Modelling Fertility Traits under Natural Mating Conditions in Beef Cattle

C. Meneses[1], M.J. Carabaño[1], R. Morales[2], A. Molina[2] and C. Díaz[1]
[1] *Dpto. de Mejora Genética Animal, INIA, Ctra. La Coruña Km 7,5. Madrid, Spain*
[2] *Dpto. Genética. Universidad de Córdoba, Córdoba, Spain*

Abstract

Fertility traits are the most economically important traits in beef cattle and in spite of having low heritabilities they ought to be included in breeding programs. The genetic selection programs in Spain are based on improving growth traits, neglecting the fertility traits up to now. In this study, a first analysis of the calving interval between first and second parities (CI_{12}) was carried out to establish a suitable selection criterion. The selected breeds were two local breeds Avileña-Negra Ibérica (ANI) and Retinta (RT), raised in extensive production with natural mating. Two models including cow and bull effects were studied. –Systematic effects were herd-year-season of first calving, age of cow at first calving and age of bull at second calving and regressions on inbreeding coefficients for cows and bulls. Then, a full model (FULL) included additive genetic and permanent environmental components for bull and an additive genetic effect for cows. A reduced model (RED) was the same as FULL but with the additive genetic component for bull excluded. Both models provided similar estimates of systematic and cow additive genetic components. Inbreeding depression was found for bulls (0.79 and 0.83 days/% inbreeding in ANI and RT, respectively) but nearly null regression coefficients on inbreeding were obtained for cows. In both breeds, heritability estimates were 0.05 for cows. For FULL, heritability estimates for bull effects were larger than the cows heritability, 0.08 for ANI and 0.10 for RT. The bull permanent component was large, with values of 0.20 and 0.31 for ANI and RT, respectively. Herd fertility in these populations can be substantially improved by bulls screening. Genetic selection can be practiced but with low efficiency, as it is commonly the case for fertility traits

Key words: fertility, extensive production, calving interval, natural mating

Introduction

In Spain there are more than thirty five local beef breeds, among those, seven have established selection programs to improve productivity (kg of calf at weaning/cow) and carcass conformation. However, productivity has been only focused on gain of kg at weaning without paying attention to numerical productivity that only depend on fertility. However, a recent report made by the Ministry of Agriculture of Spain warns about low fertility parameters in beef cattle breeds. These bad results are partly due to the absence of systematic recording of non-success and success pregnancies because of the extensive conditions in which many of these breeds are raised. Artificial insemination is very scarce and the control over the cows with this system is low. These reasons joined with the fact that fertility is one of the most economically important traits (Phocas *et al*., 1998; Urioste *et al*., 1998; Cammack *et al*, 2009; Fortes, *et al* 2013) define our objective. This is to incorporate fertility traits in beef cattle selection programs to help the farmer's profitability. To do so we will start using easy to record data, because reproductive performance is a complex trait that has many components (Rust and Groeneveld, 2001).

Materials and Methods

Data

Data from two local breeds which are the two more important breeds in the driest areas in Spain were used in this study. The breeds were Avileña-Negra Ibérica (ANI) and Retinta (RT), both raised in extensive production and with natural mating with a scant use of AI. The first breed, ANI, is mostly located in the center of Spain where many of the production areas are in high lands and RT is in the southwest, in grasslands, although both breeds share some common areas.

Calving interval (CI_{12}) between first and second parities was the trait under study. The initial data set was obtained from the Herdbook of the breeds. The editing data process consisted of selecting females whose herds were in the breeding program, and these herds had to have in the historical register a minimum of two sires. Cows with an age at first calving less than 448 days or more than 1619 days were removed. The same occurred with cows with missing sires and CI_{12} out of the range of 289-600 days. Editing criteria were established from the distribution of values of CI_{12} and checked with the breeder associations. After editing, the final data set for ANI was formed by 9 383 cows with CI_{12} data and 879 bulls, in 125 herds, and the pedigree file had 16 795 animals. In the case of RT breed, the data set was formed by 5 230 cows with CI_{12}, 743 bulls, 110 herds, and 11 445 animals in the pedigree.

Statistical Analysis

Two models were studied, a full model (FULL) and a reduced model (RED). The full model had the following equation:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Z}_1 a_1 + \mathbf{Z}_2 a_2 + \mathbf{Wp} + \mathbf{e} \, ,$$

where **y** is the vector of observed CI_{12}; **b** is the vector of systematic effects; $\mathbf{a}_1$ and $\mathbf{a}_2$ are vectors of cow and bull additive genetic effects, respectively; **p** is the vector of bull permanent environmental effects; **e** is the vector of residual effects; **X**, **Z** and **W** are the incidence matrices.

The **b** vector included the contemporary group effect (herd x year x season at first calving) with a minimum of two observation (1,969 levels ANI, 1,323 RT). There were four seasons, December to March, April to June, July and August, and, September to November, defined according to the weather characteristics of these regions. Age at first calving of the dam was also included, and it had 3 levels (age 1 < 2,5 years, 2,5 years ≤ age 2 ≤ 3 years, and age 3> 3 years). The age of the bull at the second calving was another factor in **b**, with 6 classes (age 1< 2 years, 2 ≤ age 2 < 3 years, 3 ≤ age 3 < 4 years, 4 ≤ age 4 < 5 years, 5 ≤ age 5 < 6 years and age 6 ≥ 6 years). Finally, the inbreeding coefficients for both, dam and bull, obtained by the tabular method (Tier, 1990), were included as covariates in linear regressions.

The prior distributions of $\mathbf{a} = (\mathbf{a}_1$ and $\mathbf{a}_2)$, **p** and **e** were $N(\mathbf{0}, \mathbf{A} \otimes \mathbf{G}_o)$, $N(\mathbf{0}, \mathbf{I}\sigma_p^2)$ and $N(\mathbf{0}, \mathbf{I}\sigma_e^2)$, respectively, where $\mathbf{G}_o$ is a (co)variance matrix for the additive genetic components on CI_{12} of cow and bull.

The RED model had the same effects as in FULL, except for the bull additive genetic effect.

Bayesian inference with Gibbs sampling algorithm was used to make inferences for the parameters of interest. A long chain of 10^6 iterations was obtained, discarding 500 000 rounds as burn-in, and with a thin of 10 iterations. Software TM (Legarra *et al.*, 2008) was used.

Results & Discussion

The distribution of values of CI_{12} was for ANI breed 409 days of mean and a standard deviation of 73 days, in the case of RT the values were 453 and 102 days respectively. CI_{12} was larger for RT than for ANI, which might be associated to larger herd sizes in RT associated to less control over the reproductive performance of the animals.

The difference in days between the best and the worst solutions for each effect appear in Table 1. In both models, this difference was quite similar within breed. Across breeds, RT showed larger solution ranges than ANI. The effect with the largest difference was the contemporary group, followed by the bull permanent environmental effect. This implies that the management effect makes up for most of the variability observed in $CI_{12,}$ between 380 and 545 days in ANI and RT, respectively. The bull permanent environmental effect was surprisingly large, with differences among bulls up to 150 and nearly 300 days in ANI and RT, respectively. Range of EBVs for cows was 43 and 45 days under FULL and slightly larger, 46 and 53 days for RED in ANI and RT, respectively.

Table 1. Difference in days between the best and the worst solutions for each effect and breed under full (FULL) and reduced (RED) models.

Effect	Solutions range (days)			
	FULL		RED	
	ANI	RT	ANI	RT
HYS[1]	390.1	545.5	379.8	537.1
Cow Age	20.0	18.8	20.0	18.7
Bull Age	30.5	77.7	29.3	76.3
F_i [2] Cow*	0.16 ± 0.13	0.06 ± 0.24	0.16 ± 0.13	0.07 ± 0.23
F_i [2] Bull*	0.79 ± 0.35	0.83 ± 0.56	0.76 ± 0.34	0.85 ± 0.54
Cow genetic	42. 8	45.2	45. 7	53.5
Bull permanent	121.5	229.7	149.4	284.4
Bull genetic	49.2	74.3	-	-

[1] Herd-Year-Season of first calving

[2] Inbreeding depression in days/% inbreeding

* days/% inbreeding (mean ± standard deviation)

The large effect of bulls on CI_{12} and the larger variability compared to cows, were unexpected results because the opposite has been observed in a number of species, particularly on those where AI is used (see, e.g., David *et al*., 2011). Semen screening in species with AI is likely to preclude the use of low fertility males and reduce observed variability on male fertility. On the other hand, Mackinon *et al*. (1990) found that the male component on fertility under extensive systems with a prevalence of natural mating is larger than in populations with a heavy use of AI.

An interesting result was the solution for the effect of inbreeding. In both breeds, the estimated effect of inbreeding was lager in bulls than in cows, taking the values of around 0.8 days/ % inbreeding under FULL for both breeds. For cows, the estimated effect of inbreeding was 0.16 in ANI, 0.06 in RT, which taking into account the standard errors of the estimates (Table 1) cannot be said to be different from zero. This result was somehow un-expected because effect of inbreeding on fertility traits has been found in cows (see, e.g., Sewalem *et al*. 2006 and González-Recio *et al*., 2007). Thus, this result could be associated to a different amount of pedigree information available for cows and bulls.

Table 2 shows the estimates of variance components and genetic parameters with their standard deviation for the two breeds and for FULL and RED. Estimated cow heritability for CI_{12} was low, around 0.05 for the two breeds. Similar results were found by Roughsedge *et al*. (2005) in the Limousine breed. Bull heritability from FULL was higher, around 0.1 in both breeds, than cow's heritability. As in dairy cattle, the low heritabilities for fertility make selection for fertility difficult. However, the large estimate of the bull permanent environmental effect (0.26 ANI and 0.39 RT for RED) indicate that substantial gain in fertility can be obtained in these breeds through screening of low fertility bulls. Therefore, control of semen quality and reproductive diseases that may impair male fertility are to be considered in these breeds.

Estimated genetic correlations between cow and bull components were positive but low and from the large standard errors we cannot assure that these are different from zero. David *et al*. (2011) also found close to zero estimated genetic correlations between male and female components of conception rate in several species.

Table 2. Genetic parameters estimated after discarding the burning (mean ± standard deviation).

Genetic parameters	FULL		RED	
	ANI	RT	ANI	RT
$\boldsymbol{\sigma_{a1}^2}$	233.9 ± 92. 5	525.1 ± 281.2	252.1 ± 83.5	617.0 ± 271.2
$\boldsymbol{\sigma_{a2}^2}$	401.2 ± 219.9	1225.1 ± 700.8		
$\boldsymbol{\sigma_{p2}^2}$	1026.3 ± 241.63	3775.1 ± 749.5	1250.0 ± 218.7	4566.7 ± 621.0
$\boldsymbol{\sigma_{e}^2}$	3371.9 ± 91.9	6459.0 ± 274.1	3365.0 ± 87.9	6396.9 ± 265.9
$\mathbf{h_{cow}^2}$	0.05 ± 0.02	0.04 ± 0.02	0.05 ± 0.02	0.05 ± 0.02
$\mathbf{h_{bull}^2}$	0.08 ± 0.04	0.10 ± 0.06		
$\mathbf{c^2}$	0.20 ± 0.04	0.31 ± 0.06	0.26 ± 0.03	0.39 ± 0.03
$\mathbf{r_{1\text{-}2}}$	0.24 ± 0.36	0.18 ± 0.50		

σ_{a1}^2: Cow variance, σ_{a2}^2 : Bull variance, σ_{p2}^2: variance , σ_e^2 : Residual variance, h_{cow}^2 : Cow heritability, h_{bull}^2 : Bull heritability, c^2 : Bull permanent effect, $r_{1\text{-}2}$: Correlation between cow and bull effect.

Conclusions

The male component was particularly relevant in this study, being more important the environmental than the genetic part of the bull effect. A significant inbreeding depression was detected for bulls on CI_{12}. Therefore, herd fertility in these populations can be substantially improved by bulls screening. Genetic selection could also be practiced but with low efficiency, as it is commonly the case for fertility traits.

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