Estimation Of Genetic Effects For Growth Traits Of Mexican Charolais Cattle Using Alternative Models

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Introduction

The magnitude of estimates of genetic parameters for growth traits of beef cattle may vary depending on breed group and genetic effects included in the statistical model (Meyer (1992)). It has been reported that exclusion of maternal effects (genetic and environmental) from the statistical model results in overestimation of the direct genetic variance for weaning weight (Robinson (1996)). Therefore, before performing the genetic evaluation of any economically important trait, selection of proper statistical model should be of primary interest for geneticists. The aim of the present study was to identify the most suitable model to estimate genetic parameters for growth traits of Mexican registered Charolais cattle.

Material and methods

Data. Field data for birth, weaning, and yearling weight as well as pedigree information were obtained from the Charolais Herd Book of Mexico for the period from 1997 to 2009. Weaning and yearling weight records were adjusted to a 205- and 365-days basis.

Models. Each growth trait was analyzed with six different single trait animal models to assess the importance of different genetic effects. Model 1 included direct additive genetic effects of the animal. Model 2 allowed for a common environmental effect due to the dam, fitting this as an additional random effect. Model 3 included the animal's direct genetic effect, and the dam's maternal genetic effect, assuming a covariance equal to zero between them. Model 4 was the same as Model 3 but it also allowed for a common environmental effect due to the dam. Model 5 is identical to Model 3, but included a covariance between direct and maternal genetic effects. Model 6 was fitted for all three random effects plus the covariance between direct and maternal genetic effects. Superiority of one model over another to fit significantly better birth, weaning and yearling weight data was determined via the likelihood ratio test (Dobson (1990)).

Estimation. Covariance components were estimated using the MTDFREML set of programs. Convergence was assumed to have been reached if the variance of minus twice the logarithm of the likelihood (-2logL) in the simplex was less than 10^{-8}. After first convergence, restarts were performed to verify that it was not at a local minimum.

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Results and discussion

Simple descriptive statistics are in Table 1. Number of records for growth traits evaluated ranged from 55,284 (yearling weight) to 105,599 (birth weight). Estimates of (co)variance components and genetic parameters obtained with the six different animal models for birth weight (BW), weaning weight adjusted to 205 days (WW), and yearling weight adjusted to 365 days (YW), together with values for -2logL are summarized in Table 2.

Table 1: Summary statistics and data structure for birth weight (BW), weaning weight adjusted to 205 days (WW), and yearling weight adjusted to 365 days (YW)

	BW	WW	YW
Number of records	105,599	89,111	55,284
Mean	39.0	226.6	347.5
Standard deviation	5.4	41.0	64.0
Coefficient of variation	14.0	18.1	18.4
Number of sires	3,923	3,791	3,054
Number of dams	42,960	39,701	28,982
Number of contemporary groups	13,805	11,798	7,766
Number of animals in the pedigree	131,659	131,659	131,659

Birth weight. When the permanent environmental effect (Model 2) or the maternal genetic effect (Model 3) was added, a substancial decrease in -2logL compared to Model 1 occurred (P<0.05), showing the influence of these effects on BW. However, the inclusion of the additive maternal effect instead of the permanent environmental effect did not change the estimate of the additive direct variance, resulting in similar estimates of direct heritability for both models. Compared with any of the other models, the most complete model (Model 6) substantially reduced the -2logL (P<0.05), providing the best fit to BW data. Comparison between Model 1 and Model 6 shows that Model 1 yielded a smaller estimate of the direct additive genetic variance, in contrast with results from previous studies (*e.g.*, Meyer (1992)); however, the estimate of the residual variance for Model 1 was greater than the corresponding estimate for Model 6. The direct heritability for BW was estimated to be 0.36 with the best model. Meyer (1993) obtained a lower estimate (0.21) for Charolais cattle in Australia. Working with the same beef producing breed, Grotheer *et al*. (1997) and Phocas and Laloë (2004) reported similar estimates of direct heritability for BW (0.38, 0.33). In contrast to the present estimate, greater estimates of direct heritability (0.54, 0.55, 0.45) have been reported for Charolais cattle reared in Brazil (Fernandes *et al*. (2002)), Canada (Donoghue and Bertrand (2004)) and Sweden (Eriksson *et al*. (2004)). The estimated heritability for maternal effects obtained with the best model (0.13) is comparable to and within the range of estimates (0.11 to 0.18) reported by Trus and Wilton (1988), Fernandes *et al*. (2002), Donoghue and Bertrand (2004), Eriksson *et al*. (2004) and Phocas and Laloë (2004) for Charolais cattle. The estimate of the genetic correlation between direct and maternal genetic effects for BW was -0.78, which is greater than estimates obtained in other countries for the Charolais breed (Grotheer *et al*. (1997); Donoghue and Bertrand (2004); Eriksson *et al*. (2004); Phocas and Laloë (2004)).

Weaning weight adjusted to 205 d. Considerable reductions in -2logL (Models 1 through

Table 2: Estimates of genetic parameters[a] obtained with six different animal models for birth weight (BW), weaning weight adjusted to 205 days (WW), and yearling weight adjusted to 365 days (YW) of Mexican registered Charolais cattle

Model	V_a	V_m	CO_{am}	V_{pe}	V_e	h^2_a	h^2_m	r_{am}	-2logL
BW									
1	4.0				11.3	.26±.007			357820
2	3.2			.81	11.2	.21±.008			357601
3	3.1	.73			11.3	.21±.008	.05±.004		357544
4	3.1	.46		.42	11.2	.20±.008	.03±.005		357511
5	5.6	2.7	-2.8		10.0	.36±.015	.17±.009	-.72±.08	357106
6	5.5	2.0	-2.6	.66	9.9	.36±.015	.13±.010	-.78±.09	357051
WW									
1	154				522	.23±.008			595114
2	99			59	509	.15±.008			594681
3	95	51			521	.14±.008	.08±.004		594686
4	92	24		37	512	.14±.008	.04±.006		594602
5	184	148	-124		471	.27±.015	.22±.010	-.76±.08	594340
6	180	103	-111	40	463	.27±.015	.15±.012	-.81±.10	594264
YW									
1	266				899	.23±.011			391989
2	211			61	885	.18±.012			391912
3	209	48			900	.18±.012	.04±.006		391922
4	203	22		43	889	.18±.012	.02±.007		391901
5	356	198	-197		820	.30±.020	.17±.014	-.74±.12	391781
6	352	147	-183	53	807	.30±.020	.12±.016	-.81±.14	391757

[a] V_a= direct genetic variance; V_m= maternal genetic variance; CO_{am}= covariance between direct and maternal genetic effects; V_{pe}= maternal permanent environmental variance; V_e= residual variance; h^2_a= direct heritability; h^2_m= maternal heritability; r_{am}= direct-maternal genetic correlation.

6) suggest that WW was significantly influenced by maternal genetic and permanent environmental effects, as occurred with BW. However, the most suitable model (Model 6) indicates that genetic maternal effects were more important than permanent environmental effects. The estimate of direct heritability for WW (0.27) was smaller than corresponding estimate for BW. For American and Canadian Charolais cattle, Donoghue and Bertrand (2004) estimated direct heritabilities of 0.25 and 0.27 for WW, which are similar to the present estimate obtained with the full model. In contrast, Meyer (1993) and Phocas and Laloë (2004) obtained smaller estimates (0.12 and 0.13, respectively) than the estimate in the current study. The estimated maternal heritability was 0.15 for Model 6. Similar estimates have been reported for American (Duangjinda *et al*. (2001)), French (Fouilloux *et al*. (2002)) and New Zealand (Donoghue and Bertrand (2004)) Charolais cattle. In disagreement, Meyer (1993) reported a near-zero estimate (0.04) of maternal heritability for weaning weight. The estimate of the direct-maternal genetic correlation for WW obtained with the best model was -0.81, which is similar to the estimate (-0.78) reported by Meyer (1992) for Zebu Cross cattle, but greater than the estimates reported by Grotheer *et al*. (1997), Duangjinda *et al*. (2001), Fouilloux *et al*. (2002) and Phocas and Laloë (2004). Berweger Baschnagel *et al*. (1999) reported that ignoring sire x herd effect resulted in a strong negative correlation

between additive direct and maternal effects. The estimated maternal permanent environmental variance for WW accounted for 6% of the estimate of phenotypic variance and was much smaller than the estimate of maternal heritability. For American, Canadian and New Zealand Charolais data, Donoghue and Bertrand (2004), in contrast, reported that maternal permanent environmental variance as a proportion of phenotypic variance was as important as maternal heritability.

Yearling weight adjusted to 365 d. Although maternal effects for YW were relatively less important, they remained evident after weaning. Similar to the findings for BW and WW, the most complete model that included all three random effects was the best for YW. An estimate of 0.30 was obtained for direct heritability with Model 6. This estimate is similar to the values of 0.32 and 0.33 reported for Australian (Meyer (1993)) and German Charolais cattle (Grotheer *et al*. (1997)). A low value (0.12) of estimate of maternal heritability was obtained for YW. Direct and maternal genetic effects for YW were estimated to be strongly correlated (-0.81).

Conclusion

Comparison of the different animal models showed that a model which included direct and maternal genetic effects, their correlation, and permanent environmental effects is recommended for estimation of EPD for BW, WW and YW of Mexican Charolais cattle. Genetic progress would be lessened by the strong antagonism between direct and maternal genetic effects; however, such antagonism may be a consequence of other effects in the data.

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