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Use of Multiple-trait Animal Models for Genetic Evaluation of Milk, Fat and Protein Lactation Yields of Dairy Cattle in Belgium

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Comparison of computation time between single-trait and multiple-trait evaluations showed that with the use of the canonical transformation associated with multiple diagonalization of (co)variance matrices, multiple-trait analysis for milk, fat and protein yields is not more expensive than three single-trait analyzes. Rank correlations between breeding values for 54,820 cows with records (for their 1,406 sires) estimated with the single-trait and multiple-trait models were over .98 (.99) in fat yield and over .99 (.99) in milk and protein yields. The relative gain expressed as reduction in mean prediction error variance was 3% (1%) in milk yield, 6% (3%) in fat yield, and .4% (.2%) in protein yield for cows (for sires). Relative genetic gains were 3% (1%), 6% (2%) and .5% (.2%) respectively in milk, fat and protein yields for cows (for sires). The use of multiple-trait models has therefore the advantages of improved precision and reduced selection bias. Multiple-trait analysis could be extended for the analyzes of test-day records. Results show that this or similar multiple-trait animal model could be implemented immediately in Belgium at low computing cost, using the proposed algorithms and could be the first step to new, more advanced evaluation methods.
Keywords. Dairy cattle, milk production traits, genetic evaluation, multiple-trait, computation time.

Utilisation d'un modèle animal multi-caractère pour l'évaluation génétique des quantités de lait, de matières grasses et de protéines produites pendant la lactation par des vaches laitières en Belgique. La comparaison du temps de calcul entre des évaluations génétiques uni-caractère et multi-caractère pour les quantités de lait, de matières grasses et de protéines, a montré qu'avec l'utilisation de la transformation canonique associée à la diagonalisation multiple des matrices de (co)variances, une évaluation génétique multi-caractère n'est pas plus coûteuse que trois analyses uni-caractères séparées. Les corrélations de rang entre valeurs d'élevage pour les 54 820 vaches avec enregistrements (ainsi que pour leurs 1 406 pères) estimées par modèles uni-caractère et multi-caractère ont été supérieures à 0,98 (0,99) pour les quantités de matières grasses et supérieures à 0,99 (0,99) pour les quantités de lait et de protéines. Les gains relatifs pour les vaches (respectivement pour leurs pères) exprimés en terme de réduction de la moyenne de la variance de l'erreur de prédiction sur les quantités produites ont été de 3 % (1 %) pour le lait, 6 % (3 %) pour les matières grasses et 0,4 % (0,2 %) pour les protéines. Des gains génétiques relatifs de 3 % (1 %), 6 % (2 %) et 0,5 % (0,2 %) ont été observés respectivement pour les quantités de lait, de matières grasses et de protéines chez les vaches (ou chez leurs pères). L'utilisation des modèles multi-caractères présente un certain nombre d'avantages, comme l'amélioration de la précision et la réduction du biais de sélection. De tels modèles peuvent être étendus à des analyses par jour de contrôle. Les résultats montrent que de tels modèles multi-caractères peuvent, dès à présent, être exploités en Belgique à des coûts de calcul réduits, en utilisant les algorithmes proposés. Ces modèles constituent une première étape dans la mise au point de nouvelles méthodes d'évaluation plus élaborées.
Mots-clés. Vache laitière, caractère de production laitière, évaluation génétique, multi-caractère, temps de calcul.

INTRODUCTION

Until a few years ago, genetic evaluations for yield traits of dairy cattle were made using single-trait sire models (ST-SM) (e.g., Everett, Henderson, 1972). The reason for the use of this method was the limitation of computing power that made simplifications necessary. But the ST-SM neglects the dam side of pedigrees or takes them only indirectly into account through maternal grand-sires when extended to sire-maternal-grand-sire model. Therefore single-trait animal-models (ST-AM) (e.g., Ducrocq, 1990; VanRaden, Wiggans, 1991; Leroy *et al.*, 1993) were implemented all over the world. These models take the genetic merit of mates into account and results are therefore more precise than rankings obtained by ST-SM. But such evaluations are only sub-optimal. Such models analyze 305 day yields. Those yields are already estimated out of individual test-day records with several associated problems like estimating 305 day yields when records are still in progress, based on incomplete lactations or on a reduced number of test-days.

Test-day models analyzing directly test-day yields were introduced recently. Two types of test-day models are currently investigated. A first class of models is based on the modelization of the lactation curves (Ptak, Schaeffer, 1993), eventually as random regression to address the problem of genetic persistency differences (Dekkers *et al.*, 1996). Another way of modeling test-day records is based on the use of multiple-trait animal models (MT-AM) (Wiggans, Goddard, 1996).

Besides milk yields, fat and protein information are not always recorded as such tests are more expensive. But as milk, fat and protein yields are highly correlated, flexible multiple-trait approaches may be used. From a more theoretical point of view there are at least three reasons for the use of multiple-trait animal models (MT-AM). First, such methods improve the precision of the evaluations as error variances of predictions (PEV) are reduced (Schaeffer, 1984; Thompson, Meyer, 1986), therefore gain from selection would be enhanced. Second, an MT-AM would reduce selection bias—be it for individual test-days or for milk, fat and protein lactation yields—as selection is done in dairy cattle on milk, fat and protein together (Pollak *et al.*, 1984). A last advantage is that MT-AM can be adapted for missing values, therefore the fact that one or two traits are missing can be taken into account and missing test-day yields or protein or fat records will be no problem. A recent paper discussed the feasibility of such a MT-AM for test-day records for milk, fat and protein yields in several lactations in the USA (Wiggans, Goddard, 1996).

In this study we investigated a simpler MT-AM based of 305 day, fat and protein yields, as this could be a first and very easy step towards models such as the one presented by Wiggans and Goddard (1996).

The major disadvantage of MT-AM is that programming and solving are more difficult due to complicated matrix structures. Therefore the canonical transformation can help to avoid these problems and simplify the multiple-trait evaluation into a group of single-trait evaluations. But this approach requires some conditions: traits must have the same models with a random (genetic) effect and show no missing values. Fortunately these conditions can be relaxed. Three matrices, can be simultaneously diagonalized if one is a linear combination of the two others. Lin and Smith showed in 1990 that approximate multiple-diagonalization of certain (co)variance matrices can be done even when this condition is not fulfilled. Therefore, in a lot of situations more than one random effect can be taken into account using approximate multiple-diagonalization. The condition of absence of missing values in the canonical transformation was relaxed by Ducrocq and Besbes (1993) and Gengler and Misztal (1996). Recent papers by Ducrocq and Chapuis (1995) and Gengler and Misztal (1996) showed theoretical ways to use even different models (fixed effects) per trait. But for the present study only multiple-diagonalization (MD) was used as it is absolutely necessary in order to transform current ST-AM with repeated records in MT-AM where repeated records were modeled through a permanent environment effect.

The goal of this study was to show a simple methodology that could be implemented at very low cost in Belgium instead of the ST-AM used today and to show the way to a test-day MT-AM extending and generalizing the method suggested in this paper.

MATERIAL AND METHODS

Data

The data set used for the ST and MT analyses was provided by "Élevages Information" (ÉLINFO), the data processing center of the French-speaking part of Belgium. The two major dairy breeds in this region being the Holsteins and Red and Whites, only lactations from animals belonging to these breeds were used. Records—performed between January 1990 and March 1994—were required to have a minimum of 100 days in milk and consisted of 305 day lactation yields for milk, fat and protein. Preadjustement was made for lactation length as a regression for days in milk and days in milk squared, using a fixed linear model with the same other fixed effects as for breeding value estimation but separated for first and second or later lactations. Fifteen age at calving × parity classes were defined. Records were assigned to twelve months (seasons) of calving. Eight calving interval groups were created. Each cow needed to have a first record known and herd-year classes had a minimum of five known records. After preparing and editing data, we were left with 84,019 records performed by 54,820 cows. The pedigree file contained all known ancestors, and together there were 92,501 animals. Unknown parent groups in the sense of Westell *et al.* (1988) were defined as base animals with different genetic origins. Therefore genetic groups were defined based on sex, date of birth, country of origin and Holstein genes. Groups with less than 10 animals were combined and a final number of 73 groups was obtained.

Statistical model

The same model was used for ST and MT estimation. It was written for ST as

$$y_{ijklmn} = hy_i + ap_j + s_k + cc_l + p_m + u_m + e_{ijklmn}$$

where

- hy_i is the fixed effect of herd-year i (i = 1 to 4,891);
- ap_j is the fixed effect of age-parity j (j = 1 to 15);
- s_k is the fixed effect of season of calving k (k = 1 to 12);
- cc_l is the fixed effect of calving interval l (l = 1 to 8);
- p_m is the random permanent environment effect m (m = 1 to 54,820);

- u_m is the random additive genetic effect a_m plus the corresponding random genetic group effects g_t where

$$u_m = a_m + \sum q_{mt}\, g_t$$

and q_{mt} is the coefficient linking the random genetic effect m with the genetic group effect t;
- e_{ijklmn} is the residual effect.

The model used was very similar to the one being used at the moment in Belgium (Leroy *et al.*, 1993; Farnir *et al.*, 1994), with the exceptions that all lactations were considered, and that herd-year groups replaced the management groups defined by Leroy *et al.* (1993).

Covariance components

In a preliminary step (co)variance components were estimated with the collected data. They differed significantly from the values reported by Kafidi *et al.* (1991). Therefore the (co)variance components used for this study were developed out of those given by Kafidi *et al.* (1991) in order to stick as near as possible to the current situation for genetic evaluation in Belgium. The genetic (co)variance matrix was obtained as a weighed mean of the variances for the three lactations according to the proportions found in this study. The model used was a repetition model in order to stay close to what is currently done in Belgium. Therefore after obtaining an initial residual matrix using the method explained for the genetic matrix, it was subdivided into a permanent environment matrix (25%) and a new residual matrix (75%). These proportions were rather arbitrary and were those used by Misztal *et al.* (1993). They were used as they gave us the variance components presented in **table 1** corresponding to heritabilities (and repeatabilities) of .19 (.42), .19 (.42) and .20 (.39) for milk, fat and protein yields that were near to most recent results from the literature. Kafidi *et al.* (1991) used a sire model and Henderson's method III (Henderson, 1953), therefore, in the future, new (co)variance component estimation should be done using REML (Patterson, Thompson, 1971) and an MT-AM for repeated records (e.g., Misztal *et al.*, 1995). Similar estimation would be needed for test-day milk, fat and protein yields.

Consequences of the fact that the (co)variances used might be wrong were not studied, but their possible influence on results should be recognized. Nevertheless, for this study we tried to use an approach that was as near as possible to the official approach in Belgium. Fat and protein percentages were other traits described by Kafidi *et al.* (1991) and used by Leroy *et al.* (1993). They were not considered here as they are combinations of the other traits and breeding values, and therefore can be estimated using yield traits as it is done in a lot of countries (e.g., Germany, United States, Italy).

Computation of evaluations

Single-trait evaluations were performed using an iteration on data approach explained by Schaeffer and Kennedy (1986) and Misztal and Gianola (1987). Jacobi and second-order Jacobi iterations were used for their simplicity. Approximate PEV of animal solutions were estimated indirectly by the method described by Misztal and Wiggans (1988) and Misztal *et al.* (1991). They were obtained after correcting for herd-year effects but neglecting other fixed effects. This approximation was possible due to the large number of observations for other fixed effects. The solution computations were stopped when the squared

Table 1. (Co)variance components used for the computations (in kg^2) — *Composantes de la (co)variance utilisées pour les calculs (en kg^2).*

Random effect	**Trait**	**Milk**	**Fat**	**Protein**
Permanent environment				
	Milk	187,788	7,180	5,948
	Fat	7,180	358	248
	Protein	5,980	248	206
Genetic				
	Milk	213,775	7,849	5,868
	Fat	7,849	431	224
	Protein	5,868	224	195
Residual				
	Milk	563,363	21,540	17,846
	Fat	21,540	1,075	744
	Protein	17,846	744	617

relative difference between solutions in consecutive rounds dropped below 10^{-8}. The program used was the JAA program provided by I. Misztal (Misztal, Gianola, 1987).

Multiple-trait evaluations used the following steps:

a. multiple-diagonalization of covariance matrices using the FG algorithm (Flury, Constantine, 1985);
b. transformation of data to canonical scale;
c. resolution of equations and PEV estimation as for ST evaluations;
d. back-transformation of solutions and PEV (Misztal *et al.*, 1993) to original scale.

The program used was called MTJAA and its design was based on the JAA program that was used as subroutine for step c. An advantage of the multiple diagonalization approach is that (co)variance matrices do not necessarily need to be proportional. This feature can also be used for (co)variance component estimations. For future MT evaluation of lactation or test-day yields a missing value version of MTJAA would be needed. This version was developed and used for the genetic evaluation of linear type traits of US Jersey dairy cows (*).

Approximate reliabilities were estimated for ST and MT as $1\text{-PEV}/\sigma^2_{gt}$ where PEV is the ST or MT PEV for a given animal and trait t and σ^2_{gt} the genetic variance for trait t. The correlation between estimated and real breeding values, often called accuracy, and defined by

$$\sqrt{1 - \text{PEV} / \sigma^2_{gt}}$$

was also calculated for every animal and trait for ST and MT. It should be stressed that the behaviour (possible bias) of ST-PEV and MT-PEV are not necessarily identical, but as computations were done using the same algorithm for ST and for transformed traits for MT, these differences should be small.

ST and MT programs were installed on a DECstation 5000-240 using a DECfortran compiler. A time function was added in order to assess elapsed time for every step of evaluations. No other program was run during executions.

RESULTS AND DISCUSSION

Execution times are given in **table 2**. As expected, the computation time ratio between the MT evaluation and one ST evaluation is approximately equal to the number of evaluated traits in the MT model. The multiple-diagonalization was very fast and took only 0.06 s. Writing data on fast-input/output files was only around 10 s slower (1/6th of total time) due to the canonical transformation done at the same time. One round of iteration took between 10.6 and 10.9 s. The numbers of iterations needed to obtain values below 10^{-8} for squared relative differences between solutions at consecutive round were respectively 96, 99, and 98 for milk, fat and protein yields in the ST evaluations versus 101, 97, and 75 rounds for the canonical traits

Table 2. Computing time for single-trait (ST) and multiple-trait (MT) genetic evaluations — *Temps de calcul requis pour les évaluations génétiques uni-caractère (ST) et multi-caractère (MT).*

Computation step	**ST**			**MT**	
	Milk	**Fat**	**Protein**	**One trait**	**Other steps**
Multiple-diagonalization	–	–	–	–	0.06 s
Writing to fast files **(1)**	47.4 s	50.5 s	52.8 s	62.2-60.9-60.9 s	
Iterations on data					
One iteration	10.6 s	10.6 s	10.6 s	10.9-10.6-10.9 s	
Iterations needed **(2)**	96	99	98	101-97-75	
PEV estimation					
One round PEV	3.4 s	3.4 s	3.4 s	3.4-3.4-3.4 s	
Iterations needed **(3)**	10	10	10	10-10-10	
Writing canonical solutions	–	–	–	35-35-35	
Writing solutions to files **(4)**	64.3 s	64.7 s	63.4 s	–	125.4 s
Total	1,163 s	1,189 s	1,189 s		3,463 s

(1) Including also transformation to canonical scale. **(2)** Iterations stopped when convergence expressed as squared relative differences between solutions in consecutive rounds were below 10^{-8}. **(3)** Number of iterations normally considered sufficient is between 8–10. **(4)** Including also back-transformation to original scale.

(*) Gengler N, Wiggans GR, Wright JR, Norman HD, Wolfe CW (1996). Application of canonical transformation with missing values to multitrait evaluation of Jersey type. *J. Dairy Sci.* (submitted).

in the MT evaluation. The decrease for the second and third canonical trait can be explained by the fact that they represent secondary directions of variation. PEV estimation was done with a fixed number of iterations, using a number that was found by trial and error (Misztal, 1994, personal communication). A PEV iteration took 3.4 s. Writing canonical solutions on temporary files for MT took 35 s, it saves central memory storage and allows very large models. Writing final solutions to output files took between 63.4 and 64.7 s for ST evaluations and together with the back-transformation 125.4 s in the MT case. These results show that a MT evaluation based on multiple-diagonalization and canonical transformation is not more expensive than individual ST evaluations for all the traits analyzed. In our example the time needed for three separate ST analyses was even greater than the one required to perform the MT evaluation. The memory used is very limited as only four vectors are needed for solutions and two ones for PEV estimations, therefore over 1.5 million equations can be solved with about 36 megabytes memory capacity. Computation time increases due to a higher number of equations (e.g. ten times the number used here) would be linear for writing to files and (back-)transformation, and would be quadratic for the time needed for an iteration. The number of iterations would be similar or slightly higher. Therefore maximum time would be around 33 h for a ST evaluation and 97 h for a complete MT evaluation with 1.5 million equations. The genetic evaluation carried out currently in Belgium (Leroy *et al.*, 1993; Farnir *et al.*, 1994) is of about this size.

Rank correlations between breeding values obtained from ST and MT are given in **tables 3** and **4**. We considered two subsets of animals, 54,820 cows with records and 1,406 sires having daughters with records. This was done as these animals can be considered the active part of the population. We observed a reranking of cows for fat yield because rank correlations are only .981. For protein yield as correlations are very high at .999, only very limited reranking of animals is observed for this trait by using MT. The result for milk is intermediate at .990. The corresponding rank correlations for sires are .996 for milk, .991 for fat and .999 for protein. Therefore we can assume that reranking of sires is limited compared to those observed for cows. Means and standard deviations of breeding values are similar for ST and MT evaluations.

Tables 3 and **4** show statistics concerning the approximate reliabilities for cows and sires, obtained by ST or MT models. For cows improvement of reliabilities is more important as substantial additional information provided by other traits is added. The biggest improvement is noticed for fat yields with .39 instead of .35. Improvement for milk yield is smaller with .36 instead of .34. For protein yield it is only around .003. The results for the sires are given in **table 4**. As we could expect, the improvements are smaller. For milk and fat yields, they are around .02, as for protein yield the increase of mean reliabilities is very small, below .01.

The approximate relative gain due to the use of MT instead of ST models can be estimated through different approaches. A first method is based on the relative reduction of mean PEV (Schaeffer, 1984) due to the use of MT.

Table 3. Comparison of single-trait and multiple-trait genetic evaluations of dairy yields for 54,820 cows with records — *Comparaison des évaluations génétiques uni-caractère et multi-caractère des productions laitières des 54 820 vaches avec enregistrements.*

Criteria	**Trait**		
	Milk	**Fat**	**Protein**
Breeding values			
Rank correlation	.990	.981	.998
Mean single-trait (kg)	3.6	- .04	.04
Standard-deviation single-trait (kg)	369.3	17.27	10.44
Mean multiple-trait (kg)	1.6	- .12	.01
Standard-deviation multiple-trait (kg)	373.4	17.55	10.46
Approximate reliabilities			
Mean single-trait	.344	.353	.316
Standard-deviation single-trait	.088	.088	.090
Mean multiple-trait	.363	.394	.319
Standard-deviation multiple-trait	.086	.082	.090
Minimum single-trait	.193	.202	.166
Minimum multiple-trait	.216	.251	.169
Maximum single-trait	.531	.540	.502
Maximum multiple-trait	.546	.570	.505

Table 4. Comparison of single-trait and multiple-trait genetic evaluations of sire dairy yields for 1,402 sires of cows with records — *Comparaison des évaluations génétiques uni-caractère et multi-caractère des productions laitières des 1 402 pères de vaches avec enregistrement).*

Criteria	Trait		
	Milk	Fat	Protein
Breeding values			
Rank correlation	.996	.991	.999
Mean single-trait (kg)	105.5	4.48	2.79
Standard-deviation single-trait (kg)	437.7	18.72	12.10
Mean multiple-trait (kg)	104.1	4.40	2.78
Standard-deviation multiple-trait (kg)	438.8	18.64	12.12
Approximate reliabilities			
Mean single-trait	.409	.415	.389
Standard-deviation single-trait	.253	.254	.250
Mean multiple-trait	.417	.430	.390
Standard-deviation multiple-trait	.251	.249	.249
Minimum single-trait	.049	.051	.042
Minimum multiple-trait	.054	.063	.043
Maximum single-trait	.989	.989	.987
Maximum multiple-trait	.989	.989	.987

The reductions are of 2.90% for milk, 6.34% for fat and 0.44% for protein for the 54,820 cows with records and of 1.35%, 2.56% and 0.16% for 1,406 sires (**Table 5**). Schaeffer (1984) estimated through small simulations that MT analyses for milk and fat yields would result in around 5% reduction of PEV, these results supports his hypothesis, even if in the strict sense only simulations as done by this author allow to measure exactly the benefits of MT evaluations. A second possibility is to assess the approximate improvement due to MT through the increased genetic gain (**Table 6**). As genetic gains are proportional to accuracy expressed as the correlation between estimates and real breeding values, the ratio of mean accuracy for MT to mean accuracy for ST gives the approximate relative genetic gain. We observe results similar to those found for relative reduction of mean PEV: the relative genetic gain for cows is 2.89% for milk, 5.96% for fat and .45% for protein yields, and 1.15%, 2.30% and 0.20% for sires.

CONCLUSION

Using a MT-AM for milk, fat and protein 305 day lactation yields is possible today, as multiple-diagonalization of (co)variance matrices can be used and canonical transformation simplifies the MT layout to ST situations. Extension to a MT-AM approach for individual milk, fat and

Table 5. Mean prediction error variances (PEV) for single-trait (ST) and multiple-trait (MT) models and relative approximate reduction of prediction error variance — *Variances de l'erreur de prédiction (PEV) des modèles uni-caractère (ST) et multi- caractère (MT) et réduction relative approximative de la variance de l'erreur de prédiction.*

	Trait		
	Milk	Fat	Protein
Cows with records			
Mean ST-PEV	140,236	278.9	133.4
Mean MT-PEV	136,175	261.2	132.8
Relative gain in PEV	2.90%	6.34%	.44%
Sires of cows			
Mean ST-PEV	126,341	252.1	119.1
Mean MT-PEV	124,631	245.7	119.0
Relative gain in PEV	1.35%	2.56%	.16%

Table 6. Mean accuracy (r_{TI}) for single-trait (ST) and multiple-trait (MT) models and relative improvement of genetic gain due to the use of multiple-trait model — *Précision moyenne (r_{TI}) pour modèles uni- (ST) et multi-caractère (MT) et amélioration relative du gain génétique par l'utilisation modèle du multi-caractère.*

	Trait		
	Milk	**Fat**	**Protein**
Cows with records			
Mean accuracy-ST	.582	.589	.556
Mean accuracy-MT	.598	.625	.558
Relative genetic gain	2.89%	5.96%	.45%
Sires of cows			
Mean accuracy-ST	.607	.612	.589
Mean accuracy-MT	.614	.626	.590
Relative genetic gain	1.15%	2.30%	.20%

protein test-day yields is straightforward. Comparison of time needed for computations shows that a MT analysis for lactation yields done by canonical transformation is not more expensive than several individual ST evaluations. The programs are designed to solve more than 1.5 million equations on a small workstation with 36 megabytes memory capacity within a reasonable time. Animals show an important reranking for milk and fat yields, protein yield is hardly affected. Relative improvement expressed as the reduction in PEV and as relative genetic gain is small for protein yields but between 2% and 6% for milk and fat yields for cows and between 1% and 3% for sires. Although slight, this improvement is not negligible. But the most interesting aspect of MT evaluations is the reduction of selection bias as selection is done currently on milk, fat and protein yields (Farnir *et al.*, 1994) through the use of a global index and only such a MT model would correct this type of possible bias. Recent developments show that this approach can be generalized to missing values (Ducrocq, Besbes, 1993) as prepared by the USDA-AIPL for the US Dairy Cattle Genetic Evaluation based on MT-AM for test-day records (Wiggans, Goddard, 1996). Different fixed effects per trait could also be modeled and approximate reliabilities could be obtained by the methods proposed by Gengler and Misztal (1996). A direct consequence of these developments is that genetic evaluations for dairy cattle will go in the direction of MT evaluations, grouping at least milk, fat and protein yields, eventually going to test-day yields. Further improvement of programming strategies could be needed but recent developments could show ways to do this at reasonable computing costs (e.g., Ducrocq, Besbes, 1993; Gengler, Misztal, 1995).

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Computer programs JAA and MTJAA are available electronically from anonymous FTP at num.ads.uga.edu.

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