An Autoregressive Repeatability Animal Model for Test-Day Records in Multiple Lactations

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ABSTRACT

Test-day (TD) models are becoming a standard for genetic evaluation of production traits in dairy cattle. Various approaches to model covariances between TD records include random regression, autoregressive repeatability, orthogonal polynomials, and models based on character processing. The applicability of these models is mainly associated with the number of parameters to estimate, incorporation of multiple lactations, and the accuracy of correlations generated by the cow's repeated expression of milking performance (TD yields) within and across lactations. We define and evaluate a multiple-lactation, autoregressive-repeatability model that disentangles environmental effects due to cow within and between lactations. Simulated records either included or ignored a long-term environmental effect between lactations. Our autoregressive TD animal model correctly detected presence and the absence of this effect and accurately recovered the assumed variance components and correlations underlying the data (10 parameters for three lactations). Estimates of variance components and autocorrelation coefficients were obtained using DFREML-simplex methodology. Given the value of this approach to reduce the size of residual variance components, autoregressive animal models are a preferable alternative to classical methods based on cumulative lactation yield to improve milk production in dairy cattle.

(Key words: test-day animal model, dairy cattle, autoregression, genetic evaluation)

Abbreviation key: CL = confidence limit, HTD = herd-test-date, LTE = long-term environmental effect, STE = short-term environmental effect, TD = test day.

INTRODUCTION

Analysis of daily yields on test days (TD) to calculate cumulative 305-d milk yield (Kachman and Everett, 1989; Van Tassell et al., 1992; Pander and Hill, 1993; Everett and Schmitz, 1994) was an important improvement in modeling dairy production to improve genetic gains in milk, which from 1960 to 1988 averaged 84 kg/yr in US Holstein cows (Freeman and Lindberg, 1993). These TD-adjusted cumulative yields contained similar amounts of genetic variation with smaller residual variances compared to unadjusted lactation records. Consequently, heritabilities for TD-adjusted yields of milk, fat, and protein were 11 to 17% larger than for unadjusted records, which portended more accurate genetic evaluations and greater genetic progress from selection based on TD-adjusted cumulative 305-d lactation records (Van Tassell et al., 1992).

Other approaches (Meyer et al., 1989; Ptak and Schaeffer, 1993; Schaeffer and Sullivan, 1994; Swalve, 1995; Carnevalheira et al., 1998) directly analyzed daily yields instead of TD-adjusted cumulative 305-d lactation records to genetically evaluate sires and cows for milk production. Date of test effects may explain more of the systematic environmental variations (Ptak and Schaeffer, 1993; Swalve, 1995). More TD records per cow also promote more accurate prediction of genetic merit. Especially following advice in Quaas (1984) and Wade and Quaas (1993), Carnevalheira and co-workers (1998) relaxed the usual assumption of unitary correlation between TD within cow by implementing first-order autoregressive structures within and between lactations to fit short- and long-term environmental covariances among repeated TD records. Results from this study indicated that an autoregressive TD animal model would provide larger additive genetic variance and heritability, more accurate estimates of individual genetic merit, and nearly double the theoretical annual genetic gain (200 kg) in milk for US Holstein. Consequently, our objectives were to define and evaluate a multiple lactation autoregressive repeatability model, challenging its capacity to accurately estimate the variance components and correlations underlying simu-

Received October 19, 2001.

Accepted February 26, 2002.

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lated data, which either included or ignored long-term environmental effects.

MATERIAL AND METHODS

Model Definition

Modeling TD data requires an expression that relates these observations to their underlying random genetic and environmental factors. Systematic environmental factors are typically treated as fixed effects. Smaller residual variances commonly result when groups of contemporary animals are represented using herd-test-dates (**HTD**) instead of herd-year-seasons (Kachman and Everett, 1989; Van Tassell et al., 1992; Ptak and Schaeffer, 1993; Swalve, 1995). Age at calving and the lactation of repeated daily milk yields also need to be represented. These important fixed effects (or their variants) have been explanatory variables in all TD models. The general principles outlined by Wade and Quaas (1993) were followed to incorporate a first-order autoregressive structure into mixed model methodology. Variance components and correlations were estimated with DFREML procedures (Smith and Graser, 1986; Meyer, 1988; Boldman and Van Vleck, 1991) using the simplex algorithm (Nelder and Mead, 1965) to maximize likelihood functions.

Records of daily milk yield may be depicted as repeated observations. For example, a simple repeatability TD model may be defined as:

$$y_{ijkmn} = \text{HTD}_i + \text{Age}(\mathbf{H})_j + \text{DIM}(\mathbf{H})_k + \mathbf{a}_m + \mathbf{p}_m + \mathbf{e}_{ijkmn},$$

where

- y_{ijkmn} is the observed daily yield,
- HTD_i is the fixed effect due to cows tested in the same herd (**H**) and test date,
- $\text{Age}(\mathbf{H})_j$ is the fixed effect due to the j th age class at calving within herd,
- $\text{DIM}(\mathbf{H})_k$ is the fixed effect due to cows tested in the k th days in milk (**DIM**) class within herd,
- $\mathbf{a}_m$ is the random effect of animal,
- $\mathbf{p}_m$ is the random effect accounting for environmental covariances among TDs within cow, and
- $\mathbf{e}_{ijkmn}$ is the random residual term.

When nonadditive genetic components are assumed to be negligible, a simple repeatability model is an extension of the usual breeding value model, with the further assumption of an additional nongenetic covariance from repeated observations on the same animal.

This covariance among residuals of repeated records on the same animal results in a structure typically assumed to be:

$$\text{cov}(\mathbf{e}_i, \mathbf{e}_j) = \delta_{ij}\sigma_e^2 + \sigma_p^2,$$

where δ_{ij} is the Kronecker delta, or, in matrix notation for three repeated records

$$\text{var} \begin{bmatrix} \mathbf{e}_1 \\ \mathbf{e}_2 \\ \mathbf{e}_3 \end{bmatrix} = \begin{bmatrix} \sigma_e^2 + \sigma_p^2 & \sigma_p^2 & \sigma_p^2 \\ & \sigma_e^2 + \sigma_p^2 & \sigma_p^2 \\ \text{symm} & & \sigma_e^2 + \sigma_p^2 \end{bmatrix},$$

and having the phenotypic (co)variance structure

$$\text{var} \begin{bmatrix} \mathbf{y}_1 \\ \mathbf{y}_2 \\ \mathbf{y}_3 \end{bmatrix} = \begin{bmatrix} \sigma_e^2 + \sigma_p^2 + \mathbf{a}_{mm}\sigma_a^2 & \sigma_p^2 + \mathbf{a}_{mm}\sigma_a^2 & \sigma_p^2 + \mathbf{a}_{mm}\sigma_a^2 \\ & \sigma_e^2 + \sigma_p^2 + \mathbf{a}_{mm}\sigma_a^2 & \sigma_p^2 + \mathbf{a}_{mm}\sigma_a^2 \\ \text{symm} & & \sigma_e^2 + \sigma_p^2 + \mathbf{a}_{mm}\sigma_a^2 \end{bmatrix},$$

where

σ_e^2 represents the variance unique to each observation,

σ_p^2 represents the environmental covariance between pairs of records on the same animal (assumed equally correlated for all pairs), and

$\mathbf{a}_{mm}\sigma_a^2$ represents the genetic covariance assuming unitary genetic correlation between records on the same animal, which implies that the same genes are responsible for milk production throughout the lactation.

Quaas (1984) called this the "simplistic repeatability model" because it is unlikely that all records are equally correlated regardless of adjacency. A more realistic general structure was suggested (Quaas, 1984), which would impose an autoregressive covariance structure for residuals. The simplest of these structures is a stationary first-order autoregressive process, which is applicable with equal intervals (i.e., TD records taken 1 mo apart), as shown here for three repeated observations

$$\text{var} \begin{bmatrix} \mathbf{e}_1 \\ \mathbf{e}_2 \\ \mathbf{e}_3 \end{bmatrix} = \begin{bmatrix} 1 & \rho & \rho^2 \\ & 1 & \rho \\ \text{symm} & & 1 \end{bmatrix} \sigma_e^2 = \mathbf{F}\sigma_e^2,$$

where

σ_e^2 represents the environmental variance, and ρ represents the autocorrelation with $|\rho| < 1$,

and which involves no more parameters (two in this case) than a structure ignoring the autoregressive process. Contiguous records in an autoregressive model are equally correlated if the interval between them is constant, which yields a decaying correlation between noncontiguous records with increasingly greater separation in time. $\mathbf{F}$ can be easily factored into $\mathbf{LDL}'$, where $\mathbf{L}$ ($\mathbf{L}'$) is a lower (upper) triangular matrix and $\mathbf{D}$ is a diagonal matrix. This factorization is especially useful for computing the determinant of $\mathbf{F}$, e.g., for evaluating the likelihood function.

This structure is also computationally tractable because its inverse is easily obtained without formal inversion, resulting in a tridiagonal matrix, if all contiguous observations are present and equidistantly spaced:

$$\mathbf{F}^{-1}\sigma_e^{-2} = \begin{bmatrix} (1 - \rho^2)^{-1} & -\rho(1 - \rho^2)^{-1} & 0 \\ & (1 + \rho^2)/(1 - \rho^2) & -\rho(1 - \rho^2)^{-1} \\ \text{sym m} & & (1 - \rho^2)^{-1} \end{bmatrix} \sigma_e^{-2},$$

or

$$= \begin{bmatrix} 1 & -\rho & 0 \\ & 1 + \rho^2 & -\rho \\ \text{symm} & & 1 \end{bmatrix} \frac{1}{(1 - \rho^2)\sigma_e^2}.$$

However, it may create problems for interpreting environmental influences because its structure is assumed entirely autocorrelated, which precludes independent effects peculiar to each TD record. Therefore, a potentially more realistic portrayal of random environmental effects on daily milk yield may be (for three repeated observations):

$$\text{var} \begin{bmatrix} \mathbf{e}_1 \\ \mathbf{e}_2 \\ \mathbf{e}_3 \end{bmatrix} = \text{var} \begin{bmatrix} \mathbf{t}_1 + \mathbf{r}_1 \\ \mathbf{t}_2 + \mathbf{r}_2 \\ \mathbf{t}_3 + \mathbf{r}_3 \end{bmatrix} = \mathbf{F}\sigma_t^2 + \mathbf{I}\sigma_r^2,$$

where

$\mathbf{t}$ and $\mathbf{r}$ are two environmental components resulting from partitioning the environmental variance ($\mathbf{e}$) with $\mathbf{t}$ following a first-order autoregressive process in repeated TD yields and $\mathbf{r}$ is an independent effect,

σ_t^2 represents the environmental covariance among repeated daily yields,

$\mathbf{F}$ represents the first-order autocorrelation structure associating records from each cow as defined above, and

σ_r^2 represents the residual variance common to all observations.

Thus portrayed, the two environmental components represent separate influences on each TD record. One

component (σ_t^2) comprises short-term effects (**STE**) within a lactation (e.g., dietary quality and intake, weather, minor injury, estrus). These positive or negative fluctuations may be canceled or reversed with time, thus imparting a pattern or structure (i.e., a stationary, first-order autoregressive process between equally spaced, monthly TD records), where the correlations between TD records decay in time. The other component (σ_r^2) comprises all other sources of unaccounted temporary variation that independently affect TD records.

Environmental effects that permanently influence subsequent lactations include body size, disease, and other health events, and physical injury. Conceptually, this is the classical definition of a permanent environmental effect, where close events in an autoregressive structure are assumed more highly correlated than distant events. These correlated long-term environmental effects (**LTE**) may not be separately partitioned from the STE effect (which accounts only for correlations between TD within a lactation). A repeatability TD model involving multiple lactations needs to anticipate potential covariances, including those occurring between repeated lactations. The unequal time lag between consecutive lactations (the dry period) precludes using the STE effect to also portray potential covariances between lactations. The report by Harville (1979) may have contained the earliest suggestion to model the cow's permanent environmental effect as a first-order autoregressive process to more accurately reflect temporal effects due to cow from one lactation to the next. Factors that may cause correlation between lactations have long-term influence in the sense that they should similarly influence repeated lactations (but possibly in different degrees) with noncanceling, carryover effects. Consequently, an autoregressive structure may be a realistic approach to portray these LTE effects, which relaxes the restriction (or assumption) that covariances across lactations are equal and invariant (Harville, 1979; Quaas, 1984).

Consequently, the conceptual multiple-lactation TD animal model was defined:

$$y_{ijkLmn} = \text{HTD}_i + \text{Age}_j + \text{DIM}(\mathbf{H})_{k(L)} + \mathbf{a}_m + \mathbf{p}_{m(L)} + \mathbf{t}_{n(mL)} + \mathbf{r}_{ijkLmn},$$

where

y_{ijkLmn} is the TD record,

HTD_i is the fixed effect due to measuring the milk yields of cows on the same test date in the same herd,

Age_j is the fixed effect due to the j th age at calving,

$\text{DIM}(\mathbf{H})_{k(L)}$ is the fixed effect due to cows tested in the same DIM class within herd and lactation,

$\mathbf{a}_m$ is the random effect of animal,

$\mathbf{p}_{m(L)}$ is the random effect of LTE following a first-order autoregressive process across lactations,

$\mathbf{t}_{n(mL)}$ is the random effect of STE nested within cow and lactation, assumed independent between lactations, and following a first-order autoregressive process within cow and between TD, and

$\mathbf{r}_{ijkLmn}$ is the random residual term.

The model in matrix notation is:

$$\mathbf{y} = \mathbf{X}\beta + \mathbf{Z}\mathbf{a} + \mathbf{M}\mathbf{p} + \mathbf{Q}\mathbf{t} + \mathbf{r},$$

where $\mathbf{y} \sim \mathbf{N}(\mathbf{X}\beta, \mathbf{V})$, β is the unknown vector of fixed effects that, with known $\mathbf{X}$, defines the mean; $\mathbf{a}$, $\mathbf{p}$, and $\mathbf{t}$ are vectors representing the random effects due to animal, LTE, and STE, which are, respectively, associated with records in $\mathbf{y}$ by $\mathbf{Z}$, $\mathbf{M}$, and $\mathbf{Q}$; $\mathbf{r}$ is the vector of residuals; and $\mathbf{V}$ is the (co)variance matrix. The expectations and (co)variance for this model are (for the case of $\mathbf{L}$ equal to three lactations per cow and invoking previous definitions):

$$\begin{bmatrix} \mathbf{y} \\ \mathbf{a} \\ \mathbf{p} \\ \mathbf{t} \\ \mathbf{r} \end{bmatrix} \sim \mathbf{N} \left(\begin{bmatrix} \mathbf{X}\beta \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \end{bmatrix}; \begin{bmatrix} \mathbf{V} & \mathbf{ZG} & \mathbf{MJ} & \mathbf{QS} & \mathbf{R} \\ & \mathbf{G} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ & & \mathbf{J} & \mathbf{0} & \mathbf{0} \\ & & & \mathbf{S} & \mathbf{0} \\ & & & & \mathbf{R} \end{bmatrix} \right),$$

and then

$$\begin{aligned} \mathbf{V} &= \mathbf{ZGZ}' + \mathbf{M}\mathbf{J}\mathbf{M}' + \sum_{L=1}^3 (\mathbf{Q}_L \mathbf{S}_L \mathbf{Q}_L') + \mathbf{R}, \\ \mathbf{G} &= \mathbf{A}_{q1} \sigma_a^2, \\ \mathbf{J} &= \sigma_p^2 \begin{bmatrix} 1 & \rho_p & \rho_p^2 \\ & 1 & \rho_p \\ & & 1 \end{bmatrix} \otimes \mathbf{I}_{q2}, \\ \mathbf{S}_L &= \begin{bmatrix} \mathbf{F}_{1L} & & \\ & \ddots & \\ & & \mathbf{F}_{mL} \end{bmatrix} \sigma_{tL}^2, \\ \mathbf{F}_{mL} &= \begin{bmatrix} 1 & \rho_{tL} & \rho_{tL}^2 & \dots & \rho_{tL}^{n-2} & \rho_{tL}^{n-1} \\ & 1 & \rho_{tL} & & & \rho_{tL}^{n-2} \\ & & \ddots & & & \vdots \\ & & & \ddots & \rho_{tL} & \rho_{tL}^2 \\ & & & & 1 & \rho_{tL} \\ & & & & & 1 \end{bmatrix}, \end{aligned}$$

$$\mathbf{R} = \mathbf{I}_N \sigma_r^2,$$

where q_1 equals the number of animals being evaluated, q_2 equals the number of animals having records, n equals the number of TD of a particular female, and N equals the total number of records in the analysis; $\otimes$ represents the Kronecker tensor product; $\mathbf{A}$ is the numerator relationship matrix, $\mathbf{I}$ is the identity matrix, and $\mathbf{F}$ is the autocorrelated block diagonal corresponding to the m th cow within the L th lactation. This parameterization also permits different variances of the STE effect for multiple lactations (σ_{tL}^2). Note that $\mathbf{Q} = \mathbf{I}$ with this design. Therefore, the corresponding mixed model equations are:

$$\begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{X}'\mathbf{R}^{-1}\mathbf{Z} & \mathbf{X}'\mathbf{R}^{-1}\mathbf{M} & \mathbf{X}'\mathbf{R}^{-1} \\ & \mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z} + \mathbf{G}^{-1} & \mathbf{Z}'\mathbf{R}^{-1}\mathbf{M} & \mathbf{Z}'\mathbf{R}^{-1} \\ & & \mathbf{M}'\mathbf{R}^{-1}\mathbf{M} + \mathbf{J}^{-1} & \mathbf{M}'\mathbf{R}^{-1} \\ & & & \mathbf{R}^{-1} + \mathbf{S}^{-1} \end{bmatrix} \begin{bmatrix} \hat{\beta} \\ \hat{\mathbf{a}} \\ \hat{\mathbf{p}} \\ \hat{\mathbf{t}} \end{bmatrix} = \begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{y} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{y} \\ \mathbf{M}'\mathbf{R}^{-1}\mathbf{y} \\ \mathbf{R}^{-1}\mathbf{y} \end{bmatrix}.$$

Simulated Data

Two datasets were simulated according to model assumptions to evaluate the multiple lactation autoregressive repeatability methodology, and to assess the efficiency of achieving the desired convergence. One dataset contained an LTE effect; the other one did not. The TD animal model was challenged to accurately retrieve the variance components and correlations underlying the data simulated with these different effects. Although plausible parameter estimates are not a guarantee that procedure is correct, the reverse implies incorrect or inaccurate methodology.

A pedigree file containing 50 sires and 500 cows was generated and used to simulate datasets of 15,000 records (10 TD records per cow in each of three lactations). The data were organized in groupings according to fixed effects in the model: 44 test dates, 20 DIM subclasses per lactation, and 4 age-at-calving classes. Fifty replicates of each dataset were analyzed: the one including the LTE effect had 10 parameters to estimate (six variance components and four autocorrelations), and the one ignoring it had eight parameters (five variance components and three autocorrelations). Starting values for variance components and correlations were deliberately 10% larger than the true values for every analysis. Convergence was achieved when the variance of the

Table 1. Estimates of variance components for animal (σ_a^2), long-term environmental effects (LTE, σ_p^2), short-term environmental effects (σ_t^2) and residual (σ_r^2), and autocorrelations (ρ) and their 95% confidence limits (CL) using a multiple lactation, test-day animal model either including or ignoring a LTE effect to analyze data simulated to either contain or not contain an LTE effect.

Analytical model	Parameter	Simulated data							
		Containing LTE				Not containing LTE			
		True	Estimate	+CL	−CL	True	Estimate	+CL	−CL
Includes LTE	σ_a^2	2.00	1.94	2.01	1.88	2.00	1.91	1.96	1.86
	σ_p^2	1.00	1.02	1.07	0.97	0.00	0.11	0.14	0.07
	ρ_p	0.60	0.60	0.62	0.57	0.00	0.54	0.61	0.48
	σ_{t1}^2	1.50	1.49	1.51	1.46	1.50	1.47	1.50	1.44
	ρ_{t1}	0.75	0.74	0.75	0.73	0.75	0.73	0.74	0.73
	σ_{t2}^2	2.00	2.00	2.03	1.97	2.00	1.96	1.99	1.93
	ρ_{t2}	0.80	0.80	0.80	0.79	0.80	0.78	0.79	0.78
	σ_{t3}^2	2.50	2.52	2.56	2.47	2.50	2.44	2.49	2.40
	ρ_{t3}	0.85	0.85	0.85	0.84	0.85	0.84	0.85	0.84
Ignores LTE	σ_r^2	1.00	0.99	1.00	0.98	2.00	1.98	1.99	1.97
	σ_a^2	2.00	2.85	2.91	2.79	2.00	1.99	2.03	1.96
	σ^2	1.50	1.93	1.95	1.90	1.50	1.50	1.53	1.47
	ρ_{t1}	0.75	0.83	0.84	0.83	0.75	0.75	0.75	0.74
	σ^2	2.00	2.29	2.31	2.27	2.00	1.99	2.02	1.96
	ρ_{t2}	0.80	0.84	0.84	0.84	0.80	0.79	0.80	0.79
	σ^2	2.50	3.06	3.10	3.02	2.50	2.49	2.53	2.46
	ρ_{t3}	0.85	0.89	0.89	0.89	0.85	0.85	0.85	0.84
	σ_r^2	2.00	1.04	1.05	1.04	2.00	1.99	2.00	1.98

−2 log likelihood functions from all points defining the simplex polytope was $<10^{-6}$. For each replicate, the same log likelihood (up to the fourth decimal place; Boldman et al., 1995) in each of the two last runs was obtained with three or four cold starts.

RESULTS AND DISCUSSION

Results from analysis of the simulated data are summarized in Table 1. Each model performed acceptably well for the data possessing identical effects (emboldened values, in Table 1). For these scenarios, the resulting parameter estimates were close to the true values within the limits of confidence (CL) at $\alpha = 0.05$. Furthermore, the model including an LTE effect was sensitive to the absence of this effect in the data that did not contain an LTE component. The small values obtained for $\hat{\sigma}_p^2$ and $\hat{\rho}_p$ were plausibly from a sampling effect from imposing nonzero requirements on the parameter space. However, the analytical model omitting LTE overestimated most parameters from data containing an LTE effect.

Conceptually, the LTE effect differs from the classical permanent environmental effect under the assumption that noncontiguous lactations are less correlated than adjacent ones. Many events that permanently affect a cow's capacity to express milk production occur during productive life (e.g., udder injury and infection), which

would impart a correlation structure between lactations that decays in time. This may be why Harville (1979) and Quaas (1984) considered the autoregressive approach to be a realistic way to describe this effect. Our results indicated that the least risky approach for accurate evaluation is to use a full model including an LTE effect.

The number of parameters to estimate (variance components and correlations) may restrict the applicability of a linear mixed model for TD genetic analysis. The relatively small number of parameters considered by an autoregressive model is advantageous in this sense. The additive genetic (co)variance structure in this study and analysis of field data (Carvalho et al., 1998; Carvalho, 2001) was fitted with unitary correlation between TD and lactations under assumption that the same genes similarly affect milk yield expression throughout a cow's productive life. Study is warranted to further evaluate models that would represent genetic (co)variances with autocorrelation structure.

As expected, substantial iteration was required to achieve convergence due to the number of parameters to estimate, which, as pointed out by Boldman et al. (1995), is worth considering when using DFREML with the simplex in variance component estimation. When the analytical model mismatched effects contained in the data, convergence sometimes required over 400 iterations. Therefore, besides "poor" starting values, an in-

Table 2. Average number of iterations¹ to attain convergence in a three-lactation variance component estimation problem using DFREML-simplex methodology applied to TD animal models with and without long-term environmental effects (LTE).

Analytical model	Simulated data	
	Containing LTE	Not containing LTE
Includes LTE	276	340
Ignores LTE	320	153

¹Only those replicates needing less than 400 iterations to achieve the convergence criterion (10^{-6}).

correct model may also affect convergence requirements. Table 2 shows the average numbers of iterations required to achieve convergence for the replicates requiring fewer than 400 iterations.

CONCLUSIONS

Approaches to describe covariances between TD records include random regression, autoregressive repeatability, orthogonal polynomials, and models based on character processing. The applicability of these models is mainly associated with the number of parameters to be estimated, incorporation of multiple lactations, and the accuracy of correlations generated by the cow's repeated expression of milking performance (TD yields) within and across lactations. Results showed that an autoregressive animal model containing STE and LTE autoregressive processes accurately estimated these effects and the assumed variance components and correlations regardless of presence or absence of a long-term environmental effect due to cow. This model has been applied to field data from Italy (Carvalho, 2001) and the United States, where "persistent environmental effects did not have major impact on the milking performance of Holstein cows" (Carvalho et al., 1998). Variance component estimates from these studies were consistent and revealed a potential theoretical genetic gain of nearly 200 kg/yr in milk for US Holstein herds. Therefore, this analytical approach can increase the accuracy of predicted EBV and the attendant rate of genetic gain by reducing the size of residual components of variance.

ACKNOWLEDGMENTS

This work contributes to the project POCTI/33162/CVT/2000 and to regional project S-284, Genetic En-

hancement of Health and Survival for Dairy Cattle. It was partially funded by the Fundação para a Ciência e a Tecnologia (FCT) and FEDER (EU).

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