

Partial lactations in genetic evaluation based on test day model *

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ABSTRACT

The repeatability test day model was used to run genetic evaluation of bulls based on 305-day and partial lactation records (100, 150, 200 and 250 days). A total of 170 937 test day records of 18 974 Black-and-White heifers from the Wielkopolska region were analysed. The single-trait animal model included the fixed effects (herd-test-date, linear and quadratic regression on age at test day and four fixed regression coefficients describing lactation curves) and random effects (additive genetic and permanent environment and residuals). The standard error of prediction, correlations between true and predicted breeding values, and correlations between predicted breeding values from whole and partial lactations were used as criteria in the comparison of the obtained results. Evaluation based on 200-day and shorter partial lactations leads to a slight increase of prediction error variance and decrease in reliability when compared with 250-day and 305-day lactations. Very high correlations (+0.91 – +0.98) between evaluations based on partial and 305-day lactations support the conclusion that partial records can be included in genetic evaluations.

KEY WORDS: dairy cattle, genetic value, partial lactations, test day model

INTRODUCTION

Partial lactations are usually included in genetic evaluation of dairy cattle for two reasons. First, to obtain the predicted breeding values of young bulls as

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quickly as possible with an acceptable level of accuracy. Second, because exclusion of records from abnormally terminated lactations, due to health problems, for instance, could bias the estimation by leading to overestimation of the bulls' genetic merit.

When the lactation model is employed, but complete information for lactation is unavailable, projected yields can be used (Wiggans and Van Vleck, 1979; Weller, 1998). Projection factors could be based on cumulative yield, last sample-day yield, and herd average (Wiggans and Van Vleck, 1979). In the test day model approach, prediction is based on single test day records. From a theoretical point of view, one test day record is sufficient to make a prediction when using the repeatability test model, and there is no need for estimation of any projection factors. Thus, records from short lactations as well as from lactations in progress could be used directly.

The repeatability test day model is one of several approaches to model test day records (Swalve, 1998). Jamrozik and Schaeffer (1997) proposed a random regression model (RRM) for the genetic evaluation of dairy cattle as more accurate when compared to the repeatability test day model. Generally, test day models and particularly RRM require the estimation of more (co)variance components compared to classical evaluation based on day lactation records. For more complex models it can lead to difficulties in obtaining reliable estimates of genetic parameters (Miształ, 1999). On the other hand, high correlations between test days from different stages of lactation make the repeatability model applicable to genetic evaluation (Reents et al., 1997; Rekaya et al., 1999; Strabel and Miształ, 1999).

The aim of this paper was to use the repeatability test day model to run a genetic evaluation based on a data set with partial lactations included and to study the breeding values of bulls evaluated using this kind of records.

MATERIAL AND METHODS

The data consisted of 170 937 test day observations recorded between August 1995 and July 1997 in the Wielkopolska region on 18 974 first lactations of Black-and-White cows. Brief statistical characteristics of the data-set are given in Table 1. Records from lactations shorter than 270 days were excluded from the data-set. A total of 55 083 individuals (base and recorded) were included in an additive relationship matrix. A group of 93 bulls having at least 20 but no more than 40 daughters was defined. This number of daughters was assumed as typical of young bulls in the Wielkopolska region. To simulate data sets with partial lactations, that group of bull daughters test day records taken after 250, 200, 150 and 100 days of lactation were discarded from the complete data set.

The following linear model was applied:

$$y_{ijk} = HTD_i + \sum_{l=1}^6 b_l X_{l,ijk} + a_j + p_j + e_{ijk}$$

where y_{ijk} is amount of milk for individual test day sample from cow j in first lactation; HTD_i is an effect of the herd test day; X_1 and X_2 are the linear and quadratic covariables of age on the test date, $X_3 = DIM/305$, $X_4 = (DIM/305)^2$, $X_5 = \ln(305/DIM)$, $X_6 = (\ln(305/DIM))^2$; b_l are fixed regression coefficients X_l , DIM is the number of days-in-milk; a_j is a random additive genetic effect of the j -th cow, p_j is a random permanent environment effect of the cow during lactation, e_{ijk} is random residual effect.

The following (co)variance structure of the model was assumed:

$$\text{Var} \begin{bmatrix} \mathbf{a} \\ \mathbf{p} \\ \mathbf{e} \end{bmatrix} = \begin{bmatrix} \mathbf{A} \sigma_a^2 & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{I} \sigma_p^2 & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{I} \sigma_e^2 \end{bmatrix},$$

where σ_a^2 is additive genetic variance, σ_p^2 is permanent environmental variance, σ_e^2 is residual variance, \mathbf{A} is the numerator relationship matrix and \mathbf{I} is the identity matrix.

The following criteria were used to compare results from data sets containing full and partial lactations of young bulls' daughters:

- standard error of prediction (SEP) calculated as the square root of prediction error variance (Henderson, 1975);
- correlation between true and predicted breeding values (reliability – R) (Wil-mink and Dommerholt, 1985);
- correlation between predicted breeding values based on records from partial and 305-day lactations.

Prediction of breeding values was preceded by variance component estimation. The computations of predicted breeding value, standard errors of prediction and reliabilities were performed using the MTDFREML package programs (Boldman et al., 1995).

TABLE 1

Description of the data set	
Number of records	170 937
Number of HTD classes	31 856
Average milk yield, kg	14.9
Standard deviation, kg	4.89
Average number of HTD classes in complete data set	5.37

RESULTS AND DISCUSSION

Standard errors of prediction, and correlations between the true and predicted breeding values are presented in Table 2. Generally high reliabilities were obtained for all data sets and not surprisingly, as the length of the lactation, included in earlier evaluation, increases the SEP also increases whereas the values of R decreases. The only exception was for the data set with TD records up to 250-days of lactation: SEP slightly decreased and R increased when compared to the data set with 305-day lactations. This could be explained by the fact that the magnitude of genetic variance usually changes at the periphery of lactation and if that is not accounted for in the model, it can cause bias in prediction (Swalve, 1995; Rekaya et al., 1999; Tijani et al., 1999).

TABLE 2
Standard errors of prediction (SEP), correlations between true and predicted breeding values (R)

Test day records included	SEP	R
305	0.979	0.891
250	0.975	0.893
200	1.021	0.880
150	1.062	0.869
100	1.109	0.856

Correlations between predicted breeding values for bulls based on partial records are shown in Table 3. A very high positive correlation (0.99) between the breeding values based on 250-day lactation with the breeding values based on 305-day lactation indicates that inclusion of lactation in progress is possible, and using early breeding values should not bias the prediction much. Correlation between the breeding values based on 200-day lactations and breeding values based on full lactations was also very high (+0.97) and suggests it is possible to get early proof of young bulls. Ptak and Żarnecki (1998) studied the correlation between the predicted breeding values based on partial and whole lactations

TABLE 3
Correlations between predicted breeding values for milk yield of young bulls based on test day records from whole (305) and part lactations (250, 200, 150, 100 days in milk)

Days in milk	250	200	150	100
305	0.99	0.97	0.95	0.92
250	–	0.99	0.98	0.95
200		–	0.99	0.96
150			–	0.98

and found that the correlation between the predicted breeding values based on 101-200 days and completed lactations was also high (0.919). Because not all the daughters calve at the same time, this means that some of them are in the third trimester while others have already finished their lactation. Hence, in practice including additional records of lactations in progress to the set of completed ones should yield an even higher correlation between breeding values. Moreover, it seems that breeding values should not change radically when information from lactation in progress becomes available.

Using incomplete lactation yield records in genetic evaluations of young bulls may change sire proofs when next test day data are included (Weller, 1988). It may also lead to selection on so-called "short lactation" having a drastic steep at the end of lactation (Swalve, 1994). However, Agyemang et al. (1985) found that the shape of the lactation curve would not change significantly from selection unless greatly different economic weights were assigned to the different intervals. Weller (1988) concluded that inclusion of extended records is preferable to deletion of these records from the analysis even without differential weighing confirming this. Strabel and Misztal (1999) found generally high correlations among TD within lactation. They noted that a lower correlation between TD from the periphery of lactation with the rest of lactation could be an artifact of RRM. As already mentioned, in some studies the repeatability test-day model is still considered an efficient one. In this kind of model all TD records from one lactation are considered as having the same quality of information regardless of part of the lactation they were taken from. This study confirmed that records from incomplete lactations could be used to predict accurate breeding values.

The simplicity of the repeatability model seems to be an advantage that allows including even very short lactations into the evaluations. Our research showed that this kind of lactation could be effectively used in genetic evaluations of bulls. Including young bulls' daughters lactations-in-progress could increase genetic gain by reducing calving interval. On the other hand, it should be noted that the results of this study can not be transferred to RRM where usually at least three random regressions of breeding values are required to describe the cows' genetic merit. More test day records per lactation need to be included if this model is used in order to obtain accurate predicted breeding values.

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STRESZCZENIE

Wykorzystanie laktacji cząstkowych w ocenie wartości hodowlanej na podstawie modelu dla próbnego udoju

Celem pracy była ocena możliwości przyspieszenia predykcji wartości hodowlanej buhajów na podstawie próbnego udoju ich córek w pierwszej laktacji. W badaniach uwzględniono 170 937 próbnego udoju 18 974 krów czarno-białych użytkowanych w Wielkopolsce. Predykcję wartości genetycznej przeprowadzono bazując zarówno na laktacjach 305-dniowych, jak i cząstkowych (odpowiednio: 100, 150, 200 i 250-dniowych). Zastosowano jednocechowy model zwierzęcia, uwzględniający efekty losowe (addytywny genetyczny i środowiskowy trwałe oraz resztowy) i efekty stałe: dnia próbnego udoju w stadzie, zmienne kowariancyjne liniowe i kwadratowe wieku krowy w dniu doju, a także zmienne kowariancyjne liniowe i kwadratowe (oryginalne i zlogarytmowane) liczby dni od wycielenia do próbnego udoju. Przyjęto następujące kryteria porównawcze dla uzyskanych wyników: błąd standardowy predykcji, korelację między prawdziwą a przewidywaną wartością hodowlaną, korelację między przewidywaną wartością hodowlaną w oparciu o laktację cząstkową i 305-dniową laktację.

Stwierdzono, że ocena wartości genetycznej, przeprowadzona na podstawie 200-dniowej i krótszych laktacji, prowadzi do nieznacznego wzrostu błędów standardowych przy jednoczesnym spadku dokładności oceny. Na podstawie wysokich dodatnich korelacji (+0.91 do +0.98) między predyktorami wartości hodowlanej z laktacji 305-dniowych i cząstkowych stwierdzono, że laktacje cząstkowe mogą zostać włączone do oceny wartości hodowlanej bydła mlecznego.