Study on genetic gains and karyotype of Red Chittagong cattle in Bangladesh

Md. Kabirul Islam Khan[1*], Khan Shahidul Huque[3], Gous Miah[1] and Mrs. Jannatara Khatun[2]

[1]Department of Genetics and Animal Breeding, [2]Department of Animal Science and Nutrition, Chittagong Veterinary and Animal Sciences University, Khulshi, Chittagong-4225, Bangladesh
Bangladesh Livestock Research Institute, Savar, Dhaka-1341, Bangladesh

Abstract

The study was undertaken on the Red Chittagong Cow (RCC) community farms of five Upazilla (sub-district) at Chittagong area of Bangladesh from July 2010 to June 2011 to estimate the genetic progress of RCC, local and crossbred (Holstein × Local) cows and to study the karyotype of RCC. The genetic progress per generation of individual trait of the objective in the index for RCC, Local and Holstein × Local were estimated through deterministic approach and it was indicated that RCC showed higher gains than local cows. The rate of higher genetic gains for the individual trait indicated that these traits are responsible in effective selection programme for their improvement. For karyotyping of RCC, 100 blood samples from the RC cows were collected in heparinised vacutainers from jugular venupuncture. The blood samples were cultured using standard protocols and metaphase slides were prepared and observed under microscope. The diploid chromosome complement, 58+2 (XX or XY) was observed of RCC. On the basis of the position of the centromare acrocentric chromosome was highest (42%) than telocentric and metacentric chromosome and the telocentric chromosome was lowest (17%).

Keywords: Cattle; genetic gain; karyotype and metaphase stage

Introduction

For a successful genetic improvement programme the incorporation of normal and sound animal is essential. The genetic abnormality can be identified through the observation of phenotypes and also by genetic study. However, the genetic study is more reliable, it can be conducted through karyotyping by means of chromosomal study in the cell. There is an enormous diversity in chromosome number and structure (keryotype) leads the abnormal animal (Ahmed and Khan, 2007). Genetic abnormalities are not very common in cattle. About one third of the total calves die due to various reasons, among these a significant number die from different disorder. A slight slip in chromosome number or structure brings obvious disorder though out the life, it may leads to death. Karyotype analysis is an effective way for identification of this disorder of chromosome. Generally cattle karyotype presents 60 chromosomes (2n=60), of which

58 are autosomes and 2 are sex chromosome: XX in a female subject and XY in a male subject (Melander, 1959; Khatun et al., 2011). Abnormal chromosomes can be arisen from error in chromosome replication, fertilization or early cleavage divisions of the fertilized egg. The most important effect of abnormal karyotype is their contribution to lowered reproductive performance through decreasing ability or complete failure to produce functional gametes or death of embryos. Identification of genetic disorder or unique character the karyotyping study is the initial stage. If genetic disorders are properly identified, application of possible remedy may protect the loss of cattle, which in turn increases the total productivity.

The genetic gain for economic traits leads to the total dairy farm income. More rapid genetic gains are possible if superior sires are selected and keep for breeding purpose. The sire can be selected on the basis of their dams and/or progeny performance. The genetic evaluation studies have been used to the selection of

Corresponding author: Md. Kabirul Islam Khan, Department of Genetics and Animal Breeding, Chittagong Veterinary and Animal Sciences University, Khulshi, Chittagong-4225, Bangladesh

sires and elite cows for the genetic improvement of dairy cattle.

The Red Chittagong Cattle Conservation and Genetic Improvement Project in the Chittagong area launched the RCC genetic improvement programme. In order to support the effective genetic improvement programme in future for this genotype, the current study was undertaken with the objectives (i) to estimate the per generation genetic progress of Red Chittagong cow (RCC), local and crossbred (Holstein × Local) cows; and (ii) to investigate the karyotype of RCC.

Materials and Methods

The individual cow's productive and reproductive traits data of RCC, local and crossbred (Holstein-Friesian × RCC) were collected from July 2010 to June 2011 with a designed record sheet from the selected RCC community farms of five Upazila's (Sub-district) namely, Satkania, Chadranaish, Anowara, Rowzan and Potia at Chittagong region of Bangladesh. From the recorded data, the average and the standard error of different traits of all the three genotypes were estimated using a mixed model equation through PROC GLM and PROC MIXED of SAS (SAS, 2000) and the mean differences were compared using the least significant difference (LSD) test (Steel et al., 1997).

Estimation of genetic gain

The expected genetic gain per generation in the individual traits (k) of the objective in the index can be estimated as:

$$\Delta G_T = i\beta_{TI}\sigma_I = ir_{TI}\sigma_T$$

A similar form can be used to obtain the rate of genetic gain for the individual trait:

$$\Delta G_K = i\beta_{KI}\sigma_I = ir_{KI}\sigma_{GK}$$

$$r_{KI} = Cov(G_K, I)/(\sigma_{GK}\sigma_I)$$

Therefore, $\Delta G_K = iCov(G_K, I)/\sigma_I$ where,

i = selection intensity

σ_I = standard deviation of the index and

$Cov(G_K, I)$ is the covariance of the kth trait and the index.

The required heritabilities for the individual traits in the breeding objectives are shown in Table 1.

Karyotyping of RCC

For investigating the RCC karyotype a total of 100 blood samples were collected by heparinised vacutainers through jugular venepuncture from the RCC cows. The blood samples were immediately transported in a flask maintained at 4ºC to the Genetics Laboratory at Chittagong Veterinary and Animal Sciences University. Then the supernatant were separated from the whole blood sample contains the White blood cell (WBC). The samples were cultured

using standard protocols (Ahmed et al., 2011; Ansari et al., 1999). The culture medium, RPMI-1640 with fetal calf serum, phytohema-glutinin and penicillin/ streptomycin was used in this study.

**Table 1: The heritabilities of different milk production traits for different genotypes**

Traits	Genotypes		
	RCC[1,2]	Local[1]	Holstein × Local[1]
Birth weight	0.49	0.34	0.40
Liveweight	0.54	0.49	0.52
Calving interval	0.05	0.05	0.05
Lactation length	0.35	0.40	0.40
Lactation milk yield	0.28	0.27	0.32

[1]Khan et al. (2010) and [2]Bhuiyan et al. (2008)
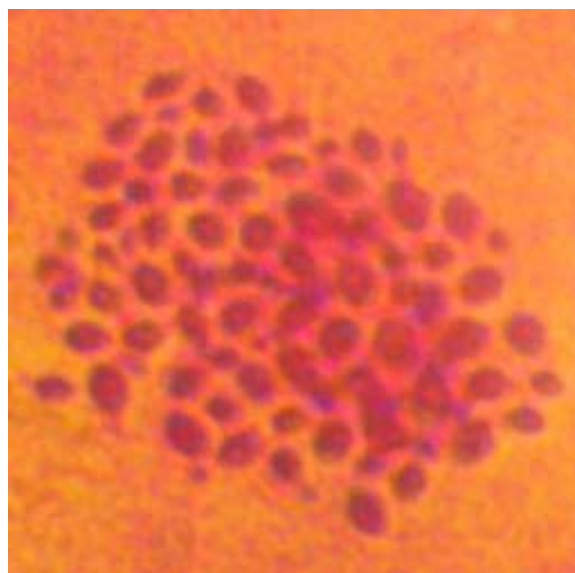
Picture 1: Metaphase chromosome spread of RCC

The culture was incubated for 72 hour at 37ºC in an incubator. In order to have a good quality metaphase cells, 2 replicates from each animal were done. At the completion of a 72 hour incubation period the culture was treated with 100 μL of colcemid and was mixed gently. The cultures were then incubated at 37ºC for 20 minutes and centrifuged at 1000 rpm for 10 minutes then the supernatant was removed, and the cells were suspended in 6-7 mL of 0.075 M KCl solution. The cultures were incubated for another 15-20 minutes and then again centrifuged at 1000 rpm for 10 minutes. The supernatant was removed just above the buffy coat, and the cultures were gently mixed. For fixing the cell a fixative (3:1 mixture of methanol and glacial acetic acid at -20ºC) were used. At least 3 times the fixatives were runs then the slide was allowed for an air drying. Each slide was then examined by phase contrast microscope connecting with a computer for the good quality metaphase spread.
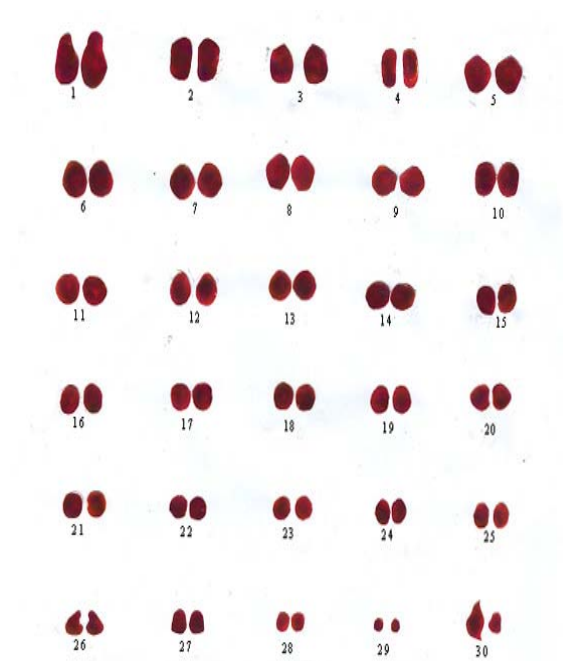
Picture 2: Karyotype of Red Chittagong Cows

Results and Discussion

Productive and reproductive traits of different genotypes

The mean and standard error of different productive and reproductive traits of different genotypes under five different Upazilla's are shown in Table 2. From Table 2, it can be seen that the Holstein × Local genotype showed superior performance than RCC and Local genotypes. Similar findings were reported elsewhere (Bhuiyan et al. 1998; Khan and Khatun, 1998). However, the lactation number showed that the RCC produced more calves than Local and Holstein × Local genotypes. Many findings (Syrstad, 1989; Madalena et al., 1990; Khan et al., 2005) from other tropical countries including Bangladesh study have shown that the first cross of temperate breeds with tropical breeds produce more milk than pure breeds in a tropical environment.

Genetic gains/progress

The genetic gains/progress (ΔG) per generation of individual trait of the objective in the index of RCC, Local and Holstein × Local in five different Upazilla's were estimated through deterministic approach and are presented in Table 3. Table 3 indicated that the genetic gains for all the traits were positive and Holstein × Local genotype showed higher gains than Local cows. However, RCC showed intermediate gains/progress per generation. The rate of genetic gains for the individual trait indicated that these traits are responsive in effective selection programme for their improvement.

Table 2: The values of different traits under five different Upazila for RCC, Local and Holstein × Local genotypes

Variables	Genotypes		
	RCC	Local	Holstein × Local
Birth weight (kg)	$16^a \pm 0.24$	$15^a \pm 0.33$	$18^b \pm 1.17$
Mature liveweight (kg)	$178^b \pm 2.03$	$160^a \pm 4.21$	$293^c \pm 8.81$
Lactation length (days)	265 ± 3.44	258 ± 7.03	272 ± 6.65
Milk production	$663^b \pm 7.77$	$461^a \pm 8.72$	$1058^c \pm 12.11$
Calving interval (days)	$466^a \pm 4.52$	$532^c \pm 4.33$	$490^b \pm 4.47$
Lactation number	$3.7^b \pm 0.18$	$1.8^a \pm 0.28$	$2.6^b \pm 0.82$
Age of the cow	6 ± 0.22	5.8 ± 0.54	5.8 ± 0.59

Means with different superscripts are different at P<0.05 between breeds

Table 3: Genetic gain (ΔG) per generation of individual traits (US$) for different genotypes of cattle

Variables	Genotypes		
	RCC	Local	Holstein × Local
Milk yield	15.55 ± 0.46^b	8.12 ± 0.63^a	19.72 ± 1.54^c
Lactation length	0.003 ± 0.18	0.35 ± 0.35	-0.05 ± 0.20
Calving interval	0.14 ± 0.07^b	0.06 ± 0.04^b	-0.02 ± 0.03^a
Liveweight	1.25 ± 1.74	0.52 ± 0.49	2.19 ± 1.96
Birth weight	0.008 ± 0.00	0.006 ± 0.00	0.007 ± 0.003

Means with different superscripts are different at P<0.05 between breeds

The rate of genetic progress was positive and differed with the breed differences. This was due to the breed effects as well as the differences of yield between individuals. Khan (2009) observed similar genetic gains for milk yield under Bangladeshi conditions but Sorensen et al. (2006) observed the lower genetic progress for milk yield from individual cows than the present study.

Karyotyping of RCC

Each metaphase cell was examined at 100x magnification under oil immersion and the observed field was photographed by a computer. A normal metaphase chromosome was spread and is shown in Picture 1. The chromosome pair was aligned in rows according to shape and size and the position of the centromere and the diploid chromosome complement was 58+2 (XX or XY) is presented in Picture 2.

From the Picture 2, it can be seen that in the RCC karyotype presents 60 chromosomes (2n=60), of which 58 are autosomes and 2 are sex chromosome: XX in a female subject and XY in a male subject, which are similar with other research (Melander, 1959; Khatun et al., 2011).

The numbers of chromosome of RCC according to the position of the centromere are shown in table 4. From this table it can be seen that on the basis of the position of the centromare acrocentric chromosome was highest and about 42% and telocentric chromosome was lowest about 17%. The similar percentages of

chromosome in bovine karyotype were detected by other researchers (Ahmed et al., 2011; Khatun et al., 2011).

Table 4: Average ± SE of different type's chromosome according to centromere position

Chromosome	Number of chromosome in metaphase spread	Percentage
Normal animals karyotype		
Acrocentric	25 ± 1.34	41.66
Metacentric	23 ± 0.78	38.33
Telocentric	10 ± 1.10	16.67
Sex chromosome	2 ± 0.87	3.33

From this study, it reveals that the Holstein × Local genotype have superior for all traits than RCC and Local. However, Holstein × Local cow's lactation number is lower than RCC under Bangladesh condition. The RCC gives birth regularly that is one calf in a year. Therefore, lifetime performance of RCC would be better than Local and Crossbred (Holstein × Local). The rate of genetic gains indicated that the achievements of milk can be obtained per generation and which is good indication for selection. The abnormal cows can be identified through karyotyping. However, for making final comments more research is needed on the identification of genetic abnormalities on the RCC population.

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