Analysis of calving traits and gestation length in UK Holstein heifers using an animal model

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Introduction

Calving traits are of importance to the dairy cattle industry being linked to impaired performance and loss of animals. Welfare of the cow during a difficult calving is compromised due to severe pain experienced during parturition, while high veterinary and labour costs lead to economic loss. A genetic evaluation of calving ease (CE) and stillbirth (SB; defined as calf mortality at, or within 48 hours after, birth) is therefore essential to restrict future increases in the occurrence of dystocia and SB. Gestation length (GL) is linked to the calving interval and, therefore, relevant to farm management. GL has been reported to be related to calving performance traits (Normal *et al* 2009). An extremely short gestation is associated with a higher frequency of SB due to under development of the fetus while a long gestation is linked to a difficult calving and SB due to the relatively oversized calf. CE, SB and GL are all examples of traits affected by both direct and maternal effects, which makes their genetic evaluation complex. Thus, the statistical approach towards analysing these traits has been the focus of many studies worldwide; especially when it comes to the inclusion and estimation of the genetic direct-maternal correlation within and across traits. Strong negative direct-maternal genetic correlations have been found regularly. Their nature, however, has been questioned (Robinson 1996), and multiple bias theories have been presented (Falconer 1965; Koch 1972; Swalve 1993; Bijma 2006). The objective of this study was to make inferences about direct and maternal heritabilities of GL, SB and CE at first calving while considering the statistical complexities arising when estimating the direct-maternal genetic relationship.

Material and methods

Direct and maternal effects Following Willhams model (1963), the phenotype of an individual *i* is the summation of the direct and maternal effects, both consisting of an additive and environmental component. The total breeding value of *i*, TBV*i,* is then the sum of its direct (expressed at birth) and maternal breeding value (expressed at calving). As the TBV represents the total heritable value of an animal, its variance represents the total heritable variance available for response to selection. In this study, we therefore also present estimates of the ratio of the total heritable variance over the phenotypic variance, represented by the parameter T^2, for all traits.

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$$P_{\mathbf{i}} = A_{\mathbf{D,i}} + E_{\mathbf{D,i}} + A_{\mathbf{M,j}} + E_{\mathbf{M,j}} \quad , \quad TBV_{\mathbf{i}} = A_{\mathbf{D,i}} + A_{\mathbf{M,i}} \quad , \quad T^2 = \frac{\sigma^2_{A_{\mathbf{D}}} + 2\sigma_{A_{\mathbf{DM}}} + \sigma^2_{A_{\mathbf{M}}}}{\sigma^2_p}$$

where *i* is the individual, *j* is its dam, *Ad* and *Am* are the direct and maternal additive effects, or breeding values, and *Ed* and *Em* are the direct and maternal environmental effects.

A potential source of the bias in the estimate of the genetic direct maternal correlation may be the presence of an environmental dam-offspring covariance (Koch, 1972) which is often ignored. his covariance (cov($E_{Di,}$ E_{Mi})) appears in the phenotypic covariance between the birth and calving record of an individual *i* and, if present, correlates the residuals of both records, as E_{Di} is expressed in the birth record of *i* and E_{Mi} in her calving record (Bijma 2006; Eaglen 2009). Ignoring the covariance can bias the remaining genetic components, and subsequently the estimated genetic parameters. To avoid this, individuals appearing both as calf and dam were deleted from all datasets in this study.

Data description CE and SB data was provided by two milk recording organizations (MRO) in the UK, the Cattle Information Service (CIS) and National Milk Records (NMR). GL was derived from the insemination and calving date and restricted to 265-295 days. Only records on single born calves were used and calving date and age at calving were checked for validity. The datasets obtained contained 43,135 records spanning 1995-2009. From this data, herds and sires with less than two observations were deleted and age at calving was restricted to 18-48 month for heifers and 30-190 months for cows. Breed of sires and dams was Holstein, Friesian or Holstein-Friesian, from different countries of origin. To avoid herds in which farmers incorrectly recorded the same CE score for most cows, the standard deviation within herd-year was studied. Herd-year classes with a standard deviation of 0, accompanied by a size outside the range of a 97.5% CI, were deleted. The final dataset consisted of 30,640 records originating from 2,098 herds and representing 2,012 (service) sires. The accompanying pedigree contained ~ 200,000 individuals and was 5 generations deep. It is important to state that the MROs have a different way of recording the calving traits (on a 4 -grade and 5 -grade scale respectively). Categories were defined by MRO A as: 1-easy, 2-assisted, 3-difficult, 4 -vet assisted, and by MRO B as: 1- normal (not assisted), 2- moderate assistance (farmer), 3- moderate assistance (vet called as precaution), 4 - difficult (extraction by farm staff), 5- very difficult calving (vet assisted).

Table 1. Freq. distributions of CE by MRO

	Frequency	
	A	B
1	77.35%	65.92%
2	20.50%	58.30%
3	1.70%	4.88%
4	0.44%	0.90%

[1] 1 = easy (non-assisted), 2 = moderate assistance (vet called as precaution), 3 = difficult, 4 = very difficult with vet assistance.

To harmonise both scales, categories 2 and 3 of the MRO B scale were merged; both referring to 'moderate assistance required'. Secondly, MRO B records CE data for the purpose of progeny testing, whereas data from MRO A is farmer-recorded which can be slightly more subjective. Table 1. shows that the frequency distributions within source and parity differ. To account for this difference, the recorded CE scores were transformed to values on the underlying normal distribution (average liability value) within source and parity. The frequency of stillborn calves in the final dataset equalled 11,6%

Statistical analyses The linear animal model used in this study was

$$\mathbf{y}_i = \mathbf{Xb} + \mathbf{Z}_d\mathbf{a}_d + \mathbf{Z}_m\mathbf{a}_m + \mathbf{e}$$

where $\mathbf{y}_i$ is a vector representing the observations for CE, SB or GL. **X**, $\mathbf{Z}_{d,}$ and $\mathbf{Z}_m$ are known incidence matrices for non-genetic, and direct and maternal genetic effects, respectively; **b** is a vector of non-genetic effects, $\mathbf{a}_d$ is a vector of the random additive genetic direct effects of the calf and $\mathbf{a}_m$ is a vector of the random additive genetic maternal effects of the dam. $\mathbf{a}_d$ and $\mathbf{a}_m$ were assumed to follow a normal distribution, with mean 0 and covariance matrix $\mathbf{G} = \mathbf{G}_0 \otimes \mathbf{A}$ where, $\mathbf{G}_0$ is a 2 x 2 direct-maternal variance-covariance matrix, $\otimes$ indicates the Kronecker product of matrices and **A** is the relationship matrix; **e** is a vector of the residuals, which are assumed to be independent, $\mathbf{e} \sim N(0, \mathbf{I}\,\sigma^2_e)$, where **I** denotes the identity matrix and σ^2_e the residual variance. Non-genetic effects fitted include sex of the calf, age of the dam (months), herd, sire breed (only for GL), interaction effect of the year and month of calving and a random effect of herd-year. Variance components were estimated using ASREML v2.0 (Gilmour *et al.* 2006).

Results and discussion

Heritabilities The estimated heritabilities for CE, SB and GL, (Table 2.) are in the range of previously published estimates of these traits in dairy cattle (Steinbock 2003; Eaglen 2008; Norman 2008) and are similar to the estimates reported by Wall *et al* (2010) on the development of calving ease evaluations for UK Holstein-Friesian cows. The estimated maternal heritability of GL seems to be slightly high as estimates in the literature range from 0.07 to 0.14. The large difference in magnitude between the direct and maternal variance of GL was expected, and reported in several studies. As the parturition is triggered by the calf, producing cortisol when experiencing space limitations, the genetic variation contributed by the calf is considerably higher than that contributed by the dam (Hansen *et al* 2004).

Genetic correlations The estimated direct-maternal genetic correlations (Table 2.) are moderate to high although the estimate for SB is not significantly different from zero ($P<0.05$). The high standard errors of the estimates are likely to be due to the low number of records. The antagonistic relationship between direct and maternal breeding value of CE has been reported in numerous studies although the strength of this relationship has stimulated some discussion, considering that previously published estimates range from zero to -0.50 in dairy and -0.72 in beef cattle (Robinson 1996). The estimated correlation in this study therefore seems be at the high end of estimates reported for dairy cattle. Considering the amount of theories presented on the direct-maternal relationship, of which one is implemented in this study (Koch 1972; Bijma 2006; Eaglen 2009), the magnitude of the estimated correlation indicates the need for further study. The high direct maternal genetic correlation estimated for GL is supported by Norman (2008). who reported a correlation of 0.83. However, other studies report low negative estimates, or close to zero (Hansen *et al.* 2004); which supports the need for further research of this particular relationship. Estimates of the genetic correlation between direct and maternal effects of SB in literature are low or close to zero (Steinbock *et al*, 2004)

Total heritability The total heritability, represented by the parameter T^2**,** in comparison to the direct heritability, shows the change in heritable variance when accounting for the maternal variance and the genetic covariance between the direct and maternal breeding value. By including the additional variance contributed by the maternal effect and accounting for the direct-maternal covariance, one obtains the true total heritable variation. Although some estimates are somewhat biased due to inaccuracy, the estimates of T^2 presented by Table 2. clearly show the impact of magnitude and sign of the maternal variance and direct-maternal covariance on the total heritable variance available for response to selection. By not, or incorrectly, estimating the total heritable variance, thereby keeping significant variation hidden, selection can lead to a different response than expected from predictions. A clear and accurate definition of this variance is therefore essential.

Table 2. Estimated genetic parameters $^{\alpha}$

	Parameter			
Trait	h_D^2	h_M^2	r_{DM}	T^2
CE	0.119 ± 0.023	0.048 ± 0.014	-0.523 ± 0.129	0.088 ± 0.018
SB	0.016 ± 0.010	0.033 ± 0.011	0.748 ± 0.438	0.083 ± 0.031
GL	0.426 ± 0.037	0.134 ± 0.013	0.758 ± 0.064	0.655 ± 0.039

α $h_D^2 = \sigma_{A_D}^2 / \sigma_P^2$, $h_M^2 = \sigma_{AM}^2 / \sigma_P^2$, $\sigma_P^2 = \sigma_{Ad}^2 + \sigma_{Adm} + \sigma_{Am}^2$

Conclusion

Estimated heritabilities of CE, SB, and GL in UK Holstein heifers are consistent with estimates reported in literature and previous conducted analyses on UK data. Although one source of potential bias in the genetic relationship between direct and maternal breeding values was eliminated, estimates show that further research will be valuable to test other bias theories. Estimates of the T^2 support the importance of this parameter as an indicator of the total heritable variation available for response to selection. The next step will be to fit a multiple trait model between CE, SB and GL.

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