.316, 0.321 and 0.560, respectively) at a medium to high magnitude. On the other hand, MYCI, CI and PPHP were weakly correlated with DP (Table 2). Moreover, genetic correlation between PPHP and CI was positive (0.250).

Conclusion

It may be stated that the present estimates of heritability and genetic correlation of different economically important traits of BCB-1 are within the normal range reported by others in different cattle population. However, the variations so far observed may be due to sample sizes, analytical models and environmental and production management systems. However, the information of present study may be used in planning future breeding activities for further improvement of the breed as well as other indigenous cattle genotypes of the country.

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