

Feasibility of a Walloon Test-Day Model and Study of its Potential as Tool for Selection and Management

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Abstract

A test-day model was developed in order to study the feasibility of a test-day model based on data from the Walloon Region in Belgium. Estimated (co)variance components reported on 305-d milk, fat and protein yield for first, second and third parities were in line with expectation. The specificity of the model used was first the use of a fixed regression on age at calving to skirt the weak number of records in each classes for that effect and secondly the use of a herd*period of calving random regression that cleans additive variances. The model was developed to allow for the joint evaluation of all the breeds recording milk production in the Walloon Region as dairy population is quite diverse and herds are composed of animals from various breeds or crossbreds. The first results from the multitrait multilactation model were promising as the model seems to behave well. Mendelian sampling variances were stable across years and genetic trends were good. Finally, the model should contribute to the understanding of the specificity of the Walloon regional data and to the evolution of genetic evaluations for dairy yields in Belgium.

Introduction

Genetic evaluation systems are undergoing a permanent evolution as there is a constant need to adapt to changing situations in the objectives and the circumstances surrounding the computations. The situation in Belgium and in particular in the Walloon Region has been challenged by new political (regionalization), scientific (new statistical methods), technological (availability of larger computer facilities) and social developments (increased importance and safeguard of local breeds). This was the starting point for a major research effort in the field of genetic evaluation for dairy cattle in Belgium. Up to now, the estimation of breeding values for production traits in dairy cattle was organized for the whole country using a single-trait repeatability lactation model (INTERBULL, 2002). This model has a certain number of shortcomings to deal with the current data situation and breed structure in the Walloon region. Also its usefulness for management purposes is very limited. The present study will present the first results on an ongoing research effort to deal with the feasibility of a test-day model using Walloon data for estimation of breeding values for milk yields. It will focus especially on particularities of this region, with a

lot of mixed breed herds, including all the local breeds, taking maximum profit of the medium size of the population. The opportunity to evaluate all the breeds in the same time including crossbreds should here be emphasized. Especially Dual Purpose Belgian Blue is still important in some regions. Interest for this breed has increased recently, also as a factor of local development and in order to support biodiversity. An alternative objective of this research was to prepare the way to advanced management tools based on test-day data.

Materials and Methods

Data

Walloon data were provided by ELINFO (ELevage INFormatique, Belgium) who manages breeding data in the Walloon Region of Belgium. Data consisted in test-day records between January 1st 1990 and December 31st 1999. Study was limited to the first three parities. Data were structured as showed in Table 1. Editing of data was done in order to exclude unlikely ages for a given lactation. There were in total 4275358 test-day records for 275041 milking cows.

Table 1. Data structure for first, second and third parities of Walloon dairy population.

Lactation	Cows with records	Animals in pedigree	Tests
First	227147	305356	1857765
Second	172475	240155	1401923
Third	126380	183856	1015670
First three	275041	345739	4275358

The breed composition of the pedigree of the cows in the first three parities is presented in Table 2. More than 63 percent of the animals in the production file have over 50 percent of Holstein (HOL) genes. The second major breed (12 percent of the cows) is constituted by animals with more than 50 percent of Dutch and German Red-Whites (MRY) genes. Already the third most important breed is Dual Purpose Belgian Blue (DP-BBB) that represents about 7 percent of the animals in production. 18 percent of the animals are reported mostly crossbreeds of these three breeds or with smaller breeds (e.g. Flemish Red Breeds). Most of the herds are composed of animals of different breeds, and the opportunity to evaluate all the breeds at the same time needed therefore to be studied.

Table 2. Breed composition of the cows with first, second and third parity test-day records.

Breed	Number of cows
Holstein (>50 %)	174029 (63.3%)
MRY (>50%)	33432 (12.2%)
Dual-purpose Belgian Blue (>50%)	18681 (6.8%)
Crossbreeds and other breeds	48899 (17.8%)

Model

The following random regression model (RRM) was used both for variance components and breeding values estimation:

$$y = Xb + Q(Wh + Za + p) + e$$

where y is a vector of milk, fat and protein test-day records, b is a vector of fixed effects (herd*test date, lactation stage, gestation stage, lactation stage*calving season*breed*calving period regressed on age at calving), h is a vector of herd * period of calving environmental random regression coefficients, a is a vector of additive genetic random regression coefficients, p is a

vector of permanent environmental random regression coefficients, e is a vector of random residual, X , W , Z are incidence matrices, Q is the covariate matrix for the second order Legendre polynomials. This model is a classical RRM except for the herd*calving period random effect and the lactation stage*calving season*breed*calving period effect regressed on age at calving. The first one was introduced because previous research highlighted that it cleaned additive variances by reorganizing (co)variances where a part of former genetic variance is now considered environmental. The second one allowed to take into account the fact that different breeds have not the same maturity patterns and are not managed similarly. Using age at calving as regressions was considered since evolution of age compared to lactation stages is easier to model and has better properties if few animals are in extreme ages.

Genetic groups were based essentially on breed of origin and efforts were made to trace ancestors as far as possible.

Genetic evaluation

Genetic evaluation was done using multiple trait multiple lactation (3 traits x 3 lactations) model (MT-ML-RRM). This type of model was chosen to allow in the future increased flexibility of testing plans. This is an important feature as the future milk records plans have to be more cost efficient (e.g., automatic milk recording, less component testing) in order to be competitive. Increased computing requirements (around 19 million equations) due to the advanced MT-ML-RRM system could be handled by the use of the Preconditioned Conjugate Gradient solver and a large computing facility (Compaq Alpha ES45 with 12GB of RAM computer).

Variance components estimation

Herds were sampled in such a way that about 10,000 cows in 2nd parity were extracted. Table 2 gives the structure of the samples. Variance components were estimated separately for milk yield, fat yield and protein yield and for each lactation using EM-REML method (Gengler *et al.*, 1999).

Table 3. Sample structure for VCE.

Lactation	Cows with records	Animals in pedigree	Tests
First	13388	25739	107089
Second	10081	20039	81157
Third	7338	15744	58189

As the MT-ML-RRM required correlations between traits and lactations the following procedure was applied:

- Three global (co)variances matrices were constructed, one per random effect, by putting together the single trait and single lactation (co)variances matrices estimated previously.
- These matrices were diagonalized and the same transformation was applied to solutions computed over the whole population for these effects.
- Raw correlations were computed between the transformed solutions and used to fill the diagonal matrices. Alternatives (e.g. based on INTERBULL methods) procedures are studied for the moment.
- The inverse transformation was then operated and few very small negative eigenvalues were forced to be slightly positive to obtain the final positive definite matrices.

Results and Discussion

Variance components estimation

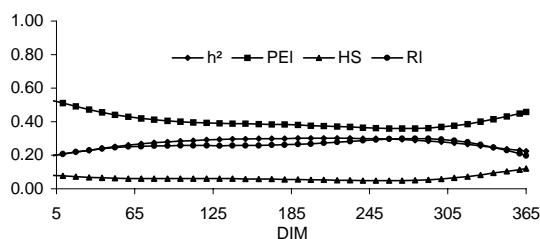


Figure 1. Evolution of the relative variances during first lactation for milk yield.

Figure 1 shows an example of intra lactation relative variances for first lactation milk yield. Heritabilities stayed above 20 percent during the whole lactation and rise slightly to a peak at about day in milk 150. The often observed artifact consisting of a brutal increase at early and late

lactation stages doesn't appear certainly because of the introduction of the herd*period of calving effect. Indeed this herd*period effect shows a little increase at the beginning and the end of the lactation, expressing the fact that variability across herds due to management is more significant at these periods.

Table 4. Heritabilities (diagonal), genetic correlations (above diagonal) and phenotypic correlations (below diagonal) for milk among first lactation.

DIM	Days in milk (DIM)				
	5	50	150	305	365
5	0.20	0.96	0.79	0.52	0.32
50	0.73	0.25	0.92	0.64	0.36
150	0.46	0.63	0.30	0.80	0.47
305	0.23	0.32	0.47	0.28	0.90
365	0.17	0.13	0.16	0.64	0.22

Genetic correlations (Table 4) between day in milk 5 and days in milk 305 and 365 are high (respectively 0.52 and 0.32) and show that the method seems to be consistent. Phenotypic correlations were lower. In order to compare correlations across traits and lactations, 305-d variance components for milk, fat and protein yield and for the three parities were computed (Table 5).

Table 5. Heritabilities (diagonal), genetic correlations (above diagonal) and phenotypic correlations (below diagonal) for milk (M), fat (F) and (P) protein for 305-d yields.

Lactation	1			2			3			
	M	F	P	M	F	P	M	F	P	
1	M	0.41	0.79	0.92	0.75	0.60	0.70	0.68	0.56	0.63
	F	0.71	0.43	0.87	0.63	0.76	0.67	0.58	0.71	0.61
	P	0.88	0.82	0.40	0.71	0.66	0.76	0.65	0.61	0.68
2	M	0.70	0.54	0.64	0.30	0.83	0.92	0.77	0.66	0.74
	F	0.43	0.61	0.49	0.59	0.37	0.88	0.65	0.79	0.70
	P	0.52	0.50	0.55	0.72	0.83	0.32	0.74	0.70	0.78
3	M	0.54	0.43	0.49	0.69	0.43	0.51	0.31	0.81	0.88
	F	0.41	0.57	0.46	0.52	0.58	0.48	0.78	0.34	0.85
	P	0.47	0.47	0.50	0.63	0.48	0.55	0.88	0.81	0.32

The values of heritabilities are in line with literature, nevertheless slightly higher. Genetic and phenotypic correlations do not differ much of what other authors published before. Given our estimation procedure they should be considered as lower bound values.

Results from genetic evaluations

Solutions for 2 classes of lactation stage*calving season*breed*calving period regressed on age at calving effect are presented at Figure 2. These solutions can also be used to adjust phenotypic test-day results in order to provide a “standard cow” to farmers.

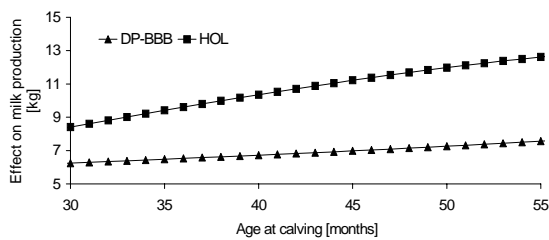


Figure 2. Effect of age on milk production for dual purpose Belgian blue (DP-BBB) and Holstein for second parity, calving in March, April or May for days in milk 60 to 90.

Differences in level of production presented here can be considered mostly management related due to the presence of genetic groups based on breed.

Genetic trends for cows and for milk yield at 305-d are presented in Figure 3. Genetic trends seem to be regular showing no abnormalities, although increasing slowly.

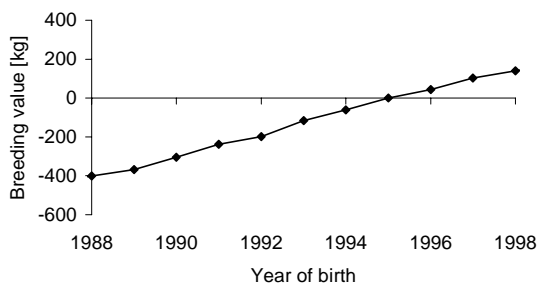


Figure 3. Genetic trends for milk yield during first parity.

Mendelian sampling standard deviations (MS SD) of the first (constant) Legendre polynomial for milk yield during first parity are presented in Figure 4. MS SD are constant from 1989 to 1997 with only slight decreases at the edges due to the limitation of the data. The model showed no major problems of estimation.

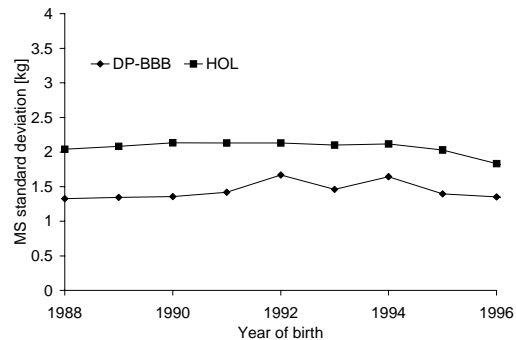


Figure 4. MS SD of the first Legendre polynomial for milk yield during first parity for Holstein and Red-Whites (HOL) and dual purpose Belgian Blue (DP-BBB).

Conclusions

This study shows that considerable progress has been made in the Walloon Region when the understanding of its specificity and the modeling of the regional test-day data is concerned. A functioning test-day model is now almost available for genetic evaluation for dairy cattle. The first results and tests are very satisfactory as the model seems to behave well. Additional tests (e.g., Interbull tests) must be conducted.

Variance components were consistent, h^2 were rather high. The proposed algorithm to compute correlations across lactations and traits behaved well but has to be refined.

Simultaneous computation of breeding values for different breeds at the same time do not seem to be a problem as the system reacted well.

Future developments

The system presented in this study is still undergoing a constant development. For example heterosis and heterogeneity of (co)variances due to breeds and heterogeneity due to environment have to be considered (e.g., Gengler & Wiggans, 2002). Efforts must also be made to compute reliabilities of breeding values. Somatic cell count will be included. Study of alternatives uses of fixed and random solution for selection and management are underway including the definition of new reported “traits”, such as persistency and maturity rates and the modification of effects in the model to increase its usefulness for management purposes (e.g., Mayeres *et al.*, 2002). The incorporation of older test-day data and of foreign information will also be studied.

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