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Estimates of genetic parameters and eigenvector indices for milk production of Holstein cows

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ABSTRACT

The objectives of the present study were to estimate genetic parameters of monthly test-day milk yield (TDMY) of the first lactation of Brazilian Holstein cows using random regression (RR), and to compare the genetic gains for milk production and persistency, derived from RR models, using eigenvector indices and selection indices that did not consider eigenvectors. The data set contained monthly TDMY of 3,543 first lactations of Brazilian Holstein cows calving between 1994 and 2011. The RR model included the fixed effect of the contemporary group (herd-month-year of test days), the covariate calving age (linear and quadratic effects), and a fourth-order regression on Legendre orthogonal polynomials of days in milk (DIM) to model the population-based mean curve. Additive genetic and nongenetic animal effects were fit as RR with 4 classes of residual variance random effect. Eigenvector indices based on the additive genetic RR covariance matrix were used to evaluate the genetic gains of milk yield and persistency compared with the traditional selection index (selection index based on breeding values of milk yield until 305 DIM). The heritability estimates for monthly TDMY ranged from 0.12 ± 0.04 to 0.31 ± 0.04. The estimates of additive genetic and nongenetic animal effects correlation were close to 1 at adjacent monthly TDMY, with a tendency to diminish as the time between DIM classes increased. The first eigenvector was related to the increase of the genetic response of the milk yield and the second eigenvector was related to the increase of the genetic gains of the persistency but it contributed to decrease the genetic gains for total milk yield. Therefore, using this eigenvector to improve persistency will not contribute to change the shape of genetic curve pattern. If the breeding goal is to improve milk production and persistency, complete sequential eigenvector indices (selection indices composite with all eigenvectors) could be used with higher economic values for persistency. However, if the breeding goal is to improve only milk yield, the traditional selection index is indicated.

Key words: eigenvalue, Legendre polynomial, persistency, random regression

INTRODUCTION

One of the main objectives in dairy cattle breeding programs is to change, genetically, the shape of the milk production curve. Total milk yield and persistency (i.e., the ability of a cow to continue to produce milk at high levels after the peak of lactation) are both of economic interest. Different statistical models have been used to genetically evaluate milk production using test-day observations. Jensen (2001) reviewed the most frequently used models for evaluating genetically the milk production.

Henderson (1982) proposed the use of random regression (**RR**) models in animal breeding for genetic evaluations on traits measured over time. Jamrozik et al. (1997) and van der Werf et al. (1998) reported that RR models were more appropriate for estimating the genetic parameters of test-day milk yield (**TDMY**) than repeatability models, because RR models are able to fit genetic and environmental changes in milk yield over the time. Schaeffer (2004) reviewed the applications of RR models to animal breeding and Dzomba et al. (2010) reported the advantages of RR models in relation to multi-trait models.

van der Werf et al. (1998), Strabel and Misztal (1999), Kettunen et al. (2000), and Pool et al. (2000) used RR with homogeneous residual variance to estimate genetic parameters for TDMY, but Jamrozik and Schaeffer (1997) and Jamrozik et al. (1997) identified

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problems in estimating the variance components of additive genetic and nongenetic animal effects, such as overestimation of the genetic variance when the RR considered this structure of residual variance. Several researchers have suggested the use of classes of heterogeneous residual variance (Olori et al., 1999; Rekaya et al., 1999; Brotherstone et al., 2000; Druet et al., 2003; El Faro and Albuquerque, 2003; Bignardi et al., 2009, 2011, 2012).

Persistency can be measured in different ways (Gengler, 1996; Swalve and Gengler, 1999). The RR models provide a way to calculate daily, partial, and whole-lactation predicted breeding values (EBV) and to define many measurements of genetic persistency of the lactation curve (Jamrozik et al., 1997; Swalve and Gengler, 1999). The economic importance of persistency is linked to a reduction of feed costs (Gengler, 1996). Dekkers et al. (1997) reported that cows with greater persistency were more profitable.

Gengler (1996) presented the most common definitions of persistency. Approaches exist to make the phenotypic measure of persistency independent of milk yield (Gengler, 1995; VanRaden, 1998; Grossman et al., 1999; Cole and VanRaden, 2006; Cole and Null, 2009). Other approaches define persistency as the difference between the peak yield and that at a test-day in the late lactation or as the ratio of these yields (Ptak and Schaeffer, 1993; Swalve, 2000). Druet et al. (2005) reported that the first and second eigenvectors of the estimated genetic (co)variance matrix in an RR model could be interpreted as latent variables for milk yield and persistency, respectively. Another approach is to develop genetic measurements of persistency from breeding values obtained with RR models (Gengler, 1996).

Togashi and Lin (2006) developed selection indices for milk production and persistency simultaneously, derived from the eigenvectors of the additive genetic coefficients of RR models. Each eigenfunction expresses the curve patterns of the mean curve of the population for a longitudinal trait in each dimension of the additive genetic RR coefficients matrix (Kirkpatrick and Lofsvold, 1992).

Selection indices to improve genetically quantitative traits have been used to summarize a group of traits in a single value, representing the breeding objective. In doing so, a selection index allows selection of these traits jointly in a weighted manner. Then, it would be interesting to study the genetic gains of total milk production and persistency using selection indices that take into account the curve pattern of the genetic lactation curve of each eigenfunction.

The objectives of the present study were to estimate genetic parameters of monthly TDMY of the first lactation of Brazilian Holstein cows using RR, and to compare the genetic gains for milk production and persistency, derived from RR models, using eigenvector indices and selection indices that did not consider eigenvectors.

MATERIALS AND METHODS

Description of the Population and Data Preparation

A data set of 3,543 first lactations of Brazilian Holstein cows from 30 herds and calving between 1994 and 2011 were used to estimate genetic parameters of monthly TDMY. They were maintained in semi-feedlot and feedlot systems, depending on the milk yield level. The cows were fed on pasture during the rainy season (October to March) and using silage during the dry season (April to September). All animals received concentrate supplementary feed according to the milk production level. The cows in confined herds received maize (corn) silage throughout the year, in addition to the other feedstuffs described above. Milking was done mechanically 3 times a day.

The monthly TDMY were measured between 5 and 305 DIM, divided into 10 classes. The first class included milk yield between 5 and 30 DIM, the second included milk yield between 31 and 60 DIM, and so on until the last class, which included milk yield between 270 and 305 DIM. The cows with no drying-off date or those that were excluded from the dairy milk evaluation were excluded from the data. Additionally, cows with at least 3 TDMY distributed throughout the lactation, even if the cows did not have all TDMY (complete lactation), were kept in the data set.

Monthly TDMY 3 standard deviations above or below the mean of the contemporary group (**CG**), defined as herd-month-year of TDMY, were also excluded from the data file. Contemporary groups that had at least 3 TDMY were kept. Table 1 shows the numbers of monthly TDMY records, CG, mean, minimum, and maximum calving age, after data editing and in the pedigree structure.

Estimates of Variance Components and Model Selection

Analyses were performed using a single-trait RR model. The model included the fixed effects of CG (herd-month-year of TDMY), the covariate calving age (linear and quadratic effect), and the additive genetic and nongenetic animal random effects. A fourth-order regression on Legendre orthogonal polynomials of DIM was used to model the population-based mean curve. The fixed effects and the covariates were significant (P