

AUTOREGRESSIVE REPEATABILITY ANIMAL MODELS FOR THE ANALYSIS OF
FIRST LACTATION TEST DAY RECORDS OF HOLSTEIN COWS

by

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DISSERTATION TITLE

Autoregressive repeatability animal models for the analysis of first

lactation test day records of Holstein cows

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AUTOREGRESSIVE REPEATABILITY ANIMAL MODELS FOR THE ANALYSIS OF FIRST LACTATION TEST DAY RECORDS OF HOLSTEIN COWS

Rami M. Sawalha, Ph.D.

University of Nebraska, 2004

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Animal models with first order autoregressive (AR(1)) covariance structures for permanent environmental effects (AR_{pe}), residual effects (AR_e) or genetic and residual effects (AR_{ae}) of test day records (TD) were examined. The models with AR(1) covariance structures were compared together and with a simple test day repeatability model with compound symmetry (CS) covariance structure for TD environmental effects and a 305-day lactation model. Data consisted of 106,472 records (TD data) of 12,071 first lactation Holstein cows (305-day data). Estimates of genetic and environmental components of variance and autocorrelation coefficients were obtained for milk, fat, and protein yields and somatic cell scores (SCS) using ASReml.

Likelihood ratio tests indicated that models with the AR(1) covariance structures were significantly more appropriate for the TD data for all traits than the CS model. Estimates of heritability were slightly less with the models with the AR_e or AR_{ae} covariance structures (0.09) than with the CS model (0.10 to 0.11) for yield traits. All TD models resulted in similar estimates of heritability for SCS (0.06).

Estimates of residual variance may have been underestimated with the CS model compared with TD models with the AR_e or the AR_{ae} covariance structures. Estimates of heritability with the 305-day model for all traits were in the range of 0.11 to 0.36.

The predicted breeding values (PBV) with different TD models were highly correlated (0.98 to 1.00). The PBV with the AR_{ae} Model were not the same at different test days and tended to decrease with advancement of the lactation for SCS. The smallest estimates of accuracy of PBV were at the beginning and at the end of lactation. The $AR(1)$ covariance structure for TD residual or for both genetic and residual effects may help to prevent overestimation of heritability and repeatability for milk, fat and protein yields and SCS compared with simple repeatability model with the CS covariance structure.

Keywords: Milk, Test day, Genetic and environmental autocorrelation.

PREVIEW

Dedicated to
My wife OLA
My father and mother

PREVIEW

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CHAPTER 1

GENERAL INTRODUCTION

Test day and 305-day records

Currently milk, fat and protein yields are routinely recorded for the enrolled cows with the Dairy Herd Improvement program in the USA. The records are taken approximately monthly and are known as test day (TD) records. Test day records can be aggregated and standardized to twice daily milking and mature equivalent basis and may be extended to 305-day lactation records.

Somatic cell count is also recorded along with other milk yield traits. Mastitis is a highly costly disease in dairy cattle but is difficult to record and to select against directly. Even with a complete clinical mastitis recording system, subclinical mastitis would still be ignored (Zhang et al., 1994). Somatic cell count may be used to improve genetic resistance against mastitis. Somatic cell count is usually transformed by \log_2 to somatic cell score (SCS). Each unit increase in the SCS indicates doubling of the somatic cell count. The SCS has an approximately normal distribution and therefore can be analyzed with less complicated statistical procedures with reasonable statistical assumptions. As with other milk traits, monthly measures of SCS can be pooled into a one lactation record utilizing TD measurements.

Multiple lactation 305-day records are currently used with a single trait repeatability animal model to estimate variance components and to predict genetic potential of sires and cows. Currently at the Animal Improvement Program Laboratory (AIPL), a maximum of 5 lactation records are included for each cow to be allowed in national dairy cattle genetic evaluation. The model used by AIPL has three random components of animal additive, permanent environment and sire by herd interaction beside the residual effects. The sire by herd interaction effect is included to account for the possible common environmental effects of paternal half sisters (Funk, 1988; and Wiggans, 1997) and may thereby help to account for preferential treatment of some daughters of certain sires.

The current scheme requires either lactation records of exact 305 day length, which is highly unlikely, or extension or adjustment of the available records. The length of a real lactation of a cow may vary considerably from the arbitrary defined length of 305 days. Variations may occur naturally among cows with different persistency levels. The optimal lactation length may not be the same under different production systems which could result in complicated extension and adjustment factors to generate the commonly defined 305-day lactation records.

With the 305-day, it may be difficult to accurately adjust for effects specific for individual test day records. Such effects may include stage of lactation, stage of pregnancy, bST treatment and production groups. These effects are assumed to be random and would thereby vanish by accumulating or averaging the TD records.

Consequently, records are corrected assuming common effects for the whole³ lactation.

Van Tassell et al. (1992) suggested correction of test day records for environmental effects specific to each test day then the records would be accumulated and evaluated as completed lactation records. This procedure is expected to account for environmental variation specific to each individual TD record and as a result may reduce residual variance of complete lactation records. This method has been adopted since 1984 as the official genetic evaluation procedure of dairy cattle in Australia (Jones and Goddard, 1990). However, even with this method, complicated extension factors are needed to generate the 305-day corrected records.

Test day records may be utilized and analyzed directly for both management and genetic improvement programs. The direct use of test day records in genetic evaluations has several advantages over the use of accumulated 305-day lactation records. Most importantly, TD records can be adjusted for the curvilinear shape of the lactation curve with models including either regression of days in milk (DIM) (Ali and Schaeffer, 1987; Ptak and Schaeffer, 1993; and Swalve, 1995c) or including a factor of classes of stage of lactation (Keown et al., 1986; and Schutz et al., 1990). Test day models may include both genetic and environmental effects specific to each individual record. Variable amounts of information from incomplete lactations and different recording schemes may also be used which may allow use of records as they are being measured for early genetic evaluation of potential breeding animals.

Thereby, generation interval and cost of testing that are of major concerns in dairy cattle breeding industry may be reduced by preliminary selection at younger ages using fewer records (Swalve, 2000).

Models for TD records are generally more complex than those for 305-d lactation records. Analysis of TD records is more computationally demanding and requires estimation of more parameters (Jensen, 2001) which may force a compromise in amount and type of data and methodology of analysis. If for these reasons estimates of parameters are biased or have high sampling variances, the expected gain from the use of TD records may not be realized (Misztal et al., 2000).

Intervals between test day records can vary considerably among herds and testing dates. Individual cows can have missing or invalid TD records which makes it difficult to agree on a universal definition of what a TD record is. One approach is to define records according to test date without considering the corresponding days in milk. The consecutive order of a test day record within the lactation would be the only determinant of its definition. This ordinal sequence was used in a research by Pander et al. (1992) to define TD records. Alternatively, a test day record can be named after the corresponding predefined DIM interval in which it is measured. Lactations are commonly divided into 10 equal intervals of 30 days (Meyer et al., 1989; Swalve, 1995c; and Wiggans and Goddard, 1996). Test day records defined according to either the first or the second approach need to be adjusted for the effect of DIM across or within intervals, respectively (Swalve, 1995b). Flexibility in defining

the TD records and the use of appropriate adjustment factors allows for utilization of⁵ TD records even with missing observations or irregular testing intervals.

Test day records may be analyzed with different models that can vary in complexity and applicability to real dairy cattle data. The most complex TD model considers each individual 'daily' observation as a separate trait correlated with other records. Fixed effects groups with such a model would mostly have only one animal per group making the information impossible to use and could result in substantial loss of data. This model would be the most complete one but is obviously over-parameterized and is computationally infeasible especially with multiple lactations and traits. Therefore, simpler and feasible models are needed (Misztal et al., 2000). On the other hand, the simplest TD models use monthly TD records as separate traits with single trait models (Swalve, 1995c). This approach explicitly assumes no genetic or environmental correlations for TD records within and across lactations.

Monthly TD records can be viewed as different but correlated traits. This allows for estimation of both environmental and genetic correlations for different TD records. No particular pattern or structure is assumed for the variances and covariances of different TD records (Trus and Buttazzoni, 1990; Meyer, 1991; and Reents et al., 1994). Generally, completed lactations may be divided into 10 environmentally and genetically correlated TD records associated with the 10 intervals. This approach requires large number of parameters to be estimated, for example, 55 estimates of variance components for additive genetic effect with 10 TD

records per cow per lactation. The computational burden may be very high especially if all 10 TD records are to be analyzed simultaneously.

For estimation of parameters, these problems may be overcome by considering two records at a time. In this case more animals can be evaluated in one analysis at the expense of greatly increasing the number of analyses of different pairs of TD records (Gadini, 1997). Another simplification is by using canonical decomposition of covariance matrices. This was shown to significantly reduce the potential number of traits to be analyzed (Ducrocq and Besbes, 1993; Wiggans and Goddard, 1997; and Misztal et al., 2000).

Test day records also can be viewed as repeated measures of a single trait within (a) lactation(s). Methods of analyses of repeated measures data have been an active area of research in the past two decades due to substantial enhancements in computing hardware and software. Statistical methods and software have been developed to more accurately deal with repeated measures data (Littell et al., 1998). The repeatability animal model however is still a common and widely investigated model in current animal breeding research. The main issues of interest are for the most part about which factors to include in the model, how to model (co)variances of repeated records and how to apply such a model to large amount of actual animal breeding data.

Factors affecting TD and 305-day records

It is important to appropriately adjust for factors influencing the records for accurate and unbiased predictions of breeding values. Ignoring influential factors may result in biased predictions whereas including unnecessary factors may reduce prediction accuracies and over-parameterize the model and increase cost of computation (Henderson, 1975a,b; and Van Bebber et al., 1997).

Both factors influencing the records and methods of modeling them should be investigated. Van Vleck (1987) demonstrated that fitting contemporary groups such as herd-year-season (HYS) as fixed factors can help in avoiding possible bias in genetic evaluations especially when sires are not randomly associated with classes of contemporary grouping. This assignment should also be the method of choice when daughters of particular sires are preferentially treated (Meyer, 1987). With fewer records per subclass, however, this approach may result in loss of otherwise valuable data. Consequently, effective numbers of records may be reduced and thereby prediction error variances may be increased. Strabel and Szwaczkowski (1999) suggested the possibility of regrouping similar or closer in time records into larger classes. Alternatively, considering such effects as random may increase the effective number of records and so may increase accuracies of predictions at the expense of possible bias. Choice of factors to include in the model is not trivial and whether to treat effects as fixed or random must take into consideration both biases and accuracies of predictions (Van Vleck, 1987).

Generally, 305-day and TD records are influenced by the same environmental factors. Herd, year and season of calving and their interactions are known to be the main non-genetic factors affecting yield traits. Models for 305-day lactation records usually account for these effects as fixed factors. Other factors that may need to be considered include parity in the case of multiple lactations, registration status, whether the cows are daughters of tested or unproven bulls, management groups within herds, treatment with bST, preferential treatment if documented and any interactions among all of these factors (Van Vleck, 1987).

Many factors may have influence of statistical significance on lactation records. The factors to include in a model may become an issue with large datasets that are not uncommon in dairy industry. However, not all factors of statistical significance are of practical interest or computationally possible to include. The current animal model implemented by USDA for both yield traits and SCS first adjusts the records for effects of season of calving, lactation length and number of milkings per day. Adjusted records are described as the sum of fixed effects of management group within herd (registry status, parity and season of calving) and age at calving; and of random effects of environmental effects common for paternal half sisters, genetic merit, permanent environment and unexplained residuals (Funk, 1988; and Wiggans, 1997).

As with 305-day lactation models, TD models can account for the main effects of herd, age at calving, lactation number, registry status, management group and

other factors in common for both types of records. Test day models have the additional capacity to adjust for effects specific to each individual TD record, most importantly adjusting for herd-test date (HTD) effects which is comparable to fitting herd-year-season of production in 305-day lactation models. Many researchers have reported smaller estimates of residual variance when fitting HTD instead of HYS with TD models (Meyer et al., 1989; Ptak and Schaeffer, 1993; and Swalve, 1995c).

Yield traits, and especially milk are known to be highly influenced by the stage of lactation. The means of TD records follow a curvilinear pattern over the course of lactation (Swalve, 1995b). A covariate for days in milk is commonly used to adjust for these variations within the lactation curve. Days in milk can also be fitted as a fixed classification factor after dividing the lactation into classes (Keown et al., 1986; and Schutz et al., 1990). The interaction between DIM classes and other effects can be modeled as well (Stanton et al., 1992).

Alternatively, the curvilinear shape of the lactation curve and variations within TD intervals may be accounted for by fitting polynomials of DIM as regression variables. The regression variables must be consistent with how TD records are defined (Meyer et al., 1989; and Swalve, 1995b). Ali and Schaeffer (1987) and Ptak and Schaeffer (1993) suggested the use of multiple regression on DIM to adjust for the effects of stage of lactation. Their TD models included linear and quadratic regression coefficients for both $DIM/305$ and $\ln(305/DIM)$.