Pre-weaning performance of Hereford, Angus, Salers and Nellore crossbred calves: Individual and maternal additive and non-additive effects

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ABSTRACT

Individual and maternal additive and non-additive effects for gestation length (GL), birth (BW) and weaning weights (WW) were estimated in Hereford (H/H), Aberdeen Angus (A/A), Salers (S/S) and Nellore (N/N) breeds. Data were recorded on 4474 calves of 39 genotypes (pure- and cross-bred) which were sired by 141 bulls and born in two connected crossbreeding experiments carried out between 1993 and 2004. Five crossbreeding parameter models were compared. The best fit, assessed by the Akaike Information Criterion, was obtained by the additive model for GL and by the Dickerson full model for BW and WW. The individual additive effect of N/N increased GL by 12.0 days compared to H/H, whilst the maternal additive effect reduced it by 3.1 days. The individual additive effects of A/A and N/N for BW were +1.8 kg and −2.3 kg, respectively. Maternal effects had opposite sign to the individual effects (A/A, +3.6 kg; N/N, −8.3 kg). Additive effects of S/S were not significant (P>0.10). Maternal heterosis increased BW in all crosses with H/H (from +1.8 to +5.1 kg) but the individual heterosis was only significant in the crosses with N/N (2.3 kg). In the case of WW, maternal additive effects as well as individual and maternal heterosis improved WW by 18.5, 5.3 and 11.9 kg, respectively. Additive effects of N/N decreased WW (individual, −12.1 kg; maternal, −34.6 kg) whilst the individual and maternal heterosis had a favourable effect (+20.2 kg; +63.1 kg). In both N/N and S/S breeds, maternal recombination losses increased WW (30.7 and 48.2 kg) and individual recombination losses have the opposite effect (from −12.1 to −27.0 kg). In general terms, additive and non-additive effect of European breeds did not increase GL or have any effect on BW. However, increasing proportions of Nellore were associated with longer GL compared to H/H. The use of Nellore as paternal breed may be related to heavier BW which may increase the incidence of dystocia. Positive effects of crossbreeding on WW were mainly due to the use of crossbred dams given the significant magnitude of maternal heterosis. The best combination of individual additive effects came from the utilisation of European breeds, whilst the greater magnitudes of both heterosis and recombination losses were observed in the Nellore crosses.

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1. Introduction

Beef production depends on the joint effect of genetic resources, environment and the interaction between both factors. Crossbreeding is one effective tool for the optimal use of genetic resources according to the specific environments, allowing the combination of local genetic resources and others that may be more productive from the economic point of view. It is possible to define the most appropriate crossbreeding system based on the use of crossbreeding genetic models. Parameters for these models can be estimated from the performances of crossbred animals of few genetic

groups recorded in crossbreeding experiments. The representativeness of these estimates relies on the use of a large and representative sample of sires commercially available for the different breeds (Madalena, 2001).

Crossbreeding experiments provide the basis for the estimation of the crossbreeding parameters for both additive (differences between breeds) and non-additive genetic effects (dominance and epistasis) (Dickerson, 1969). The use of crossbreeding and the optimal system depends, amongst other factors, on the magnitude of individual and maternal components of additive and non-additive effects and their interaction with the environment. Crossbreeding parameters are not only relevant for the optimization of crossbreeding systems but also for the genetic evaluation of multibreed populations. The use of crossbreeding parameters allows the comparisons amongst the estimated breeding values of crossbred animals used as seedstock, as well as those estimated for different breeds evaluated together (Pollak, 2006).

The estimation of the crossbreeding parameters may be limited by the type and numbers of genetic groups included in the crossbreeding experiment, in addition to possible multicollinearity problems amongst genetic groups. Estimability problems have restricted the number of published parameters available for dominance and epistatic effects, and for more complex traits involving maternal effects (i.e. pre-weaning and weaning traits). The number of published crossbreeding parameter estimates varies amongst breeds. More estimates are available in the literature for Hereford and Angus amongst the British breeds. Similarly, the, Continental and Zebu breeds with more information are Charolaris and Brahman, respectively (Dillard et al., 1980; Olson et al., 1993; Peacock et al., 1981).

Pre-weaning performance is recognised as one of the most important factors determining the economic returns of beef production, and its overall productivity (Cunningham and Henderson, 1965). High birth weights and/or low weaning weights due to low calf growth potential or poor maternal ability of cows have a negative effect on the productivity of cow/calf enterprises.

The aim of this study was to estimate additive and non-additive crossbreeding parameters for gestation length and birth and weaning weights for Hereford, Aberdeen Angus, Salers and Nellore breeds under temperate grazing conditions.

2. Materials and methods

2.1. Experimental design and animal management

Data were recorded in two crossbreeding experiments carried out between 1993 and 2004 at a commercial farm "Capilla Vieja" owned by Caja Notarial de Seguridad Social, which is located near to Pandule in the department of Paysandú (Uruguay) at 32°13′ South latitude and 57°21′ West longitude.

The animals were raised on natural pastures (approximate production: 5500 kg dry matter/ha/year), which are characterised by a very seasonal pattern of production (62% produced in spring–summer), with short peaks of high quality forage in spring and the highest production volume in summer. There is a severe reduction of both quality and quantity of the forage available in winter (13.9% of the annual production) (Saldanha, 2005). Neither cows nor calves were supplemented at any time of the year in these experiments.

2.1.1. Breeds and experiment design

Four breeds that are representative of different cattle origins or types were included in the two crossbreeding experiments: Hereford (H/H) and Aberdeen Angus (A/A) as representative of British breeds, Salers (S/S) as a Continental breed and Nellore (N/N) as Zebu breed.

Experiment one was designed with the objective of estimating crossbreeding genetic parameters for the crosses British × British, Zebu × British and Continental × British (Gimeno et al., 1995). The genetic groups feasible to be produced were evaluated considering the Dickerson full genetic model with maternal effects. The design of experiment was optimised using the Optimum Design Crossbreed Experiments (ODCE) software (Sölkner and Fucks, 1994). The starting point was a herd of adult H/H cows. As result of the optimization it was decided to include in the experiment pure A/A cows in addition to the H/H (females S/S and N/N were not available), to breed F1 males to obtain a F2 generations, and to produce first and second backcrosses (Gimeno et al., 1995) (Table 1).

Experiment one had two groups of dams. Group A comprised adult (multiparous) H/H cows that were open in the previous year which were inseminated with the four breeds (H/H, A/A, S/S and N/N) and second parity A/A cows inseminated with A/A. Group B included the different female genotypes produced by group A. These cows were inseminated when they were 2 years old, with the four purebreds and F1 bulls (A/H, S/H and N/H) born in the experiment. Females born in experiment 2 were also included in group B with the aim of increasing the numbers of animals produced in the later generations of the experiment.

Table 1
Number of animals born between 1993 and 2004 by paternal and maternal genetic groups[a].

Maternal genetic groups	Paternal genetic groups							
	H/H	A/A	S/S	N/N	A/H	S/H	N/H	Total
H/H	821	850	852	596	14	17	19	3169
A/A		201			20			221
A/H	111	92			96			299
S/H	138		129			98		365
N/H	86			87			54	227
H/AH		20						20
A/AH	21							21
AH/H					3			3
AH/A	1				7			8
H/SH			34					26
S/SH	8		18					34
H/NH				18				18
N/NH	5			7				12
NH/H				1			2	3
AH/AH					12			12
SH/SH						13		13
NH/NH							6	6
SH/H						9		9
H/A(AH)		3						3
A/H(AH)		3						3
S/H(SH)			1					1
S/S(SH)			1					1
Total	1191	1169	1035	709	152	137	81	4474

[a] Sire and dam genotypes at the left and right of the slash, respectively.