Genetic evaluation of lactation persistency for five breeds of dairy cattle

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ABSTRACT

Cows with high lactation persistency tend to produce less milk than expected at the beginning of lactation and more than expected at the end. Best prediction of lactation persistency is calculated as a function of trait-specific standard lactation curves and linear regressions of test-day deviations on days in milk. Because regression coefficients are deviations from a tipping point selected to make yield and lactation persistency phenotypically uncorrelated it should be possible to use 305-d actual yield and lactation persistency to predict yield for lactations with later endpoints. The objectives of this study were to calculate (co)variance components and breeding values for best predictions of lactation persistency of milk (PM), fat (PF), protein (PP), and somatic cell score (PSCS) in breeds other than Holstein, and to demonstrate the calculation of prediction equations for 400-d actual milk yield. Data included lactations from Ayrshire, Brown Swiss, Guernsey (GU), Jersey (JE), and Milking Shorthorn (MS) cows calving since 1997. The number of sires evaluated ranged from 86 (MS) to 3,192 (JE), and mean sire estimated breeding value for PM ranged from 0.001 (Ayrshire) to 0.10 (Brown Swiss); mean estimated breeding value for PSCS ranged from −0.01 (MS) to −0.043 (JE). Heritabilities were generally highest for PM (0.09 to 0.15) and lowest for PSCS (0.03 to 0.06), with PF and PP having intermediate values (0.07 to 0.13). Repeatabilities varied considerably between breeds, ranging from 0.08 (PSCS in GU, JE, and MS) to 0.28 (PM in GU). Genetic correlations of PM, PF, and PP with PSCS were moderate and favorable (negative), indicating that increasing lactation persistency of yield traits is associated with decreases in lactation persistency of SCS, as expected. Genetic correlations among yield and lactation persistency were low to moderate and ranged from −0.55 (PP in GU) to 0.40 (PP in MS). Prediction equations for 400-d milk yield were calculated for each breed by regression of both 305-d yield and 305-d yield and lactation persistency on 400-d yield. Goodness-of-fit was very good for both models, but the addition of lactation persistency to the model significantly improved fit in all cases. Routine genetic evaluations for lactation persistency, as well as the development of prediction equations for several lactation end-points, may provide producers with tools to better manage their herds.

Key words: best prediction, genetic evaluation, persistency

INTRODUCTION

Persistency of lactation is typically defined as the rate of decline in production after peak milk production has been reached. High lactation persistency is associated with a slow rate of decline in production, whereas low lactation persistency is associated with a rapid rate of decline. Cows with greater lactation persistency are more profitable than average cows when yield and lactation persistency are correlated, although the differences are relatively small unless reproductive performance is very poor (Dekkers et al., 1997). Most previous studies of lactation persistency have focused on its relationships with yield traits, but persistent cows may have lower health care and reproductive costs because of reduced stress at peak lactation (Zimmermann and Sommer, 1973). Muir et al. (2004) reported favorable relationships among lactation persistency and some measures of fertility (e.g., 56-d nonreturn rate), and unfavorable relationships with others (e.g., calving interval). Persistent animals require less energy in early lactation, allowing greater utilization of cheap roughage (Sölkner and Fuchs, 1987). Appuhamy et al. (2007, 2009) reported that diseases tend to significantly affect lactation persistency, rather than persistency affecting disease occurrence, and that there are undesirable genetic correlations among persistency of milk and fat yields and several metabolic diseases. Harder et al. (2006) also reported unfavorable genetic correlations among persistency and metabolic diseases.

Lactation persistency is not currently included in International Bull Evaluation Service evaluations and there considerable variation among countries in how it is evaluated. Gengler (1996) reviewed several definitions of lactation persistency, including those independent of yield, differences between peak yield and yield on some arbitrary day in late lactation, and ratios of peak to late-lactation test-day yields. Druet et al. (2005) and

Togashi and Lin (2006) have described measures of lactation persistency based on eigenvectors of the genetic (co)variance matrices of random regression models, although their biological interpretation is unclear.

Cole and VanRaden (2006) described the evaluation of persistency of lactation yield for Holstein cows using national data and best prediction (VanRaden, 1997), demonstrating the feasibility of routine genetic evaluations for these traits. Best prediction (**BP**) of lactation persistency (VanRaden, 1998) is calculated as a function of a trait-specific standard lactation curve and the linear regression of a cow's test-day deviations on DIM. They also suggested that lactation persistency might be used to improve predictions of yield.

Objectives of the current study were to calculate (co)variance components needed for routine evaluations of lactation persistency in Ayrshire (**AY**), Brown Swiss (**BS**), Guernsey (**GU**), Jersey (**JE**), and Milking Shorthorn (**MS**) cattle and to develop equations for the prediction of 400-d actual milk yield for each breed from 305-d actual milk yield and persistency of milk yield.

MATERIALS AND METHODS

Persistency

For a given lactation, individual daily yield can be modeled as the expected value of a management group plus a deviation from that mean:

$$y_i = E(y_i) + t_i,$$

where y_i is an individual yield on test-day i, $E(y_i)$ is the expected yield for an animal in the same management group (Wiggans et al., 1988) on the same test day, and t_i is a deviation from the group mean on the same test day. Suppose that $\boldsymbol{\mu}$ is a vector of expected values for each day of lactation for a single trait, $\mathbf{t}_{365 \times 1}$ is a vector of 365 test-day deviations for the trait, and $\mathbf{t_m}_{ntd \times 1}$ is a vector of only the measured deviations (ntd). The means and variances of $\mathbf{t}$ and $\mathbf{t_m}$ are assumed known with $V(\mathbf{t}) = \mathbf{V}_{365 \times 365}$ and $V(\mathbf{t_m}) = \mathbf{V_m}_{ntd \times ntd}$. The covariance between $\mathbf{t}$ and $\mathbf{t_m}$, $\mathbf{C}_{365 \times ntd}$, is assumed known and is calculated using a mathematical function that accounts for daily measurement error, biological changes over time, and parity (Cole et al., 2009). The elements of $\mathbf{t}$ are calculated using herd-specific lactation curves whose average yields may vary. Vectors and matrices are dimensioned for 365 d rather than 305 d because test days falling between 305 and 365 d are used to improve the prediction of 305-d yield.

Lactation persistency may be measured by multiplying test-day deviations by a linear function of DIM (VanRaden, 1998). Let $\mathbf{d}_{365 \times 1}$ represent a vector whose elements, d_i, represent the DIM on the ith day of lactation. A measure of lactation persistency that is phenotypically uncorrelated with lactation yield may be obtained by defining coefficients $q_i = d_i - d_0$, where d_0 is a constant which acts as a tipping point between yields in early and late lactation and the vector $\mathbf{q}_{365 \times 1}$ indicates how far apart in time individual DIM are from the trait-dependent tipping points. Lactation persistency is then calculated as:

$$p = \mathbf{d'}\boldsymbol{\mu} - d_0 E(\mathbf{y}) + \mathbf{q'CV_m}^{-1}\mathbf{t}_m$$

where p is the predicted lactation persistency, which represents the component of lactation persistency that is independent of yield. Values of d_0 were calculated separately for first and later parities, and the same d_0 were used for all breeds. The tipping points are distinct from the lactation curves ($\mathbf{d'}\boldsymbol{\mu}$), and are used only in the calculation of persistency. Lactation persistency was converted to a unit normal scale with a mean of 0 and a variance of 1.

The $\mathbf{d'}\boldsymbol{\mu}$ term represents a breed- and parity-specific standard lactation curve, $d_0 E(\mathbf{y})$ represents the expected yield of a cow in the same breed-parity group, and the $\mathbf{q'CV_m}^{-1}\mathbf{t}_m$ term represents an individual cow's expected deviation from the herd test-day average. Lactation persistency may be thought of as the regression of adjusted yield deviations on DIM for a particular trait, with cows producing greater yield in the first part of lactation (DIM $< d_0$) having negative lactation persistency and cows producing greater yield in the second part of lactation (DIM $> d_0$) having positive lactation persistency. Additional details on the derivation of lactation persistency are provided in Cole and VanRaden (2006).

Data

Data consisted of lactations for AY, BS, GU, JE, and MS dairy cattle initiated by calvings on or after January 1, 1997, stored in the national dairy database (**NDDB**) at the Animal Improvement Programs Laboratory (USDA, Beltsville, MD). All cows were required to have a first lactation, only the first 5 lactations were used, and lactation persistency that exceeded $\pm$ 4.0 (4 SD) was rounded to an absolute value of $\pm$ 4.0. Days open less than 50 were set to 50, and days open greater than 250 were set to 250. Phenotypic reliabilities, the ratio of predicted to true lactation persistency (VanRaden, 1997), of at least 50% were required for all milk (**PM**),