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

J.P. Gutiérrez [a,*], I. Fernández [b], I. Alvarez [b], L.J. Royo [b], F. Goyache [b]

[a] *Dpto. de Producción Animal, Facultad de Veterinaria, Universidad Complutense, Avda. Puerta de Hierro s/n, E-28040-Madrid, Spain*
[b] *SERIDA-Somió, C/ Camino de los Claveles 604, E-33203 Gijón (Asturias), Spain*

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Abstract

Although a number of recent studies have focused on the existence of a non-negligible sire × 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.

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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* Corresponding author. Tel./fax: +34 913943767.
E-mail address: gutgar@vet.ucm.es (J.P. Gutiérrez).

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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 × 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 theses effects. However, simulations including a sire × 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 × 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 × 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 insem-