Estimated Additive and Non-additive Breed Effects and Genetic Parameters for Ultrasound Scanned Traits of a Multi-breed Beef Population in Tropical Australia

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ABSTRACT: Direct additive, dominance and genetic parameters for ultrasound scan traits of a multi-breed population involving European, British, Sanga and Brahman breed types were estimated. A generalized ridge regression technique was used to eliminate high associations among some of the genetic effects in the model. Clear breed type effects were observed for all scanned traits. European breeds had negative and positive direct additive genetic effects for fat and eye muscle area, respectively in both heifers and bulls. British, Sanga and Brahman had positive direct additive effects for scan traits in heifers and bulls. Estimated heterosis of Brahman crosses were higher than non Brahman crosses for fat traits and ranged from 2% to 13%. The estimated heritabilities for rump fat, rib fat and eye muscle area of heifers were 0.36, 0.34 and 0.36 and for bulls 0.33, 0.23 and 0.39, respectively.
Keywords: additive effect; heterosis; multi-colinearity; BREEDPLAN

Introduction

Adaptive advantage of Brahman and Brahman cross cattle in the harsh tropical climatic conditions has lead to their domination in northern Australian beef industry. However, their lower fertility rate and poorer meat quality compared to *Bos taurus* cattle led to subsequent crossing with British, European and African breeds to improve the productive and reproductive performances in the northern Australian beef herds. This has also lead to the development of various composite breeds (Belmont Red, NAPCO composite and AACO composite) with the breed composition generally 50% *Bos taurus* and 50% adaptive breeds (African or *Bos indicus* breeds). Therefore, implementation of a genetic evaluation system to such a multi-breed population requires the estimation of genetic parameters while accounting for breed additive, maternal breed additive, dominance and maternal dominance effects However, many of the genetic effect variables are highly correlated (multi-colinearity) and this introduces numerical instability and inaccuracy into the estimates. Ridge regression has been used to overcome these muliti-colinearity problems (Hoerl, 1962). The objective of this work reported here was to estimate genetic effects and genetic parameters for scan traits of a multi-breed population after accounting for multi-colinearity of the genetic effects.

Materials and Methods

Data used for this study were submitted by breeders to the Belmont Red Breed Society for use in BREEDPLAN and came from a range of composite herds of varying breed composition. Real time ultrasound scan measurements included fat depth at the P8 (rump) site for bulls (BP8) and heifers (HP8), rib fat in bulls (BRF) and heifers (HRF) and eye muscle area in bulls (BEMA) and heifers (HEMA), with age at recording for all traits ranging from 300 to 800 days. Number of records for HP8, HRF, HEMA, BP8, BRF and BEMA were 4042, 4159, 4936, 2984, 2965 and 4697, respectively. Breed composition of the different composite breeds was identified from the pedigree and animals were classified into four breed types, namely the British (BRI), European (EUR), Sanga (SAN) and Brahman (BRA), based on their origin and similarities. Coefficients for direct additive effects were equal to the proportion of each breed in the breed composition of the calf. Direct dominance was estimated by assuming a linear function of the mean direct heterozygosities at all loci influencing the traits. Different heterosis effects for crosses with and without Brahman genotype were estimated. Maternal direct and maternal dominance effects were found to be not significant and were not included in further analyses. Given the limited number of records for each trait, epistatic loss was not considered in this analysis. Multi-colinearity between the genetic effect variables was assessed by calculating variance inflation factor (VIF) and condition index (CI) by using COLLINONT option of the PROC REG procedure of the SAS (SAS, 2011). Genetic parameters for scanned traits were estimated using a univariate linear animal model as given below,

$$Y_{ijkl} = cg_i + \beta_1 age_j + \beta_2 age_j^2 + \beta_3 hf_j + \beta_4\, age_k\,(sex_k) + \beta_5\, A + \beta_6\, D_B + \beta7\, D_{NB} + a_k + e_{ijkl}$$

where Y_{ijkl} is the trait measured in animal k in a fixed contemporary group i (cg_i), age_j is the age of dam j at calving deviated from five years of age, hf_j (heifer factor) is the additional dam age function fitted to improve the fit for offspring of dams less than 2.5 years old, age_k is the age of animal k nested within sex of animal k, β_1, β_2 and β_3 are the regression coefficients for linear, quadratic and heifer factor effects of dam age, β_4 is the regression coefficient for age of animal, β_5 is the partial regression coefficient representing the direct additive (breed) effect A, β_6 is the partial regression coefficient representing the dominance effect of crosses with Brahman genotype D_B, β_7 is the partial regression coefficient representing the dominance effect of crosses with non Brahman genotype D_{NB}, a_k is the random genetic effect of animal k and e_{ijkl} is the random error associated with each observation. The age was deviated from 500 days and contemporary groups were as defined by Graser *et al*. (2005). A generalized ridge regression was used in estimating the direct additive effect of breeds in which a constant K value was added to the diagonal of direct additive effect as given in Roso et al. (2005). Direct

additive effects, heterosis and genetic parameters were estimated in ASReml (Gilmour et al. (2009)).

Results and Discussion

Average breed type composition of animals for the six scan traits are given in Table 1. The proportion of Brahman breed was 44 to 46% of the total breed composition. The BRI and SAN breeds contributed 77% to 81% of the breed composition of the cattle, reflecting the Belmont Red predominance in the data.

Table 1. Average coefficient of breed type components for the six ultrasound scan traits.

Traits[1]	Average coefficient of breed types[2]			
	EUR	BRI	SAN	BRA
HP8	0.03	0.41	0.40	0.16
HRF	0.03	0.41	0.40	0.16
HEMA	0.03	0.41	0.39	0.17
BP8	0.04	0.41	0.41	0.14
BRF	0.04	0.41	0.41	0.13

[1] HP8 and BP8, P8 fat in heifers and bulls; HRF and BRF, rib fat in heifers and bulls; HEMA and BEMA, eye muscle area in heifers and bulls.
[2] EUR, European; BRI, British; SAN, Sanga; BRA, Brahman.

Accurate estimation of additive and non-additive effects requires a large number of crossbred groups and their purebred counterparts in a properly designed experiment (Sölkner, (1991)). A commercial multi-breed dataset, such as the one analyzed for this study, does not have all the desirable properties of a properly designed experiment. Nevertheless, the estimated additive and non-additive effects were in agreement with the previous studies (Cundiff and Gregory (1999); Cundiff et al. (1999)). Estimated direct breed additive genetic effects and heterosis for the fat traits in heifers and bulls are given in Table 2. Breed type differences were observed for the fat traits in heifers and bulls. The direct additive effect of EUR was negative and was significant ($P \leq 0.05$) for scan fat of heifers. In contrast, for scan fat traits, the direct additive effects of BRI, SAN and BRA were positive but not significant ($P > 0.05$). The direct additive effect of SAN was the highest among the four breed groups. As observed with the scanned fat traits in heifers, the direct additive effect of EUR decreased the scan fat content in bull while the BRI, SAN and BRA increased it. Except for the EUR effect on BP8, the direct additive effects of all breed groups on scan fat traits of bulls were not significant ($P > 0.05$). Estimates of direct genetic effects were in agreement with the findings of Cundiff and Gregory (1999) and Cundiff et al. (1999). They found that EUR were lower in fat content than BRI and BRI, SAN and BRA were more similar in their fat contents.

For eye muscle area in heifers, the direct additive effect of EUR and SAN were positive and for BRI and BRA were negative. For bulls, the direct additive effects of EUR and BRA were positive and of BRI and SAN were negative. However, except for EUR effect on HEMA, the direct additive effects of all breeds were not significant ($P > 0.05$). This study shows that including EUR increased growth and reduced fat thickness in these multi-breed calves.

Table 2. Estimated additive and non-additive genetic effects for ultrasound scanned traits (standard error in parenthesis)

Traits[1]	Direct additive of breed types[2]				Heterosis[3] (%)	
	EUR	BRI	SAN	BRA	NBR	BR
HP8,mm	-1.71 (0.70)	0.20 (0.70)	0.98 (0.75)	0.52 (0.71)	8.0	13.1
HRF,mm	-1.1 (0.43)	0.19 (0.43)	0.44 (0.46)	0.44 (0.44)	3.6	8.2
HEMA,cm^2	4.28 (1.90)	-2.61 (1.93)	0.27 (2.09)	-1.94 (1.91)	3.2	4.1
BP8,mm	-0.94 (0.39)	0.13 (0.24)	0.07 (0.25)	0.01 (0.24)	-3.8	-4.5
BRF, mm	-0.60 (0.32)	0.10 (0.32)	0.42 (0.34)	0.08 (0.33)	1.9	3.6
BEMA,cm^2	3.08 (1.81)	-2.59 (1.79)	-1.11 (1.89)	0.63 (1.67)	8.5	8.1

[1] See Table 1.
[2] See Table 1.
[3] NBR, crosses without Brahman genotype; BR, crosses with Brahman genotype.

Estimated heterosis for the scan traits were higher for crosses with Brahman genotypes than crosses with non Brahman genotypes. Except for the crosses with non Brahman genotypes, the estimates were in agreement with the value of 10.1% reported by Marshall (1994) for crosses involving *Bos tarus and Bos indicus* cattle in a tropical environment. Estimated heterosis for scan fat traits of bulls was lower than those of heifers indicating the bulls were leaner than heifers at the time of recording. Estimated heterosis for HEMA was in agreement with the estimate of 4.1% obtained by Marshall (1994). However, the estimated heterosis for BEMA was higher than the value reported by Marshall (1994).

Estimated heritabilities and the genetic correlations of the six scan traits are given in Table 3. All ultrasound scanned traits of heifers and bulls were moderately heritable with estimated heritability ranging from 0.23 to 0.39. Estimated heritabilities for the fat traits were lower than those for temperate breeds and higher than those of tropically adapted breeds reported by Johnston et al. (2003). The genetic correlations between P8 fat and rib were high for both heifers and bulls. The genetic correlation between the P8 fat and rib fat of heifers and bulls were 0.88 and 0.80, respectively. They were both very similar to the estimate of 0.82 reported by Johnston et al. (2003) for P8 and rib fats in tropically adapted breeds. The P8 fat and rib

fat measured in heifers were also highly correlated with the respective traits measured in bulls. However, the non-unity correlation between them suggests that fat traits measured in heifers and bulls need to be analyzed separately. The genetic correlation between scanned fat traits of heifers and bulls and eye muscle areas were low, except between HRF and HEMA in bulls. Very low genetic correlation between fat traits and eye muscle areas were also reported by Johnston et al. (2003).

Table 3. Estimated heritabilities (diagonal) and the genetic correlations (above diagonal) for ultrasound scanned traits in heifers and bulls.

Traits[1]	HP8	HRF	HEMA	BP8	BRF	BEMA
HP8	0.36 (0.06)	0.88 (0.11)	0.03 (0.10)	0.81 (0.11)	0.79 (0.10)	0.02 (0.11)
HRF		0.34 (0.05)	0.03 (0.10)	0.69 (0.11)	0.87 (0.10)	0.00 (0.11)
HEMA			0.36 (0.05)	-0.11 (0.10)	0.23 (0.11)	0.82 (0.10)
BP8				0.33 (0.06)	0.80 (0.06)	0.06 (0.12)
BRF					0.23 (0.06)	0.24 (0.10)
BEMA						0.39 (0.10)

[1] See Table 1.

Given the significant breed type effects on ultrasound scanned traits of heifers and bulls in this study, it is important that appropriate genetic groups are fitted in BREEDPLAN to account for these breed effects. Furthermore, the non-additive effects also need to be modelled in BREEDPLAN to adjust the phenotypic records for these effects. Estimated breeding values along with predicted progeny hybrid vigour will be required to make selection decisions in multi-breed populations.

Conclusions

Breed type effects and heterosis were observed for ultrasound scanned traits of multi-breed beef cattle. Furthermore, moderate heritability for all traits after adjusting for the direct additive and dominance effects confirmed that scan traits could be improved through selection. Estimated additive and non-additive effects and genetic parameters need to be incorporated in the BREEDPLAN evaluation to improve the productivity of Northern Australian beef herds.

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