USE OF TEST-DAY MILK YIELD FOR GENETIC EVALUATION IN DAIRY CATTLE: A REVIEW

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ABSTRACT

The use of appropriate method for genetic evaluation of dairy animals is an important aspect of dairy cattle production. Traditional 305-day lactation model does not account for the changes in environmental factors within 305-day lactation and may involve unjustified projection of incomplete lactations. The use of test-day model in the recent past has made it possible to economize the genetic evaluation with a better accuracy. This paper reviews the recent developments in genetic evaluation of dairy cattle in the developed production set ups and explores the possibility of using test-day model for genetic evaluation of dairy cattle in Pakistan. Different options within test-model approach are also discussed.

Key words: Test-day milk yield, genetic evaluation, dairy cattle, test-day model.

INTRODUCTION

In dairy cattle, selection for milk yield focuses on the use of 305-day lactation records. However, recently, records from single and early test days (TD) have been used to enable earlier selection decision. The standardization of lactation yields to 305-day seems to be arbitrary; furthermore, the simple compilation of TD records into 305-day lactation records, as practiced in most countries, is contrary to the improvement of evaluation models by removal of as much environmental influence as possible through highly accurate correction factors and optimal definition of contemporary groups. The Australian evaluation system for dairy cattle is an exception, because TD records are first adjusted for age and stage of lactation, deviated from their respective TD average, and finally, combined into an index defining the lactation yield (Jones and Goddard, 1990). A similar approach has been suggested in the United States (Van Tassell, 1992).

This paper reviews the recent developments in genetic evaluation of dairy cattle in the developed production set ups and explores the possibility of using test-day model for genetic evaluation of dairy cattle in Pakistan. Different options within test-model approach are also discussed. This is expected to provide food for thought in countries like Pakistan where production recording and genetic evaluation systems are being introduced.

FACTORS AFFECTING TEST-DAY MILK YIELD

The TD milk yields for cows are affected by factors such as breed, region of the country, herd management and management group within a herd (Everett et al., 1994; Reents et al., 1995; Jamrozik et al., 1997a), day of the year (including weather conditions), lactation number (Jamrozik et al., 1997b; Swalve and Gengler, 1998, De Roos et al., 2001), age at calving (Kaya et al., 2003), month of calving (Borman et al., 2003), days in milk (Hamed, 1995; Kaya et al., 2003), pregnancy status (Amin, 2003) and milking times per day (Wiggans, 1986). Yield for complete 305-day lactation is composed of 7 to 10 TD yields so that the factors affecting TD yields are averaged together. Averaging would be appropriate if the factors are the same for each TD and represent random environmental variation. But these factors show a changing pattern from one TD to the other. Changes in environment within 305-day lactation are usually ignored, and a simple herd-year-season effect is often used to account for the average of environmental effects on each test day. Incomplete lactations are projected from the available TD records to 305-day lactation milk yields with the requirement that the cow has been milked for a minimum number of days or has at least two TD records. The projection factors assume a standard shape of the lactation curve for a cow of a particular breed and lactation number. Cows that have greater persistency are generally underestimated, and cows that are less persistent are generally overestimated. This situation can cause a problem for sire evaluation if persistency is heritable. The daughters of a bull would tend to be more similar for persistency, and, if evaluations are based on projected 305-day lactation milk yields and if all first daughters are in approximately the same stage of lactation when their records are projected, then sires could be misevaluated. Test day models (TDM) have been proposed to model TD milk yields directly. It accounts for all the factors affecting TD yields on each test-day.

TEST-DAY MODEL AND ITS ADVANTA- GES OVER TRADITIONAL METHODS

Test-day models are the statistical procedures that consider all genetic and environmental effects directly on a test-day basis (Ptak and Schaeffer, 1993). A brief overview of developments in genetic evaluation and test-day model in the recent past is given in Table 1. The use of test-day yield depends on the relative amount of genetic variation during lactation. A test-day model (TDM) improves the accuracy of genetic evaluation, provides better modeling and extending of part lactation is no more needed. It maximizes the amount of information to be gathered for each animal. Moreover, it avoids the use of factors to extend partial lactation records (Wiggans and Goddard, 1996). It includes factors that are specific to each test-day, such as management groups within a herd on a test-day (Jamrozik *et al.*, 1997a; Reents *et al.*, 1995). In addition, it is a possible solution for the problem of differences in the amount of information contributing to the 305-day prediction (Reents *et al.*, 1995). TDM reduces the cost of milk recording by making fewer measurements. It results in longer intervals between milk recording and less frequent collection of milk samples. Regardless of the length of the interval between tests, a TDM can appropriately weigh the recorded TD information by considering the covariances among TD yields.

Two distant TD yields can contribute more information than those which are close and highly correlated. Use of TD data allows the use of information from lactations with long intervals between milk recordings because estimation of yields for unrecorded intervals would not be required. On the other hand, a test-day model cannot overcome the loss in accuracy from fewer TD and allows yields from any combination of TD to be included appropriately (Wiggans and Goddard, 1997). In TDMs, records from individual test days are used to determine lactation production instead of aggregating records. TDMs are more flexible in handling records from different recording schemes. TDMs reduce the generation interval through frequent genetic evaluations with the latest data compared to 305-day complete lactation. TDMs can predict total production more accurately by accounting for time-dependent environmental effects (Swalve, 2000).

APPROPRIATE MODELS FOR TEST-DAY MILK YIELD ANALYSIS

Test-day records are analyzed using various proposed statistical models. The most widely used model is a repeatability TDM (Reents *et al.*, 1998). The repeatability model has been the most extensively used model (Ptak and Schaeffer, 1993; Kaya *et al.*, 2003). Under this model, consecutive test-day samples from the same lactation are considered as repeated observations on the same trait, and a permanent environmental effect accounts for environmental similarities between different test-days within the same lactation (Vargas *et al.*, 1998). A major disadvantage of the repeatability model is the heterogeneity of the residual variance during the lactation (Ptak and Schaeffer, 1993). The residual variances are smaller when herd TD is used as a definition for contemporary groups instead of herd-year-seasons (Ptak and Schaeffer, 1993; Ilatsia *et al.*, 2007). The extension of records can be avoided; cows can be grouped into different contemporary groups within herd according to their stage of lactation, as it is actually done on any farm, and accuracy of evaluations can increase if heritabilities of TD records are in the range of 305-day records. This TDM has been applied to somatic cell score (SCS) in Canada (Reents *at al.*, 1995).

Schaeffer and Dekkers (1994) presented an extension of TDM. The shape of the lactation curve differed for individual cows by including random regression coefficients for each animal (Henderson, 1982). The lactation curve for an individual cow could be viewed as two sets of regressions on days in milk (DIM). Fixed regressions for all cows belonging to the same subclass of age-season of calving describe the general shape for that cow, and the random regressions for a cow describe the deviations from the fixed regressions, which allowed cows to have differently shaped lactation curves. This extension of the TDM was a random regression model (RRM) which also modelled TD yields. Schaeffer (2000) introduced a random regression TDM, which allows the fitting of lactation curves to individual lactations. Because curve parameters are treated as random variables, reasonable estimates are obtained even with few data points. It is a better model with more comprehensive description of animal genotype e.g. persistency. The random regression models have become common for the analysis of longitudinal data or repeated records on individuals over time. Applications in animal breeding research are emphasized while recognizing that RRMs are used in many biological situations including human health. The best known application of RRM has been to genetic evaluation of dairy cattle using test-day production records (Schaeffer, 2004). Lidauer *et al.* (2003) presented a reduced rank which had negligible effect on breeding value estimation but clearly improved the solving properties of mixed model equations.

Table 1: Reaching to test day model - some examples

Year	Method of evaluation	Particular features
1974	Modified contemporary comparison (MCC)	It was a sire model. This procedure incorporated many improvements over the previously used herd-mate comparison. The major advantages were: 1) consideration of the merit of herd-mates, 2) inclusion of genetic groups based on pedigree index, and 3) improved weighting of information. The MCC was shown to produce bull evaluations essentially identical to those derived using a linear model with BLUP properties when both models included the same fixed and random effects.
1989	Animal model (AM)	The MCC was a sire model and was replaced in 1989 with an AM. Canada also adopted AM in 1989 and by 1992 AM was the standard method. A key technique used in AM computing is "iteration on the data." The advantages of the AM were that it considered all relatives, no matter how distant, and all animals of a breed, male and female, were evaluated simultaneously.
1993	Test day model (TDM)	The test-day model (TDM) is also an animal model but focuses on each test-day observation rather than on lactation data. The TDM, first introduced in Australia in 1984, models each test-day observation instead of the lactation record, or pre-adjust lactation records for the test-day effect. A TDM allows for a more exact specification and consideration of the environment (a day vs. lactation). Often, TDM includes consideration of persistency of lactation and rate of maturity. Although test-day data have been collected in the United States since 1905 for management and have contributed to national genetic evaluations since 1936, the TDM was patented in the United States in 1993, later in Canada, and a patent was applied for in Europe. This has forestalled its use in the United States except for regional and unofficial evaluations by the patent holder. Many other countries besides Australia have now adopted a TDM [Belgium, Canada, Estonia, Finland, Germany-Austria, Italy (Holstein), The Netherlands, Switzerland, and South Africa (Guernsey and Jersey, Powell and Norman, 2006)
1993	Repeatability TDM	Under this model, consecutive test-day samples from the same lactation are considered as repeated observations on the same trait, and a permanent environmental effect accounts for environmental similarities between different test-days within the same lactation. A major disadvantage of the repeatability model is the heterogeneity of the residual variance during the lactation (Ptak and Schaeffer, 1993; Reents *et al.*, 1998; Kaya *et al.*, 2003).
2000	Random Regression model (RRM)	Random regression test day model allows the fitting of lactation curves to individual lactations. Because curve parameters are treated as random variables, reasonable estimates are obtained even with few data points. It is a better model with more comprehensive description of animal genotype e.g. persistency. The RRM has become common for the analysis of longitudinal data or repeated records on individuals over time. Applications in animal breeding research are emphasized while recognizing that RRM are used in many biological situations including human health. The best known application of RRM has been to genetic evaluation of dairy cattle using test-day production records (Schaeffer *et al.*, 2000; Schaeffer, 2004).
2000	Multiple trait reduced rank TDM	It allows to half the number of parameter without reducing the goodness of fit considerably. It was suggested for further extension of the random regression test-day model for the traits like milk fat and protein yields. (Pool, 2000)
2000	Multiple trait TDM	A multitrait (MT) approach together with continuous covariance function was used to derive reference for random regression estimates. Due to the statistical complexity of random regression test-day models, use of multiple-trait model is a more feasible approach for the estimation of (co)variance components for covariance function coefficients (Kettunen *et al.*, 2000)..
2003	Multiple trait reduced rank TDM	Reduction of rank in the random regression test-day model decreases memory requirements and improves convergence in iteration when solving the mixed model equations (Lidaur *et al.*, 2003)..
2007	Multiple-trait multiple-lactation TDM	Variance components were estimated using animal models based on a derivative free restricted maximum likelihood procedure. Various univariate and multi-trait fixed regression TDM were used that defined contemporary groups either based on the year-season of calving or on the year-season of TD milk sampling. A multiple-trait model was suggested to be more ideal in determining the genetic merit of dairy sires and bulls based on daily yield records (Ilatsia *et al.*, 2007; Muir *et al.*, 2007).

Swalve (2000) reported that test-day models might be separated into three groups. First, two-step models under which corrections were carried out at TD level and subsequently corrected TD records were processed in an aggregated form as lactation records. Second, fixed regression models assumed that TD records within lactation were repeated records. Because yields in the course of the lactation followed a curvilinear pattern, this curve could be considered by using suitable covariates. Third, random regression models additionally defined the animal's genetic effect by using regression coefficients and allowing for covariances among them. The difference between random regression and fixed regression models was that the genetic merit of an individual was allowed to differ in the course of the lactation in random regression models. Random regressions were related to the approach of defining covariance functions for longitudinal data. Computationally, TDMs are very demanding. For evaluations on a national scale, the size of the equation system could go to hundreds of millions of equations, depending on the size of the database and the specific model defined.

ESTIMATES OF GENETIC PARAMETERS OBTAINED FROM VARIOUS TEST-DAY APPROACHES

Genetic parameters have been estimated for TD milk yields using various methods. It was observed that the heritability of TD milk yields remained low during early or late lactation because of greater residual variation and was higher during midlactation (Meyer *et al*., 1989; Swalve, 1995; Mechado *et al*., 1998; Druet *et al*., 2003; Kaya *et al*., 2003; Gengler *et al*., 2005; Shadparvar and Yazdanshenas, 2005; Silvestre *et al*., 2006; Bilal *et al*., 2008). Such studies have often analyzed TD records in sequential order by which the first TD record includes cows that might have DIM from 4 to 40 days. If the model for the analysis of the first TD record had no variable to account for DIM, then the estimate of heritability could be biased. During the first 40 days of lactation, the yield of a cow increases toward the peak, and the difference in yield for the same cow between 4 and 40 days could be large simply because of the shape of the lactation curve during that period. If the known differences in yield that were due to the shape of the lactation curve are not included in the analysis and the yield on each day is assumed to have the same mean, then the residual variation would be very large for the analysis of that first TD record and heritability would be low. The range of DIM was also a problem for remaining TD analysis because the differences in yields of cows included differences in persistency and because some cows might no longer be milking. Genetic correlations between adjacent TD records have been shown to be high and to decrease as interval between TD increases (Swalve, 1995; Eslamil *et al*., 2004; Bilal *et al*., 2008). The high genetic correlations have been due partially to the shape of the lactation curve, which has been ignored in many analyses. Estimated breeding values have been estimated using test day milk yield and these values were compared to the estimated breeding values (EBVs) obtained from 305-day lactation milk yields in many studies. Swalve (1995) estimated breeding values for 305-day and test-day yields and comparison of both sets of breeding values indicated only minor changes in sire rank, but more drastic re-ranking for individuals. Schaeffer *et al*. (2000) observed a strong positive correlation of yield EBV with previous 305-day lactation model EBV for Holstein bulls (0.97) and cows (0.93). Similarly, there was a strong positive rank correlation observed between ranking of sire and cows on the basis of test day and 305-day yield (Kaya et al., 2003; Sawalha *et al*., 2005).

Misztal *et al*. (2000) reported that analysis of parameters in test-day models involved two types of models i.e: random regression model and multiple-trait model. In random regression model, various functions described variability of (co)variances with regard to days in milk. On the other hand, in multiple-trait model, observations in adjacent days in milk were treated as one trait. The methodologies used for estimation of parameters included Bayesian via Gibbs sampling, and restricted maximum likelihood (REML) in the form of derivative-free, expectation-maximization, or average-information algorithms. The first method was simpler and used less memory but might need many rounds to produce posterior samples. In REML, however, the stopping point was well established. Pool (2000) opined that a multiple-trait random regression test-day model with three parities and a full fit was huge (i.e., 2x15 parameters to be estimated per animal) and probably over parameterized. Therefore, a stepwise-reduced rank procedure, which allows to half the number of parameter without reducing the goodness of fit considerably, was suggested for further extension of the random regression test-day model for the traits like milk fat and protein yields.

Lidaur *et al*. (2003) applied a multiple-trait reduced rank random regression TDM for the breeding value estimation for first parity milk, protein, and fat yield of Finnish dairy cattle. This model was compared with three other models: a similar multiple-trait random regression TDM without rank reduction, a multiple-trait repeatability TDM, and a multiple-trait 305-day lactation yield model. Required covariance parameters were derived from the same covariance functions for all four models. For both random regression models, standard deviations of breeding values were the same and correlations between breeding values were between 0.995 and 0.998, resulting in only slight differences in the ranking of animals. Genetic trends were identical

for the random regression test-day models and very similar to those estimated by the 305-day lactation yield model. The repeatability test-day model gave a slightly different genetic trend and inflated standard deviations for breeding values of cows with lactations in progress. Reduction of rank in the random regression test-day model decreased memory requirements and improved convergence in iteration when solving the mixed model equations.

INCLUSION OF VARIUOUS FACTORS IN TEST-DAY MODEL TO IMPROVE ACCURACY

A more refined approach is to consider herd production level in the TDM. Veerkamp and Goddard (1998) concluded that failure to consider herd production level in a TDM evaluation might result in overweighting of early lactation information from high production herds compared with information coming from bulls tested across all production levels. Strabel and Misztal (1999) observed a high correlation between most of test-day records across lactations and suggested that a repeatability model could be considered as an alternative to a multiple-trait model to analyze multiple parities. Kettunen et al. (2000) suggested that due to the statistical complexity of random regression TDMs, use of multiple-trait model was a more feasible approach for the estimation of covariance components for covariance function coefficients. Norman et al. (2000) suggested that some improvement in accuracy of genetic evaluations could be achieved by adjusting lactations for effect of herd-test-day. There was a clear influence of stage of lactation on variation in test-day yield and its progressive nature with increasing length of lactation period; therefore, inclusion of stage of lactation in the model was suggested for greater accuracy (Amin, 2003). Furthermore, accuracy of genetic evaluations could be improved by including herd stage effects in the model for milk fat, and protein, but not for somatic cell score (Borman et al., 2003).

More selection errors and less genetic gain would be expected from selection decisions based on an analysis of first lactation only (Kaya et al., 2003; Bilal et al., 2008), and greater accuracy would be achieved from multiple lactations (Carvalheira et al., 1998). The multiple-trait model has been proposed as a solution to problem of heterogeneity of residual variance during a lactation faced in repeatability model. Ilatsia et al. (2007) suggested that a multiple-trait model was more ideal in determining the genetic merit of dairy sires and bulls based on daily yield records. Fujii and Suzuki (2006) suggested that there was no need to consider heterogeneous residual variances in genetic evaluations, because the heterogeneity of residual variance over the years did not affect the ranking of top sires and cows. However, the increase in the amount of information, which can be nearly 10 times higher than with the traditional schemes, represents a large computational burden (Meyer et al., 1989; Ptak and Schaeffer, 1993; Wiggans and Goddard, 1996). Presently, this computation burden no more exists due to the substantial increase in computer memory which can handle very complex models involving huge data sets, although it needs technical experts in data handling and processing with suitable computers.

SCOPE OF TEST-DAY MODEL UNDER LOCAL CONDITIONS

The major part of work on test-day model has been carried out in countries with well-established breeding programme, official milk recording schemes and accurate pedigree information. In Pakistan, the pre-requisites for the application of test day model are lacking because official milk recording schemes have only been implemented in a small proportion of the population, pedigree information is not always available and breed variation is high at the farm level. However, Research Centre for the Conservation of Sahiwal Cattle (RCCSC) at Distt. Jhang and Buffalo Research Institute (BRI) at Pattoki Distt. Kasur are making efforts to register cattle and buffaloes for effective performance recording of large as well as small herds. There is a dire need of adept personnel in animal breeding and genetics and reproductive biotechnology to make these two projects effective and more productive. The recording system currently involves recording of test-day milk yield only which is then combined to 305-day lactation milk yield and used for the selection of dairy sires and cows/buffaloes. From the previous discussion, it is evident that the selection on the basis of 305-day lactation milk yield is less accurate and reliable rather it gives under and overestimation of certain factors. It can be replaced with a system similar to the Australian evaluation system where age and stage of lactation is accounted for and TD milk yield is adjusted for these factors. This is more convenient to get one step closer to TDM which should replace the traditional 305-day lactation milk yield approach.

CONCLUSION

The test-day models have been suggested as the method of choice for the analysis of milk yield traits in order to maximize the use of all available information. This method becomes even more important in countries with smaller herd size and without well-established milk recording schemes. In fact, the test day model appears to be a better alternate of 305-day lactation model because early selection on the basis of test-days could reduce generation interval. It could economize the genetic evaluation of dairy animals and improve accuracy of evaluation. Among the various models used

for test-day milk yield analysis, the most recommended model under local conditions could be the multi-trait (multiple lactation) random regression test-day model (MT-RRTDM). This model has the ability to fulfill all the requirement of a comparatively accurate model and accounts for the deficiencies in traditional models in one way or the other. However, under Pakistani condition (where 305-day lactation model has been used for genetic evaluation), it would be difficult to directly shift from 305-day lactation model to MT-RRTDM. Australian evaluation system may be more appropriate where TD milk yield records are first adjusted for age and stage of lactation, deviated from their respective TD average and finally combined into an index defining the lactation. It is however, suggested that standard operating procedures be developed to make the implementation procedure transparent.

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