

Estimates of genetic parameters for economic traits in dairy buffalo

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ABSTRACT: This study aims to verify the existence of genetic variation in economic traits of dairy buffalo in Brazil. Variance components were estimated by restricted maximum likelihood method. Heritability estimates for milk yield (MY); fat, protein, lactose and total solids percentages; somatic cell count, lactation length and calving interval were 0.31, 0.28, 0.38, 0.23, 0.36, 0.20, 0.08 and 0.19, respectively. Genetic correlations between MY and the other traits were -0.26, -0.25, 0.11, -0.21, -0.14, 0.78 and -0.09, respectively. The results show that most traits, except for lactation length, display enough additive genetic variability to respond to a breeding program. Furthermore, applying simultaneous selection for MY may result in undesirable impact on milk constituents.

Keywords: buffaloes; genetic correlation; heritability; Milk yield

Introduction

The worldwide buffalo population is estimated at approximately 195 million, mostly located in Asia. In Brazil, there are about 1 million 200 thousand buffaloes (FAO, 2011). Buffaloes are an important species from a socioeconomic viewpoint, especially in developing countries, for their meat, milk and working ability. Furthermore, buffaloes have become a good economic option worldwide due to dairy production and preparation of *mozzarella* cheese (Tonhati et al. 2000a).

Buffalo milk is characterized by high fat, protein and total solids contents, thus reaching high yields in dairy products manufacturing and high revenues for the producers. However, selection for increased milk production causes milk quality and livestock reproductive efficiency to decrease. According to Malhado et al. (2009), older age at first calving in the tropics is one of the factors that has a negative impact on buffalo dairy farms since this trait is indicative of sexual precocity and life potential of the female herd.

Knowing heritability, as well as genetic and phenotypic correlations of economic traits is necessary for planning and choosing the proper techniques for genetic improvement of buffaloes. In Brazil, this information is still scarce (Tonhati et al. 2000b). This study aims at determining the genetic variation of productive and reproductive traits that can be used for breeding selection in order to improve the buffalo population in Brazil.

Materials and methods

This study analyzes the traits: milk yield at 270 days (MY); percentages of fat (%F), protein (%P), lactose (%L), total solids (%TS); somatic cell count (SCC); lactation length (LL); and, age at first calving (AFC). The data used in the study were from 2,531 first lactation Murrah buffaloes, between 24 and 48 months old, daughters of 203 sires, belonging to 12 herds in São Paulo state and calving between 2005 and 2013. Milk yield was obtained from the 5th day while the first control was considered up to the 45th day after calving. The contemporary groups, which should contain at least three animals, were grouped according to herd, birth year and season for the AFC trait, and herd, calving year and season for all other traits. A pedigree dataset with 10,088 animals was used for all analyses. Table 1 shows the dataset structure and descriptive statistics of each studied trait.

Variance components were estimated by restricted minimum likelihood method using the Wombat software (Meyer 2006) and the multi-trait animal model. The model can be represented by the following matrix:

$$y = X\beta + Za + e$$

where y is the vector of the observed trait, X in the incidence matrix of fixed effects, β is the vector of fixed effects (CG, number of milkings and as linear and quadratic covariates, buffalo calving age), Z is the incidence matrix of random additive genetic effects, a is the vector of random additive genetic effects, and e is the vector of random residual effects.

Results and Discussion

The estimated heritability for the traits milk yield and fat and protein percentage varied from moderate to high (Table 2). This result suggests enough genetic variability to respond well to breeding selection programs. Similar results are reported by Malhado et al. (2013) who found 0.28 for MY, for buffaloes in Brazil. Aspilcueta-Borquis et al. (2010) reported heritability estimates for %F and %P of 0.32 and 0.39, respectively, also for buffaloes in Brazil.

Heritability estimates were moderate for the traits lactose percentage and somatic cell counts. Moreover, high heritability was found for total solids percentage (Table 2). These results indicate that these traits respond well to selection programs. Aspilcueta-Borquis

Table 1. Dataset structure and descriptive statistics of the traits milk yield (MY), lactation length (LL), and percentages of fat (%F), protein (%P), lactose (%L), total solids (%TS), age at first calving (AFC) and somatic cell count (SCC)

	MY (Kg)	%F	%P	%L	%TS	SCC	LL (days)	AFC (days)
Total data	2531	861	860	626	531	656	2531	2436
Mean	1699.95	6.64	4.25	5.00	17.14	2.19	269.57	1140.05
Standard deviation	572.58	0.95	0.27	0.18	0.93	0.71	65.12	171.83

Table 2. Estimates of heritability (diagonal), genetic correlation (above the diagonal) and phenotypic correlation (below the diagonal) between the traits milk yield (MY), lactation length (LL), percentage of fat (%F), protein (%P), lactose (%L), total solids (%TS), age at first calving (AFC) and somatic cell count (SCC)

	MY	%F	%P	%L	%TS	SCC	LL	AFC
MY	0.31	-0.26	-0.25	0.11	-0.21	-0.14	0.78	-0.09
%F	-0.08	0.28	0.52	-0.40	0.96	-0.35	0.01	0.02
%P	-0.22	0.23	0.38	-0.47	0.65	0.18	0.07	-0.24
%L	0.15	-0.39	-0.33	0.23	-0.30	-0.26	0.01	-0.15
%TS	-0.07	0.92	0.44	-0.26	0.36	-0.38	-0.26	-0.14
SCC	-0.21	0.08	0.02	-0.28	-0.02	0.20	0.22	0.44
LL	0.63	0.01	-0.09	0.11	0.007	-0.15	0.08	0.12
AFC	-0.004	0.07	-0.02	-0.07	0.02	-0.01	0.01	0.19

et al. (2010) reported similar heritability value (0.25) for SCC.

On the other hand, the heritability value estimated for lactation length is low (Table 2), indicating that much of the variation of this trait is due to environmental differences among individuals and, therefore, improving management and feeding could also improve the trait indices. The same values have been reported by Malhado et al. (2009) and Rodrigues et al. (2010).

The age at first calving displayed a moderate estimate of heritability (Table 2), suggesting that this trait responds reasonably well to selection. This value was higher than the 0.07 value reported by Seno et al. (2010). However, lower than the values of 0.20 and 0.41 obtained by Tonhati et al. (2000b) and Malhado et al. (2009), respectively.

Table 2 shows the genetic and phenotypic correlations among studied traits. The genetic correlations between MY and the percentages of fat, protein and total solids were moderate and negative, indicating that direct selection for increasing milk production would result in reduced constituents. According to Seno et al. (2007), including the selection of milk quality traits is not advantageous when the purpose of the herd is exclusively to produce milk for sale. However, if *mozzarella* is also being produced, it is advisable to make the selection for fat and protein, given the importance of these milk constituents for the product yield. Nevertheless, only the genetic correlation between milk yield and lactose percentage was positive, suggesting that direct selection for one trait would result in correlated genetic

gain in another. The genetic correlation between milk yield and somatic cell count (Table 2) was low and negative; also negative and lower (-0,06) value was reported by Aspilcueta-Borquis et al. (2010).

The genetic correlation between the traits MY and lactation length (LL) was high and positive. Therefore, direct selection to increase MY would also increase LL. Malhado et al. (2009) reported a similar result, 0.89.

Genetic correlation between MY and age at first calving was close to zero. This result shows that the selection process for any of these traits is independent, that is, selection for MY has no impact on age at first calving. Malhado et al. (2009) reported a genetic correlation value of -0.02 for these traits. However, Tonhati et al. (2000b) reported 0.63 for the same traits.

Conclusion

Most of the studied traits, except for lactation length, showed enough genetic variation between animals and, therefore, selection is a viable tool to provide genetic gain via breeding programs. However, direct selection for milk yield results in decreased fat and protein percentages, hampering the simultaneous selection for these traits. Therefore, the objective of the buffalo herd should be taken into account in the selection. If the only objective is milk sale, the selection should be for MY, but if the goal is to manufacture dairy products, the selection should be for milk constituents.

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