

## PAPER

## Genetic parameters for milk yield analyzed by test-day models in Murrah buffaloes in Brazil

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### Abstract

New statistical models for genetic parameters estimation based on longitudinal data have been proposed. In this study, we considered the data of 47,614 test-day milk yields from 1,578 buffaloes, with 4,757 complete lactations, calving from 1985 to 2006. Single-, two- and multiple trait analyses were used and variance components were estimated by Restricted Maximum Likelihood. The model used to evaluate the milk yield trait at 305 days (MY305) included: i) herd-year-calving season (contemporary group) and milking number as fixed effects; ii) buffalo age at calving as covariate (linear and quadratic effect); iii) additive genetic, permanent environmental, residual and the animal as random effects. The same effects were included in the test-day milk yield model except the contemporary group, defined as herd-year-test day. The heritability estimations for TDMY vary from 0.13 to 0.23 for single-trait analyses, from 0.13 to 0.24 for two-trait analyses and from 0.15 to 0.24 for the multiple-trait analyses. The results obtained for each of the three models showed that the higher heritability estimations were always obtained in the third test month. The genetic correlations between the TDMY and MY305 were high and positive. In conclusion, the TDMY trait use into the selective process will promote genetic changes similar to the ones obtained through the MY305.

### Introduction

The dairy bubaline genetic evaluation has been performed by focusing the milk yield at 305 days (MY305), at 270 days (MY270) or at partial periods of lactation, traditionally estimated by repeatability models (Rosati and Van Vleck, 2002; Hurtado-Lugo, *et al.*, 2006; Malhado, *et al.*, 2007). In order to calculate the MY305, measures are taken by averaging 30 days. In case of short or incomplete lactation, the milk yield is calculated by formulas or by extended factors; its accuracy prediction depends on the quality of these factors and on the quantity of the available information during the lactation.

However, some methodological approaches have been proposed to modulate repeated measures during a period of time, such as the milk yield. These methodologies are called Test-Day Models (TDM); the measuring parameter is the total milk yield during the test day, named "test-day milk yield" (TDMY). These methods have been used in genetic evaluation for milk yield in many countries (Interbull, 2009). By using the TDMY parameter there is no need to extend the lactation period for animals not reaching 305 lactation days, by means of adjusting factors. The TDMY models may consider: the effect of the lactation duration in days, the peculiar effect of the test-day, the milking number, the duration of the preceding dry period, the period of lactation and the diseases (Ferreira *et al.*, 2003).

The results obtained using TDM models in dairy cattle show that the selection based on partial controls should be done in the fourth or fifth control, as these have the higher heritability values (Jamrozik and Schaeffer, 1997; Bignardi *et al.*, 2008). The TDMY heritability value is equal or slightly lower than the one obtained by MY305 (Machado *et al.*, 1999; Bignardi, *et al.*, 2008). Besides, the correlations between TDMY and MY305 vary from medium (0.3) to high (1.0) values (Ferreira *et al.*, 2003; Melo *et al.*, 2005; Bignardi *et al.*, 2008).

The aim of the present research was to estimate the genetic parameters to test-day milk yield (TDMY) and milk yield at 305 days (MY305) traits, using single-, two-, and multiple-trait, intending to provide useful data to the dairy bubaline genetic improvement programs.

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### Materials and methods

In this study, data of the Dairy Bubaline Test Program developed by the Animal Science Department of São Paulo State University, Jaboticabal-SP, Brazil were used. Experimental data were provided by 12 dairy herds of Murrah breed. The animals were raised in *Brachiaria spp* and *Panicum sp* pastures and supplemented with 1 kg of concentrate feed for each 3 kg of milk produced. In the dry season (April to October), they were also supplemented with forage, specially sugar cane and mineral salt, *ad libitum*. The milking test controls were performed keeping the calves closer to the dams in order to stimulate buffaloes' milk production. Milk yield was measured monthly.

Lactations with less than 90 days or more than 400 days were eliminated, as well as milk yields under 300 kg or over 3500 kg. The calving seasons were divided as: April to September (season 1) and October to March (season 2). The contemporary groups were so defined: i) as herd-year-test day in order to evaluate the trait test-day milk yield (TDMY); and ii) as herd-year-calving season to milk yield at 305 days (MY305). The contemporary

groups with less than four observations were eliminated in both cases. After the relevant eliminations for each trait, the analyzed data consisted of 47,614 registers of TDMY, 4,757 lactations of 1,578 Murrah buffaloes, daughters of 140 sires, with calving from 1985 to 2006; consistency of the data was performed by statistic package SAS (1997). Calving ages were considered from 2 to 11 years. In all the analyses, it was used a pedigree archive with 11,760 animals positioned in a relative matrix.

The TDMYs were separated in nine classes of 30 days each, for total of nine test-day controls (TDMY1 to TDMY9). The traits were analyzed by single- and two-traits animal models comparing TDMY with MY305 parameters. A multiple-trait analysis was also performed with all the TDMY and the MY305. The model used in the TDMY analysis included the additive genetic and permanent environment as random effects; and the contemporary group and the milking number as fixed effect. The buffalo age at calving was considered as covariate (linear and quadratic regression). The model used in the MY305 analysis has the same effects of the TDMY analysis, but the contemporary group was defined as herd-year-calving season.

The animal model can be represented as:

$$y = X\beta + Z\alpha + W\alpha + \varepsilon$$

where:  $y$  is the vector of observations (MY305 and TDMY);  $\beta$  is the vector of fixed effects;  $\mu$  is the vector of additive genetic random effect;  $\alpha$  is the vector permanent environment random effect;  $X$ ,  $Z$  and  $W$  are incidence matrices relating to  $\beta$ ,  $\mu$  and  $\alpha$ , respectively;  $\varepsilon$  is the vector of residual effects.

This model has the following assumptions:

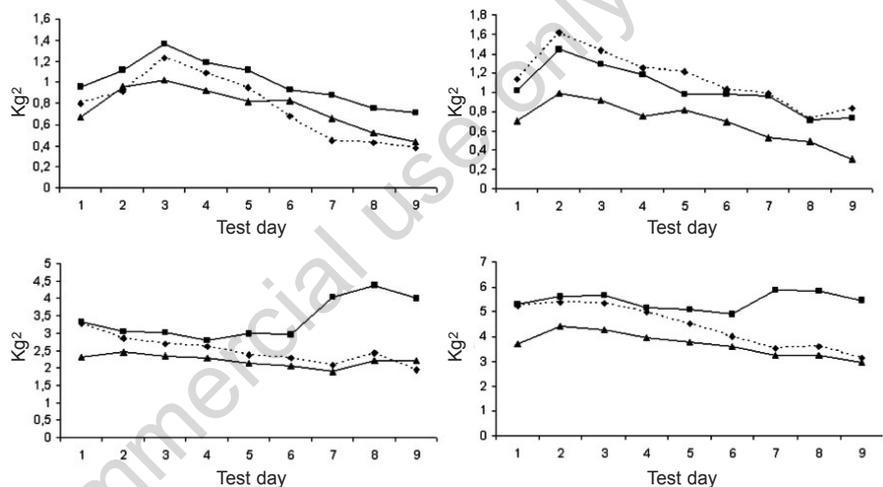
$$E(y) = X\beta \quad \text{e} \quad \text{Var}(y) = ZGZ' + WPW' + R$$

In single-trait analyses, the random effects have a normal distribution with zero as mean and variance as  $G = \text{var}(\mu) = A\sigma^2_\mu$ ,  $P = \text{var}(\alpha) = I\sigma^2_\alpha$  e  $R = \text{var}(\varepsilon) = I\sigma^2_\varepsilon$ . The symbols  $\sigma^2_\mu$ ,  $\sigma^2_\alpha$  and  $\sigma^2_\varepsilon$  correspond to additive, permanent environment and residual variances, respectively. In multiple-trait analyses, the variance of random effects are defined by  $G = G_0 f A$ ,  $P = P_0 f I$  and  $R = R_0 f I$ . The symbols  $A$  and  $I$  correspond to relative and identity matrixes, respectively;  $G_0$ ,  $P_0$  and  $R_0$  correspond to additive, permanent environment and residual (co)variance matrixes, respectively.

The (co)variances components in the single- and two-traits analyses were estimated by restricted maximum likelihood method, using the MTDFREML statistical package (Boldman *et al.*, 1993). In order to analyze the multiple-traits, the REMLF90 program was used (Misztal, 2001). It was assumed that the convergence was achieved when the relative quad-

**Table 1.** Number of observations (N), means (kg), standard deviation (SD, Kg) and coefficients of variation (CV, %) to TDMY (TDMY1 to TDMY9) and MY305.

Trait	Number of observations		Milk yield	
	N	Means, kg	SD, kg	CV, %
TDMY1	6.153	8.12	3.14	36.49
TDMY2	6.175	8.61	3.17	34.95
TDMY3	6.032	8.30	3.10	35.49
TDMY4	5.862	7.74	2.92	35.88
TDMY5	5.580	7.17	2.72	36.65
TDMY6	5.211	6.56	2.55	37.50
TDMY7	4.816	5.94	2.30	37.91
TDMY8	4.075	5.43	2.17	39.25
TDMY9	3.710	4.76	1.96	39.83
MY305	4.865	1,813.15	697.40	38.37



**Figure 1.** Additive genetic variance (lower, left), permanent environmental variance (lower, right), residual genetic variance (upper, left) and phenotypic variance (upper, right) estimated in single-trait analyses (♦), two-trait analyses (■) and multiple-trait analyses (▲) for TDMY.

ratio differences among the consecutive estimates were lower than  $1 \times 10^{-9}$ .

Spearman correlations among predicted breeding values obtained in single- two- and multiple-traits analyses and the coincidence of rank of 5% best sires (7) were calculated.

## Results and discussion

The observed means, the standard deviation and the coefficients of variation for the TDMY and for the MY305 are showed in Table 1. The means for TDMY (Table 1) revealed a typical lactation curve initializing with 8.12 kg, followed by a short increase in milk yield until the peak of the lactation, occurred in the second test-day (8.61 kg), and a subsequent decrease until the end of lactation with a production of

4.76 kg in the ninth lactation month. The means observed for MY305 were higher than the ones obtained by Tonhati *et al.* (2000 a,b), which were 1,259.47 kg e 1,496.00 kg, respectively. However, the MY305 means were similar to the ones obtained by Ramos *et al.* (2006) and Malhado *et al.* (2007), being 1,650.00 kg and 1,863.50 kg, respectively. All of these studies were carried out in Brazil with Murrah buffaloes and indicated an increase in milk yield during lactation, due to management improvement and to a selection for the milk yield trait. Shabade *et al.* (1993), analyzing information of Murrah buffaloes in India, showed a MY305 value of 1,892.21 kg. Rosati and Van Vleck (2002), analyzing Mediterranean breed in Italy, observed for MY305 a mean value of 2,286.80 kg. This higher value could be due to a management improvement, as well as to the results of the milk program test and genetic

evaluation carried out in the country for decades.

The MY305 observed in Colombia (1,064.59 kg) were lower than the ones obtained in the present study (Hurtado-Lugo *et al.*, 2006). These differences can be explained not only by different environmental conditions, but also because of the herds genetic constitution. In Colombia, buffalo management is recent and these were the first evaluations on this specie in that country. It should be pointed out, from the results presented, that Brazilian bubaline have a great potential for milk yield.

Additive genetic, permanent environmental and phenotypic variance estimates for TDMY in single-, two- and multiple-traits models are shown in Figure 1. The additive genetic variance estimates in the analyses had an increase from the lactation beginning until the third lactation month, then decreasing until the lactation end. These results differ from the ones obtained by Hurtado-Lugo *et al.* (2006), who estimated higher variances in the fifth test-day. On the other hand, researches using the TDMY model in dairy bovine found a greater additive genetic variance between the third and fourth lactation month (Ferreira *et al.*, 2003; Rodrigues *et al.*, 2005 and Bignardi *et al.*, 2008).

The permanent environmental variances estimates in the analyses (Figure 1) were higher in the second lactation month and decreasing afterward until the end of the lactation. The phenotypic and residual variances had the same behavior of the previous ones and in both cases the variances were lower in multiple-trait analyses.

The heritability estimates for TDMY (Figure 2) vary from 0.12 to 0.23, from 0.13 to 0.24 and from 0.15 to 0.24 by using the single-, two- and multiple-trait analyses, respectively, with a higher value in the third lactation month. The heritability estimates were higher in two- and multiple-trait analyses; these are higher than the ones obtained by Hurtado-Lugo *et al.* (2006), who have estimated heritability from 0.01 to 0.20, with the higher values found in the intermediate lactation period (Machado, 1999; Ferreira *et al.*, 2003; Bignardi *et al.*, 2008), indicating that selection has to be performed in this period, with the higher heritability.

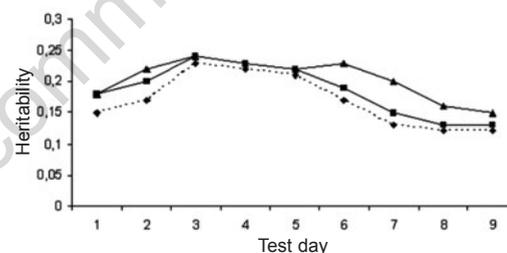
The genetic and residual correlations among the test-days obtained by multiple-trait analyses are in Table 2. The genetic correlations between MY305 and TDMY are high and positive, varying from 0.87 to 0.99. Similar estimates in dairy bubaline were related by Hurtado-Lugo *et al.* (2006) and varied from

**Table 2. Genetic correlations estimates (over the diagonal) and residual correlations estimates (under the diagonal) among the test days obtained in multiple-trait analyses.**

	TDMY1	TDMY2	TDMY3	TDMY4	TDMY5	TDMY6	TDMY7	TDMY8	TDMY9	MY305
TDMY1	-	0.96	0.97	0.95	0.91	0.82	0.80	0.76	0.79	0.93
TDMY2	0.63	-	0.99	0.99	0.96	0.89	0.86	0.84	0.87	0.90
TDMY3	0.50	0.70	-	0.98	0.96	0.88	0.85	0.82	0.86	0.99
TDMY4	0.44	0.60	0.69	-	0.96	0.88	0.85	0.82	0.86	0.99
TDMY5	0.39	0.54	0.62	0.68	-	0.97	0.94	0.92	0.94	0.92
TDMY6	0.31	0.45	0.53	0.59	0.69	-	0.98	0.97	0.95	0.94
TDMY7	0.24	0.37	0.44	0.52	0.54	0.64	-	0.97	0.96	0.91
TDMY8	0.22	0.29	0.33	0.41	0.44	0.46	0.64	-	0.96	0.87
TDMY9	0.16	0.18	0.24	0.29	0.28	0.34	0.44	0.55	-	0.88
MY305	0.21	0.30	0.26	0.37	0.42	0.46	0.44	0.39	0.39	-

**Table 3. Spearman correlation coefficients (rg) among sire estimated breeding values, applying 5% selection intensity for test-day milk yield (TDMY1 to TDMY9), obtained by single-, two- and multiple-trait analyses.**

Trait	Single vs Two-trait		Single vs Multiple-trait		Two vs Multiple-trait	
	rg	5%	rg	5%	rg	5%
TDMY1	70.74	68.00	67.34	61.00	77.75	74.00
TDMY2	78.18	72.00	73.54	70.00	83.35	81.00
TDMY3	83.22	79.00	80.45	72.00	90.33	98.00
TDMY4	82.25	79.00	80.26	72.00	92.21	98.00
TDMY5	81.41	73.00	79.23	68.00	89.78	88.00
TDMY6	80.41	73.00	79.08	64.00	82.76	83.00
TDMY7	79.28	70.00	72.75	60.00	80.24	81.00
TDMY8	72.94	67.00	70.19	60.00	78.34	80.00
TDMY9	70.17	64.00	63.29	53.00	72.63	78.00



**Figure 2. Heritability estimates to TDMY obtained by single- (●), two- (■) and multiple-trait analyses (▲).**

0.87 to 1.00. For dairy cattle, the genetic correlations among the analyzed traits were high and positive, too (Ali and Schaeffer, 1987; Ferreira *et al.*, 2003; Bignardi *et al.*, 2008). The results obtained from the analysis of the genetic correlations between MY305 and TDMY suggest that the direct selection based on partial production will bring correlated gains to MY305.

The genetic correlation estimates (Table 2) for TDMY varied from 0.76 to 0.99, being higher in adjacent test-days. Melo (2005) and Bignardi *et al.* (2008) related a variation from 0.64 to 1.00 and from 0.30 to 1.00, respectively. The lower genetic correlation estimates were found between TDMY1 and the following TDMYs. This could be due to the difficulty of modeling the milk yield at the lactation begin-

ning. The residual correlations were all positive and the estimated values varied from 0.24 (TDMY1 to TDMY9) to 0.70 (TDMY2 to TDMY3). The residual correlation proportion obtained among all TDMY was lower than 0.60 in 77.78% of the analyses. The bigger the test-days intervals were, the smaller the residual correlations resulted, and this occurred gradually.

Sires rank correlations among breeding values for single- two- and multiple-traits analyses are shown in Table 3. The biggest coincidence occurred in TDMY3 and TDMY4, where heritability estimates were higher. The rank correlations of the bulls were high, indicating reasonable maintenance of rank position of the sires, when the two- and multiple-traits were compared.

In an empirical comparison of the single-, two- and multiple-traits models used to evaluate the TDMY, the two- and multiple-trait models seemed to be the best, when the genetic evaluation objective was to analyze the MY305. However, one of the disadvantages in utilizing multiple-trait models is that these models cannot always be used to analyze the TDMY, because of the high computer demand required by this method. Therefore, the utilization of this methodology could not be feasible in genetic evaluation systems using a huge amount of data.

Although there is scarce information about the use of TDMY in dairy bubaline, the results obtained showed that this methodology could be an interesting alternative to be used in Brazil; especially since test-day milk yield is not commonly adopted in bubaline management. A further advantage could be the application of these evaluation strategies in spaced-out month milk tests, trying to reduce the generated costs.

## Conclusions

The results indicate that the two- and multiple-trait models, including registers for month test-day milk yield and milk yield at 305 days, are the most convenient to perform a genetic evaluation for the studied traits in bubaline.

The selection performed according to the month tests (second to sixth) can promote changes towards the same direction of the milk yield at 305 days.

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