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Investigation of the Genetic and Phenotypic Potential of Productive Traits Using the Uni and Multiple Traits Animal Model in River Buffalo

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Abstract: The main objective of this study was to estimate genetic and phenotypic potential of milk yield, fat yield and fat percentage traits. Data analyzed were 3350 records from buffalo during 1989-2008 were collected. Co-variance components were estimated using uni and multiple traits of animal model with the Restricted Maximum Likelihood method. In this method with constant effects of season-city-year and lactation period and additive genetic was taking as Random effect. The mean and standard deviation for milk yield, fat yield and fat percentage were 964.14±18.28, 52.35±1.88 and 5.58±0.03, respectively. The heritability of milk yield, fat yield and fat percentage were 0.22, 0.18 and 0.13, respectively using univariate model. The repeatability of milk yield, fat yield and fat percentage were 0.55, 0.41 and 0.39, respectively using univariate model. The genetic and phenotypic correlation between milk yield-fat percentage, milk yield-fat yield, fat yield-fat percentage was -0.25 and -0.30, 0.75 and 0.25, 0.29 and 0.41, respectively. The heritability for milk yield trait was moderate, so selection on the basis of this trait may cause a desirable genetic gain.

Key words: Genetic and phenotypic potential, productive traits, buffalo, animal model, univariate model, milk yield

INTRODUCTION

The world population of domestic buffaloes, *Bubalus bubalis* is estimated to be >150 million (Bhat, 1992). Two main types of domestic buffalo are the river buffalo and the swamp buffalo. River buffalo live in a geographical belt from India in the east to Italy in the west, passing through Pakistan, Iran, Turkmenistan, Iraq, Syria, Egypt, Azerbaijan, Turkey, Greece, Bulgaria and the former Yugoslavia. The river buffalo is mainly reared for milk production. Murrah in India, Nili Ravi and Kundi in Pakistan, Beheri and Saidiin Egypt and Italian and Shumen in Europe are well known types of river buffalo. About half of the world's buffalo population lives in India. Swamp buffaloes are reared for draught and for meat. Because buffaloes are able to stay in water when temperature is high, they are more adapted to hot and humid climates than many breeds.

Buffalo is one of economic domestic animal in Iran. There are >465000 individuals in Iran from them, 114335 individuals are in Khouzestan Province. Despite the fact that buffalo breeding is an important source of income in the north, north-west and south area of Iran, specially in Khouzestan Province, there are few studies in genetic and phenotypic potential buffaloes in Iran but there are many studies of cattle in some areas of Iran. Most genetic analyses of productive traits of buffaloes have been conducted in India and Pakistan. Significant effects of parity order for milk yield were found by Arona *et al.* (1962). Milk yield was also reported to increase from 1-6th parity (Sane *et al.*, 1972). Another study showed an increase in milk yield from the first to a peak in the fourth lactation (Patro and Bhat, 1979) and that milk yield even in the ninthe lactation is relatively close to peak production. Significant effects of year and season of milk yield have been reported (Patro and Bhat, 1979; Reddy and Taneja, 1984; Mahdy *et al.*, 1999). Heritability estimates for the Indian population of buffaloes for first lactation milk yield have ranged from 0.08-0.65 (Bhat, 1992).

In an Egyptian experiment heritability estimates ranged from 0.03±0.08-0.20±0.13 for total milk yield in parities 1-5 and repeatability across parities was 0.50±0.03. The estimated heritability across parities for total milk yield was 0.11±0.05 (Mourad and Mohamed, 1995). Milk produced by buffalo cows is usually rich in fat (Table 1). Buffalo milk is richer in fat percentages than dairy cattle. Singh *et al.* (1979) found fat percentage was influenced by year and season while the effect of parity was not found

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Table 1: Summary of production for records in the analyses

Parameters	Average±SD	Min.	Max.	Records
Milk yield (kg)	964.14±18.28	900	1045.0	3350
Fat yield (kg)	52.35±1.88	44	65.0	3350
Fat (%)	5.58±0.03	5	6.3	3350

to be significant. In the same analysis repeatability estimates were 0.71 for fat and 0.74 for protein percentages. Phenotypic correlations among all constituents (fat, protein, lactose, ash) were positive, ranging from 0.28-0.97. Negative estimates were found for phenotypic correlations between milk yield and all percentage components while estimates of phenotypic correlation were positive between all component yields and milk yield.

Estamation of genetic and phenotypic potential of milk yield, fat yield and fat percentage traits is necessary to monitor and evaluate selection programs. Evaluation of important traits other than milk yield should provide buffalo producers with more useful information upon which to base their genetic decisions (Mahoney *et al*., 1986). The objective of this study was to estimate genetic and phenotypic parameters of milk yield, fat yield and fat percentage traits.

MATERIALS AND METHODS

Records of buffaloes milk yield were obtained from monthly test day from 1989-2008 in Khouzestan Province. No records after the twelfth parity were considered. Only 3,350 records were usable after editing. Milk yield, fat yield and fat percentage were measured monthly. All traits were analyzed using the same animal model.

In this method with fixed effects of season-city-year and lactation period and additive genetic was taking as Random effect. Animal genetic and permanent environmental random effects were associated with cows. The statistical model in matrix notation can be expressed as:

$$Y = Xb + Zu + Wp + e$$

Where:

- Y = Vector of one of the traits with repeated records
- X = The matrix that associates b with y
- b = Vector of fixed effects
- Z = The matrix that associates u with y
- u = The vector of breeding values for direct genetic effects with numerator relationship matrix, A
- W = The matrix that associates p with y
- p = The vector of permanent environmental effects of the cows
- e = The vector of residual temporary environmental effects not explained by other parts of the model

Variance and covariance components were estimated by the multiple-trait Derivative-Free Restricted Maximum Likelihood method (DFREML) using the REML 3.1 program (Meyer, 1995). Heritabilities and repeatability were obtained by uni-trait analyses and the genetic and phenotypic correlation between milk yield-fat percentage, milk yield-fat yield, fat yield-fat percentage were obtained by multiple-trait analyses. For the 6 traits analyzed the multiple-trait animal model was an expansion of the single-trait model. The covariances parameters were estimate from bivariate analyses of pairs of traits.

RESULTS AND DISCUSSION

The mean and standard deviation for milk yield, fat yield and fat percentage were: 964.14±18.28, 52.35±1.88 and 5.58±0.03, respectively (Table 1). Effects of season-city-year of milk yield, fat yield and fat percentage were significant ($p<0.05$). These results were similar as the values reported in the literature (Patro and Bhat, 1979; Reddy and Taneja, 1984; Mahdy *et al*., 1999). Variance components and heritability estimates obtained by uni-trait analyses are shown in Table 2.

All estimates of genetic parameters seem to below, especially if compared to estimates from similar analyses 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 can be addressed. There is traditionally considerable variability in management both among and inside herds. The model can only partially account for management variability. The variation in production can be assigned mainly to environmental effects causing low heritability estimates. The low estimate of heritability for all traits indicates that progress due to selection might be slow if traditional selection schemes are used to improve quantity and quality of milk. Better identification will improve the genetic trend of the population.

Estimates of genetic, phenotypic and residual correlations are shown in Table 3 and 4. Estimates of genetic correlations between traits are similar to those that can be found in the literature for dairy cattle.

The genetic, residual and phenotypic correlations were similar as the values reported in the literature (Rosati and Van Vleck, 2002).

Large estimates for genetic correlations between milk and fat yields are commonly reported for dairy cattle (Barker and Robertson, 1966). The ssmall negative genetic correlations between milk yield and fat percentages indicate that milk yield can be increased through selection without large decreases in quality of milk. A selection goal for the buffalo population is production of milk. The

Table 2: Estimates of variance components and genetic parameters

Varience of components	Milk yield (kg)	Fat yield (kg)	Fat (%)
σ_u^2	7303.40	42.35	0.15
σ_p^2	32217.80	233.20	1.10
σ_e^2	24914.40	190.85	0.88
σ_{pe}^2	10416.39	53.26	0.27
σ_{te}^2	14498.10	137.59	0.61
h^2	0.22	0.18	0.13
r	0.55	0.41	0.39

σ_u^2: variance due to additive genetic effects; σ_p^2: total phenotypic variance; σ_e^2: total residual variance; h^2: heritability of genetic effects; σ_{pe}^2,: variance due to permanent environmental effects; σ_{te}^2: temporary environmental effects; r: repeatability

Table 3: Estimates of genetic correlations among traits

Parameters	Milk yield (kg)	Fat yield (kg)	Fat (%)
Milk yield (kg)	-	0.75	-0.25
Fat yield (kg)	-	-	0.39
Fat (%)	-	-	-

Table 4: Estimation of phenotypic (above diagonal) and residual correlations (below diagonal) among traits

Parameters	Milk yield (kg)	Fat yield (kg)	Fat (%)
Milk yield (kg)	-	0.86	-0.48
Fat yield (kg)	0.65	-	-0.31
Fat (%)	-0.20	0.28	-

objective of selection can be reached by increasing the production of milk with optimum percentages of fat to be processed to make cheese.

CONCLUSION

Milk yield estimated from observations on other traits can be used as a selection criterion to improve overall economic return. Relatively small estimates of genetic variance were found for all traits analyzed, resulting in low heritability estimates. Small estimates might be due to inaccurate identification of true paternity. Utilization of artificial insemination needs to be increased in order to increase genetic exchange among herds and to increase rate of genetic improvement. Consideration should be given to further study of the fraction of incorrect parental identification. Improvement in identification of parents might be a cost-effective way to increase heritability and to increase the rate of genetic improvement. Then, it seems new strategies for selection may need to be found in order to improve buffalo for milk production more rapidly than with traditional means.

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