

# Implementation of a Test Day Model for Production Traits in the UK

**R. A. Mrode, G. J. T. Swanson and M. F. Paget**

*MDC Evaluations Ltd, Fox Talbot House, Greenways Business Park, Chippenham, Wiltshire, SN15 1BN, England*

*Tel: 01249 467 272. Fax: 01249 467 273. Email: [raphm@mdcevaluations.co.uk](mailto:raphm@mdcevaluations.co.uk)*

## Introduction

The Test day model (TDM) has become the method of choice for genetic evaluation of production traits in dairy cattle. Various researchers have outlined its advantages which include better correction of environmental effects, ability to model individual cow lactation curves and produce persistency evaluations. However, in the UK, complete test day (TD) records are only available from 1995 compared with 305d yields utilised in the current repeatability animal model (IAM) which are available since 1975. The recent guide for National and International evaluation systems by Interbull (2001) recommended that genetic evaluation for production traits should be based on at least 15 years of data. The span of TD records in the UK does not meet this requirement. Moreover, analysis of only TD records would exclude the dams of cows with

records prior to 1992 and this could affect the accuracy of cow evaluations. Mäntysaari (2002) presented a random regression (RR) model that could be used for the joint analysis of TD and lactational records.

This paper describes the RRM being implemented in the UK for the joint analysis of TD and 305d records and presents some results from its application to the Jersey and Holstein Friesian breeds.

## Material and Method

A multiple trait multi lactation reduced rank random regression TDM has been fitted to analyse milk, fat and protein in the first three lactations. The model for TD records for trait  $k$  in the  $j^{th}$  lactation is

$$y_{ijklmnopst} = htd_{jkl} + mps_{jkm} + dop_{jkn} + het_{jko} + recom_{jkp} + \sum_{r=1}^5 \beta_{jksr} v_{tjkr} + \sum_{r=1}^6 q_{tjkr} a_{ijr} + \sum_{r=1}^6 w_{jkr} pe_{ijr} + e_{ijklmnopst} \quad [1]$$

where  $y_{ijklmnopst}$  is the TD yield of trait  $k$  in the  $j^{th}$  lactation of cow  $i$  made on day  $t$  in milk, within herd-test-day (htd) subclass  $l$  and which belongs to subclasses  $m, n, o, p$  and  $s$  for month pregnant by stage of lactation (mps), days open (dop), heterosis (het), recombination (recom) and age by season effects respectively;  $mps_{jkm}$  is the effect of the month in which cow became pregnant by stage of lactation interaction with 44 subclasses,  $\beta_{jks}$  are the fixed regressions coefficients specific to subclass  $s$  of age by season effect for the  $k^{th}$  trait in the  $j^{th}$  lactation. There were 30 age by season subclasses,  $\mathbf{v}$  is the vector of the first 5 Legendre polynomials for day  $t$  in milk,  $\mathbf{a}_{ij}$  and  $\mathbf{pe}_{ij}$  are vectors of

RR coefficients for animal and permanent environmental effects respectively for animal  $i$  in the  $j^{th}$  lactation and  $e$  is the random error. The vectors  $\mathbf{q}_{tjk}$  and  $\mathbf{w}_{tjk}$  contain co-variables associated with  $\mathbf{a}_{ij}$  and  $\mathbf{pe}_{ij}$  respectively and obtained from eigen functions as described in the section below on rank reduction. TD records from different recording schemes such as 6 weekly, 8 weekly or am/pm were weighted by factors reflecting their accuracies relative to 4 weekly recording. The model for 305d yield for trait  $k$  in the  $j^{th}$  lactation was similar to that in equation [1] with htd being replaced by herd-year-season.

## Rank Reduction

A genetic co-variance matrix (G) of order 27 was obtained for milk, fat and protein yields in the first 3 parities from a RR model fitting Legendre polynomials of order 2 for each trait (I White, R Thompson, S Brotherstone, pers. comm.) Eigenvalue decomposition of  $G_j$  (order 9) for the  $j^{\text{th}}$  lactation was carried out and eigenfunctions corresponding to the 6 largest eigenvalues were used to describe the additive genetic covariance matrix for animal effect. Thus for the  $j^{\text{th}}$  lactation:-

$$G_j = T_{(9,6)} D_{(6,6)} T'_{(6,9)}$$

The co-variables contained in Q in equation (1) for milk, fat and protein in lactation j were then calculated as  $Q = [\Phi \otimes I_{(3,3)}] T$ , where  $\Phi$  is matrix of Legendre polynomials. Then Q can be partitioned as

$$Q = [Q_{(j\text{Milk})} \quad Q_{(j\text{Fat})} \quad Q_{j\text{Protein}}]$$

A similar reduction in rank was carried out for the covariance matrix for permanent environmental effects.

In the case of 305d records, yields were assumed to be obtained from 10 TD yields recorded at standardised DIM of 5,35,65 ..., 275. Thus for 305-d records the matrix of co-variables for the  $k^{\text{th}}$  trait in lactation j were accumulated over these standardised 10 stages

$$\text{of lactation as } Q_{305jk} = \sum_{i=1}^{10} \sum_{r=1}^6 (Q_{ijk} \cdot 30)$$

Correspondingly, residual variances for 305d records in lactation j were computed as  $10 \times 30^2 R_j$  (Mäntysaari, 2002), where  $R_j$  is the average co-variance matrix of residual variance for TD over the whole of the lactation.

## Solving the MME

The system of equations were solved using the software, Mix99 (Lidauer, *et al.*, 1999) on a Sun Workstation with 4 processors and 16 GB

RAM. The convergence criterion was the relative difference between right-hand and left-hand sides of the MME. Equations were assumed to have converged when it was lower than  $10^{-7}$ . The data analysed for the Jersey and Holstein Friesian breeds is shown in Table 1. The results presented for the Holstein breed are from single trait across lactation analysed and carried out before upgrade of computer to 16 GB.

After convergence breeding values (BV) for lactation (305d) yields were computed from the random regression co-efficients. Thus for the  $k^{\text{th}}$  trait in the  $j^{\text{th}}$  lactation  $BV_{kj}$  was calculated as  $1'Q_{jk} a_j$  where the  $Q_{jk}$  contains co-variables for DIM 4 to 305 for the  $k^{\text{th}}$  trait. The estimated BVs were averaged across the three lactations and compared with current single trait repeatability IAM evaluations.

## Results and Discussions

Convergence was obtained after about 698 iterations for the Jersey breed, with real time per round of iteration being 0.15 minute. Each trait for the Holstein breed converged after approximately 220 iterations and real time per iteration was 5.8 Minutes.

The correlation of Bull PTAs from the TDM and the IAM were high at about 0.97 for milk, fat, and protein for Jersey Bulls, with a reliability of at least 50% in the IAM. This correlation increased to 0.99 for bulls with reliability of at least 90% (Table 2), indicating very little average changes in PTAs for Bulls with large numbers of daughters. These correlations are similar to those reported in Canada (Van Doormaal and Kistemaker, 1999) and in Finland (Lidauer *et al.*, 2000).

Correlations between cow PTAs from the TDM and IAM varied from 0.91 to 0.93 for the Jersey breed. The slightly lower correlations for cows with reliability of at least 65% (Table 3) could be due to the fact these cows include up to 5 lactations in the IAM while the TDM has 3 lactations presently. The correlations for the cows are similar to those reported for Jerseys and Holstein (VanDoormaal and Kistemaker, 1999) but higher than estimates by Lidauer *et al.* (2002).

Figures 1 and 2 show the graphs of genetic trends for milk yield for Jersey Cows and Holstein Bulls. These are very similar to the IAM.

## Conclusion

The joint analysis of TD and 305d records, using the multiple-trait, multi-lactation rank reduction model looks feasible. It overcomes the problem of blending results from the 2 different evaluations. The less than unity correlations implies that there will be changes when the TDM evaluation is introduced. Some of the differences would be due to better correction of environmental factors, differences in parameters and in addition to changes in model e.g. omission of herd sire interaction in the TDM.

## References

- Lidauer, M.I., Strandén, I. & Mäntysaari, E. 1999. *Mixed Model Equations Solver. MIX99 Manual*. Animal Production Research, Jokioinen, Finland.
- Lidauer, M., Mäntysaari, E.A., Strandén I. & Poso, J. 2002. Multiple-Trait Random Regression Test-Day Model for all lactations. *Interbull Bulletin* 25, 81-86.
- Mäntysaari, E.A. 2002. Combining Test Day and Full Lactation Records in Prediction of Breeding Values. 7 *WCGALP*, Montpellier. Communication No 01-01.
- Van Doormaal, B.J. & Kistemaker, G.J. 1999. Application of the Canadian Test Day Model. *Interbull Bulletin* 22, 100-103.

## Acknowledgement

Thanks are due to R. Thompson, S. Brotherstone, and I. White for the genetic parameters.

**Table 1.** The Data Structure for Jersey and Holstein/Friesian Breeds.

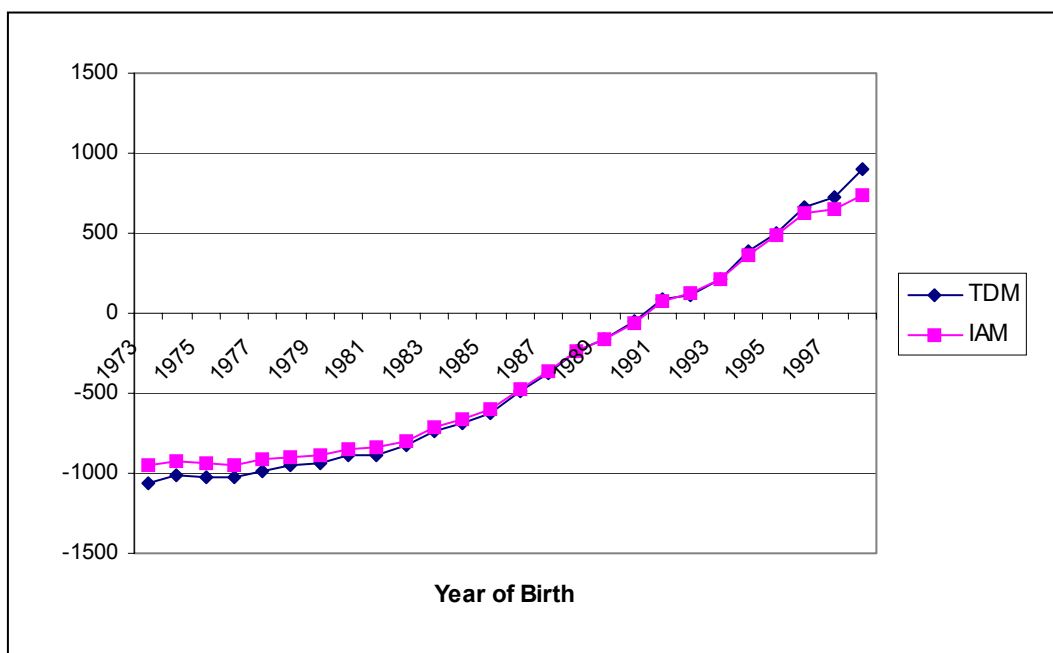
Parity	Jersey			Holstein		
	Cows	TD Records	Cows 305d Records	Cows	TD Records	Cows 305d Records
1	45,441	396,524	73,122	2,189,809	19,578,122	2,453,386
2	35,168	304,536	59,683	1,693,304	15,007,854	1,938,007
3	27,466	235,275	48,614	1,289,446	11,322,635	1,479,662

**Table 2.** Correlations Between Bull Evaluations from the TDM and IAM.

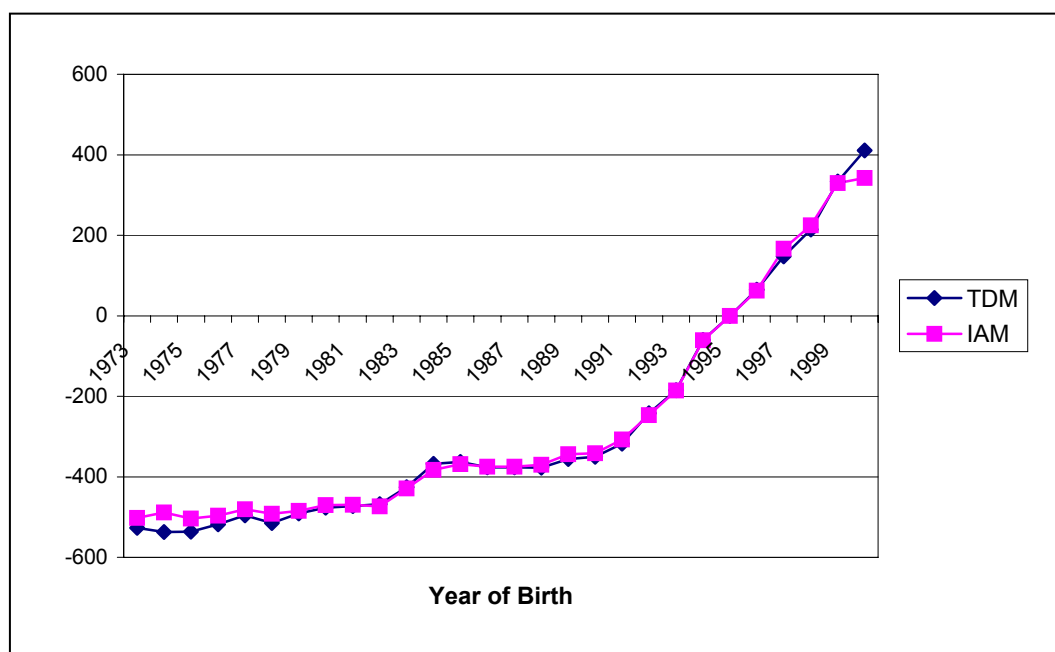
Jersey					Holstein				
N	Rel%	Milk	Fat	Protein	N	Rel %	Milk	Fat	Protein
2,171	≥ 50	0.97	0.97	0.97	40711	≥50	0.96	0.97	0.97
185	≥90	0.99	0.99	0.99	4750	≥90	0.98	0.98	0.98

**Table 3.** Correlation Between Cow Evaluations from the TDM and IAM.

Jersey					Holstein				
N	Rel%	Milk	Fat	Protein	N	Rel %	Milk	Fat	Protein
34,583	30-49	0.93	0.95	0.94	508,512	30-49	0.92	0.89	0.93
5,718	≥65	0.91	0.93	0.93	128,894	≥65	0.89	0.86	0.90



**Figure 1.** Comparison of Trends from TDM & IAM (Holstein Bulls).



**Figure 2.** Comparison of Trends from TDM & IAM (Jersey Cows).