



Original article

Estimation of genetic parameters using a random regression monthly test-day model in an Ethiopian dairy cattle population

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ABSTRACT

Monthly test-day milk records ($n = 50,839$) from 2045 cows born from 312 sires and 1169 dams in Bako, Debre Zeit and Holetta (Ethiopia, 1977 to 2010) were used to estimate the variance components and genetic parameters for monthly test-day milk yield. Cows were Horro (H), Boran (B), Friesian (F) crossbreds, Jersey (J) crossbreds, and Simmental (S) crossbreds. Lactations were modeled with a log-transformed, modified, incomplete, gamma function. The random regression, animal repeatability model considered herd-year-test-day subclass, parity, H, B, F, J, and S cow fractions, $F \times B$, $F \times H$, $J \times B$, $J \times H$, $S \times B$ and $S \times H$ cow heterozygosities as fixed effects. Random effects were additive genetic, permanent environmental and residual. Variance components were estimated using restricted maximum likelihood procedures. Additive genetic, permanent environmental and phenotypic variances, heritabilities (0.17–0.42) and repeatabilities (0.84–0.94) for test-day milk yields increased as lactation progressed. Additive genetic, permanent environmental and phenotypic correlations were higher between adjacent than non-adjacent monthly test-days, and decreased as interval between test-days increased. The results suggested that a random regression, animal repeatability model using a modified, incomplete, gamma function would be appropriate for genetic evaluation in this multibreed population.

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Introduction

Selection for milk yield in dairy cattle is generally based on the analysis of 305 d lactation records. Test-day milk yields are used to estimate 305 d lactation yield. The accuracy of 305 d yields depends on the number of test-day records, the number of days between tests and the methods of estimating 305 d yield. However, genetic evaluation in developing countries is constrained by the lack of an appropriate data recording system. The use of test-day data would offer practical solutions where there is a lack of necessary infrastructure and resources required for milk recording throughout the lactation period.

Models that use 305 d lactation milk yield do not account for the changes in environmental factors within 305 d of lactation. Test-day models, however, allow more accurate estimation of

environmental effects from including the influence of a particular day of recording, account for variation in the numbers of tests recorded per animal, enable optimal use of information from all test-days (especially for lactations with long intervals from calving to the first test-day or between test-days) and greater stability of bull evaluations through accounting for genetic differences among daughters in the shape of the lactation curve and maturity rate (Swalve, 1995; Wiggans and Goddard, 1997).

Test-day records are expressions of a trait that change over time. Genetic correlations between individual test-days and 305 d milk yield ranged from 0.78 to 1.00 (Machado et al., 1999). Ptak and Schaeffer (1993) indicated that a genetic evaluation using four or more test-days yield per lactation is more accurate than from just one 305 d record. Estimated breeding values for 305 d and test-day yields and comparison of both sets of breeding values indicated only minor changes in sire ranking (Swalve, 1995). Similarly, a strong positive rank correlation was observed between the ranking of sires and cows on the basis of test-day and 305 d yield (Kaya et al., 2003; Sawalha et al., 2005).

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Variance components and genetic parameters are needed for a genetic improvement program to predict selection response, to choose among breeding plans and to predict the breeding values of candidates for genetic selection. The methods of estimation of variance components and genetic parameters depend on the type of data. Random regression models are widely used for the estimation of variance components and prediction of breeding value for traits repeatedly recorded over time because they are more flexible and accurate than multiple trait models (Cobuci et al., 2005). Random regression models predict breeding values for cumulative milk yield throughout the lactation and for milk yield at any specific day of lactation in contrast to multi-trait models that only permit point predictions (Bignardi et al., 2011). The estimated genetic parameters depend on the type of regression functions utilized and the covariance structures assumed for animal additive genetic, permanent environment and residual effects in random regression models (Bignardi et al., 2011). Many different models (for example, Legendre polynomials, splines and lactation curve functions) have been proposed for test-day regression. However, it is unlikely that a single “best model” exists because local circumstances determine which effects should be included in the model. In principle, the model that maximizes genetic progress in the population should be chosen for genetic evaluation (Jensen, 2001). The objective of this study was to estimate genetic parameters for monthly test-day milk yields in an Ethiopian multibreed dairy cattle population using a random regression, animal repeatability model.

Materials and methods

Description of the study area, animals and breeding system

The study was based on monthly test-day milk data from the Bako, Debre Zeit and Holetta Research Centers, Ethiopia. Details of the research centers have been reported elsewhere (Gebreyohannes, 2013).

Data and statistical analysis

Lactation milk yields for the period 1977 to 2010 for Bako and Holetta and from 1989 to 2006 for the Debre Zeit research center were used for the study. Monthly test-day milk data were extracted from the daily records of each cow for every 30 day interval starting from the date of calving. The dataset used for this study consisted of 50,839 monthly test-day records. The data were from 2045 cows born from 312 sires and 1169 dams. Records from only parities 1 to 5 were included in the analysis. Lactations shorter than 90 d (less than three monthly test-day records) were excluded from the analysis.

Different functions can be used in regression models. To be suitable for a random regression model, a function must be linear in the parameters and should have as few parameters as possible (Jakobsen et al., 2002). The modified, incomplete, gamma function (MIG) was chosen for this study because it was found to accurately fit monthly test-day milk data and provide excellent predictions of lactation milk yields (Gebreyohannes, 2013). The MIG is represented as $y_t = ate^{-ct}$, where y_t is the monthly test-day milk yield (in kilograms) at time t (in days) after calving, and a and c are parameters of the function. The MIG function was log-transformed to a linear form ($\ln(y/t) = \ln(a) + (-ct)$) with the intercept equal to $\ln(a)$ and the slope equal to $-c$. This log-transformed MIG function was used to model random, animal genetic and permanent environmental effects in the random regression, animal repeatability model.

The random regression, animal repeatability model included the fixed effects of year-season and parity subclasses, regression on the Horro (H), Boran (B), Friesian (F), Jersey (J), and Simmental (S) breed fraction of the cow, regression on $F \times B$, $F \times H$, $J \times B$, $J \times H$, $S \times B$ and

$S \times H$ heterozygosity fractions of the cows and the animal additive genetic, permanent environmental and residual random effects. Animal additive genetic and permanent environmental effects were modeled using a log-transformed MIG function. The residual variance was assumed to be constant throughout the lactation.

The random regression animal repeatability model used here can be described using Equation (1):

$$y_{jkmt} = HTM_j + P_k + \beta DIM_t + \sum_{i=1}^5 f(g_{im})g_{it} + \sum_{i=1}^5 f(h_{im})h_{it} + \sum_{n=0}^1 a_{mn}z_{mnt} + \sum_{n=0}^1 pe_{mn}z_{mnt} + e_{jkmt} \quad (1)$$

where y_{jkmt} represents $\ln(y/t)$ of milk recorded from cow m on monthly test-day t in herd-year- test-day subclass j , and parity subclass k . The HTM_j is the fixed effect of the j th herd-year-monthly test-day subclass ($j = 1$ to 1017); P_k is the fixed effect of parity subclass ($k = 1$ to 5), and β is the regression coefficient for DIM_t , where DIM_t represents the days in milk at day t after calving ($t = 30, 60, 90, 120, 150, 180, 210, 240, 270$ and 300 d). The g_{im} are additive breed regression coefficients, and the h_{im} are heterosis regression coefficients. The $f(g_{im})$ is the i th breed fraction of cow m ($i = 1, \dots, 5$; B, H, F, J and S), and $f(h_{im})$ is the i th heterozygosity for cow m ($i = 1, \dots, 6$; $F \times B$, $F \times H$, $J \times B$, $J \times H$, $S \times B$ and $S \times H$). The i th breed fraction for cow m was computed as $f(g_{im}) = 0.5(p_i^s + p_i^d)$ and the i th heterozygosity for cow m was computed as $f(h_{im}) = p_i^s p_j^d + p_i^d p_j^s$, where p_i^s and p_i^d denote the proportion of breed i or j in the sire and dam of cow m (Dickerson, 1973; Elzo and Famula, 1985; Koch et al., 1985). The a_{mn} are the random regression coefficients for animal additive genetic effects for cow m , the pe_{mn} are the random regression coefficients for permanent environmental effects for cow m , and e_{lmjk} is the residual associated with each test-day observation. The z_{mnt} represent the n th coefficient of the log-transformed MIG function for monthly test-day records at time t for animal m (i.e., $z_{mt0} = 1$, and $z_{mt1} = t$).

The random regression model in matrix notation can be described using Equation (2):

$$y = X\beta + Qg + Z_1a + Z_2pe + e \quad (2)$$

where y is the vector of $\ln(y/t)$ of monthly test-day observations on day t , β is a the vector of fixed effects for herd-year-test-day subclasses (htm), parity subclasses and fixed regression of milk yield on days of lactation, g is the vector of fixed cow breed and heterosis effects, a is the vector of random regression coefficients for animal additive genetic effects, pe is the vector of random regression coefficients for permanent environmental effects, X is the matrix relating observations to fixed effects, Q is the matrix relating observations to cow breed effects (through B, H, F, J, and S breed fractions of the cows) and cow heterosis effects (through $F \times B$, $F \times H$, $J \times B$, $J \times H$, $S \times B$ and $S \times H$ heterozygosity fractions of the cows). Matrices Z_1 and Z_2 are incidence matrices that relate observations to random regression coefficients for the animal and permanent environmental effects, respectively; and e is the vector of residuals. The expected value of y is $X\beta + Qg$. The expected values of random animal additive genetic, permanent environmental and residual effects is zero. The variance of the vector of random regression coefficients for animal additive genetic effects is $G \otimes A$, the variance of vector of random regression coefficients for permanent environmental effects is $P \otimes I$ and the variance of the vector of residuals is $R = I\sigma_e^2$, where G and P are 2×2 matrices of variances and covariances between random regression coefficients for animal additive genetic effects and for permanent environmental effects,

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