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

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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 have been used in genetic evaluation for milk yield in many countries (Interrull, 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.

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 sp pastures and supplement-fed 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 to 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-trait 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:

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

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

This model has the following assumptions:

- $E(y) = X\beta + Z\alpha + W\epsilon + \epsilon$
- $Var(y) = ZGZ^\prime + WPW^\prime + R$

In single-trait analyses, the random effects have a normal distribution with zero as mean and variance as $G = var(\alpha) = A\sigma^2_\alpha$, $P = var(\epsilon) = I\sigma^2_\epsilon$ and $R = var(\epsilon) = I\sigma^2_\epsilon$. The symbols $\sigma^2_\alpha$, $\sigma^2_\epsilon$ and $\sigma^2_\epsilon$ correspond to additive, permanent environment and residual variances, respectively. In multiple-trait analyses, the variance of random effects are defined by $G = G_0 I + A$, $P = P_0 I + I$ and $R = R_0 I$.

Table 1 shows the 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       |
| TDMY2 | 6.175                  | 8.61       |
| TDMY3 | 6.032                  | 8.30       |
| TDMY4 | 5.862                  | 7.74       |
| TDMY5 | 5.580                  | 7.17       |
| TDMY6 | 5.211                  | 6.56       |
| TDMY7 | 4.816                  | 5.94       |
| TDMY8 | 4.075                  | 5.43       |
| TDMY9 | 3.710                  | 4.76       |
| MY305 | 4.865                  | 1,813.15   |

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 Malheiro 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.

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Spearman correlations among predicted breeding values obtained in single- two- and multiple-trait 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 Malheiro 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 species 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-trait 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., 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 fifth lactation month. For dairy cattle, the higher heritability estimates were 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 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 beginning. 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 77.76% 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-trait 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-trait were compared.

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

| Trait          | 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 es Two-trait | Single es Multiple-trait | Two es Multiple-trait |
|---------------|---------------------|-------------------------|-----------------------|
| TDMY1         | 70.74               | 68.00                   | 67.34                 |
| TDMY2         | 78.18               | 72.00                   | 73.54                 |
| TDMY3         | 83.22               | 79.00                   | 80.45                 |
| TDMY4         | 82.25               | 79.00                   | 80.26                 |
| TDMY5         | 81.41               | 73.80                   | 79.23                 |
| TDMY6         | 80.41               | 73.80                   | 79.08                 |
| TDMY7         | 79.28               | 70.00                   | 72.75                 |
| TDMY8         | 72.94               | 67.00                   | 70.19                 |
| TDMY9         | 70.17               | 64.00                   | 63.29                 |

Figure 2. Heritability estimates to TDMY obtained by single- (●), two- (●) and multiple-trait analyses (●).
In an empirical comparison of the single-, two- and multiple-trait 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 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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