



SHORT COMMUNICATION

Estimates of Genetic Parameters of Production Traits for Khuzestan Buffaloes of Iran using Repeated-Records Animal Model

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ARTICLE HISTORY

Received: November 09, 2011

Revised: December 25, 2011

Accepted: January 03, 2012

Key words:

Animal model

Buffalo

Heritability

Repeatability

ABSTRACT

Buffalo milk yield records were obtained from monthly records of the Animal Breeding Organization of Iran from 1992 to 2009 in 33 herds raised in the Khuzestan province. Variance components, heritability and repeatability were estimated for milk yield, fat yield, fat percentage, protein yield and protein percentage. These estimates were carried out through single trait animal model using DFREML program. Herd-year-season was considered as fixed effect in the model. For milk production traits, age at calving was fitted as a covariate. The additive genetic and permanent environmental effects were also included in the model. The mean values (\pm SD) for milk yield, fat yield, fat percentage, protein yield and protein percentage were 2285.08 \pm 762.47 kg, 144.35 \pm 54.86 kg, 6.25 \pm 0.90%, 97.30 \pm 26.73 kg and 4.19 \pm 0.27%, respectively. The heritability (\pm SE) of milk yield, fat yield, fat percentage, protein yield and protein percentage were 0.093 \pm 0.08, 0.054 \pm 0.06, 0.043 \pm 0.05, 0.093 \pm 0.16 and zero, respectively. These estimates for repeatability were 0.272, 0.132, 0.043, 0.674 and 0.0002, respectively. Lower values of genetic parameter estimates require more data and reliable pedigree records.

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To Cite This Article: Baharizadeh M, 2012. Estimates of genetic parameters of production traits for Khuzestan buffaloes of Iran using repeated-records animal model. *Pak Vet J*, 32(4): 618-620.

INTRODUCTION

The world population of domestic buffalo, *Bubalus bubalis*, is estimated about 180.70 million. Of these, 96.4% are in Asia and 74.81% are in south west Asia (Anonymous, 2010). Two main types of domestic buffalo are the river buffalo and the swamp buffalo. Iranian buffaloes have also some similarity to Iraqi buffaloes. All of the Iranian buffaloes are riverine. Water buffaloes have an effective and important role in the economy of rural families in the areas where they are bred due to their abilities for production of milk, meat and draft power. The value of multiparous water buffaloes in Iran is nearly equal to a pure Holstein cow. More than 75% of these buffaloes are milch type. It has been estimated that 16% of the Iranian buffaloes are slaughtered for meat production. The water buffalo in Iran will remain a considerable component of the animal farming, contributing to sustainable agriculture system and rural development for many decades to come (Naserian and Saremi, 2007).

In Iran, there are few studies on genetic potential of buffaloes as compared to cattle. Most genetic analyses of

productive traits in buffaloes have been conducted in India and Pakistan. In spite of implementation of recording and breeding scheme in 1993 by the Animal Breeding Organization of Iran, no within- or across-herd genetic evaluation programs have been carried out on these animals. The main problem associated with the use of genetic evaluation is lack of knowledge of the genetic parameters for economically important traits. In literature, the estimates of these parameters for various traits are different. For example, the heritability and repeatability estimations for milk yield varied from 0.05 to 0.25 and 0.07 to 0.38, respectively in Egyptian buffaloes under different production systems (Abdel-Salam *et al.*, 2009).

Due to different methods, populations, seasons and regions, the heritability and repeatability values vary considerably. Estimation of genetic parameters is necessary to monitor and evaluate selection programs. The present investigation has been undertaken to estimate the genetic parameters for milk yield, fat yield, fat percentage, protein yield and protein percentage in buffaloes from the Khuzestan province of Iran.

MATERIALS AND METHODS

Data on 4248 Khuzestan buffaloes, collected by Animal Breeding Organization from 1992 to 2009, were used to estimate variance components, heritability and repeatability, for milk yield, fat yield, fat percentage, protein yield and protein percentage. All traits were analyzed using the same animal model. The model included the fixed effect of herd-year-season; the age at calving was taken as covariate for all traits. The additive genetic and permanent environmental effects were also included in the model. History sheets of individual buffalo, milk recording registers and breeding registers were scrutinized and requisite information was obtained. The following data were collected from the records: identification number of each animal, date of birth, date of calving, lactation milk yield, herd and sire. In addition to morning and evening milk yield, milk yield, protein & fat yield, fat and protein percentages were recorded monthly. Only normal and complete records of the buffaloes were included in the analysis. Incomplete lactations showing any abnormality were not used. The animals with lactation length less than 60 days and calving interval shorter than 300 days or longer than 800 days were excluded.

Statistical analysis: The statistical model in matrix notation can be expressed as:

$$Y = Xb + Za + Wpe + e \quad \text{Where:}$$

Y= Vector of observations for each trait

X= The matrix that associates b with y

b = Vector for fixed effect

Z = The matrix that associates a with y

a = The vector for direct additive genetic effect

W = The matrix that associates pe with y

pe = Vector of permanent environmental effect

e = Vector of residual error terms

Variance components were estimated for each trait using Restricted Maximum Likelihood procedures via a derivative-free algorithm using the repeated-record animal model by DFREML method, using REML 3.1 (Meyer, 2000). Heritability and repeatability estimates were obtained by uni-trait analysis.

RESULTS

The mean values and standard deviation for milk yield, fat yield, fat percentage, protein yield and protein percentage were 2285.08±762.47 kg, 144.35±54.86 kg, 6.25±0.90%, 97.30±26.73 kg and 4.19±0.27%, respectively (Table 1).

Estimates of variance components, heritability and repeatability for milk yield, fat yield, fat percentage, protein yield and protein percentage are shown in Table 2. The heritability and standard errors of milk yield, fat yield, fat percentage, protein yield, protein percentage, were 0.093±0.08, 0.054±0.06, 0.043±0.05, 0.093±0.16 and zero, respectively. These estimates for repeatability were 0.272, 0.132, 0.043, 0.674 and 0.0002, respectively.

DISCUSSION

All estimates of genetic parameters seem to be low, especially if compared to estimates from similar analysis for dairy cattle. Buffaloes have not been intensively selected in the past, so greater genetic variability among animals would be expected. Some possible causes of low estimates of genetic parameters might be the non-genetic effects, limitation of the size of data set, the state of nutrition and other managerial conditions. The model can only partially account for management variability. The variation in production can be assigned mainly to environmental effects causing low heritability estimates. Though editing on data was done before the analysis to exclude cows without information about sire and dam, some wrong genealogy may be present. Misleading paternity identification with the animal model would result in assigning part of the genetic variability to environmental effects and would reduce the estimate of heritability for direct genetic effects. The low estimate of heritability for all traits indicated that progress due to selection might be slow if traditional selection is used to improve quantity and quality of milk yield. Better identification will improve the genetic parameters of the population. Alternative selection schemes to overcome the problem of misleading genealogies may need to be further developed.

Table 1: Data structure used in the analysis and means observed for milk yield, fat yield, fat percentage, protein yield and protein percentage

Traits	Milk yield (kg)	Fat		Protein	
		Yield (kg)	Percentage	Yield (kg)	Percentage
Records	4248	3659	3659	1527	1527
Animals	1439	1434	1434	1129	1129
Sires	67	67	67	50	50
Dams	166	166	166	103	103
Mean±SD	2285.08±762.47	144.35±54.86	6.25±0.90	97.30±26.73	4.19±0.27

Table 2: Estimation of variance components, and genetic and phenotypic parameters for milk yield, fat yield, fat percentage, protein yield and protein percentage

Parameters/Traits	Milk	Fat		Protein	
	yield (kg)	Yield (kg)	Percentage	Yield (kg)	Percentage
σ_a^2	24389.81	71.707	0.01586	34.50	0.000
σ_{pe}^2	47212.43	104.197	0.000	215.077	0.000
σ_e^2	191438.30	1153.556	0.350	120.486	0.027
σ_p^2	263040.54	1329.460	0.366	370.063	0.027
$h^2 \pm SE$	0.093±0.08	0.054±0.06	0.043±0.05	0.093±0.16	0.000
R	0.272	0.132	0.043	0.674	0.0002

σ_a^2 , additive genetic variance; σ_{pe}^2 , permanent environmental variance; σ_e^2 , error variance; σ_p^2 , phenotypic variance; Pe^2 , permanent environmental effects; h^2 , heritability; R, repeatability.

Results of the present study are in agreement with the findings reported by Farhangfar *et al.* (2005) and Morammazi *et al.* (2007). Farhangfar *et al.* (2005) showed that heritability and repeatability estimates of milk yield were 0.071 and 0.075 for Khuzestan buffaloes of Iran. In the other study on the same breed, heritability estimates of milk yield, fat yield and fat percentage were 0.077, 0.056 and 0.030, respectively. In the same study repeatability for milk yield, fat yield and fat percentage were 0.217, 0.184 and 0.030, respectively (Morammazi *et al.*, 2007). These results were lower than the estimates reported by other authors. For example, Aspigueta-Borquis *et al.* (2010) showed heritability for milk yield, fat yield, fat percentage, protein yield and protein percentage as 0.22, 0.21, 0.33, 0.23 and 0.39, respectively. Tonhati *et al.* (2010) reported that heritability estimates for milk yield, fat percentage and protein percentage were 0.25, 0.30 and 0.48 respectively, in dairy buffaloes in Brazil. Nazari *et al.* (2010) showed heritability in Khuzestan buffaloes for milk yield, fat yield and fat percentage as 0.22, 0.18 and 0.13, respectively. These estimates for repeatability were 0.55, 0.41 and 0.39, respectively. Barbas *et al.* (2010) found that heritability and repeatability estimates for milk yield in Murrah buffaloes were 0.39 and 0.46, respectively. These differences may be attributed to the different breeds, structure of the data, models and methods of analysis.

Conclusion: Estimates of heritability and repeatability obtained from the present study were generally not consistent. These estimates for all traits were low and therefore further analyses are needed through the collection of more data and providing adequate linkages across herds to make firm conclusions.

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