

Genetic Evaluation of Calving Ease for Walloon Holstein Dairy Cattle

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Abstract

Calving complications have an incidence on the economic profitability of dairy herds. In the Walloon Region of Belgium, calving ease data recording is being done on voluntary basis since 2000. This allows now the implementation of a genetic evaluation of Holstein dairy cattle addressing the need of dairy breeders to select bulls in order to reduce frequency of calving problems.

Calving ease scores were analyzed using univariate animal linear models, which were fitted with the genetic correlation between direct and maternal additive genetic effects either estimated or constrained to zero. Variance components and related genetic parameters were estimated from a dataset including 33,155 calving records. Included in the models were fixed season effects, fixed herd effects and fixed sex of calf*age of dam classes*group of calvings interaction effects, random herd*year of calving effects, random maternal permanent environment effects, and random animal direct and maternal additive genetic effects.

For both models, direct and maternal heritabilities for calving ease were about 8% and about 2%, respectively. Genetic correlation between direct and maternal additive effects was found to be non-significantly different from zero. So, an animal linear model with genetic correlation between direct and maternal effects constrained to zero was adopted for the routine genetic evaluation of calving ease for Walloon Holstein dairy cattle. This model was validated by Interbull in January 2013 and, since April 2013, the Walloon Region of Belgium has officially participated to the international MACE evaluation for calving traits.

Key words: calving ease, animal model, Holstein

Introduction

Calving complications impact production, fertility and cow and calf morbidity and mortality and affect negatively economic profitability in dairy herds (Dematawena and Berger, 1997; Eaglen *et al.*, 2011). Calving ease (CE) measures the presence or absence of calving problems and their intensities. This trait is generally scored on a categorical scale by the breeder, what makes it more sensitive to subjectivity (Dekkers, 1994).

Additionally, CE is affected by two additive genetic components, the ability of the calf to be easily born (direct effect) and the ability of the dam to easily give birth (maternal effect).

The direct effect is expressed only once, when the calf is born whereas the maternal effect is expressed several times, each time a cow calves.

Considering the categorical nature of the trait, from a theoretical point of view, application of a threshold model is the correct choice (Gianola, 1982), whereas, from a practical point of view, linear model is a more easily applicable choice (Varona *et al.*, 1999; Ramirez-Valverde *et al.*, 2001; Phocas and Laloë, 2003). This is evidenced by the fact that different Interbull members use a linear approach for the genetic evaluation of categorical calving traits (Interbull, 2013).

The aim of this research was to estimate the genetic parameters for direct and maternal additive effects based on an animal linear model and to report the implementation of a routine genetic evaluation for CE in the Walloon Holstein dairy cattle.

Materials and Methods

Data material for calving evaluation

CE is scored by dairy breeders on voluntary basis and collected by the Walloon Breeding Association (AWE). CE scores ranged from 1 to 4 (1=caesarean and embryotomy, 2=hard pull, 3=easy pull, and 4=normal). The original dataset comprised 138,144 calving records and presented a typical distribution of CE; most of the records fell into category 4 (69%) and few records into category 1 (about 1%).

Records from Holstein calves born between 2000 and 2012 were used. Edits were done for out-of-range values for CE and records with missing information related to the factors in the statistical model, were removed. Multiple births and calf without dam known were excluded. Records were limited to first five parities. Age at calving must be 21-48 months for heifers (1st parity) and 31-142 months for cows (2nd-5th parities) with specific limits depending on parity. Since dairy breeders use their own judgment to assign scores for CE, data quality depends highly on them. Therefore, herds with a standard deviation for scores smaller than 0.05 were deleted in order to avoid herds where breeders put all scores in the same category. Herds had to report at least, in average, four calvings per year calculated on the first two parities. The full dataset contained CE records from 85,118 calves born from 62,265 dams in 862 herds. Pedigree data were extracted from the database used for the official Walloon genetic evaluations. The final pedigree file included 233,882 animals. More details in Table 1.

Estimation of (co)variance components and related parameters

To ensure an appropriate data structure for the parameter estimation, some extra edits were applied. Calves were required to have known sire and dams were required to display a CE record in 1st parity. Only data from continuous calvings per dam were kept (*e.g.* if a dam displayed CE records from its first, second and fourth calving only CE records from first and second calving were kept). Herds had to display at least, in average, four calvings per year calculated on the 1st parity only. A final edit required in average more than one calving per dam per herd in order to avoid the presence of herds where only heifers were recorded. Based on these edits, in order to estimate (co)variance components, CE records from 33,155 calves born from 25,240 dams and 2,215 sires in 492 Walloon herds were used. The final pedigree contained 120,374 animals. Table 1 displays characteristics of this dataset.

Table 1. Characteristics of full and variance component estimation datasets.

	Full dataset		VCE dataset	
	N	%	N	%
CE records	85,118		33,155	
Female calves	66,511	78.1	26,177	78.9
Male calves	18,511	21.9	6,978	21.1
Herds	862		492	
Sires with progeny records	3,148		2,215	
Dams	62,265		25,240	
Final pedigree file	233,882		120,374	
CE scores				
1. Caesarean and embryotomy	781	0.9	443	1.3
2. Hard pull	4,006	4.7	2,179	6.6
3. Easy pull	23,461	27.6	10,114	30.5
4. Normal	56,870	66.8	20,419	61.6

Models for calving ease evaluation

Preliminary analyses were carried out using general linear model procedure of SAS. Different linear models were fitted aiming to identify fixed effects that affected variation of calving scores.

The ultimate model included the fixed effects of season (4 classes), herd and sex of calf*age of dam classes (11 classes)*group of parities (2 classes: 1st parity and 2nd-5th parities). These effects were included in the following univariate animal linear model; where CE was modeled as continuous trait; to estimate (co)variance components:

$$y = X\beta + Z_h h + Z_a a + Z_m m + Z_p p + e \quad [1]$$

where β are fixed effects, h are random herd*year of calving effects, a are random direct additive genetic effects, m are random maternal additive genetic effects, p are random permanent maternal environmental effects, X , Z_h , Z_a , Z_m and Z_p are known incidences matrices linking data with respective effects, and e are the residuals. This model was fitted with the genetic correlation between direct and maternal additive genetic effects either estimated or constrained to null called **Model L1** and **Model L2**, respectively, in the remainder of this paper.

Procedures based on a Bayesian approach using the Gibbs sampling algorithm were used to estimate (co)variance components and related genetic parameters by using programs gratefully provided by Ignacy Misztal (Misztal *et al.*, 2002). No genetic grouping was used.

Genetic Evaluation system

For routine genetic evaluation of CE, model [1] was applied on the full dataset and solved by sparse inversion. CE breeding values were expressed in expected differences in percentage of “normal” calving. Reliability

(**REL**) of breeding values was defined as the squared correlation between true and predicted breeding values. It was estimated based on the diagonal elements of the mixed model equations, as shown by Henderson (1984). Prediction Error Variance (**PEV**) given by direct inversion of the coefficient matrix allowed the estimation of correct reliabilities:

$$REL_x = \frac{\sigma_x^2 - PEV_x}{\sigma_x^2}$$

where σ_x^2 is the additive genetic variance for genetic component x (*i.e.* direct or maternal effect).

Results and Discussion

Estimates of (co)variance components and of related genetic parameters

Results for the (co)variance components, related genetic parameters, and fraction part of variances in phenotypic variance for Models L1 and L2, are reported in Table 2.

Parameters can generally be considered as significantly different from zero, posterior means being greater than twice the posterior standard deviation, except for genetic correlation between direct and maternal additive genetic effects for Model L1.

The additive genetic variance due to direct effects was greater than that due to maternal effects for both models. Indeed, heritabilities for direct effects were nearly four times higher than for maternal effects. Heritabilities estimates were in the range of previously published estimates of this trait in dairy cattle, which ranged from 0.03 to 0.17 for direct heritability and from 0.02 to 0.12 for maternal heritability (Weller and Gianola, 1989; Steinbock *et al.*, 2003; López de Maturana *et al.*, 2007; Eaglen *et al.*, 2012).

Table 2. Posterior mean (PM) and posterior standard deviation (PSD) of (co)variance components and related genetic parameters.

Parameter ^a	Model L1		Model L2	
	PM	PSD	PM	PSD
σ^2_h	.042	.002	.042	.002
σ^2_a	.027	.004	.028	.004
σ^2_m	.008	.003	.009	.002
σ^2_p	.018	.004	.017	.005
σ^2_e	.269	.005	.269	.005
$r_{u(a,m)}$.088	.194	.000	.000
h^2 direct	.074	.012	.078	.012
h^2 maternal	.023	.007	.024	.007
C_h	12%		12%	
C_p	5%		5%	
C_e	74%		74%	

^aThe terms σ^2_h is the herd*year of calving variance, σ^2_a is the direct additive genetic variance, σ^2_m is the maternal additive genetic variance, σ^2_p is the permanent maternal environmental variance, σ^2_e is the residual variance, $r_{u(a,m)}$ is the genetic correlation between direct and maternal effects. C_h , C_p and C_e are the herd*year of calving fraction, permanent maternal environmental fraction and residual fraction in the phenotypic variance, respectively.

The herd*year of calving effects represented 12% of the phenotypic variance, which was the largest contributor to the phenotypic variance after the residual effects (74%). Effects of herd*year of calving take into account biological differences among herds and years of calving but also subjectivity of CE scores.

The maternal permanent environment effects represented 5% of the phenotypic variance in each model and were greater than the genetic maternal effects. Preliminary analyses to this study have established that maternal genetic variance tended to be overestimated by models taking not into account the existence of a maternal permanent environment effects. Hence, most of the observed variability due to the maternal effects was found to be of a non (additive) genetic origin. As a special care was taken to get useful data for variance component estimation (e.g. maximizing repeated calvings), this result should not be an artefact of the sparseness of repeated records used.

Estimates of variance components and related genetic parameters were similar between Models L1 and L2; though genetic correlation between direct and maternal additive genetic effects was estimated or constrained to zero, indicating that the value of this correlation had no large influence.

Although a low positive genetic correlation was estimated between genetic effects with Model L1, it seemed more relevant to consider no genetic correlation according to its posterior standard deviation.

Genetic evaluation results

According to previous statements, the second version of model [1] (i.e. Model L2) was applied on the full dataset. Figure 1 shows trends in direct and maternal genetic effect breeding values in Holstein AI bulls. Those bulls were required to have a minimal REL of .35.

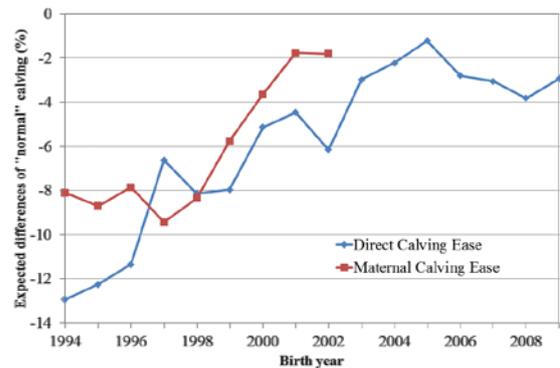


Figure 1. Genetic trends of direct and maternal breeding values in Holstein bulls with a minimal REL of .35

The number of bulls selected for this figure was 1,171 and 202 for direct and maternal genetic effects, respectively. Mean, standard deviation, minimum and maximum of these bulls’ breeding values are shown in Table 3.

Few bulls did meet the REL requirement for maternal genetic effect and so there were not enough bulls to provide reasonable results after a birth year of 2002.

Table 3. Descriptive statistics of direct and maternal CE breeding values for bulls from trends.

	Mean	SD	Min	Max
Direct	-5.11	9.21	-40.09	30.66
Maternal	-6.55	8.64	-31.10	18.47

There were clear positive genetic trends for both effects although there was no genetic evaluation system of CE for Walloon dairy cattle. As currently the testing of young sires is extremely limited in the Walloon Region of Belgium this reflects the preselection done in exporting countries before these sires are used.

Figure 2 shows that similar genetic trends were observed in Holstein cows and calves. Animals used to realize these trends were required to have a minimal REL of .15. This can be explained by the fact that foreign scale calving information for used sires was known before and most likely used by breeders. Even if this information was suboptimal it allowed avoiding sires with major CE problems.

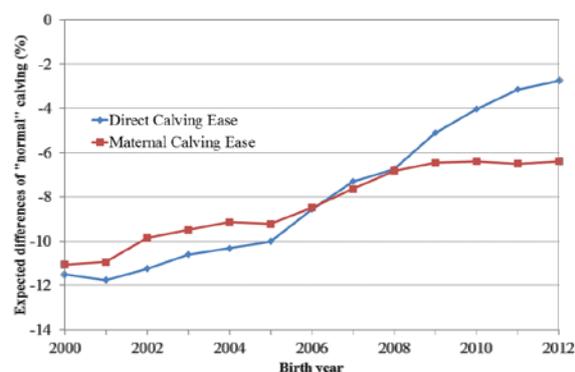


Figure 2. Genetic trends of direct and maternal breeding values in Holstein cows and calves with a minimal REL of .15

Based on these results using Model L2, Region Walloon of Belgium participated in Interbull January 2013 MACE test run for Holstein breed. This model was validated with Interbull trend validation method III. Genetic correlations with other countries were estimated for direct and maternal genetic effects of CE. On average, country correlation was .62 for direct CE and .64 for maternal CE, respectively. The highest country correlation was with Switzerland Red and White Holstein

(.73) for direct CE and with Germany (.75) for maternal CE, respectively.

Conclusions

A univariate animal linear model was developed for routine genetic evaluation of CE for Walloon Holstein dairy cattle. No relevant genetic correlation between direct and maternal effects on ease of calving was found. Model L2 was therefore implemented in routine in April 2013 to provide, to our dairy breeders, breeding values of CE for their Holstein animals.

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