The Direct and Maternal Genetic Relationships Between Calving Ease, Gestation Length, Milk Production and Selected Type Traits

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Abstract

Focus in cattle breeding is shifting from traits that increase income, towards traits that reduce costs. As a result, an increasing number of functional traits, of which calving ease (**CE**) is an example, are included in national breeding indices. Yet, knowledge of genetic relationships between **CE** and other traits of interest is scarce. The same applies to gestation length (**GL**), a potential novel selection trait. Linear type traits often assumed to be associated with calving traits due to their function of describing the visual characteristics of an animal. Therefore, genetic relationships are estimated between **CE**, **GL**, selected type traits and milk production using a national dataset of 27,845 primiparous cow performance records separating genetic direct and maternal effects. Traits chosen cover type traits that have previously been associated with calving performance: udder depth (**UD),** chest width **(CW),** rump width **(RW),** rump angle **(RA),** mammary composite **(MAMC),** stature **(STAT),** and body depth **(BD**). The milk production trait chosen is the 305-d milk yield (**MY-305**). Multi-trait linear trivariate sire models were fitted using ASREML v3.0 where an additional random sire of the calf effect was included to account for the direct effect of **CE** and **GL**. Results show that high yielding individuals are genetically prone to spend a shorter time *in utero* of their primiparous dams (-0.19±0.09) and be born more easily (-0.45±0.14). Individuals experiencing a longer first gestation period are likely to be larger animals (0.48±0.14) with wider rumps (0.52±0.15) which have gestated shorter before being born (-0.30±0.13). And finally, heifers having a difficult calving are likely to be deeper individuals (0.47±0.18) with wider rumps (0.41±0.20) and chests (0.55±0.20) and lower pin bones (0.51±0.20). This study further shows that it is feasible, and valuable, to separate direct and maternal effects when estimating genetic correlations between calving traits and other traits of interest. Differences in direct and maternal genetic correlations indicate that genetic relationships between **CE**, **GL** and type traits are clearly present but careful consideration is needed if these traits are utilised in national breeding indices.

1. Introduction

Worldwide, awareness is growing that, in order to maintain or improve economic efficiency, genetic emphasis on fitness traits is needed when selection decisions are made (De Maturana *et al*., 2007). Calving is a major event in a cow's life with complications during calving leading to a potential loss and/or impaired performance of the animal and compromised animal welfare. Reducing the number of difficult calvings by genetic selection is therefore highly beneficial for the cows and for the dairy cattle industry. Investigation into the genetic relationships between calving traits and other (non-calving) traits is however noticeably lacking. Furthermore, direct and maternal genetic effects are rarely separated when genetic correlations are estimated which can lead to estimation bias. Type traits are among present selection traits that have primarily phenotypically been associated with calving traits. Any estimated genetic relationships are scarce.

The aim of this study is therefore to estimate the direct and maternal genetic relationships of CE and GL with selected type traits and milk yield.

2. Material and Methods

2.1 Data description

This study was restricted to first parity **CE** records that were collected and provided by two milk recording organizations (MRO) in the UK from 1995 to 2009. After merging the CE data from both sources the data were validated for duplicates and invalid dates. Data contained only single birth calvings. The age of the dam at calving, parity and breed of dam and sire were checked for inconsistencies and incorrect records were discarded. **GL** was derived from the last recorded insemination and calving date and was restricted to 265-295 days. After editing, the **CE** dataset consisted of 43,135 records originating from 2,824 herds. Unrealistic scoring of **CE** (the same **CE** score for most or all calvings) was avoided by a correction on standard deviation within herd-year contemporary group. Herd-year classes with a standard deviation of 0, accompanied by a size outside the range of a 97.5% confidence interval, were deleted.

The number and definitions of categories on the **CE** scoring scale differed between the MRO's therefore harmonization of the scales needed to take place. Furthermore, purpose of the collection of **CE** data differs between MRO's (farmer recorded vs. progeny testing).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 edited dataset, consisting of 30,640 records, was subsequently matched to trait data in the lactation following the recorded calving. Six out of seven type traits were objectively scored from 1 to 9 by a classifier at inspection, where 1 and 9 are applied to the extremes of the trait. Scores at the extreme end of the scale represent the following conformation: **CW**: 1-narrow, 9-wide; **RW**: 1-narrow, 9 wide; **RA**: 1 – high pin bones, 9 – low pin bones; **BD**: 1-shallow, 9-deep; **STAT**: 1-small, 9-tall; **UD**: 1-below hock, 9-above hock. **MAMC** is a composite type trait which covers the strength and quality of the fore and rear attachment, strength of central ligament, teat quality and udder texture. **MAMC** is scored with a pointing system which ranges from <64 – poor to 100 – excellent. Subsequently, all type records were adjusted for classifier before data was provided for this study (Brotherstone *et al.*, 1990). Validity checks were performed on the matched dataset to ensure all data was correctly linked. Erroneous records were removed and age of heifer was restricted between 18-40 months to ensure only first parity records. Contemporary groups with fewer than two records (herd, herd-year, sire and maternal grandsire) were discarded. Time between calving and inspection was restricted to be between 0-8 months. Editing led to a final dataset of 27,845 heifer performance records, originating from 1,751 herds representing 1,699 (service) sires and 2,543 maternal grandsires.

2.2 Statistical analysis

Trivariate linear mixed models were fitted using REML, by ASREML version 3.0 (Gilmour *et al.*, 2009) after optional fixed effects and potential interaction effects were tested on significance in SAS V9. An extended sire model was fitted where the sire of the dam (sd) accounts for the normal additive (direct) effect for all non-maternally affected traits. For the maternally affected traits, **CE** and **GL,** this same sire acts as the maternal grandsire (MGS) of the calf thereby accounting for the additive maternal effect (**CEm, GLm**). To allow separation of all direct and maternal genetic (co)variances, sire of the calf (sc) was additionally fitted to account for the additive direct effect of **CE** and **GL (CEd, GLd).**

The general linear statistical model fitted therefore equalled

$$\mathbf{y}_i = \mathbf{X}_i\mathbf{b}_i + \mathbf{Z}_{i\_sd}\mathbf{a}_{i\_sd} + \mathbf{Z}_{i\_sc}\mathbf{a}_{i\_sc} + \mathbf{e}_i$$

where $\mathbf{y}_\mathrm{i}$ is a vector representing the observations for trait *i*, (trait 1 is always either **CE** or **GL** and trait 3 is always **MY-305**). **X**, $\mathbf{Z}_{\mathrm{i\_sd}}$, and $\mathbf{Z}_{\mathrm{i\_sc}}$ are known incidence matrices for non-genetic, and direct and maternal genetic effects, respectively; **b** is a vector of non-genetic effects, $\mathbf{a}_{\mathrm{i\_sd}}$ is a vector of the random additive genetic direct effects of the sire of the dam for all traits. $\mathbf{a}_{\mathrm{i\_sc}}$ is a vector of the random additive direct effects of the sire of the calf for maternally affected traits, and is therefore equal to 0 for the non-maternally affected traits. $\mathbf{a}_{\mathrm{i\_sd}}$ and $\mathbf{a}_{\mathrm{i\_sc}}$ were assumed to follow a normal distribution, with mean 0 and covariance matrix $\mathbf{G} = \mathbf{G}_0 \otimes \mathbf{A}^{-1}$ where, $\mathbf{G}_0$ equals a 4 x 4 symmetrical direct-maternal variance-covariance matrix, $\otimes$ indicates the Kronecker product of matrices and $\mathbf{A}^{-1}$ is the inverted relationship matrix. Residuals between traits are assumed independent and therefore follow $\mathbf{e}_i \sim N(0, \mathbf{I}\sigma^2_{e\,i})$, where $\mathbf{I}$ denotes the identity matrix and $\sigma^2_{e\,i}$ is the residual variance of trait *i*.

Non-genetic effects fitted included sex of the calf, herd, sire breed (only for **GL**), year*month of calving, year*month of inspection, stage of lactation at inspection, age at calving (covariate), age at inspection (covariate), (age at inspection)^2 and a random effect of herd-year. Analyses yielded sire and MGS variances which were algebraically converted into direct and maternal variance components.

3. Results and Discussion

3.1 Data description

Frequency distributions of CE per data source are given in Table 1 which also shows the harmonized scoring scale. Frequencies differences between MRO's validate the transformation of CE scores prior to analyses.

Table 1. CE frequencies per data source.

Trait		Data source		
		Total	MRO A	MRO B
CE[1]	1	73.13%	79.62%	66.04%
	2	23.05%	17.97%	28.61%
	3	3.17%	1.86%	4.60%
	4	0.65%	0.56%	0.74%

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

Table 2 presents the descriptive statistics for all traits.

Table 2. Descriptive statistics of all traits.

Trait	Statistic	
	Mean	σ^2_P
CEd	1.31 (0.56)	0.43 (0.01)
CEm	1.31 (0.56)	0.43 (0.01)
GLd	280.67 (5.00)	24.55 (0.56)
GLm	280.67 (5.00)	24.55 (0.56)
Production		
MY-305 (kg)	7522.94 (1577.52)	1.42 (0.02)
Conformation		
UD	5.91 (1.28)	1.37 (0.02)
MAMC	80.03 (5.04)	21.54 (0.36)
RW	5.52 (1.38)	1.60 (0.03)
RA	4.33 (1.28)	1.53 (0.03)
CW	5.23 (1.47)	1.81 (0.03)
STAT	6.13 (1.37)	1.31 (0.02)
BD	5.8 (1.30)	1.39 (0.02)

3.2 Genetic correlations between calving traits

Table 3 presents the heritabilities of and genetic correlations between, **CE** and **GL**. Heritabilities of **CE** are low and the direct heritability is approximately twice the maternal heritability. In this study, the direct-maternal genetic covariance of **CE** is not significantly different from zero therefore, from this study, we cannot conclude that there is a genetic relationship between the direct and maternal genetic effect of **CE**. Estimated heritabilities of **GL** show a considerable difference between the direct and maternal heritability, which is thought to originate from the biological fact that the foetus triggers parturition. The significant maternal heritability of **GL** proves however that **GL** is a maternally affected trait. A general consensus exists that **GL** is related to **CE**. Results of this study, however did not detect any significant genetic correlations of **CE** and **GL** in first parity, direct nor maternal.

3.3 Genetic correlations between calving and type traits

Linear type traits describe biological extremes for a range of visual characteristics of an animal (Berry *et al.,* 2004). It is therefore not strange that conformation is thought to be associated with calving traits. Results of this study (Table 3) show that **CEm** and **GLm** are genetically related to the selected type traits. Estimated genetic relationships of type and length of gestation conform to the literature where larger animals with wider rumps are associated with a longer gestation period (Pozveh *et al.,* 2009). Individuals with a wider chest and a deeper body were genetically more prone to a difficult calving. Surprisingly however, are the positive genetic correlations found between **CEm**, **RW** and **RA** which suggest that difficult calvings are related to low pinbones and wider rumps. In the literature, high pin bones are thought to tilt the vaginal canal causing it to lie at an angle which might cause difficult calvings (Wall *et al.,* 2005). Support however comes from Ali et al. who in 1984, reports a low positive correlation between hip width and **CE.** In addition, genetic correlations estimated by Ali et al. suggest that cows with large slopes from hip to thurl and consequently low thurls in relation to hip bone tend to have more problems during calving. The positive genetic correlations found in this study between **CEm**, **RA** and **RW** therefore might seem surprising but should not be disregarded. Other genetic correlations estimated in the same analyses conform to the literature which supports the model. Interestingly, Berry *et al.* hypothesizes in 2004 that estimated genetic correlations between milk yield and type traits may reflect past emphasis on milk production simultaneously with increased cow stature, width depth and angularity in Holstein breeding programs of which the outcome is taller wider deeper cows. In combination with the results of this study, which show that larger, wider and deeper heifers are genetically prone to longer gestations and more difficult calvings, it could be hypothesized that historical selection decisions may be indirectly linked to the current problems in calving performance.

3.3 Genetic correlations between milk yield and other traits

Multi-trait analyses conducted between a variety of traits, calving traits and MY-305 show that higher yielding cows are genetically prone to have lower udders, better mammary composition, wider rumps, higher stature and deeper bodies (Table 3). The relationship of milk yield and conformation found in this study is nearly identical to that reported in Berry *et al.* 2004.

4. Conclusions

This study shows that CE and GL are genetically related to other important selection traits which need to be taken into account when CE and GL are implemented into national breeding indices. Significant results show that high yielding individuals are genetically prone to spent a shorter time *in utero* of their primiparous dam and be born more easily. Individuals experiencing a longer first gestation period are likely to be larger animals with wider rumps which have gestated shorter before being born. And finally, heifers having a difficult calving are genetically predisposed to be deeper individuals with wider rumps and chests and lower pin bones. Further, this study shows that it is feasible and valuable to separate the direct and maternal effects when estimating genetic correlations between calving and other traits. Besides being statistically more appropriate, the estimation of both direct and maternal genetic correlations allows evaluating genetic relationships in more detail which may aid to explain the current state of calving performance in UK Holstein-Friesian heifers and develop more appropriate selection indices.

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Table 3. Genetic correlations between calving traits and type traits .

		Genetic correlation with CE		Genetic correlation with GL		Genetic correlation with MY-305
Trait	h_d^2	r_d	r_m	r_d	r_m	
Calving						
CE – Direct	0.057 (0.02)*	-	-0.20 (0.27)	0.09 (0.13)	0.23 (0.22)	-0.42 (0.16)*
CE – Maternal	0.028 (0.01)*	-0.20 (0.27)	-	-0.06 (0.20)	-0.12 (0.26)	0.27 (0.18)
GL - Direct	0.49 (0.05)*	0.09 (0.13)	-0.06 (0.20)	-0.30 (0.13)*	-	-0.19 (0.09)*
GL - Maternal	0.09 (0.03)*	0.23 (0.22)	-0.12 (0.26)	-	-0.30 (0.13)*	0.04 (0.14)
Milk yield						
MY-305	0.50 (0.04)*	-0.45 (0.14)*	0.31 (0.17)	-0.19 (0.09)*	0.04 (0.14)	1.00 (0.00)
Conformation						
UD	0.19 (0.04)*	0.03 (0.24)	-0.44 (0.23)	-0.07 (0.14)	0.31 (0.18)	-0.45 (0.09)*
MAMC	0.24 (0.04)*	0.03 (0.21)	-0.26 (0.22)	-0.14 (0.13)	0.19 (0.18)	0.41 (0.09)*
RW	0.30 (0.05)*	-0.06 (0.21)	0.41 (0.20)*	0.09 (0.13)	0.52 (0.15)*	0.21 (0.09)*
RA	0.41 (0.06)*	0.01 (0.20)	0.51 (0.20)*	0.09 (0.12)	-0.18 (0.16)	0.10 (0.09)
CW	0.21 (0.04)*	0.04 (0.22)	0.55 (0.20)*	-0.09 (0.14)	0.35 (0.18)	-0.03 (0.11)
STAT	0.41 (0.06)*	0.17 (0.19)	-0.03 (0.21)	-0.11 (0.12)	0.48 (0.14)*	0.20 (0.08)*
BD	0.32 (0.05)*	-0.04 (0.21)	0.47 (0.18)*	-0.10 (0.12)	0.28 (0.16)	0.25 (0.09)*

* $P< 0.05$ as judged by 1.96 x s.e.