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Sire \times contemporary group interactions for birth weight and preweaning growth traits in the *Asturiana de los Valles* beef cattle breed

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Abstract

Although a number of recent studies have focused on the existence of a non-negligible sire \times contemporary group interaction effect (s) affecting the estimation of genetic parameters for maternally influenced traits in beef cattle, the assessment and interpretation of this effect using field data remains poorly understood. In this study 27,639 records of both birth weight (BW) and weaning weight (WW) from the *Asturiana de los Valles* breed were used to assess the consequences of the inclusion of an s effect on the estimation of genetic parameters for BW, WW and average daily gain (ADG) fitting univariate and bivariate models. Estimations of s^2 for BW, WW and ADG were 0.040, 0.070 and 0.077 regardless of the fitted model. Inclusion of s in the estimation models induced a reduction of both the direct and the maternal heritability, varying between 8 and 28% with the trait and the estimation model employed. As expected, the correlations between both direct and maternal genetic effects for each trait were less negative when s was included in the estimation model. The estimated correlations between the s effect affecting BW, WW and ADG were 0.108, -0.038 and 0.616 for the pairs BW–WW, BW–ADG and WW–ADG, respectively. These results suggest that misidentification of individuals cannot be the sole cause of the effect of s and that this effect is of a different nature and origin for different traits (i.e. selective matings for low BW's and unaccounted management practices for preweaning growth traits). Models including the s effect should be accepted as working models in beef improvement schemes. © 2005 Elsevier B.V. All rights reserved.

Keywords: Preferential treatment; Heritability; Maternal effect; Genetic correlation; Birth weight; Weaning weight; Average daily gain

1. Introduction

Selection for direct and maternal effects is necessary for most economically important traits in beef cattle. For this purpose, selection programs based on genetic evaluations require accurate estimates of ge-

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netic and environmental parameters. However, models involving maternal genetic effects are usually considered deficient. The estimations of direct and maternal genetic effects tend to be imprecise due to large sampling correlations between parameters (Meyer, 1997). When the covariance between direct and maternal genetic components is not negligible, the genetic effects estimated under an animal model are forced to be higher by the action of inflated negative correlation between both genetic components (Gutiérrez et al., 1997; Meyer, 1997). Some causes, such as differential non-random mating among herds (Notter et al., 1992) or unaccounted differences in management within contemporary groups (Meyer, 1997; Berweger Baschnagel et al., 1999), may be at the root of these inflated estimations. Robinson (1996a,b) reporting on simulated data and Berweger Baschnagel et al. (1999) on field data suggested possible confusion between environmental and genetic effects linked to sire resulting in an overestimation of the additive genetic variance. A non-negligible effect of the sire \times contemporary group interaction has also been described in dairy cattle (Meyer, 1987; Calus et al., 2002) and in meat sheep (Hagger, 1998; Konstantinov and Brien, 2003).

Using simulation, misidentification of the animals has been identified as a major source of bias in the estimation of the genetic parameters affecting preweaning growth traits in beef cattle (Lee and Pollak, 1997a,b; Senneke et al., 2004). Misidentification produces spurious environmental variance linked to sire biasing the estimations of both the heritability of the direct and the maternal genetic components and of the covariance between these effects. However, simulations including a sire \times year interaction in the estimation model do not always correct the spurious direct–maternal covariance produced, implying that general statements for analysis of real datasets cannot be made (Lee and Pollak, 1997a,b). In addition, sire selection programs use parameters obtained from the analysis of field data, in which misidentification is likely but whose level is unknown. Moreover, an environmental effect linked to sire does not affect genetic parameter estimation on all the traits in which maternal influence is not negligible (Goyache et al., 2003a). It is thus of major importance to test the effect of the inclusion of the interaction between the sire and the contemporary

group in the models of estimation of genetic parameters using field data (Dodenhoff et al., 1999).

The purpose of the present analysis is to study how the inclusion of a sire \times contemporary group interaction effect influences the estimation of genetic parameters, especially for the direct–maternal genetic correlation, for birth weight (BW), weaning weight (WW) and preweaning average daily gain (ADG) using a sample of field data of the *Asturiana de los Valles* beef cattle breed. This aim focused basically on ascertaining whether a sire \times contemporary group interaction effect is the same at birth and weaning ages.

2. Materials and methods

Productive data and pedigree information of the *Asturiana de los Valles* breed were obtained from the performance recording database (the CORECA database) implemented by the Regional Government of the *Principado de Asturias* (Northern Spain), through the *Asturiana de los Valles* Breeders Association (ASEAVA). Performance recording had been implemented based on nuclei, grouping farms according to their proximity and their production system, owing to the reduced size of the farms (Gutiérrez et al., 1997; Goyache et al., 2003a). Animals with identification errors or ambiguous birth dates were eliminated. The contemporary group was defined as nucleus-year of calving. Productive data included only single calving records. A total of 27,639 records with both BW and WW were obtained. Age of calf at weaning (AGE) of the available records ranged from 90 to 270 days. ADG was simply computed as $ADG = (WW - BW) / AGE$.

The structure of the analysed records is summarised in Table 1. The analysed database included a total of 59,813 animals, of which 1889 were sires and 16,966 dams. A total of 1153 sires and 11,375 dams had progeny in the data. The number of sires and dams with their own record as well were 168 and 1043, respectively. The analysed dataset included 10,176 and 4318 sire–offspring and dam–offspring record pairs, respectively. The average number of progeny records per sire was 47.7. Due to the small average size of the farms, maintenance of sires is costly, thus leading to a wide use of artificial insemination.

Table 1

Structure of data used for the estimation of genetic parameters for birth weight (BW), weaning weight (WW) and average daily gain (ADG) in the *Asturiana de los Valles* beef cattle breed

Structure of data	
Number of animals	59,813
Animals with record	27,639
Sires with progeny in data	1153
Cows with progeny in data	11,375
Sires with record and offspring	168
Cows with record and offspring	1043
Nucleus-year (levels)	484
Calving season (levels)	2
Calf sex (levels)	2
Creep feeding (levels)	2
Age of cow at calving (linear covariate) (levels)	1
Age of calf at weaning (linear covariate) (levels)	1
Sire \times contemporary group interaction (levels)	5928
Mean \pm S.D. for BW (kg)	40.6 \pm 7.2
Mean \pm S.D. for WW (kg)	224.3 \pm 61.2
Mean \pm S.D. for ADG (g/day)	958.5 \pm 366.2
Mean \pm S.D. for AGE (days)	197.0 \pm 59.0

ination (about 25%, ranging from 9% to 57% depending on areas) (Gutiérrez et al., 1997). Consequently, good genetic connections between herds were achieved (Gutiérrez and Goyache, 2002; Goyache et al., 2003a, 2005). The dataset analysed here included 32 sires producing calves in more than 20 contemporary groups. These 32 sires summed a total of 9293 calves.

Genetic parameters were estimated via a univariate or bivariate REML procedure applied to a mixed linear model. All runs were carried out using the DF-REML program (Meyer, 1998). All the fitted models included the following fixed effects: herd-year of calving as contemporary group (484 levels), calving season (two levels: from January 1st to June 30th and from July 1st to December 31st), sex of calf (male or female) and the age of the dam at calving in days as a linear covariant. Models fitted for the analysis of WW and ADG also included the effect of creep feeding (two levels: creep and non-creep) and the age of calf at weaning, in days, as a linear covariant. As regards random effects, four different models were defined:

Model 1: A univariate animal model including the additive genetic effect (u), the maternal genetic effect (m), the covariance between them (cov_{um}), all three effects being depen-

dent on the relationship matrix, and the residual (e).

Model 2: Like Model 1, but also including a sire \times contemporary group interaction (s) as a random permanent environmental effect independent of the additive relationship matrix.

Model 3: A bivariate animal model, where BW, WW and ADG are analysed sequentially with each of the other traits, including the direct genetic effect, the maternal genetic effect, the covariance between them (cov_{um}) and the residual as random effects in the model for each trait besides the covariance between either direct (cov_{uu}) or maternal (cov_{mm}) genetic effects.

Model 4: Like Model 3, but also including a sire \times contemporary group interaction (s) as a random permanent environmental effect independent of the additive relationship matrix and the covariance between either s environmental effects (cov_{ss}).

A permanent maternal environmental effect was not included in the fitted models in the present analysis because of restrictions in the DF-REML program as to the number of random effects that may be estimated. It may affect the estimates of maternal genetic variances and direct–genetic correlations because ignoring the maternal permanent environmental effect inflates the maternal genetic variances (Meyer, 1992). However, since the primary goal of the study is to assess the influence of an environmental effect linked to sire on direct–maternal genetic covariances, the non-inclusion of this effect (which is likely to exist) most probably does not affect the main conclusions of the present study. Gutiérrez et al. (1997) in the *Asturiana de los Valles* breed did not find differences in the direct–maternal genetic covariances estimated for BW, WW and ADG, regardless of whether a maternal permanent environmental effect was included in the fitted models or not. In addition, Berweger Baschnagel et al. (1999) in Swiss Angus and Hagger (1998) in meat sheep found that, as expected, the inclusion of the maternal permanent environment effect did not affect the estimations of the effect of the sire \times contemporary group interaction since no relationship is likely to exist between the environmental effects linked to both sire and cow.

Table 2

Heritability for the direct (h^2) and maternal (m^2) genetic effects, genetic correlations between these effects (r_{um}), sire \times contemporary group interaction variance as a proportion of phenotypic variance (s^2), phenotypic variance ($\text{Var}(p)$) and likelihood ($-2 \log L$) for birth weight (BW), weaning weight (WW) and average daily gain (ADG) in the *Asturiana de los Valles* beef cattle breed estimated using two univariate models

Trait		h^2	m^2	r_{um}	s^2	$\text{Var}(p)$	$-2 \log L$
BW	Model 1	0.401 (0.033)	0.224 (0.024)	-0.348 (0.090)		46.345	-64513.213
	Model 2	0.343 (0.033)	0.207 (0.024)	-0.271 (0.099)	0.040 (0.005)	46.251	-64047.005
WW	Model 1	0.434 (0.036)	0.115 (0.022)	-0.403 (0.112)		1724.736	-113347.030
	Model 2	0.313 (0.034)	0.091 (0.020)	-0.199 (0.134)	0.070 (0.006)	1715.202	-113221.577
ADG	Model 1	0.323 (0.031)	0.012 (0.009)	-0.733 (0.226)		114135.908	-170571.040
	Model 2	0.231 (0.031)	0.010 (0.009)	-0.522 (0.284)	0.077 (0.007)	114639.849	-170474.165

Standard errors of the estimates are in parentheses.

The matricial notation of the sets of mixed model equations to be solved are $\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{Nm} + \mathbf{e}$ for Model 2 and $\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{Nm} + \mathbf{Ws} + \mathbf{e}$ for Model 4, with:

$$\begin{pmatrix} \mathbf{y} \\ \mathbf{u} \\ \mathbf{m} \\ \mathbf{s} \\ \mathbf{e} \end{pmatrix} \sim \mathcal{N} \left(\begin{pmatrix} \mathbf{Xb} \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix}, \begin{pmatrix} \mathbf{V} & \mathbf{ZG} & \mathbf{NM} & \mathbf{WS} & \mathbf{R} \\ \mathbf{ZG} & \mathbf{G} & \mathbf{C} & 0 & 0 \\ \mathbf{NM} & \mathbf{C} & \mathbf{M} & 0 & 0 \\ \mathbf{WS} & 0 & 0 & \mathbf{S} & 0 \\ \mathbf{R} & 0 & 0 & 0 & \mathbf{R} \end{pmatrix} \right)$$

where $\mathbf{V} = \mathbf{ZGZ}' + \mathbf{ZCM}' + \mathbf{MCZ}' + \mathbf{NMN}' + \mathbf{WSW}' + \mathbf{R}$, $\mathbf{G} = \mathbf{A}\sigma_u^2$, $\mathbf{M} = \mathbf{A}\sigma_m^2$, $\mathbf{S} = \mathbf{I}_s\sigma_s^2$, $\mathbf{C} = \mathbf{A}\sigma_{um}$, $\mathbf{R} = \mathbf{I}_e\sigma_e^2$, in Model 2 and, $\mathbf{G} = \mathbf{A} \otimes \mathbf{G}_0$, $\mathbf{M} = \mathbf{A} \otimes \mathbf{M}_0$, $\mathbf{S} = \mathbf{A} \otimes \mathbf{S}_0$, $\mathbf{C} = \mathbf{A} \otimes \mathbf{C}_0$, $\mathbf{R} = \mathbf{I}_e \otimes \mathbf{R}_0$, in Model 4, and \mathbf{y} is the vector of observations, \mathbf{X} the incidence matrix of fixed effects, \mathbf{Z} the incidence matrix of animal effect, \mathbf{N} the incidence matrix of maternal effect, \mathbf{W} the incidence matrix of sire \times contemporary inter-group interaction effect, \mathbf{b} the vector of unknown parameters for fixed effect, \mathbf{u} the vector of unknown parameters for direct animal genetic, \mathbf{m} the vector of unknown parameters maternal genetic, \mathbf{s} the vector of unknown parameters for sire \times herd-year interaction, \mathbf{e} the vector of residuals, \mathbf{I}_e the identity matrix of equal order to the number of records, \mathbf{I}_s the identity matrix of equal order to the number of sire \times herd-year subclasses, \mathbf{A} is the numerator relationship matrix, \mathbf{R}_0 the residual covariance matrix among measurements on the same animal, \mathbf{G}_0 the covariance matrix for additive genetic effects, \mathbf{C}_0 the diagonal covariance matrix between direct additive and maternal genetic effects, \otimes the Kronecker product, σ_u^2 the direct genetic variance, σ_m^2 the maternal genetic variance, σ_{um} the direct-maternal genetic covariance, σ_s^2 the environmental variance associated with the sire \times contemporary group inter-

action, and σ_e^2 is the error variance. As described above, Models 1 and 3 are, respectively, like Models 2 and 4, although excluding the sire \times contemporary group interaction effect.

The superiority of the estimates obtained using Model 2 with respect to the corresponding Model 1 was determined by the likelihood ratio test as described in Gutiérrez et al. (1997).

3. Results

The parameters estimated (and their standard errors) using univariate and bivariate models for the analysed traits are given respectively in Tables 2 and 3. The complete set of estimated (co)variances is available on request. Heritability for the direct effect using Model 1 was 0.401, 0.434 and 0.323 for BW, WW and ADG, respectively, while m^2 for the same traits was in turn 0.224, 0.115 and 0.012. Genetic correlation between direct and maternal effects estimated using Model 1 was negative for all the traits, ranging between -0.348 for BW and -0.733 for ADG. The inclusion of s in the estimation model (Model 2) did not substantially affect the estimations of phenotypic variances, although it did lead to a reduction in direct heritability of 14% for BW and 28% for WW and ADG. Maternal heritability was also reduced roughly by 8%, 21% and 23% for BW, WW and ADG, respectively. Genetic correlation between direct and maternal effects in Model 2 was less negative than in Model 1, being -0.271 for BW, -0.199 for WW and -0.522 for ADG. This substantial reduction in the estimates of the genetic parameters in Model 2 is accompanied by an estimation of s^2 of 0.040, 0.070 and 0.077 for BW, WW and ADG,

Table 3
Heritability for the direct (h^2) and maternal (m^2) genetic effects, sire \times contemporary group interaction variance as a proportion of phenotypic variance (s^2), genetic correlations between direct and maternal genetic effects (r_{um}), genetic correlations between either direct (r_{uu}), maternal (r_{mm}) and sire \times contemporary group interaction (r_{ss}) effects, phenotypic variance ($\text{Var}(p)$) and likelihood ($-2 \log L$) for birth weight (BW), weaning weight (WW) and average daily gain (ADG) in the *Asturiana de los Valles* beef cattle breed estimated using two bivariate models

		h^2	m^2	s^2	r_{uu}	r_{mm}	r_{um}	r_{ss}	$\text{Var}(p)$	$-2 \log L$
Model 3	BW	0.392 (0.032)	0.217 (0.024)	0.352 (0.060)	0.067 (0.102)	-0.321 (0.089)	46.279	-177389.370		
	WW	0.438 (0.036)	0.119 (0.022)	0.422 (0.075)	0.107 (0.117)	-0.416 (0.111)	1728.112			
Model 4	BW	0.336 (0.032)	0.192 (0.023)	0.040 (0.005)	0.167 (0.080)	-0.247 (0.099)	46.295	-234925.973		
	WW	0.211 (0.034)	0.096 (0.021)	0.070 (0.006)	0.666 (0.075)	-0.488 (0.289)	114562.714			
Model 3	BW	0.397 (0.033)	0.219 (0.024)	0.154 (0.247)	0.888 (0.336)	-0.100 (0.121)	1717.323	-278703.900		
	ADG	0.320 (0.031)	0.013 (0.009)	0.077 (0.007)	0.952 (0.336)	-0.267 (0.199)	112752.581			
Model 4	BW	0.343 (0.033)	0.198 (0.024)	0.040 (0.005)	0.705 (0.103)	-0.014 (0.136)	1718.719	-278502.280		
	ADG	0.227 (0.030)	0.010 (0.010)	0.077 (0.007)	0.077 (0.007)	-0.207 (0.231)	113983.510			
Model 3	WW	0.402 (0.032)	0.052 (0.015)							
	ADG	0.244 (0.025)	0.020 (0.011)							
Model 4	WW	0.319 (0.033)	0.056 (0.016)							
	ADG	0.186 (0.028)	0.023 (0.012)							

Standard errors of the estimates are in parentheses.

respectively. The likelihood ratio test carried out to compare the superiority of the estimates obtained using Model 2 with respect to Model 1 for each trait was always significant for $p < 0.0005$.

Models 3 and 4 (Table 3) were used to ascertain the influence of the s effect on the genetic relationships existing between each pair of the analysed traits. Estimated heritabilities for both direct and maternal genetic effects were substantially the same as those obtained using the corresponding univariate models (accounting for the inclusion of s or not). The estimates of s^2 obtained using Model 4 were also the same for each trait as those obtained using Model 2. Genetic correlations between either direct or maternal genetic effects were always positive and varied from moderate to low regardless of the estimation model except for the pair WW–ADG, in which r_{uu} and r_{mm} were 0.666 and 0.888 for Model 3 and were 0.705 and 0.952 for Model 4, respectively. In all cases, the inclusion of s in the estimation model always led to less negative estimations of the genetic correlations between either direct or maternal genetic effects. The direct–maternal genetic correlations were, in all cases, less negative when the estimation model included s . The changes in the estimations of these genetic correlations were of the same order for the univariate and bivariate models. However, r_{um} estimated for the pair WW–ADG was substantially higher than those obtained using the univariate models, reaching -0.100 and -0.014 for WW and -0.267 and -0.207 for ADG for Models 3 and 4, respectively.

Models 3 and 4 were also used to ascertain the relationships between the s effect affecting either of the analysed traits. The correlations between the environmental effects linked to sire (s) affecting each analysed trait estimated using Model 4 showed substantial differences: 0.108 for the pair BW–WW, -0.038 for the pair BW–ADG and 0.616 for the pair WW–ADG.

4. Discussion

In general, the estimates reported in the present study for genetic parameters affecting BW, WW and ADG are slightly higher than those usually observed in the literature for the heritability of the direct effect, of the same order or lower for the heritability of the

maternal genetic effect and more negative for the genetic correlation between the direct and the maternal genetic effects. The literature reports that the *Asturiana de los Valles* breed presents high genetic variability for most of the productive analysed traits (Gutiérrez et al., 1997, 2002; Gutiérrez and Goyache, 2002). Koots et al. (1994a), weighting various published estimates by the inverse of their sampling variance, obtained mean heritabilities of the direct effect of 0.31, 0.24 and 0.296 for BW, WW and ADG, respectively. The corresponding average estimates for the maternal genetic effect were 0.14, 0.13 and 0.25 for BW, WW and ADG, respectively (Koots et al., 1994a). Moreover, Koots et al. (1994b), averaging published estimates of genetic correlations between direct and maternal genetic effects, reported negative average values of -0.35 , -0.25 and -0.30 for BW, WW and ADG, respectively. In all cases, the present estimates are substantially lower than those previously reported for the *Asturiana de los Valles* breed using an animal model including both direct and the maternal genetic effects and their correlation (Gutiérrez et al., 1997; Goyache et al., 2003b). This is particularly true for the r_{um} estimated for WW and ADG in the aforementioned articles, which ranged, respectively, between -0.65 and -0.76 and between -0.75 and -0.82 . The databases analysed by Gutiérrez et al. (1997) and Goyache et al. (2003b) were substantially smaller and with worse data structure than the one available here, thus resulting in more realistic estimates in the present study because of a more correct data structure.

This is the first study in which the effect of s has been estimated for BW (0.04) in an outbred beef population. Senneke et al. (2004), testing the effect of different levels of misidentification of sires on the estimation of variance components for BW, reported that the proportion of phenotypic variance estimated for an environmental random effect linked to sire was negligible. However, said estimations were carried out on an inbred line and the authors consider that the consequences of misidentification (as a cause of the s effect) on estimates of genetic parameters may be less severe than in an outbred population. Moreover, the proportion of the phenotypic variance estimated for the s effect in the present study for WW and ADG is substantially the same as that reported by Berweger Baschnagel

et al. (1999) and Dodenhoff et al. (1999) with field data of, respectively, Swiss Angus and American Angus cattle.

The corresponding Models 3 and 4 cannot be directly compared, although the behaviour of Model 4 tends to follow that observed for Model 2, which, as reported, performs significantly better than Model 1. Hence, the genetic and environmental parameters estimated with Model 4 may be more 'realistic' than those estimated using Model 3. The inclusion of the s effect in the bivariate models produces less negative estimates in the genetic correlations estimated between either direct or maternal genetic effects (Table 3). Both the r_{uu} and the r_{mm} estimated using Model 4 are closer to those reported by Koots et al. (1994a,b), averaging published estimates of 0.50, 0.26 and 0.98 for the correlation between direct effects for the BW–WW, BW–ADG and WW–ADG pairs, respectively, and of 0.39 for the correlation between maternal genetic effects for the WW–ADG pair. This finding also allows us to assume that estimates from Model 4 may be closer to the 'true' population (co)variances than those obtained with the model not including the s effect.

Estimates of large and negative direct–maternal genetic correlations may be due to large sampling correlations between the genetic parameters (Meyer, 1997). However, if this were the sole cause of these large estimates, the use of more information to assess genetic parameters using bivariate models would by itself improve the quality of the estimations. The present results show how estimates of r_{um} obtained using bivariate models are consistently the same as those obtained with univariate models for the corresponding traits. In contrast, the direct–maternal genetic correlations estimated in the present study are less negative when the s effect is included in the estimation models. This change in the correlation estimates follows a similar pattern in univariate and bivariate analyses (Senneke et al., 2004), although the estimates of the direct–maternal genetic correlation were less negative with the bivariate models. The present results lead us to conclude that the effect of s is not negligible and should be taken into account into estimation models, at least until evidence identifying without uncertainty the environmental effects at the root of these inflated estimations appears.

A major issue of the present study was the estimation of the correlations between the s effect affecting BW, WW and ADG. As the effect of s is non-negligible for the three analysed traits, the present results suggest that the causes originating an environmental effect linked to sire are not the same for BW and for WW and ADG. Deficiencies in identification of individuals have been pointed out as a source of spurious sire \times year interaction (Lee and Pollak, 1997a,b; Senneke et al., 2004). However, if this was the sole cause of the effect of s estimated here, the values of r_{ss} found between BW and the other traits would be near 1, as all the available individuals have records for the analysed traits. Robinson (1996a) suggests that a possible cause of the s effect is the variation existing between sires of different genetic origins, which is not likely to occur in the *Asturiana de los Valles* breed. Other explanations for the s effect are a possible unadjusted influence of both selective matings and preferential management practices within a contemporary group of calves leading to the obtaining of the highest growth performance (Notter et al., 1992; Meyer, 1997; Berweger Baschnagel et al., 1999). Farmers may have planned to use some sires only on a given type of dam (i.e. heifers) so as to avoid calving problems. In this respect, since animals with higher BW's tend to show higher growth abilities, selective matings for low BW's would tend to produce an s effect varying in the opposite sense to that caused by unaccounted preweaning management practices. This might explain the low (or virtually inexistent) correlation between the s effect affecting BW and both WW and ADG. Of course, the possibility that a part of the estimated effect of s might be caused by animal misidentification cannot be rejected, although the present results suggest that, in all probability, s has a different nature and origin for different traits.

The effect of the sire \times contemporary group interaction is a well-known problem in dairy cattle. Meyer (1987) and Calus et al. (2002) reported estimations of this interaction of between 2.5% and 3% of the phenotypic variance, thus leading to this effect being included in some dairy cattle evaluation programs (Powell et al., 1994). The cause of this interaction effect does not seem to be the heterogeneity of variances (Canavesi, 1993), which leads to the con-

sideration that this is a result of the existence of an environmental covariance between the daughters of a given sire within a given contemporary group because of preferential treatment. This could be more important when some sires are used and evaluated in a small number of herds (Powell et al., 1994). This scenario may be compatible with a common situation in beef cattle improvement programs, thus leading to a more intense effect of the environmental covariances existing among sires and herds.

5. Conclusions

This study presents evidence as to a possible different origin of the sire \times contemporary group effect affecting different preweaning growth traits in beef cattle. The effect of s on BW may be dependent on non-random matings, while that affecting both WW and ADG may be dependent on preferential management practices. Nevertheless, when field data are analysed s would be more likely to result from the effect of environmental covariances affecting contemporary calves than misidentification of individuals. As pointed out by Hagger (1998) in meat sheep, not accounting for a sire \times contemporary group interaction effect in models describing preweaning growth traits in beef cattle may lead to inflated estimates of direct and maternal genetic (co)variance components and result in a strong negative correlation among them, thus biasing genetic evaluations. In this respect, field data analysis such as the present study seems to provide good reasons for accepting models including the s effect as working models in beef improvement schemes, at least until substantial evidence for an improved model should appear.

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