Estimates Of Genetic Parameters Of Milk Yield And Milking Speed Of Holstein Cows

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Introduction

Milk yield is the main trait evaluated in Brazil for dairy cattle. The system of official milking recording is expensive and inefficient. Dairy breeders of taurine breeds import semen from countries where genetic evaluations are longer implemented. Many traits can be recorded and used for research using information from dairy producers, mainly those who have good information system and electronic milking machines. Nowadays information about other productive traits (fat and protein yields), somatic cell count, mastitis and milking flow are being collected by some producers. The potential of using electronically recorded data for genetic evaluation for dairy sires for milk speed is assessed in this paper. Milking speed, milking duration, milkability, milking flow are functional traits similar but measured by different ways (Boettcher, P.J., Dekkers, J.C.M. and Kolstad, B.W., 1998; Vicario, D., Carmier, P. and Degano, L., 2005). Milking speed accounts more than 50% of routine work in a dairy herd and this trait can be related to mastitis and high somatic cell count (Luttinen and Juga, 1997). Slow milking animals increase the management costs of dairy herd, but faster milking animals could be more susceptible to mastitis. Random regression models (RRM) applied to test-day records have been adopted for genetic evaluation of dairy cattle, mainly for test-day milk yields. Orthogonal Legendre polynomials (LP) have been used in modeling the covariance structure of TD records in dairy cattle. More recently multiple trait RRM have been adopted for some traits, but difficulties of modeling has been encountered (Strabel and Misztal, 1999). The objective of this study was to compare one-trait and bi-trait random regression models for first lactation test-day milk yields and milk speed of Holstein cows.

Material and methods

Data were provided by Agrindus Corporation that is one of the most important farms of São Paulo state, in Southeast of Brazil. The data of monthly milk yields and milking speed pertained to 2,175 first lactation Holstein cows, calving from 1997 to 2005. Cows were daily recorded by electronic milking machine milked three times a day. The management herd was totally intensive and cows had high genetic potential for milk yield. Data set comprised 18,666 records from 5 to 305 days in milk distributed to 10 classes of days in milk. Cows with records were daughters of 211 sires and 1,562 dams and the relationship matrix included 7166 animals after pedigree have been pruned. A total of 1,867 cows (from 2,175)

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had at least 7 records and the majority (1,140 cows) had 10 monthly records for both traits. Traits were analyzed by one-trait and two-trait random regression animal models (RRM) and multiple trait (MT) analysis. Firstly, one-trait analysis was performed for test day milk yields (TDMY) and milking speed (TDMT), by fitting covariance functions for additive genetic and permanent environmental effects on Legendre polynomials. Residual variances were fitted by a cubic variance function on ordinary polynomial. Five RRM were performed for each trait, ranging the order of polynomials from 4 to 6. The models included the fixed effects of contemporary group (year-month of test), management group, age of cow at calving (linear and quadratic effects). The average trend of population was fitted by a cubic Legendre polynomial on days in milk. Variance components were estimated by REML using the "Wombat" package (Meyer, 2006). Models were compared by Akaike’s (AIC) and Schwarz’s Bayesian (BIC) information criteria. After the choice of best orders for random effects, a bi-trait RRM was performed using REML method by REMLF90 package (Misztal, 2001), also using Legendre polynomials for additive genetic and permanent environmental effects, for both traits. To make easy to perform the analysis, orders of ka and kc was respectively 5 and 6, for both traits. Multi-trait animal models for both traits (10 milk yields and 10 milking speed, with 110 parameters each model) were performed using the same fixed and random effects firstly described, except permanent environmental effects. Analysis using an animal model with 20 trait simultaneously did not converge. Average and standard deviation for TDMY and TDMT were 29.35 and 7.02 kg, and, 13.05 and 3.47 minutes, respectively.

**Results and discussion**

Results from AIC and BIC tests for one-trait RRM suggested that for TDMY a RRM containing order 5 for both additive genetic and 6 for permanent environmental effects, with 40 parameters, adjusted best. For TDMT a RRM with order 5 for both covariance function and 34 parameters was sufficient to adjust trends according to BIC (Table 1), while according to AIC the order 6 for permanent environmental effect could be better. The residual variances were fitted by a cubic variance function according to previous results. For milk yields the residual variances described increasing trend from first (7.13kg$^2$) to eighth (12.0kg$^2$) month, decreasing to values close to 11.37kg$^2$ afterwards. For milking speed the values described a linear trend, decreasing from 2.37min$^2$ in the first month to 1.46min$^2$ in the last test-day record. After the choice of orders for additive genetic and permanent environmental covariance functions using one-trait RRM for milk yield and milking speed, a two-trait RRM was performed simultaneously for both traits. For this analysis it was not possible to adjust heterogeneous residual variances using variance function because the convergence criteria were not attained. In this case, homogeneity of residual variances was considered in the two-trait analysis whose values were 9.41 kg$^2$ for milk and 1.60 min$^2$ for time, throughout the lactation. The pattern of heritability estimates for both analyses was very close in trends, but not in values. For milk yield the estimates were higher at the end of lactation than in the start period. Moreover the heritability estimates of one-trait analysis were higher than that of the
two-trait in almost all test-day records, mainly at the end of lactation with values were close to 0.6. For milking speed the same trend was observed as milk yields. The estimates of one-trait analysis were almost ever higher than 0.4 while the values of two-trait analyses were close to 0.30 through all period. In general heritabilities for milking speed tended to be higher than that for milk yields, except in the last months of lactation.

The estimates of the ratio of permanent environmental were also higher for one-trait than that for two-trait analysis, following the same trend observed for additive genetic effect. Two-trait analysis seemed to diminish problems observed when random regression models are used to fit trends in milk yields (Bignardi, A. B., El Faro, L., Cardoso, V. L. et al. 2009), with high estimates in the extremes of lactation. The heritability estimates seemed to be smoothed, mainly for milking speed. Using a multiple trait analysis with the same data set for both traits, the estimates were lower than that observed for one-trait RRM (not shown). Even though the estimates were higher at the end of lactation they were closer to that obtained for two-trait RRM analysis.

Table 1: Number of parameters (p), log likelihood function (-2 LogL), Akaike’s Information Criterion (AIC) and Schwarz’s Bayesian Information Criterion (BIC), by one-trait random regression models for milk yields and milking speed

<table>
<thead>
<tr>
<th>k_a</th>
<th>k_c</th>
<th>p</th>
<th>Test-day milk yield</th>
<th>Test-day milking speed</th>
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<td></td>
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<td></td>
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<td>AIC</td>
</tr>
<tr>
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<td>24</td>
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<tr>
<td>5</td>
<td>6</td>
<td>40</td>
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</tr>
</tbody>
</table>

*best model, k_a: order for additive genetic effect; k_c: order for permanent environmental effect

Figure 1: Heritability estimates for test-day milk yields (TDMY) and milking speed (TDMT) by one-trait (left) and two-trait (right) random regression models
Higher heritability estimates for milking speed, around 0.40 were estimated close to third month of lactation. In the studied herd, milking speed is an important management trait because of the great number of animals in lactation, the number of milking (3 times a day) and finally, because of functionality of electronic milking machine. Therefore, milking speed is an important breeding goal to be included in a selection index for this herd. Moreover, genetic correlation for milking speed were all positive and higher than 0.60, except among first and the three last milking speed, with values around 0.40 to 0.55 suggesting that selecting for third test-day milking speed would improve milking speed in all other periods. Lower heritability estimates have been shown in literature for this trait (around 0.25 and less), maybe explained by the models of fitting, by the number of measurements within lactation and by the way this trait is expressed (milking flow, milking speed, milking duration, milkability) and measured (objectively or scored subjectively).

On the other hand, milk yields had shown a less interesting genetic pattern than milking speed throughout the lactation, with much higher heritability estimates at the end of lactation. The estimates, however, are close to that reported in literature with Holstein cows. Genetic correlations among test-day milk yields were all positive except between first and tenth test-day milk yields (-0.10). In general first month had shown small genetic correlation with the rest, mainly in the second part of lactation, which was around 0.30. Given the high genetic potential of the Holstein cows of this farm, milk yield seems to be less relevant as a breeding goal, but some caution related to persistency of lactation is important.

Electronic milking machines and computational management programs may help to improve collecting of data records, mainly in countries which official milking record have not allowed genetic evaluation for dairy sires on a large scale.

Conclusion

Modeling repeated test-day milk yields and milking speed with multiple-trait random regression models is possible, but convergence problems were encountered when fitting heterogeneous residual variances. One-trait random regression models for both traits seemed to overestimate heritability throughout the lactation period.

References