Testday models for production traits in dairy cattle

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Abstract

Methodology has been developed to implement testday models in the national genetic evaluation of dairy breeds for production traits in South Africa. Positive definite covariance matrices have been estimated, using multitrait, multi-lactation, fixed regression testday BLUP animal models, including testday records of the first three lactations as repeated measures for the Holstein and Jersey breeds. Heritability estimates were 0.40 ± 0.007 for milk yield, 0.25 ± 0.006 for butterfat yield and 0.37 ± 0.006 for protein yield for the Holstein breed and 0.39 ± 0.004 for milk yield, 0.21 ± 0.002 for butterfat yield and 0.34 ± 0.002 for protein yield for the Jersey breed. These estimates are well in the range of estimates reported by countries participating in INTERBULL evaluations.

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Introduction

Dairy sires in South Africa were first genetically evaluated through progeny groups, using data recorded by the National Livestock Improvement Scheme. This led to the utilization of contemporary comparison methods to estimate the breeding values of sires. Dairy animals received breeding values from BLUP (Best Linear Unbiased Prediction) Methodology for the first time in 1987, when breeding values were estimated, using a Sire Model. In 1992 the Animal Model was fitted to dairy records to estimate breeding values in single trait analyses. Since 1999 multitrait analyses were developed for the South African dairy breeds, where 305-day milk, butterfat and protein first lactation yields were evaluated together in order to utilize the genetic correlations between the traits to estimate breeding values even more accurately (Loubser *et al.*, 2001). Genetic groups were also incorporated into the pedigrees in order to qualify in 2000 for participation in INTERBULL runs for the estimation of MACE (Multiple Across Country Evaluation) breeding values. Using only completed first lactation records in genetic analyses have of course several disadvantages. A cow that did not participate in milk recording during her first lactation or for some reason her first lactation was terminated before 240 days in milk, never receive a breeding value based on performance, regardless of her performance in later lactations. Furthermore, the performance of the cows in second and third lactations is never included, rendering less accurate genetic evaluations especially for "late bloomers". The basis of a 305-day yield is a set of testday yields taken approximately every 30 days in milk. Incomplete lactations are extended to a 305-day basis following a set of well-defined rules (Ptak & Schaeffer, 1993). Such projection procedures usually assume a fixed shape of lactation curves for cows and tend to underestimate 305-day yields from early testdays for more persistent cows and overestimate yields for the less persistent cows (Mrode *et al.*, 2002). One way to avoid the problem of extension of testday yields into a 305-day record would be to use testday yields for genetic evaluation of dairy sires and cows, rather than 305-day yields. The aim of this study was therefore to develop a genetic model and to estimate covariance matrices that could be used to evaluate sires and cows in South Africa, based on testday yields from lactations 1 to 3.

Materials and Methods

Data consisted of testday records for milk, butterfat and protein yields for lactations 1, 2 and 3 of Holstein and Jersey cows calving from 1995 to 2002. These records were downloaded from the INTERGIS for cows participating in the South African Dairy Animal Improvement Scheme. Basic edits were done on the data and in order to ensure a well-linked data structure for variance component estimation, the data were strictly selected according to the study of Haile-Mariam *et al.* (2000). After research was done on the estimation of breeding values for somatic cell count using testday models in South Africa (Mostert *et al.*, 2004), it was decided to include records from the first three lactations as repeated measures of the first lactation, assuming a genetic correlation of 1 across lactations. By using this methodology, it was still

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possible in terms of computer capacity and time, to do multitrait analyses for production traits. Starting with the Holstein data a subset of 34 662 testday records were used from the abovementioned selection for variance component estimation. This included 10 955 testday records for lactation 1, 14 955 records for lactation 2 and 8 752 for lactation 3. This is the data of 3 093 cows, representing 250 sires and 3 052 dams. For the Jerseys the selection ended with 88 572 testday records for the first lactation, 70 009 records in the second lactation and 30 870 records in the third lactation, representing 17 758 cows, 473 sires and 14 941 dams. (Co)variance components were estimated using VCE4 (Groeneveld & Garcia-Cortes, 1998) with the following genetic model:

$$y_{ijklmnp} = \mu + HTDLM_{im} + A_j + PE_{jm} + S_{km} + AC_{lm} + wilmink(S_{km}) + CI_{jm} + e_{ijklmnp}$$

Where

$y_{ijklmnp}$	=	p^{th} test-day milk, butterfat or protein yield of cow j in lactation m,
μ	=	mean yield
$HTDLM_{im}$	=	fixed effect of herd x testdate x parity x number of milkings effect
A_j	=	animal additive genetic effect
PE_{jm}	=	permanent environmental (random) effect within lactation to account for common effects of environment associated with all testday records of cow j in lactation m
S_{km}	=	fixed effect of calving season in lactation m
AC_{lm}	=	fixed effect of ageclass in lactation m
$wilmink(S_{km})$	=	Wilmink curve (Wilmink, 1987) modelled on days in milk within season in lactation m (regression)
CI_{nm}	=	fixed effect of calving interval class in lactation m
$e_{ijklmnp}$	=	random residual error

Season was defined as winter (April – September) *versus* summer (October – March), while the same ageclasses were allocated as in the derivation of standard lactation curves by Mostert *et al.* (2001). Calving interval classes were allocated using standard deviation units. A series of univariate and bivariate analyses were run as well as a trivariate analysis for each breed. Heritabilities and genetic correlations from the trivariate analyses are indicated in Table 2.

Results and Discussion

The advantages of a testday model include a more accurate correction for environmental effects relevant to each testday record (Ptak & Schaeffer, 1993); the ability to model the shape of the lactation curve to differ for each cow, estimation of persistency evaluations (Jamrozik *et al.*, 1997), as well as the use of early predictors of genetic merit for selection decisions, thereby decreasing the generation interval. Other advantages are that records do not need to be extended, erasing debates over extension factors; better modelling of the effect of pregnancy can occur because a testday can directly be linked to whether or not a cow is pregnant and that further subdivision of the contemporary group into management groups is feasible if they are recorded (Swalve, 2000). Testday models, however, are computationally very demanding. For evaluations on a national scale, the size of the equation system can go to hundreds of millions of equations, depending on the size of the database and the specific model defined. Furthermore, all the individual testday yields on every cow need to be stored. All analyses converged with status 1, giving positive definite matrices. Heritabilities were slightly higher for the Holstein breed for all traits, while the genetic correlation between milk and butterfat yields was similar (0.84) and between milk and protein yields was slightly higher for the Holstein breed (0.94 *vs.* 0.92) compared to the Jersey breed. Only the genetic correlation between butterfat and protein yields was higher for the Jersey breed compared to the Holstein breed (0.91 vs. 0.88). As can be expected, the genetic correlations between the permanent environmental effects were high for both breeds, while the direct estimates for permanent environment for the Holstein breed were nearly half of that of the Jerseys for all traits. Residual estimates (direct and correlations) were higher for the Holsteins compared to the Jerseys for all traits. Both breeds showed the same pattern regarding residual correlations, namely correlations in the sixties between milk and butterfat yields and between butterfat and protein yields, whereas the correlations between milk and protein yields were in the nineties for both breeds.

These estimates are within the range of estimates reported by countries participating in INTERBULL evaluations (obtainable at www-interbull.slu.se) (Table 2).

Table 1 Variance ratios (on the diagonal) and correlations (above the diagonal) for milk, butterfat and protein yield (kg/day) of Jersey and Holstein cattle, using fixed regression testday models

	Holstein			Jersey		
Additive	**Milk**	**Butterfat**	**Protein**	**Milk**	**Butterfat**	**Protein**
Milk	*0.40 ±0.007*	0.84 ± 0.006	0.94 ± 0.002	*0.39 ±0.004*	0.84 ± 0.002	0.92 ± 0.001
Butterfat		*0.25 ±0.006*	0.88 ± 0.005		*0.21 ±0.002*	0.91 ± 0.002
Protein			*0.37 ±0.006*			*0.34 ±0.002*
Perm Env	**Milk**	**Butterfat**	**Protein**	**Milk**	**Butterfat**	**Protein**
Milk	*0.13 ±0.008*	0.98 ± 0.005	0.99 ± 0.002	*0.23 ±0.003*	0.96 ± 0.002	0.98 ± 0.001
Butterfat		*0.09 ±0.006*	0.99 ± 0.004		*0.16 ±0.002*	0.96 ± 0.002
Protein			*0.11 ±0.007*			*0.20 ±0.002*
Residual	**Milk**	**Butterfat**	**Protein**	**Milk**	**Butterfat**	**Protein**
Milk	*0.47 ±0.006*	0.67 ± 0.002	0.93 ± 0.001	*0.39 ±0.002*	0.64 ± 0.001	0.91 ± 0.00
Butterfat		*0.67 ±0.007*	0.66 ± 0.003		*0.63 ±0.002*	0.62 ± 0.001
Protein			*0.53 ±0.007*			*0.46 ±0.002*

Table 2 Heritability estimates for Holsteins reported by countries participating in INTERBULL evaluations

Country	Model	Milk	Butterfat	Protein
Canada	MT-ML-RR-TD	0.36-0.39	0.33-0.37	0.35-0.37
Estonia	ST-ML-FR-TD	0.27	0.23	0.24
Germany	ST-ML-RR-TD	0.49	0.48	0.48
NLD/BEL	ST-ML-RR-TD	0.59	0.58	0.52
Switzerland	ST-ML-FR-TD	0.36	0.30	0.32

MT=Multitriat ML=Multi-lactation RR=Random Regression TD=Testday ST=Single trait FR=Fixed Regression

Conclusion

Methodology has been developed to implement testday models in the national genetic evaluation of dairy breeds for production traits in South Africa. Positive definite covariance matrices have been estimated, using multitrait, multi-lactation, fixed regression testday BLUP animal models, including testday records of the first three lactations as repeated measures for the Holstein and Jersey breeds. These methods will be implemented after participation in the test runs of INTERBULL in Sweden during March and September 2004.

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