

Genetic Evaluation of Female Fertility for Walloon Dairy and Dual Purpose Cows Using a Parity Random Regression Model: First Results

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Abstract

The genetic evaluation of female fertility is under development for the Walloon Region of Belgium. Pregnancy rate was chosen for this study, and two models compared. The first one is a classical multi-trait model, the 3 traits being the pregnancy rates for the first three parities. The second one is a random regression model, using random regressions based on parity differences. Parity differences were based on phenotype differences and applied to all random effects. Mean heritabilities across first three parities was 4.26 and 4.28 for the first respectively second model. Parity differences seemed to model very consistently when compared to multi-trait models for residual, additive genetic and permanent environmental effects, larger differences appeared for a herd x period effect. Genetic correlations between second and successive parities were close to unity with both models. Certain computational advantages of using parity differences could be lost if additional computations confirm these results, as dimensions of matrices would be similar. However the flexibility of a random regression model to group fixed effects across parities would still favor this type of model.

Introduction

Fertility traits definition differ greatly across countries. Jorjani (2005) regrouped these traits in three categories for Interbull international evaluation: submitted traits should be related to the animal ability to become pregnant (e.g. non return rate), to the animal ability to re-cycle after calving (e.g. interval calving – first AI), or to a combination of these two abilities (like calving interval or days open).

Calving interval can be regarded as an interesting measurement for predicting fertility as it is available from milk recording and genetically correlated with various direct measures of fertility (Pryce *et al.*, 1997; 1998). Pregnancy rate (PR) is defined as the percentage of nonpregnant cows that become pregnant during each 21-d period (VanRaden *et al.*, 2004). This measure, derived from days open (DO), has the characteristic to put a large emphasis to short DO records, while DO are largely affected by long DO records. Oseni *et al.* (2004) showed that PR is more stable across DO threshold, what makes it potentially a better choice for genetic evaluation for fertility.

Most genetic evaluations of fertility consider a genetic correlation of 1 across parities. Even if this simplification is very convenient for technical reasons, it may not be the case in practice. Indeed Olori *et al.* (2003) used a multi-parity approach with calving interval to account for genetic correlation among the first three parities: genetic correlations of .85 to .94 were so estimated.

Random regression (RR) is a very flexible approach to model evolution of genetic parameters along a time function (e.g. DIM in milk production test-day model). A major problem in RR models (RRM) is that it is not always obvious what type of regressions to use (Gengler *et al.*, 2005). Biological based functions are often better for describing the mean of biological process, while polynomials based functions are better for describing their variance.

In the setting of multi-parity models another alternative method was proposed by Wiggans and VanRaden (2004). They defined biological changes among repeated records as an approximation of expected a priori change in genetic merit across parities. The parameter so defined was called parity differences (PD).

Implicitly this approach models also differences in correlation among these repeated records. While Wiggans and VanRaden (2004) used a linear function of these biological differences to describe variances, Gengler *et al.* (2005) implemented in the Walloon genetic evaluation of longevity a quadratic function in order to allow a quadratic variation of genetic merit according to biological differences.

The objective of this paper was to present the current status of the development of the new genetic evaluation of female fertility in Walloon Region of Belgium. Pregnancy rate (PR) was chosen for the study and two models studied. The first considered the first three parities as correlated traits, the second kept all parities and modeled variances changes across parities with PD.

Materials and methods

Data

Data for fertility was provided by regular milk recording system. DO and then PR were estimated according to calving and insemination date. When the last was not available, next calving date minus 280 days was used for insemination date estimation. DO below 35 days were considered suspect and deleted. DO after 355 days were limited to 355 days. PR was expressed as percentage and computed as $21/(DO - 45 + 11)$ where 45 represents the voluntary waiting period in our production circumstances and 11 half of a reproductive cycle. Left censored records were not included in the analysis: all information from animals without first parity PR were discarded and all parities following a missing PR were removed as this might indicate some special treatments. A total of 1,027,595 PR were estimated for 399,305 cows.

The breed composition of cows in data set is given in Table 1. The repartition is similar to the one presented by Auvray and Gengler (2002) for Walloon cows milk recorded from 1990 to 1999, excepted for non Holstein breeds. Indeed Dual-Purpose Belgian Blue, and to a less extent Dutch and German Red-Whites (MRY) cows, were more popular before 1990 than they are nowadays.

In order to estimate (co)variances components, 85 herds having at least 75 cows with records were randomly selected in order to have a sample of 14,916 cows with PR. Therefore 38,190 records were used in the study. The complete pedigree after extraction consisted in 43,055 animals.

Table 1. Breed composition of the cows with pregnancy rate (PR) records.

Breed	Number of cows
Holstein (>50%)	260,904 (65.3%)
MRY (>50%)	73,920 (18.5%)
Dual-Purpose Belgian Blue (>50%)	52,602 (13.2%)
Crossbreds and other breeds	11,879 (3.0%)

Definition of Parity Differences

Mean PR were then estimated for each parity and adjusted according a fifth order regression on parity (Table 2). PD were then estimated based on differences in pregnancy rates compared to the third parity that were scaled in a way that the difference between PR in first and third parity represented - 1.

Table 2. Definition of parity differences (PD) based on differences in adjusted mean pregnancy rates (PRadj) among parities.

Parity	PR (%)	PRadj (%)	Δ PR (%)	PD	PD ²
1	37.48	37.47	-2.57	-1.00	1.0000
2	39.91	39.92	-0.12	-0.05	0.0022
3	40.06	40.04	0.00	0.00	0.0000
4	39.83	39.81	-0.23	-0.09	0.0080
5	39.70	39.77	-0.27	-0.11	0.0110
6	39.76	39.68	-0.36	-0.14	0.0196
7	39.56	39.20	-0.84	-0.33	0.1068
8-10	38.58	38.57	-1.47	-0.57	0.3272

Multi-trait and Random Regression Models

A RRM and a nearly equivalent multi trait model (MTM) were defined. The following 3 parities model was used:

$$y = Xb + Wh + Za + p + e \quad (1)$$

A nearly equivalent RRM based PD was defined as:

$$y = Xb + Q_{rr} (Wh + Za + p) + Q_{rr} e \quad (2)$$

where \mathbf{y} is a vector of PR records (in parity 1 to 3 for the MTM and in parity 1 to 10 for the RRM), \mathbf{b} is a vector of fixed contemporary effects based on regression of major breeds inside year \times month of calving \times parity group (1, 2 and more), season of calving (3 month seasons) \times age at calving (2 month classes) \times parity group (1, 2, 3, 4, 5 and more), herd \times parity group (1, 2 and more); \mathbf{h} is a vector of herd \times year of calving environmental random effects (MTM) or random regression coefficients (RRM); \mathbf{a} is a vector of additive genetic random effects (MTM) or random regression coefficients (RRM); \mathbf{p} is a vector of permanent environmental random effects (MTM) or random regression coefficients (RRM); \mathbf{e} is a vector of random residual effects (MTM) or random residual regression coefficients (MRM); \mathbf{X} , \mathbf{W} and \mathbf{Z} are incidence matrices linking observation to the effects and \mathbf{Q}_{rr} is a matrix of constant, linear and quadratic regressions based on orthogonalized PD (PD^0 , PD^1 , PD^2). Estimations of variance components were done using EM and AI-REML.

Results

Table 3 shows variance components estimated with model (1). The estimated mean heritability across first three parities, 4.26%, is consistent with results found in literature.

Table 3. Relative variances (diagonal) and herd-period (h), permanent environment (e) and additive genetic (a) correlations across parities with model (1).

Parity	h			p			a		
	1	2	3	1	2	3	1	2	3
1	5.04	0.73	0.88	0.75	0.85	0.84	4.76	0.92	0.91
2		3.87	0.96		1.82	1.00		4.22	1.00
3			3.46			1.82			4.24

For each random effect, estimated correlations between second and third parities were close to 1. Correlations between first and successive parities were decreasing, except for herd \times year effect, where third parity seemed more correlated with first one.

With model (2), the mean heritability for first three parities was 4.28. Figure 1 and Figure 2 give evolutions of random effects across PD and parities respectively.

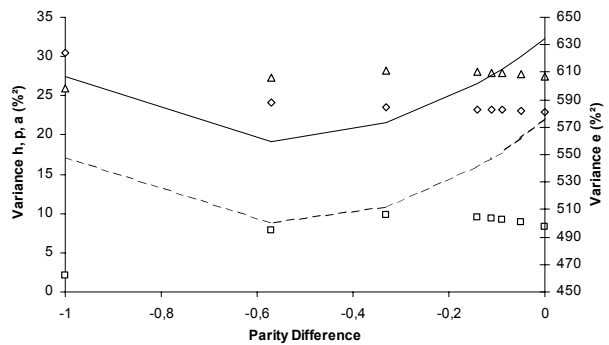


Figure 1. Evolution of herd-year (h, \diamond), permanent environment (p, \square), additive genetic (a, \triangle), residual (e,dash line) and phenotypic (P,solid line) variances across parity differences with model (2).

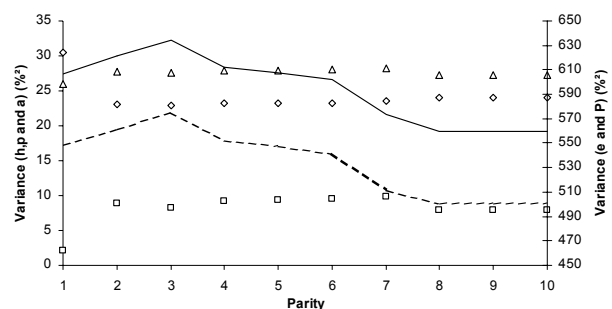


Figure 2. Evolution of herd-year (h, \diamond), permanent environment (p, \square), additive genetic (a, \triangle), residual (e,dash line) and phenotypic (P,solid line) variances across parities with model (2).

The use of a quadratic function of PD allowed to model the non linear evolution of random effects across PD. Residual effect showed a bigger range of variation in comparison to other random effects: residual variances increased from first to third parity, and then decreased continuously until parity 8. For \mathbf{h} , \mathbf{p} and \mathbf{a} effects, estimated variances dropped from first to second parity, and was then more stable.

Table 4 shows relative variances and correlations estimated with model (2).

Table 4. Relative variances (*rv*, in italic) and herd-period (*h*), permanent environment (*e*) and additive genetic (*a*) correlations across parities with model (2).

Parity	1	2	3	4	5	6	7	8
h	<i>rv</i> 5,02	3,71	3,61	3,78	3,82	3,87	4,10	4,31
1	1.00	0.76	0.75	0.77	0.78	0.78	0.84	0.92
2		1.00	1.00	1.00	1.00	1.00	0.99	0.96
3			1.00	1.00	1.00	1.00	0.99	0.95
p	<i>rv</i> 0,34	1,42	1,31	1,50	1,54	1,59	1,72	1,40
1	1.00	0.75	0.76	0.74	0.74	0.74	0.74	0.77
2		1.00	1.00	1.00	1.00	1.00	1.00	1.00
3			1.00	1.00	1.00	1.00	1.00	1.00
a	<i>rv</i> 4,28	4,47	4,34	4,56	4,60	4,66	4,91	4,87
1	1.00	0.94	0.94	0.93	0.93	0.93	0.93	0.95
2		1.00	1.00	1.00	1.00	1.00	1.00	1.00
3			1.00	1.00	1.00	1.00	1.00	1.00

Correlations between second and consecutive parities were still close to 1. Differences in correlations between first and subsequent parities were very close to these of PD. Correlation between parity 1 and 3 for **h** effect was smaller than with model (1). Even if this could be due to the exclusion of parities superior to 3 in model (1), another explanation may be the very small parity differences between parity 2 and 3 (-0.05).

Evolution in relative variances between parities 1, 2 and 3 was similar with the two models for **h** and **p** effects. For additive genetic effect, this is not the case: heritability was smaller in parity 1 with model (2), while it is the opposite with model (1).

Discussion and perspectives

Use of PD could be a very interesting new approach to model means and variances across parities. Differences in parity were defined based on the phenotype, and then applied to all random effects. While it seemed to model very consistently when compared to multi-trait models for residual, additive genetic and permanent environmental effects, larger differences appeared for herd x period effect. Even a quadratic function of PD might not sufficient to avoid this problem.

Both models estimated a very high correlation between parity 2 and 3. Additional estimations with model 2 found a correlation of 1 among all parities following the second. The biggest source of variation after the third parity seemed to be the residual variation, resulting in changes in relative variances.

Olori *et al.* (2002) found a genetic correlation of 0.90 between second and third parity. Additional studies, with new samples, have to be done to check the correlation of 1 after second parity. If it is confirmed, certain computational advantages of using PD could be lost since matrices would have the same dimension between both approaches. The use of a 3 x 3 multi-trait approach, with all parities superior to 3 considered as repetitions of third one, and PR weighted by function of residuals variances (parity 1 to 8) will then be a good way to model PR across all parities. However this model lacks the flexibility of a random regression model to group fixed effects across parities.

In the near future a joint evaluation with non return rate and direct longevity will be tested in Walloon Region.

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