LACTATION CURVE IN TROPICAL MILKING CRIOLLO USING RANDOM REGRESSION TEST-DAY MODELS

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INTRODUCTION

The search for dairy productivity in the tropical areas of Latin America has renewed the attention on the Tropical Milking Criollo (CLT, by its spanish acronym) cattle (de Alba and Kennedy, 1994; Rosendo-Ponce and Becerril-Pérez, 2002). The future value of these cattle should be based on parallel genetic and environmental improvement. The study of tropical lactation curves becomes fundamental in view of the debate on whether tropical and template curves are similar. Studies of lactation curves under tropical conditions have been limited; in Mexico only very few studies have been conducted using information from tropical grazing systems (Galaviz-Rodriguez *et al.,* 1998, Osorio-Arce and Segura-Correa, 2005). The direct use of test day (TD) yields instead of 305-day lactation yields have been used in the genetic evaluation for dairy animals (Jamrozik *et al.*, 1997; Gengler *et al.*, 1999). Two types of TD models have been suggested: multitrait analysis proposed by Wiggans and Goddard (1997) and random regression test day models (RRTDM) by Schaeffer and Dekkers (1994). Although a challenge for both types of methods is to obtain correct variance components, accuracy on the evaluation in multitrait models decreases because records made within specific time intervals need to be preadjusted to fixed times, and records outside the time intervals are not used (Nobre *et al*., 2003). RRTDM have become a popular choice for improving the accuracy of genetic evaluations, as well as evaluating persistency of lactation (Jamrozik *et al.,* 1997). The objective of this study was to compare three different random regression functions, applying the TD analysis to lactation curves of the CLT cattle.

MATERIAL AND METHODS

Data source. The study was carried out considering an initial data base of 1,480 lactations from 410 CLT cows, born between 1965 and 2001. Edited data base contained 925 lactations from 299 cows, making a total of 9,968 TD records. Elimination criteria were lactations with less than three records, records under illness, lactations from cows milked without the calf presence and records obtained from the same lactation in two herds. Period of lactation was considered between 6 and 400 days in milk. Data were collected from three CLT herds located in the tropical low lands of the Gulf Coast of Mexico. Climatic conditions are hot subhumid and humid, average temperatures are about 25 $°C$, rainfall ranges from 1120 to 1600 mm per year, and maximum altitude is 16 m (García, 1988). Cows were fed mostly on grazing native and introduced pastures, like *Cynodon plectostachyus, Brachiaria mutica* and *Panicum maximum*; cows were milked manually once a day with the calf presence.

Statistical analyses. All random regression models analyzed had a basic structure as follow (Schaeffer, 2004):

$$y_{ijkn:t} = F_i + f(t)_j + r(a,x,m_1)_k + r(pe,x,m_2)_k + e_{ijkn:t} \; ,$$

where $y_{ijkn:t}$ is the nth observation on the kth animal at time t belonging to the ith fixed factor and the jth group. F_i are the fixed effects; $f(t)_j$ is a fixed regression function that accounts for the phenotypic trajectory across all animals in the jth group; $r(a,x,m1)_k = \sum_{l=0}^{m1} a_{kl} x_{ijk:l}$ represents a random regression function, in which a is the additive genetic effect of the kth animal, x is the vector of time covariates and m_1 is the order of the regression function, $x_{ijk:l}$ are the covariables related to time t, and a_{kl} are the animal additive genetic regression coefficients to be estimated; $r(pe,x,m2)_k = \sum_{l=0}^{m2} p_{kl} x_{ijk:l}$ is the correspondent random regression function for the permanent environmental effects of the kth animal; and $e_{ijkn:t}$ is the random residual effect with mean null and variance σ^2. The following (co)variance structure was assumed:

$$Var\begin{pmatrix} a \\ p \\ e \end{pmatrix} = \begin{pmatrix} A \otimes G & 0 & 0 \\ 0 & I \otimes P & 0 \\ 0 & 0 & I\sigma^2 \end{pmatrix},$$

where **A** is the numerator relationship matrix; **G** is the (co)variance matrix for the additive genetic random regression coefficients of order m_1+1; **P** is the (co)variance matrix for the permanent environmental random regression coefficients of order m_2+1; and **I** is a identity matrix.

The fixed effects were the same for all models: herd-year-calving season with 98 levels, test day season with three levels (Jan-Apr, May-Aug and Sep-Dec) and lactation number with three levels (1, 2 and 3 or more).

Based on earlier examination of the shape of lactation curves using local regression (LOESS), a non-parametric approach (Cleveland and Loader, 1996), three random regression functions were chosen for this study. The first model used random regression coefficients on covariables defined from Wilmink's function (WI), (Wilmink, 1987), and the other two models used coefficients on covariables defined through first (L1) and second order (L2) Legendre polynomials (Kirkpatrick *et al.,* 1990). Residual variance (RV) and Akaike information criterion (AIC) were used as criteria for model comparison. Variance components, solutions of effects and likelihood were estimated with REMLF90 (Misztal, 2002).

RESULTS AND DISCUSSION
The magnitudes of daily additive genetic variance and daily permanent environmental variance were similar for the three functions in the middle of the lactation (between 100 and 350 days in milk); however, differences were observed at the beginning and end of the lactation (Figure 1).
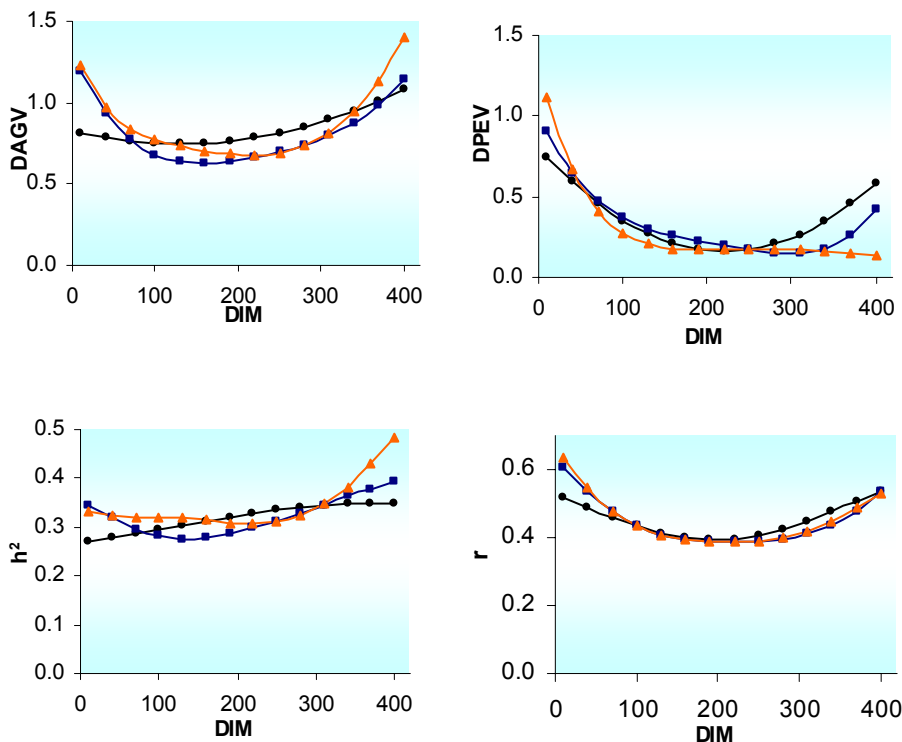
Figure 1. Estimated daily additive genetic variance (DAGV), daily permanent environmental variance (DPEV), heritability (h^2) and repeatability (r) for random regression test day model with first order Legendre polynomial (─●─L1), second order Legender polynomial (─■─L2) and Wilmink's function (─▲─WI). DIM=days in milk.

As a consequence of different variances estimated among functions, heritabilities and repeatabilities were different in some parts of the lactation curve (Figure 1). In general, WI function estimated higher heritabilities at the end of the lactation, L1 lower at the beginning and the end of the lactation, while L2 observed intermediate estimations. This behavior have been found by other authors (e.g. Rekaya *et al.*, 2000; Lopez-Romero and Carabaño, 2003), who attributed these results to modelling problems and the use of polynomials.

Repeatability showed a more consistent behavior among the three models, being similar for all models between 100 and 250 days in milk with differences in only .01 units. The different magnitudes among genetic parameters, throughout the lactation, show the advantage of RRM to evaluate different points of the curve, and the possibility of using this methodology to make genetic evaluations and modify the shape of the lactation curve in CLT (initial yield, peak of yield, persistence, etc.).

The residual variances were 1.441, 1.359 and 1.363 for L1, L2 and WI models, respectively. L2 had the smallest AIC (32803.5) followed by WI (32841.5) and L1 (33221.4). These results suggest model L2 could be the best option to use in lactation curves of the CLT cattle. López-Romero and Carabaño (2003) comparing a great variety of models, found that random regression models based on Legendre polynomials showed a better performance than the model based on Wilmink's function.

CONCLUSION

The use of random regression test day models allowed estimating milk yield heritability and repeatability for several days in milk during the lactation curve of the Tropical Milking Criollo. Based on residual variance and Akaike information criterion, the second order Legendre polynomials seemed to fit the data better. Further studies with more data and examination of other random regressions functions are needed to improve the shape of the lactation curve for the Tropical Milking Criollo cattle in Mexico.

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