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Genetic relationships among calving ease, gestation length, and calf survival to weaning in the Asturiana de los Valles beef cattle breed[1]

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ABSTRACT: The aim of this paper was to estimate the genetic relationships among calving ease (CE), calf survival (CS), and gestation length (GL) to assess the possibility of including this information in beef cattle breeding programs. A total of 35,395 field records were available for CE, 30,684 for GL, and 36,132 for CS from the Asturiana de los Valles beef cattle breed. The 3 traits were analyzed as traits of the calf fitting a multivariate linear mixed model. Estimates of heritability (±SE) for the direct genetic effects (CEd, GLd, and CSd) were 0.325 ± 0.022, 0.331 ± 0.026, and 0.226 ± 0.018, respectively, whereas the estimates for maternal genetic effects (CEm, GLm, and CSm) were 0.066 ± 0.018, 0.066 ± 0.017, and 0.034 ± 0.011. The estimates for the ratio of permanent environmental variance to phenotypic variance were CEc 0.090 ± 0.011, GLc 0.066 ± 0.011, and CSc 0.024 ± 0.007. Genetic correlations between direct, maternal genetic, or permanent environmental effects involing CE and GL were, in general, positive and moderate, whereas those involving CE and CS were high. All were significant except for the pair CEm-GLm (0.277 ± 0.172). Correlations between GL and CS were nonsignificant. Genetic correlations for CEd-CEm, GLd-GLm, and CSd-CSm were negative and high, ranging from -0.461 ± 0.120 for GLd-GLm to -0.821 ± 0.145 for CSd-CSm. The genetic correlations for CEd-CSm and for CSd-CEm were negative, significant, and high, whereas that for GLd-CEm was moderate (-0.323 ± 0.124) and that for GLd-CSm was nonsignificant. The genetic correlations for GLm with the direct effects of the other traits were non-significant. Strong selection for CE will result in a significant correlated response in CS. Therefore, CE can be considered an early indicator of CS performance. The benefit of using GL as a correlated trait in a genetic evaluation with CE and CS seems limited.

INTRODUCTION

Calf survival (**CS**) has a major influence on the profitability of suckling cow production systems (Phocas et al., 1998). Mortality of calves reduces beef income and adds significantly to beef production costs (Meijering, 1984; Wittum et al., 1993). Dystocia negatively affects CS via multiple mechanisms including prolonged hypoxia and potential traumas (Lombard et al., 2006). In dairy cattle, a calving ability index including CS (stillbirth) and calving ease (**CE**) for sire selection has been proposed (Cole et al., 2007).

Genetic studies on CS in beef cattle are scarce (Goyache et al., 2003; Tarrés et al., 2005; Guerra et al., 2006). Moreover, the available information on the genetic relationships between CE and CS is basically found in dairy cattle (Eriksson et al., 2004; Hansen et al., 2004; Cole et al., 2007).

Crews (2006) reported important genetic associations between gestation length (**GL**) and birth weight (**BrW**), which has, in turn, a significant genetic relationship with CE (Gutiérrez et al., 2007; Phocas, 2009). In dairy cattle, Hansen et al. (2004) suggested the inclusion of GL in sire selection programs due to its potential genetic associations with stillbirth and CE (Meijering, 1984; McGuirk et al., 1999).

We have estimated genetic parameters for CS at different calf ages (Goyache et al., 2003) and the genetic relationships between CE and BrW, weaning weight, and calving interval in the Asturiana de los Valles beef cattle breed (Gutiérrez et al., 2007). Our interest now is to establish the genetic basis affecting traits that have been shown to be economically important in beef cattle

Table 1. Number of records by calving ease score, percentage of the total number of recorded scores, and percentage alive at weaning and means and SD of gestation length (GL) by calving ease score class

Calving ease score[1]	n[2]	%	GL, d		Calves alive at weaning	
			Mean	SD	n	% of calves alive
1	16,313	45.3	286.9	5.8	15,206	93.2
2	15,900	44.2	287.3	5.7	14,957	94.1
3	2,889	8.0	289.0	5.6	1,666	57.7
4	893	2.5	288.9	5.9	718	80.4

[1]Calving ease was scored as: 1 (no assistance), 2 (minor assistance), 3 (hard assistance), and 4 (caesarean section).
[2]Number of records.

so as to include these in the breeding objective (Gutiérrez et al., 2002, 2006; Goyache et al., 2005). The aim of this study was to estimate the genetic relationships among CE, GL, and CS to weaning so as to evaluate the possibility of including this information in beef cattle improvement programs. The consequences due to correlated responses are also discussed.

MATERIALS AND METHODS

Animal Care and Use Committee approval was not obtained for this study because the data were obtained from an existing database under the custody of SERIDA, a research organization dependent on the government of Principado de Asturias.

Asturiana de los Valles is a local beef cattle breed basically exploited under semi-extensive conditions in the mountainous Cantabrian Range (northern Spain; Gutiérrez et al., 1997, 2007; Gutiérrez and Goyache, 2002). Production data and pedigree information of the Asturiana de los Valles breed were obtained from the performance record database (the CORECA database) implemented by the Regional Government of the Principado de Asturias (northern Spain), through the Asturiana de los Valles Breeders Association. The database includes records from the beginning of the performance recording in the second half of the 1980s to the beginning of 2000. Due to the small size of the farms, performance recording was implemented on nucleus farms, grouping farms according to their proximity and their production system, further considering the nucleus as the management unit (Gutiérrez et al., 1997; Goyache and Gutiérrez, 2001). Contemporary groups were defined based on nucleus-year of calving. Animals with identification errors or ambiguous birth dates were excluded from the analysis.

Calving ease was recorded using the following scores: 1 (no assistance; 16,313 records), 2 (minor assistance; 15,900 records), 3 (hard assistance; 2,889 records), and 4 (caesarean section; 893 records). The management system requires the presence of the farmer for a significant time during calving (basically in winter), and, therefore, the assistance of the farmer is unavoidable. As a consequence, the percentage of calvings scored

as 2 is greater than in other breeds and only scores greater than 2 are considered difficult births. Abnormal presentations were not considered in the present analysis. Gestation length was computed as the interval, in days, from the last mating date (one-third of them AI) to calving. Following previous studies, only GL records ranging from 269 to 305 d were included and used for further analyses (Goyache and Gutiérrez, 2001; Goyache et al., 2005). Calf losses were recorded in the CORECA database with the following scores: 1 (calf alive at weaning), 2 (calf sold before weaning), 3 (calf alive at 72 h but dead before weaning), 4 (calf alive at birth but dead within 72 h), and 5 (calf dead at birth). From these scores, CS was defined as a dichotomous variable considering calf loss scores 3, 4, and 5 as 1 and scores 1 and 2 as 0 (Goyache et al., 2003). Altogether, total records available were as follows: 35,395 CE, 30,684 GL, and 36,132 CS. Further description of data for each CE score class is given in Table 1.

Calving ease and CS have a discrete nature, which theoretically would suggest fitting a threshold model that would better account for the probabilistic structure of the data. However, following previous analyses, we modeled CE and CS as continuous traits assuming multivariate normal distributions [see Goyache et al. (2003) and Gutiérrez et al. (2007) for a detailed justification of this procedure].

The 3 traits were analyzed as traits of the calf. The analyzed database included a total of 51,561 animals, and the final structure of the data was dependent on the traits involved in each analysis (Table 2). Genetic parameters together with their SE were estimated via a multitrait REML procedure applied to mixed linear models. All runs were carried out using the DFREML program (Meyer, 1998). The fitted models included the following fixed effects: nucleus-year of calving as contemporary group, calving season (2 levels: from January 1 to June 30 and from July 1 to December 31), sex of calf (male or female), and age of the dam at calving in days as a linear and quadratic covariant.

Genetic analyses were carried out using a multivariate model involving CE, GL, and CS. The matrix notation for the model to be solved was $\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{Nm} + \mathbf{Wp} + \mathbf{e}$, with

Table 2. Structure of data used for estimation of genetic parameters for calving ease (CE), gestation length (GL), and calf survival at weaning (CS)

Structure of data	CE	GL	CS
No. of animals	51,561	51,561	51,561
Animals with record	35,395	30,684	36,132
Sires with progeny in data	1,266	1,221	1,281
Cows with progeny in data	13,448	12,432	13,635
Sires with record and offspring	193	172	203
Cows with record and offspring	1,349	1,200	1,390
Sire-offspring pairs	6,874	6,006	7,812
Dam-offspring pairs	2,953	2,445	3,080
Nucleus-year (levels)	396	395	397
Calving season (levels)	2	2	2
Calf sex (levels)	2	2	2
Age of cow at calving (order of covariate)	2	2	2
Mean	1.65[1]	287.3[2]	0.09[3,4]
SD	0.71[1]	5.76[2]	0.28[3]

[1]In the corresponding scoring units: 1 (no assistance), 2 (minor assistance), 3 (hard assistance), and 4 (caesarean section).

[2]In days.

[3]In the corresponding scoring units: 1 (calf death at weaning) and 0 (calf alive at weaning).

[4]Indicates the mean calf loss.

$$
\begin{bmatrix} \mathbf{u} \\ \mathbf{m} \\ \mathbf{p} \\ \mathbf{e} \end{bmatrix} \sim N \left(\begin{bmatrix} \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \end{bmatrix}, \begin{bmatrix} \mathbf{G} & \mathbf{C} & \mathbf{0} & \mathbf{0} \\ \mathbf{C} & \mathbf{M} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{P} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{R} \end{bmatrix} \right),
$$

where $\mathbf{G} = \mathbf{A} \otimes \mathbf{G_0}$, $\mathbf{M} = \mathbf{A} \otimes \mathbf{M_0}$, $\mathbf{C} = \mathbf{A} \otimes \mathbf{C_0}$, $\mathbf{P} = \mathbf{I_p} \sigma_p^2$, $\mathbf{R}$ is the covariance matrix of order equal to the number of records, with the diagonal elements equal to the residual variance of the involved trait and nondiagonal elements equal to the residual covariance between traits if the element corresponds to records of different traits belonging to the same animal, and zero otherwise, $\mathbf{y}$ is the vector of observations, $\mathbf{X}$ is the incidence matrix of fixed effects, $\mathbf{Z}$ is the incidence matrix of animal effects, $\mathbf{N}$ is the incidence matrix of maternal genetic effects, $\mathbf{W}$ is the incidence matrix of permanent environmental effects, $\mathbf{b}$ is the vector of fixed effects, $\mathbf{u}$

Table 3. Total variance and heritabilities estimated for calving ease (CE), gestation length (GL), and calf survival at weaning (CS; SE are in parentheses)

Item[1]	GL	CE	CS
$V_{(p)}$	$3.79 \cdot 10^{-5}$	$4.42 \cdot 10^{-1}$	$7.79 \cdot 10^{-2}$
h^2	0.331 (0.026)	0.325 (0.022)	0.226 (0.018)
m^2	0.066 (0.017)	0.066 (0.018)	0.034 (0.011)
c^2	0.066 (0.011)	0.090 (0.011)	0.024 (0.007)

[1]$V_{(p)}$ = phenotypic variance in squared units of the trait: GL in days; CE: 1 (no assistance), 2 (minor assistance), 3 (hard assistance), and 4 (caesarean section); CS: 1 (calf death at weaning) and 0 (calf alive at weaning); h^2 = heritability for the direct genetic effect; m^2 = heritability for the maternal genetic effect; c^2 = estimate for the ratio of permanent environmental variance to phenotypic variance (c^2).

is the vector of direct animal genetic effects, $\mathbf{m}$ is the vector of unknown maternal genetic effects, $\mathbf{p}$ is the vector of permanent environmental effects, $\mathbf{e}$ is the vector of residuals, $\mathbf{I_p}$ is the identity matrix of order equal to the number of dams, σ_p^2 is the permanent environmental variance, $\mathbf{A}$ is the numerator relationship matrix, $\mathbf{G_0}$ is the covariance matrix for additive genetic effects, $\mathbf{M_0}$ is the covariance matrix for maternal genetic effects, $\mathbf{C_0}$ is the covariance matrix between direct additive and maternal genetic effects, and $\otimes$ is the Kronecker product.

RESULTS

Table 3 shows the total variance, the heritabilities, and c^2 (ratio of permanent environmental variance to phenotypic variance) estimated for CE, CS, and GL. Estimates of heritability ($\pm$SE) for the direct genetic effect (**CEd**, **GLd**, and **CSd**) were 0.325 ± 0.022, 0.331 ± 0.026, and 0.226 ± 0.018, respectively, whereas the estimates for maternal genetic effects (**CEm**, **GLm**, and **CSm**) were 0.066 ± 0.018, 0.066 ± 0.017, and 0.034 ± 0.011. The estimates for c^2 were CEc 0.090 ± 0.011, GLc 0.066 ± 0.011, and CSc 0.024 ± 0.007.

Genetic correlations among direct, maternal genetic, or permanent environmental effects across traits are given in Table 4. Correlations involving CE and GL were, in general, positive and moderate, whereas those involving CE and CS were large. Correlation for CEc-CSc was positive and large (0.676 ± 0.142), showing that the relationship between CE and CS is more than genetic. All of the pairs were significant except for the pair CEm-GLm (0.277 ± 0.172). Correlations between GL and CS were nonsignificant.

Genetic correlations for CEd-CEm, GLd-GLm, and CSd-CSm were negative and high (Table 5), ranging from -0.461 ± 0.120 for GLd-GLm to -0.821 ± 0.145 for CSd-CSm. The genetic correlations for CEd-CSm and for CSd-CEm were negative, significant, and high

Table 4. Genetic correlations between direct (d), maternal (m) genetic, and permanent environmental (c) effects resulting from the analysis of the genetic relationships among calving ease (CE), gestation length (GL), and calf survival at weaning (CS) carried out using the multivariate model (SE are in parentheses)

Item	CEd	CSd
GLd	0.389 (0.039)	0.074 (0.038)[1]
CEd		0.644 (0.037)
	CEm	**CSm**
GLm	0.277 (0.172)[1]	0.003 (0.238)[1]
CEm		0.730 (0.171)
	CEc	**CSc**
GLc	0.351 (0.108)	0.214 (0.195)[1]
CEc		0.676 (0.142)

[1]Nonsignificant estimate for $P < 0.05$.

Table 5. Genetic correlations between direct (d) and maternal (m) genetic effects (SE are in parentheses) for calving ease (CE), gestation length (GL), and calf survival at weaning (CS)

Item	GLm	CEm	CSm
GLd	−0.461 (0.120)	−0.323 (0.124)	−0.251 (0.144)[1]
CEd	−0.154 (0.120)[1]	−0.585 (0.090)	−0.654 (0.120)
CSd	0.078 (0.160)[1]	−0.515 (0.102)	−0.821 (0.145)

[1]Nonsignificant estimate for $P < 0.05$.

(Table 5). The genetic correlation between GLd-CEm was moderate, significant, and negative (−0.323 ± 0.124), whereas that for GLd-CSm was nonsignificant. The genetic correlations for GLm with the direct effects of the other traits were nonsignificant. In general, SE of the genetic correlations estimated between direct and maternal genetic effects of different traits were large.

DISCUSSION

Genetic Parameters Within Traits

The current estimates of heritability for the direct genetic effects (CEd, GLd, and CSd) are substantially greater than others previously reported for the same traits in the Asturiana de los Valles breed. Heritability reported here for CEd (0.325) is nearly twice that recently reported by Gutiérrez et al. (2007) of 0.191. The present estimate also is greater than the mean heritability of 0.16 in adult cows reported by Koots et al. (1994), although this value is within the range reported for 4 British beef breeds (from 0.13 to 0.39; Roughsedge et al., 2005). Also, the estimate of heritability reported here for CSd (0.226) is approximately 2-fold those of 0.106 and 0.142 reported previously in the breed (Goyache et al., 2003) and also greater than recent estimates reported in multibreed beef cattle populations (from 0.049 to 0.190; Guerra et al., 2006), Brahman cattle (0.06, Riley et al., 2004), and Danish Holsteins for stillbirth (0.10; Hansen et al., 2004). Moreover, heritability estimated here for GLd (0.331) is roughly 3-fold greater than the values of 0.115 (Goyache et al., 2005) and 0.15 (Goyache and Gutiérrez, 2001) previously reported for the Asturiana de los Valles breed considering GL as a dam trait, and twice the estimates recently reported for Canadian Charolais, which ranged from 0.61 to 0.64 (Crews, 2006). Given that these papers analyzed GL as a trait of the dam, the values obtained cannot be directly compared with the current estimates for this trait.

Estimates for the maternal genetic effects of the analyzed traits did not show a very clear behavior. In contrast with CEd, heritability estimated for CEm (0.066) was one-half that of 0.140 recently reported in the breed (Gutiérrez et al., 2007) and also slightly less than other estimates available in the literature, which, in most cases, ranged from 0.09 to 0.12 (see Gutiérrez et al., 2007, for a recent review). Published estimates for CSm are scant. The current estimate for CSm (0.066) is 2-fold

greater than those ranging from 0.016 to 0.039 previously reported in the Asturiana de los Valles breed. However, it is roughly one-half that reported for perinatal survival (stillbirth) in Danish Holstein by Hansen et al. (2004). The GLm has been estimated here for the first time in the Asturiana de los Valles beef cattle breed. Previous estimates of the direct genetic effect for GL using a similar model to that used here, but considering GL as a trait of the dam (0.115; Goyache et al. 2005), is expected to include all of the maternal genetic effects and also one-half of the direct genetic effects due to the calf. Consequently, these estimates cannot be directly compared.

Genetic correlations for CEd-CEm, GLd-GLm, and CSd-CSm were negative, as usually found in the literature. The genetic correlation estimated here for CEd-CEm is roughly 3-fold greater than that recently reported in the breed (−0.219; Gutiérrez et al., 2007) and substantially greater than most other estimates reported in the literature (Phocas and Laloë, 2004; Roughsedge et al., 2005). Also, the genetic correlation estimated for GLd-GLm is greater than that of −0.13 estimated in Holsteins (Hansen et al., 2004), −0.18 estimated in a composite beef cattle herd (Bennett and Gregory, 2001), and −0.37 reported in Canadian Charolais cattle (Crews, 2006). Yet, the genetic correlation for CSd-CSm is greater than that of −0.697 previously reported in this breed and similar to that of −0.85 reported by Cubas et al. (1989), in Angus cattle under a sire-maternal grandsire model. Clearly, a female calf with a greater genetic ability to survive to weaning will have poor maternal genetic ability to make its offspring survive.

Genetic Correlations Between Traits

Estimates of genetic correlations involving the 3 traits analyzed here are scarce in the literature. In our study, correlations between genetic effects involving GL are not significant, in general, except for GLd-CEd (0.389 ± 0.039) and GLd-CEm (−0.323 ± 0.124). The current estimate for GLd-CEd is similar to those reported in Danish (0.38 ± 0.05; Hansen et al., 2004) and UK (0.34 ± 0.05; McGuirk et al., 1999) Holsteins. Consistent with our nonsignificant estimate for GLd-CEm, Hansen et al. (2004) reported a null genetic correlation for this pair of traits (−0.01 ± 0.06). In our analysis, the genetic correlation for GLd-CSd is low, positive, and not significant. However, previous estimates for GLd-CSd (actually stillbirth or perinatal mortality) were significant (0.22 ± 0.07; McGuirk et al., 1999; 0.18 ± 0.06; Hansen et al., 2004). Genetic correlations involving CE and CS are more frequent in the literature. Our results for CEd-CSd and CEm-CSm were positive and high (0.644 ± 0.037 and 0.730 ± 0.171). Hansen et al. (2004) reported similar significant estimates for CEd-CSd (actually stillbirth) and CEm-CSm of, respectively, 0.83 ± 0.04 and 0.62 ± 0.05. Regarding genetic correlations for CEd-CSm and CSd-CEm, we obtained negative and

significant values (-0.654 ± 0.120 and -0.515 ± 0.102, respectively), whereas the values obtained by Hansen et al. (2004) for CEd-CSm and CSd-CEm where non-significant (0.08 ± 0.08 and 0.07 ± 0.09).

General Discussion

It was expected that current estimates of the genetic effects associated with GL would be greater than previously reported in the breed. Gestation length seems to be under control more in the fetus than in the dam (Kirkpatrick, 1998). When GL is treated as a trait of the dam, most estimated heritabilities are low, whereas, if GL is analyzed as a trait of the calf, estimates of heritability tend to be moderate to high (Andersen and Plum, 1965; Kirkpatrick, 1998). However, the greater values estimated here for the within-trait genetic parameters may be due more to a generally admitted deficient performance of the models involving maternal genetic effects than to underlying biological reasons. When covariance between direct and maternal genetic components is not negligible, the genetic effects estimated under an animal model tend to be greater by the action of inflated negative correlation between direct and maternal effects (Gutiérrez et al., 1997; Meyer, 1997). Additionally, the current analysis includes simultaneous estimation of a considerable number of highly correlated parameters, particularly between CE and CS. It is usually admitted that this scenario can give marked increases in the estimated variance components, therefore leading to inflated estimates of genetic and permanent environmental parameters (Meyer, 1994). This may be the basis of the high heritability estimated here for CEd when compared with other estimates previously found in the same breed (Gutiérrez et al., 2007).

In our analysis, GL had a moderate genetic correlation with CE, but not with CS. Genetic relationship between GL and CE is likely to be dependent on the genetic relationship between GL and BrW. In Canadian Charolais (Crews, 2006), GLd and BrWd (direct effect of birth weight) were positively correlated (0.34 ± 0.04) and GLd-BrWm (maternal effect of birth weight) were negatively correlated (-0.20 ± 0.07). These estimates are consistent with those reported here for GLd and CE. Although our estimates of genetic correlation for GLm and CE were not significant, Crews (2006) reported significant genetic correlations between GLm and the direct and maternal genetic effects for BrW. In any case, the genes determining GL and CE (and, probably, BrW) are not likely to be the same as those affecting CS. In general, GL can be considered a trait genetically independent of most economically important traits in beef cattle (except BrW). Gestation length has been shown to have near-zero genetic correlations with direct and maternal effects for weaning weights and postweaning BW gain (Bennett and Gregory, 2001; Crews, 2006). Recently, Yagüe et al. (2009) have also shown that GL (analyzed as a trait of the cow) was not significantly correlated with the genetic effects associated with major reproduction traits such as days to first insemination, days from first insemination to conception, number of inseminations per conception, days open, and calving interval. Therefore, inclusion of GL in sire selection programs in beef cattle is not advocated.

Some correlations estimated here, mainly those involving GL and maternal effects, were not significant. However, this may not reflect a lack of between-trait biological relationships, but insufficient information to obtain fair estimates of the effects. The number of dam-offspring pairs may not be sufficient to obtain significant values for CSd-GLm, GLd-CSm, and CEd-GLm. The value estimated for GLm-CEm (0.277 ± 0.172) can be explained by the low maternal heritabilities estimated for these effects. On the contrary, we consider that the low estimates (and increased SE) obtained here for GLd-CSd and GLm-CSm suggest that they can be considered as essentially null.

Genetic correlations between calf survival and other traits are scant in the literature and basically refer to mortality in the perinatal period. However, the genetic basis affecting calf losses at any age between the perinatal period and weaning seems to be substantially the same (Goyache et al., 2003) and can be compared with those reported in this study. The overall scenario discussed above with respect to the CE-CS genetic (and permanent environmental) correlation suggests that strong selection for one of these traits will result in a significant correlated response in the other trait. The response to direct selection is $R = ih^2\sigma_p$ (where σ_p is the phenotypic SD and i the selection intensity) and the correlated response in a trait Y when using a different trait X as the selection criterion is $CR_Y = ih_X h_Y r_A \sigma_{pY}$, with r_A being the additive genetic correlation between traits (Falconer and Mackay, 1996). Table 6 includes a summary of the responses of comparing CE and CS. Direct selection for CEd would give roughly three-quarters of the expected response on CSd, if this effect was the selection criterion. On the other hand, direct selection on CSd would only give, as correlated response, one-half the direct response on CEd. Using CEd or CSd as the selection criterion, there is a detrimental effect

Table 6. Genetic response obtained for direct (d) and maternal (m) genetic effects of calving ease (CE) and calf survival at weaning (CS)

Response	Genetic effect under selection			
	CEd	CSd	CEm	CSm
CEd	216.2[1] i	116.1 i	−57.0 i	−45.7 i
CSd	48.7 i	63.1 i	−17.6 i	−20.1 i
CEm	−57.0 i	−41.8 i	4.4 i	23.0 i
CSm	−19.2 i	−20.1 i	9.7 i	9.5 i

[1]To make the results of the traits easier to view, they are given as a score of × 1,000 (i: selection intensity).

on CEm and CSm, which is similar in magnitude regardless of the selection criterion actually applied. Taking this into consideration, CE appears to be a key trait for selection aimed at avoiding calf losses. The trait CE is relatively easy to score, requires little additional recording effort, and would work as an early indicator of ability of the calf to survive to weaning.

In this paper we present joint estimates of genetic parameters associated with calving ability and survival in beef cattle. The present results provide additional information on the nature of genetic effects associated with the traits analyzed, especially for the relationships between CE and CS. Strong selection for CE will result in a significant correlated response in CS. Moreover, CE recording is less time-consuming and CE could be considered as an early indicator of CS performance. Also, GL had weak genetic correlations with the other traits. Therefore, the benefit of using GL as a correlated trait in a genetic evaluation with CE and CS seems limited. This information may be useful in beef cattle breeding programs.

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