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Genetic parameters for direct and maternal calving ease in Walloon dairy cattle based on linear and threshold models

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Summary

Calving ease scores from Holstein dairy cattle in the Walloon Region of Belgium were analysed using univariate linear and threshold animal models. Variance components and derived genetic parameters were estimated from a data set including 33 155 calving records. Included in the models were season, herd and sex of calf \times age of dam classes \times group of calvings interaction as fixed effects, herd \times year of calving, maternal permanent environment and animal direct and maternal additive genetic as random effects. Models were fitted with the genetic correlation between direct and maternal additive genetic effects either estimated or constrained to zero. Direct heritability for calving ease was approximately 8% with linear models and approximately 12% with threshold models. Maternal heritabilities were approximately 2 and 4%, respectively. Genetic correlation between direct and maternal additive effects was found to be not significantly different from zero. Models were compared in terms of goodness of fit and predictive ability. Criteria of comparison such as mean squared error, correlation between observed and predicted calving ease scores as well as between estimated breeding values were estimated from 85 118 calving records. The results provided few differences between linear and threshold models even though correlations between estimated breeding values from subsets of data for sires with progeny from linear model were 17 and 23% greater for direct and maternal genetic effects, respectively, than from threshold model. For the purpose of genetic evaluation for calving ease in Walloon Holstein dairy cattle, the linear animal model without covariance between direct and maternal additive effects was found to be the best choice.

Introduction

All dairy cows must give birth to begin producing milk. In most cases, calving proceeds normally but problems may happen before or during the calving and cause various problems. The major problem is dystocia which may be defined as calving difficulty resulting from prolonged spontaneous calving or prolonged or severe assisted extraction. Mee (2008) provides a good review of the different types of dystocia and their associated risk factors in dairy

cattle. Calving complications impact production, fertility, and cow and calf morbidity and mortality and thus can negatively affect economic profitability in dairy herds (Dekkers 1994; Dematawena & Berger 1997; López de Maturana *et al.* 2007b; Eaglen *et al.* 2011). Calving-related infections affect also indirectly human health as they require increased use of antibiotics, leading potentially to microbial resistance. Besides, animal welfare is compromised by these calving complications and so consumer acceptability of dairy production systems (Mee 2008).

Calving ease measures the presence or absence of dystocia and its intensity. This trait is generally scored on a categorical scale by the breeder, which makes it more sensitive to subjectivity (Dekkers 1994). Furthermore, this trait is affected by two additive genetic components, the calf's contribution (direct effect; e.g. arising from size, birthweight, hormonal balance...) and the dam's contribution (maternal effect; e.g. arising from pelvic opening, uterine influence of the dam on her calf's birthweight...). The direct additive effect is expressed only once, when the calf is born, whereas the maternal additive effect is expressed several times, each time a cow calves.

From a theoretical point of view, threshold models are preferred over linear models as a method for genetic analysis of such categorical traits displaying a discrete probability distribution (Gianola 1982), and this was confirmed with simulated data by Hoeschele (1988). However, several studies in sheep, beef and dairy cattle using field data found no clear advantage of threshold over linear models (Weller & Gianola 1989; Olesen *et al.* 1994; Matos *et al.* 1997; Varona *et al.* 1999; Ramirez-Valverde *et al.* 2001; Phocas & Laloë 2003). Some of these studies reported greater computational requirements with threshold than with linear models. This might explain why most of the routine genetic evaluations of categorical calving traits are based on linear models (Interbull 2013), although such data violate the assumption of normality. Calving traits are evaluated with a threshold approach only in France, Italy and the USA (Ducrocq 2000; Canavesi *et al.* 2003; Wiggans *et al.* 2003).

Models used for routine genetic evaluation of calving ease range from sire (-maternal grandsire) models to animal models in univariate or multitrait form that either allow a covariance between direct and maternal genetic effects or fix this covariance to zero (Interbull 2013). Many threshold models are implemented as models with sire-maternal grandsire effects to avoid convergence problems and biased estimation of genetic parameters due to the well-known extreme category problem, particularly in the presence of numerous fixed effect classes (Luo *et al.* 2001). However, because some cows with calving records that also have their own direct calving records as a calf, an animal model seems more appropriate to include information on the cows themselves and so generates directly breeding values for direct and maternal effects for bulls and cows.

The purpose of this research was to compare linear and threshold animal models for the prediction of breeding values for calving ease and to estimate the genetic parameters for direct and maternal additive

effects for calving ease in the Walloon Holstein dairy cattle. Models were compared on the basis of their predictive abilities to determine the most suitable model for current Walloon data.

Materials and methods

Data

In the Walloon Region of Belgium, calving ease is scored by dairy breeders on a voluntary basis and collected by the Walloon Breeding Association (AWE). Calving ease scores range from 1 to 4 (1. Caesarean and embryotomy, 2. hard pull, 3. easy pull and 4. normal). The original data set comprised 138 144 calving records and presented a typical distribution of calving ease; most of the records fell into category 4 (69%) and few records into category 1 (approximately 1%). From this original data set, two data sets were created, one for the (co)variance components estimation (data set I) and one for the validation/comparison of models (data set II). Records from Holstein calves born between 2000 and 2012 were used for this research, and data editing was almost identical for both data sets.

Data were edited to remove all suspect records, which included records with out-of-range values for calving ease or missing information related to the factors in the statistical model, including animal identification, birth date, herd identification, calving date, parity number, calving scores and sex of calf. Only records on single born calves were used. Records were limited to first five parities. Calving age of dams was restricted to be between 21 and 48 months for primiparous (1st parity) cows and between 31 and 142 months for multiparous (2nd to 5th parities) cows. Percentage of records for dams outside these ages was relatively small (<0.2%). Data quality depends highly on dairy breeders' own judgement to assign scores for calving ease. Therefore, only herds with a standard deviation for scores >0.05 were kept to avoid herds where breeders put all scores in the same category. In addition to all the general edits, some specific edits were applied to each data set.

For the data set I, all calves had to have sire and dam identified and every dam had to have a calving record in first parity. Herds displaying less than four first calvings on average per year were deleted. In each herd, only data from continuous calvings per dam were kept (e.g. if a dam displayed records from its first, second and fourth calvings, only records from first and second calvings were kept). A final edit required on average more than one calving per dam

per herd. The objective was to create a reliable data set without unnecessarily reducing the available data. The final data set I included records from 33 155 calves born in 492 Walloon herds from 2215 sires, 25 240 dams and 2031 maternal grandsires. The total number of animals including ancestors without records was 120 374.

For the data set II, all calves had to have only dam identified and herds had to display at least, on average, four calvings per year calculated from the first two parities. The final data set II included records from 85 118 calves originating from 862 Walloon herds, from 3148 sires, 62 265 dams and 3352 maternal grandsires. The total number of animals in the pedigree was 233 882.

For both data sets, calving ages of dam were divided into eleven classes: 21–24, 25–26, 27–28, 29–30, 31–35, 36–38, 39–48, 49–56, 57–65, 66–81 and more than 81 months at calving. Calving seasons were divided into four seasons: winter season from January to March, spring season from April to June, summer season from July to September and autumn season from October to December.

Models of analysis

All the fitted models included the three following fixed effects: season effects, herd effects and combined effects of sex of calf by age of dam classes by group of parities (two groups: first parity and the 2nd to the 5th parity).

Univariate linear animal model

Calving ease was modelled as a continuous trait:

$$\mathbf{y}_{\text{CE}} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}_h\mathbf{h} + \mathbf{Z}_a\mathbf{a} + \mathbf{Z}_m\mathbf{m} + \mathbf{Z}_p\mathbf{p} + \mathbf{e}$$

where \mathbf{y}_{CE} is a vector of observed calving ease scores, $\boldsymbol{\beta}$ is a vector of fixed effects, \mathbf{h} is a vector of random herd \times year of calving effects which were included to account for the variability in the frequency of dystocia among herds and years within herds, \mathbf{a} is a vector of random direct additive genetic effects, \mathbf{m} is a vector of random maternal additive genetic effects, \mathbf{p} is a vector of random permanent maternal environmental effects; \mathbf{X} , \mathbf{Z}_h , \mathbf{Z}_a , \mathbf{Z}_m and \mathbf{Z}_p are incidences matrices linking observations with respective effects; \mathbf{e} is a vector of residual effects. There might be some statistical problems and convergence issues with the estimation of fixed herd \times year of calving with a threshold model when dealing with herd \times year of small size or with some scores not registered (i.e. the extreme category problem). A random herd \times year effect was fitted to avoid this problem (Misztal *et al.* 1989). Even if this

issue is less a problem in linear models, the same random herd \times year effect was kept.

Model indicated as Model L1 was fitted with an estimated genetic correlation between direct and maternal additive genetic effects. Model indicated as Model L2 was fitted with a genetic correlation between genetic effects constrained to zero.

Univariate threshold animal model

The same fixed and random effects as in the linear model were considered, but this model assumed the existence of a latent or underlying unobservable normal variable – that is, a liability (L) – modelling the response of calving ease with the following distribution:

$$\begin{aligned} f(y_{\text{CE}}|L) &= \prod_{i=1}^n f(y_{\text{CE}}|L_i) = \prod_{i=1}^n [I(L_i < t_1)I(y_{\text{CE}_i} = 1) \\ &\quad + I(t_1 < L_i < t_2)I(y_{\text{CE}_i} = 2) \\ &\quad + I(t_2 < L_i < t_3)I(y_{\text{CE}_i} = 3) \\ &\quad + I(L_i > t_3)I(y_{\text{CE}_i} = 4)] \end{aligned}$$

where \mathbf{y}_{CE} are the observed calving ease scores, t_1 , t_2 and t_3 are thresholds that categorize the four categories of response and I is an indicator function that takes value 1 if the condition specified is true and 0 otherwise. A response in a given category is observed, if the actual value of liability falls between the thresholds defining the appropriate category.

Just as Wang *et al.* (1997), thresholds t_1 and t_2 were assumed to be known and t_3 was assumed to be unknown in order to simplify the sampling scheme rather than the one defined by setting the residual variance of the categorical trait to one. Therefore, the values of t_1 and t_2 were based on the observed frequencies of calving ease scores in the considered categories, and residual variance was assumed to be unknown.

Model indicated as Model T1 was fitted with an estimated genetic correlation between direct and maternal additive genetic effects. Model indicated as Model T2 was fitted with a genetic correlation between genetic effects constrained to zero.

Variance components were estimated based on the data set I, for the four models by a Bayesian approach using the Gibbs sampling algorithm with flat priors for (co)variances. Gibbs sampling was used to obtain the marginal posterior distribution for variance components of each random effect from the model from 400 000 samples, after discarding 50 000 samples as the burn-in period. The stationary stage was confirmed by graphical inspection of plots of sampled values versus iterations. Every fifth sample was

retained to compute mean and standard deviation of the marginal posterior distribution. The estimation and the post-Gibbs analysis were performed using programs kindly provided by Ignacy Misztal (Misztal *et al.* 2002).

Comparison of models

Models were compared on their goodness of fit but also on their ability to predict 'future data'. For this purpose, the entire data set II was split into two parts. One-half of the calving ease records was randomly set to missing in the first data subset and the remaining one-half was set to missing in the second data subset. So, each calving ease record was only present in one of the two subsets. For these two subsets, direct and maternal breeding values and expectations of calving ease score were computed with a BLUP approach for linear and threshold models. This strategy was repeated five times to get ten subsets, *that is*, five paired subsets.

Within each model and for each of the ten data subsets, mean square errors (MSEs) were computed between expectations from the predictive distribution and the observed calving ease records which had been randomly set to missing.

The MSE was defined for linear model as:

$$\text{MSE} = \frac{1}{n} \sum_{i=1}^n (y_{\text{CE}i} - \hat{y}_{\text{CE}i})^2$$

where y_{CE} and \hat{y}_{CE} correspond to the observed and predicted calving ease scores, respectively; n is the number of data points in a data subset.

With the threshold model, MSE was computed, based on López de Maturana *et al.* (2009) as:

$$\text{MSE} = \frac{1}{n} \sum_{i=1}^n (y_{\text{CE}i} - \sum_{C=1}^{\text{ncat}} C \times P_{Ci})^2$$

where the probability (P_{Ci}) that observation i falls in category C was computed as:

$$P_{Ci} = \Phi\left(\frac{t_C - L_{\text{CE}i}}{\hat{\sigma}_e}\right) - \Phi\left(\frac{t_{C-1} - L_{\text{CE}i}}{\hat{\sigma}_e}\right)$$

with $\Phi(\cdot)$ is the cumulative distribution function of a normal variable evaluated at (\cdot) ; t_C is the inferred value of the appropriate threshold, and $L_{\text{CE}i}$ is the posterior mean of the liability to calving ease for an individual i .

Within each model and for each of the ten data subsets, Pearson's correlation between observed and predicted scores was calculated as:

$$r(y_{\text{CE}}, \hat{y}_{\text{CE}}) = \frac{\text{COV}(y_{\text{CE}}, \hat{y}_{\text{CE}})}{\sigma_{y_{\text{CE}}} \sigma_{\hat{y}_{\text{CE}}}}$$

where $\text{COV}(y_{\text{CE}}, \hat{y}_{\text{CE}})$ is the estimate of covariance between the observed and predicted calving ease scores, and $\sigma_{y_{\text{CE}}}$ and $\sigma_{\hat{y}_{\text{CE}}}$ are the estimates of standard deviations of observed and predicted calving ease scores, respectively.

Three groups of sires with progeny were created depending on their accuracy as follows: low: sires $>0 \leq 50$ progeny, medium: sires $>50 \leq 100$ progeny and high: sires >100 progeny. For each of these three groups of sires, correlations between sire breeding values were calculated for each of the five paired data subsets within each model to assess model prediction performance. A higher correlation estimate implied a better stability of the model to predict breeding values for animals whose records were randomly set to missing.

Finally, Spearman's rank correlations were computed between sire breeding values estimated from linear model and from threshold model for sires with progeny.

Results and discussion

The descriptive statistics of the data set I and data set II are displayed in Table 1. Disproportionate sex ratios were observed in records, and there were fewer male calves than female calves in both data sets. Further investigation suggested there may be a bias in recording of the sex of the calf as some breeders prefer to record female calves than male calves due to the difference in value between a male and a female calf in dairy cattle. This recording bias in the number of female and male calves can lead to an underreporting of difficulty to calve (score < 4) because the calving of male calves is known to be more difficult (Mee 2008).

(Co)Variance components and derived genetic parameters

Results for the (co)variance components and derived genetic parameters are reported in Table 2. Parameters generally were significantly different from zero because posterior means were more than two posterior standard deviations from zero, except for genetic correlation between direct and maternal additive genetic effects for Model L1 and Model T1 (i.e. models fitted with an estimated genetic correlation).

Table 1 Summary of edited data set used to estimate (co)variance components (data set I) and edited data set used for validation of models (data set II)

Item	Data set I		Data set II	
	No. of observations	Percentage	No. of observations	Percentage
Final data file	33 155	–	85 118	–
Female calves	26 177	78.9	66 511	78.1
Male calves	6978	21.1	18 511	21.9
Final pedigree file	120 374	–	233 882	–
Herds	492	–	862	–
Sires with progeny records	2215	–	3148	–
>0 ≤ 50 progeny	2067	–	2785	–
>50 ≤ 100 progeny	90	–	180	–
>100 progeny	58	–	183	–
Dams	25 240	–	62 265	–
Maternal grandsires	2031	–	3352	–
Calving ease				
1. Caesarean and embryotomy	443	1.3	781	0.9
2. Hard pull	2179	6.6	4006	4.7
3. Easy pull	10 114	30.5	23 461	27.6
4. Normal	20 419	61.6	56 870	66.8

Table 2 Posterior mean (PM) and posterior standard deviation (PSD) of (co)variance components and related genetic parameters estimated with each of four models

Parameter ^b	Model L1 ^a		Model L2 ^a		Model T1 ^a		Model T2 ^a	
	PM	PSD	PM	PSD	PM	PSD	PM	PSD
σ_h^2	0.042	0.002	0.042	0.002	0.146	.012	0.146	0.012
σ_a^2	0.027	0.004	0.028	0.004	0.085	0.015	0.082	0.013
σ_m^2	0.008	0.003	0.009	0.002	0.027	0.008	0.024	0.008
σ_p^2	0.018	0.004	0.017	0.005	0.035	0.012	0.034	0.010
σ_e^2	0.269	0.005	0.269	0.005	0.411	0.049	0.413	0.048
$r_u(a,m)$	0.088	0.194	–	–	–0.071	0.190	–	–
h_a^2	0.074	0.012	.078	.012	0.121	0.024	0.117	0.020
h_m^2	0.023	0.007	.024	.007	0.039	0.012	0.034	0.011
C_h	12%		12%		21%		21%	
C_p	5%		5%		5%		5%	
C_e	74%		74%		59%		59%	

^aModel L1 is the linear animal model with estimated covariance, Model L2 is the linear animal model with covariance constrained to zero, Model T1 is the threshold animal model with estimated covariance, and Model T2 is the threshold animal model with covariance constrained to zero.

^bThe terms σ_h^2 is the herd × year of calving variance, σ_a^2 is the direct additive genetic variance, σ_m^2 is the maternal additive genetic variance, σ_p^2 is the permanent maternal environmental variance, σ_e^2 is the residual variance, $r_u(a,m)$ is the genetic correlation between direct and maternal effects, h_a^2 and h_m^2 are the direct and the maternal heritabilities, respectively. 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 additive genetic variance due to direct effects was greater than that due to maternal effects for all models. On average, direct heritabilities were approximately three to four times as large as maternal heritabilities. All heritabilities estimated with all models were within 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 & Gianola 1989; Steinbock *et al.* 2003; Wiggans *et al.* 2003; López de

Maturana *et al.* 2007a; Eaglen *et al.* 2012). These estimates are not directly comparable because of different models (animal versus sire and maternal grandsire, linear versus threshold, univariate versus bivariate) that were used. However, most previous estimates tended to show that direct heritability was greater than maternal heritability.

Effects of herd × year of calving represent differences among herds and years of calving, which can be partly due to differences in subjective scoring of

calving ease. Fitting herd \times year effects as random allows more effective use of the data when applying the threshold model. The herd \times year of calving effects represented 12 and 21% of the phenotypic variance for the linear and threshold models, respectively, which was the largest contributor to the phenotypic variance after the residual effects (74 and 59%).

The maternal permanent environment effects represented 5% of the phenotypic variance in each model and were greater than the genetic maternal effects. Preliminary analyses based on the current data showed that maternal genetic variances tended to be overestimated by models that ignored permanent environmental effects.

Estimates of variance components and derived genetic parameters were similar within model type (linear versus threshold). A positive genetic correlation was found with Model L1 and a negative one with Model T1, but in both cases, the genetic correlation was not significant. Therefore, it seemed more appropriate to consider no genetic correlation between direct and maternal additive genetic effects in the subsequent stage of this study.

The analysis of calving ease with linear models yielded variance estimates that were consistently smaller than those obtained with threshold models. Particularly, variance of herd \times year of calving effects showed a marked decrease from threshold models to linear models. Threshold model heritability estimates were greater than linear model heritability estimates (0.117 versus 0.078 and 0.034 versus 0.024 for direct and maternal heritabilities, respectively), but these heritabilities cannot be directly compared because they were estimated on different scales, on a visible probability scale and on an underlying normal scale for linear and threshold models, respectively. Furthermore, heritability estimates are frequency dependent when a linear model is used to fit categorical traits. Dempster & Lerner (1950) proposed transformations to make heritabilities comparable. As reported by several studies, higher heritabilities are usually expected with threshold models than linear models (Luo *et al.* 1999; Phocas & Laloë 2003).

The best fit of the model, measured by the percentage of residual variance in the phenotypic variance, was achieved for threshold models, approximately 59% against 74% with linear models.

Comparison of models

The MSE for Model L2 and Model T2 used to predict the calving ease records set to missing in the ten data

subsets is provided in Table 3. Models with the smaller MSE had better predictive ability. In general, MSE was similar for both models with only very small differences. Based on the average MSE, the threshold model did not perform better than linear model (0.294 versus 0.293). These results were consistent with those obtained by Varona *et al.* (1999) who also used differences in MSE as a criterion for comparison of models. They found small differences between univariate linear and threshold models based on field and simulated data in beef cattle.

Table 3 also displays Pearson's correlation estimates between observed and predicted calving ease scores by Models L2 and T2 for the ten subsets. Similar to MSE, differences in correlation between models were very small. For all subsets, the threshold model performed slightly better than the linear model (0.502 versus 0.497). These results were expected because the threshold model is considered as being strategy better model to fit such categorical traits.

Table 4 contains the average correlation estimates between the five paired data subsets for genetic direct and maternal calving ease breeding values from Models L2 and T2 considering sires with 50 or fewer progeny (low-accuracy sires), sires with between 51 and 100 progeny (medium-accuracy sires) and sires with more than 100 progeny (high-accuracy sires). The differences between linear and threshold models decreased as the number of progeny records available for sires increased, especially for differences between sire breeding values for maternal effects. So, if the number of calving records per sire is limited,

Table 3 Mean squared error (MSE) and Pearson's correlation estimates between observed and predicted calving ease scores for Model L2 and Model T2 for the ten replicates

Subset	MSE		Correlation	
	Model L2 ^a	Model T2 ^a	Model L2 ^a	Model T2 ^a
1	0.292	0.292	0.497	0.502
2	0.296	0.297	0.493	0.497
3	0.295	0.294	0.497	0.503
4	0.292	0.293	0.495	0.499
5	0.291	0.292	0.501	0.507
6	0.294	0.295	0.494	0.498
7	0.293	0.293	0.494	0.500
8	0.292	0.293	0.501	0.506
9	0.292	0.292	0.494	0.500
10	0.294	0.294	0.499	0.505
Average	0.293	0.294	0.497	0.502

^aModel L2 is the linear animal model with covariance constrained to zero, and Model T2 is the threshold animal model with covariance constrained to zero.

Table 4 Average, standard deviation (SD), minimum and maximum of correlation estimates between split data sets^a for calving ease breeding values of sires with progeny (N = 3148) from Model L2 and Model T2

Category ^b	Model L2 ^c							
	Direct genetic effect				Maternal genetic effect			
	Mean	SD	Min	Max	Mean	SD	Min	Max
Sires >0 ≤ 50	0.635	0.028	0.604	0.663	0.465	0.057	0.369	0.506
Sires >50 ≤ 100	0.647	0.047	0.605	0.698	0.369	0.037	0.329	0.407
Sires >100	0.689	0.030	0.644	0.721	0.394	0.073	0.290	0.460
Model T2 ^c								
Sires >0 ≤ 50	0.507	0.030	0.475	0.536	0.360	0.047	0.279	0.392
Sires >50 ≤ 100	0.549	0.057	0.478	0.610	0.282	0.032	0.238	0.316
Sires >100	0.599	0.038	0.538	0.634	0.334	0.069	0.226	0.406

^aIn five paired data subsets.

^bSires >0 ≤ 50: sires with 50 or fewer progeny records in data file, sires >50 ≤ 100: sires with 51–100 progeny records in data file, sires >100: sires with more than 100 progeny records in data file.

^cModel L2 is the linear animal model with covariance constrained to zero, and Model T2 is the threshold animal model with covariance constrained to zero.

differences in the ranking of sires might occur using the linear versus threshold model. For all groups of sires, greater correlations were observed with Model L2 than with Model T2 for direct and maternal genetic effects. On average, correlations from the linear model was 17 and 23% higher than from the threshold model for direct and maternal breeding values, respectively. Thus, the linear model appeared to have a higher stability for predicting breeding values of animals whose records were randomly set to missing. These results were not in line with those obtained in beef cattle by Ramirez-Valverde *et al.* (2001) who found a better stability with a threshold approach. As expected, lower accuracy was observed for maternal effects.

The most likely reasons for the linear model showing consistently better results could be due to the fact that in the threshold model, additional parameters (thresholds) needs to be estimated leading potentially to lower estimation accuracies, especially for animal models. The threshold model fitted slightly better and explained more variance; however, breeding values were less stable between paired subsets especially for maternal additive genetic effects.

Fitting herd × year effect as random can lead to biased estimates of breeding values (Visscher & Goddard 1993). Phocas & Laloë (2003) stated that when a non-random association exists between sires and contemporary groups, the correlation between true and predicted breeding values can be affected. However, it is unsure to what degree this non-random association has to exist to create this behaviour.

Spearman's rank correlations between sire breeding values from Model L2 and Model T2 were 0.972 and 0.971 for direct and maternal calving ease breeding values, respectively, indicating that the ranking of sires was nearly identical between the linear and the threshold models. This was in agreement with results from similar comparisons involving categorical traits in cattle (Weller *et al.* 1988; Clutter *et al.* 1989; Ramirez-Valverde *et al.* 2001) and in sheep (Olesen *et al.* 1994; Matos *et al.* 1997).

Conclusions

(Co)variance components and derived genetic parameters for calving ease were estimated with univariate linear and threshold animal models. The direct–maternal genetic correlation was positive for the linear model and negative for the threshold model, but neither was significantly different from zero. The heritability estimates were consistent with those found in other studies on calving ease in dairy cattle. The threshold models showed a better goodness of fit than linear models. However, in terms of predictive ability, no clear advantage of the threshold models over the linear models was found with our data. Accordingly, it would be preferable and more technically feasible to use a linear model to perform genetic evaluation of calving ease. Thus, the linear animal model without covariance between direct and maternal additive genetic effects (i.e. Model L2) would be the model of choice to implement the routine genetic evaluation of calving ease for the Walloon dairy cattle.

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