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COMPARISION OF GENETIC PARAMETERS FOR CALVING DIFFICULTY IN ANGUS, CHAROLAIS, HEREFORD AND LIMOUSIN.

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SUMMARY

Data on Angus (ANG), Charolais (CHR), Hereford (HER) and Limousin (LIM) cattle were used to estimate genetic parameters for calving difficulty (CD) and to quantify genetic relationships among CD, birth weight (BWT) and gestation length (GL). Bayesian analysis was carried out using Gibbs sampling to obtain means of marginal posterior distributions. Estimated heritabilities for direct genetic effect of CD were 0.24, 0.22, 0.31 and 0.22 for ANG, CHR, HER and LIM, respectively while maternal heritabilities ranged from 0.13 to 0.20. Genetic correlations between direct genetic effects of CD with BWT were highly positive and with GL were moderately positive for all four breeds. Low to moderate negative correlations of maternal genetic effect of CD with direct genetic effects for BWT and GL were estimated. This study showed that CD was moderately heritable in all four breeds and therefore, genetic progress is possible through selection. The ANG and HER had similar genetic correlations. Among the four breeds, LIM had slightly higher direct and maternal genetic correlation for CD and higher correlations between the maternal genetic effects of all three traits. However, moderate to high positive correlation between direct genetic effects of CD, BWT and GL show selection for lower BWT and GL would decrease CD in all four breeds.

INTRODUCTION

Calving difficulties (CD) cause significant economic losses in beef enterprises through death of calves and cows, increased labour and veterinary cost and reduced reproduction rate (Brinks *et al.* 1973). In BREEDPLAN, calving outcome is scored as a categorical trait and analysed as calving ease with BWT and GL in a multi trait evaluation to produce calving ease EBV. In the past, for computational simplicity, the genetic parameters used to predict breeding values were derived using linear models. However, because of the categorical nature of CD, non linear models to estimate genetic parameters are more appropriate. A Bayesian approach using Monte Carlo technique allows the easy implementation of combined linear with threshold models, which is necessary for combining categorical with normally distributed traits. Therefore, the aim of this study was to estimate genetic parameters for CD and quantify the genetic association of CD with BWT and GL of different beef breeds to update genetic evaluation of CD of beef cattle in Australia.

MATERIALS AND METHODS

Data used for this study were submitted by breeders to their breed societies for use in BREEDPLAN. The breeds included Angus (ANG), Charolais (CHR), Hereford (HER) and Limousin (LIM). Data included CD score, birth weight (BWT, kg) and gestation length (GL, days) records of calves born to females below 12 years of age.

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A univariate threshold animal model was developed to estimate genetic parameters for CD in all four breeds. Model used in the estimation of genetic parameters was

$$Y_{ijk} = CG_i + AGE_j + GD_j + S_k + a_k + m_j + pe_j + e_{ijk}$$

Where Y_{ijk} is the CD score of animal k in a fixed contemporary group i (CG_i), AGE_j is the age of dam j at calving as class effect, GD_j is the grade of dam as class effect fitted for LIM only, S_k is the sex of animal k, a_k is the random additive genetic effect of animal k, m_j and pe_j are the random maternal genetic and random permanent maternal environment effects of dam j, and e_{ijk} is the random error associated with this observation. Contemporary group was defined by Graser *et al*. (2005). For analyses, the CD, which was scored on a 1 to 5 scale were grouped into three categories *viz* score 1 to represent unassisted birth or no difficulty, score 2 to represent easy pull or minor difficulties and score 3 to represent hard pull or mechanical assistance were used. Ten dam age classes were identified as fixed effect. Records from contemporary groups with only one score for CD were excluded to avoid the extreme category problem. The random error variance was fixed at 1.

A trivariate animal model was used to combine a threshold model (with two threshold) for CD with linear models for BWT and GL. Birth weight and GL records were pre-adjusted for sex of calf, linear and quadratic age of dam deviated from five years of age nested within season (Autumn and Spring) and linear heifer effects nested within heifer class and season (Graser *et al*. 2005). Model fitted for CD had the same effects as univariate evaluation. Models for BWT and GL had fixed contemporary groups, random additive genetic effect of animal, random maternal genetic and random permanent maternal environment effects of dam. Complete pedigree information going back to six generations was used. Bayesian analysis was carried out using Gibbs sampling to estimate the means of marginal posterior distributions. The analysis was carried out using THRGIBBSF90 (Misztal *et al*. 2002). Post Gibbs analyses were done using POSTGIBBSF90. Single chains of 200,000 iterations were sampled and the first 20,000 samples were discarded. A stationary state was confirmed by plotting sample values against iterations as suggested by Kass *et al.* (1998). Every 20th sample was stored and a total of 9,900 were kept to compute posterior means and highest posterior density interval (95%) credible regions.

RESULTS AND DISCUSSION

Table 1. Data characteristics for the estimation of genetic parameters for calving difficulty (CD), birth weight (BWT) and gestation length (GL).

Breed	**CD**[1]						**BWT**			**GL**		
	N	**Mean**	**SD**	**Proportion of scores (%)**			**N**	**Mean**	**SD**	**N**	**Mean**	**SD**
				1	**2**	**3**						
Angus	273568	1.1	0.3	96.2	2.6	1.2	750633	36.5	5.1	220592	280.8	5.1
Charolais	39572	1.1	0.4	91.0	6.5	2.5	58973	43.3	5.7	17700	286.1	5.5
Hereford	228787	1.1	0.4	93.0	4.8	2.2	459460	38.8	5.4	66767	284.8	5.2
Limousin	38605	1.2	0.5	88.7	7.0	4.3	57269	38.3	4.8	27065	288.7	5.5

[1] Records from contemporary groups with only one score for CD were excluded

Raw means by breed are presented in Table 1, and show a range in liability for CD (88.7 to 96.2%) and differences in raw means for BWT (37.7 to 43.3kg) and GL (281 to 289 days). Estimates of direct heritability for CD (h_a^2) were very similar for ANG, CHR and LIM and ranged from 0.22 to 0.24 (Table 2). However, HER had a significantly ($P \leq 0.05$) higher heritability (0.31). Estimated heritability for maternal genetic effect (h_m^2) of CD for ANG, HER and LIM were the same (0.13). Estimated h_a^2 for CHR and HER were in agreement with the estimates of Eriksson *et al.* (2004). The 95% highest posterior density regions for the heritabilities were centred around the point estimates of the traits. However, the h_a^2 and h_m^2 estimates for the four breeds were lower than the estimates presented by Bennett and Gregory (2001) with linear model evaluation. Estimated genetic correlation between direct and maternal genetic effects for all four breeds were negative and ranged from -0.06 (LIM) to -0.48 (CHR) and, except for LIM, they were in agreement with values reported by Koots e*t al.* (1994). Estimated r_{am} of CD for LIM was higher than the mean values reports by Koots e*t al.* (1994).

Table 2. Estimated heritabilities for direct genetic (h_a^2) and maternal genetic (h_m^2) effects, variance ratio for permanent environmental effect of dam (p_e^2) and genetic correlation between direct and maternal genetic effects (r_{am}) with 95% highest posterior density interval (HPD) for calving difficulty using univariate threshold model.

Breed	h_a^2	**HPD**		h_m^2	**HPD**		p_e^2	**HPD**		r_{am}	**HPD**	
		Low	**High**		**Low**	**High**		**Low**	**High**		**Low**	**High**
Angus	0.23	0.19	0.28	0.13	0.11	0.15	0.08	0.06	0.10	-0.35	-0.49	-0.22
Charolais	0.22	0.13	0.30	0.20	0.13	0.27	0.11	0.07	0.15	-0.47	-0.64	-0.28
Hereford	0.31	0.29	0.33	0.13	0.11	0.15	0.06	0.04	0.08	-0.45	-0.52	-0.38
Limousin	0.22	0.15	0.30	0.13	0.07	0.17	0.19	0.13	0.24	-0.06	-0.27	0.16

The genetic correlations between direct genetic effects of CD and BWT were high for all the breeds compared and ranged from 0.64 to 0.69 (Table 3). Eriksson *et al*. (2004) also estimated genetic correlation of similar magnitude between direct genetic effects of CD and BWT for CHR and HER breeds. The direct genetic correlations between CD and GL were also positive ranging from 0.13 (HER) to 0.44 (LIM). Correlations between maternal genetic effect for CD with BWT and GL were also moderate and positive. Low negative correlations and low or no genetic correlations were observed between maternal genetic effect of CD and direct genetic effects of BWT and GL, respectively. However, negative correlation between direct genetic effect of CD and maternal genetic effect of all three traits were observed for all four breeds. Estimated genetic correlation between direct genetic effect of CD and maternal genetic effect of BWT ranged from -0.31 to -0.19 and the estimates for the four breeds were not significantly ($P \leq 0.05$) different from each other. The estimates were in agreement with values reported by Eriksson *et al*. (2004). The consistent low to moderate negative correlations between direct and maternal effects indicates a slight antagonism and to improve CD would require selection based on both components. High genetic correlation between direct genetic effects of CD and BWT and moderate correlation between direct genetic effects of CD and GL indicates that selection for reduced BWT and GL will decrease CD. This study showed that ANG and HER had more similar genetic correlations than the other two breeds.

Table 3. Estimated genetic correlations between calving difficulty (CD) and birth weight (BWT) and gestation length (GL) (95% highest posterior density interval in parenthesis).

Breed		**Genetic correlation**			
		Direct		**Maternal**	
	CD	**BWT**	**GL**	**BWT**	**GL**
Angus	Direct	0.67	0.25	-0.25	-0.09
		(0.58 to 0.72)	(0.18 to 0.32)	(-0.37 to -0.13)	(-0.22 to -0.02)
	Maternal	-0.12	0.01	0.41	0.26
		(-0.24 to 0.02)	(-0.07 to 0.10)	(0.34 to 0.44)	(0.19 to 0.31)
Charolais	Direct	0.64	0.34	-0.31	-0.20
		(0.55 to 0.70)	(0.18 to 0.44)	(-0.46 to -0.13)	(-0.35 to 0.04)
	Maternal	-0.19	-0.10	0.48	0.30
		(-0.31 to -0.07)	(-0.25 to 0.05)	(0.26 to 0.65)	(0.12 to 0.49)
Hereford	Direct	0.64	0.13	-0.19	-0.06
		(0.65 to 0.64)	(0.01 to 0.22)	(-0.31 to -0.09)	(-0.27 to 0.07)
	Maternal	-0.26	-0.03	0.39	0.21
		(-0.36 to -0.17)	(-0.17 to 0.07)	(0.33 to 0.44)	(0.08 to 0.26)
Limousin	Direct	0.69	0.44	-0.23	-0.20
		(0.66 to 0.83)	(0.33 to 0.56)	(-0.40 to -0.04)	(-0.46 to -0.02)
	Maternal	-0.15	-0.02	0.52	0.42
		(-0.32 to 0.04)	(-0.20 to 0.14)	(0.28 to 0.75)	(0.17 to 0.59)

CONCLUSIONS

Calving difficulty measured in ANG, CHR, HER and LIM were moderately heritable, with very little difference in their genetic parameters for CD and correlations with BWT and GL. Combining CD with positively correlated BWT and GL will improve the accuracy of genetic evaluation of CD in all four breeds. Birth weight and GL are highly correlated with CD and indicating that BWT and GL could be used as indirect selection criteria to improve CD in all four breeds. Genetic parameters obtained by combining linear with threshold models are more appropriate to use in the genetic evaluation of calving ease for BREEDPLAN.

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