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Describing Variation in Carcass Quality Traits of Crossbred Cattle

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Abstract: In order to investigate variation in carcass quality traits, during a four-year period, mature Hereford cows (637) were mated to 97 sires from seven breeds (Jersey, Wagyu, Angus, Hereford, South Devon, Limousin and Belgian Blue), resulting in 1144 calves. Carcass production traits (carcass weight = HCWt, fat depth = P8, eye muscle area = EMA, intramuscular fat = IMF) were obtained from these cattle that constitute the Australia's Southern Crossbreeding Project. Data were analysed using multi-variate sire model containing fixed effects of sex, sire breed, slaughter age nested within sexes. Random effects were sire, dam, management (location-year-post-weaning groups) and environmental effects. HCWt of South Devon, Belgian Blue, Limousin and unexpectedly, Angus were the heaviest on the average. Hereford calves were intermediate and Jersey and Wagyu were lighter on the average than others. Carcasses of the Belgian Blue and Limousin had low P8 and IMF, carcasses of Hereford and South Devon were intermediate and Angus, Jersey and Wagyu had high P8 and IMF. Management group effects were greatest especially for EMA and IMF. The sire variation was about 6, 6, 4 and 2% of total variation for HCWt, P8, EMA and IMF. Heritability ranged from 0.20 to 0.37 (carcass weight). The genetic correlation between the two fat depots was not as high (0.18) as expected. Results from this study suggest that strategies to increase genetic potential for HCWt would increase the genetic potential for EMA but may reduce marbling and tend to slightly increase P8. All phenotypic correlations were positive, although not large.

Key words: Crossbred cattle, multi-trait model, carcass quality traits

INTRODUCTION

Beef producers face the challenge of using diverse resources to produce cattle that are profitable to all segments of the industry and to produce meat products that target consumer demand (Capps *et al.*, 2006; Mennecke *et al.*, 2007). Moreover, a better understanding of the relationship between fat and meat quality in relation to production characteristics of beef breeds would enhance income sustainability. Therefore, producers and breeders need information from a broad spectrum of marketing end points to implement effective breeding and management plans (Gaden and Peter, 2008; Parnell, 2007). The information required includes genetic and non-genetic (co)variation for all economically important traits of interest. Specifically, producers utilise both between and within breed genetic variation and management strategies to produce a live calf and then a high quality carcass. Practically, there are some advantages in estimating variance components from a multi-trait model instead of separate uni-variate models, especially in breeding programme. Generally, carcass quality traits used

for animal breeding programs are correlated, so that considering only one trait will likely result in a physiological imbalance for instance (Eriksson, 2003; Kahi *et al.*, 2007; Liinamo, 2000; Wolfová *et al.*, 2005). Therefore, it makes sense to analyse those traits together. The objective of this study was to present (co)variance components, through the multi-trait model, that would summarise the primary information of importance to beef producers.

MATERIALS AND METHODS

Animals and management: The data from the Southern Crossbreeding Project (1994-2000) have been used for this research. The Southern Crossbreeding Project was designed to characterise between and within breed variations with the aim of improving utilisation of existing breeds for meeting a range of market specifications in southern Australia. It used a topcross design and has been described by Pitchford *et al.* (2002). Purebred Hereford cows (581) were artificially inciminated with semen of sire breeds Angus (11 sires), Belgian Blue

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(16 sires), Hereford (10 sires), Jersey (12 sires), Limousin (16 sires), South Devon (15 sires) and Wagyu (17 sires) over four years. There were generally 12-15 progeny per sire, with an average of 13 calves per sire and 14 sires per breed. Sires were generally used in one year only with a few exceptions, whereas dams were commonly used for more than one year. The number of sires per breed used in this project was lower but there were approximately twice the number of progeny per sire than in the United States Department of Agriculture Germ Plasm Evaluation in Cattle Project (Cundiff *et al.*, 2008; MacNeil and Northcutt, 2008). All cows were 3 years or older when calving, so no maiden heifers were used. The average number of calves per dam in this project was under 2, with a range of 1-4 calves. They were artificially inseminated in June and July and if they did not conceive after two insemination attempts they were removed from the experiment until the next mating.

The research used data from 1141 of the heifers (569) and steers (572) born in autumn (average birth date 3rd April). The cattle in this project were raised in a typical Mediterranean environment characterized by cool, wet winters and hot, dry summers. Pasture growth generally occurs between April and November. Calves were born when there was minimal pasture availability (average birth date 3rd April). Live calves were also tagged and castrated (bulls only) within three days of birth. Additional measurements (e.g., height) were also taken but are not reported in this study. Calves were born on two South Australian properties (Struan and nearby Wandilo) in three management groups. Calves were weaned in summer (mid December-early January) at 250-300 days of age, each year, i.e., in most years the last weight represented a weaning weight. Some variation in weaning dates was necessitated by seasonal conditions. At weaning, all calves born at Wandilo were transferred to Struan. Calves stayed with their dams on pasture until weaning, were pasture fed until 12-18 months of age and then transported to a commercial feedlot for finishing and randomly allocated to between one and three post-weaning management groups, except the 1997 steers which, after a good pasture season in 1998, reached marketable weight without requiring grain finishing (Pitchford *et al.*, 2002). In the feedlot, they were fed a minimum of 60% grain (various, but primarily barley) with approximately 12 MJ kg^{-1} DM ME and 13% protein for 70-90 days (heifers) or 150-180 days (steers). The exception to this was the 1997 steers that, after a good pasture season in 1998, reached marketable weights without requiring grain finishing. All cattle were slaughtered commercially at abattoirs and they were processed depending on which market they were to be sent.

Carcass quality traits: Calves were slaughtered when the majority of heifer carcasses were more than 200 kg (average 16 month) and steer carcasses more than 300 kg (average 23 month) at various commercial abattoirs throughout Southeastern Australia (Table 1). They were assessed for hot standard carcass weight (HSCW) based on a standard trim (AUSMEAT®, 1995), fat depth over the rump at the P8 position (P8) as described by Arthur *et al.* (2001), eye (loin) muscle area (EMA) at the site of quartering and various other traits not included in this study.

Number of observations 572, 569 and 1141 for steers, heifers and pooled dataset [a]HCWt = Hot standard carcass weight (kg), [a]P8 = Fat depth at P8 site (mm), [a]EMA = Eye muscle area (cm²), [a]IMF = Intramuscular fat content (%), [b]standard deviation.

Throughout the project there was some variation in site of quartering. Most carcasses were quartered at the 10-11th rib so when done otherwise, they were adjusted to the expected area at that site. Adjustment equations have been developed (Rutley *et al.*, 2002) to cope with this. Equation 1 was developed using ten diverse breed combinations ranging from purebred Jersey to purebred Limousin. The shape of the muscle did not differ between breeds so a simple logarithmic function was sufficient. The result is that the area at the 8/9th site is 78% of the area of the area at the 10/11th site, 9/10th is 91%, 11/12th is 104%, 12/13th is 102%.

$$Ln(EMA) = 0.772 + 0.643(site) - 0.0288(site)^2$$

Statistical analysis: Data were analysed using ASREML version 1.10 following (Gilmour *et al.*, 2002). The aim was to develop multivariate mixed model was developed for the four traits (HCWt, P8, EMA and IMF). The carcass traits were log-transformed because of a scale effect on the variance. The following mixed model was fitted using REML:

$$Ln(carcass) = X\tau + Zu + e$$

Table 1: Description of traits and summary of data

Carcass quality traits	Mean	Median	SD[b]
Heifer			
HCWt	218	216	32
P8	10	10	4
EMA	62	65	21
IMF	4	4	2
Slaughter age	495	483	75
Steer			
HCWt[a]	324	328	51
P8[a]	14	14	5
EMA[a]	74	74	15
IMF[a]	4	4	3
Slaughter age	684	720	103

where, τ is the vector of fixed effects, u is the vector of random effect and e is the vector of random residual effect (temporary environmental effect or measurement error), NID $(0, \sigma^2)$.

Fixed effects were sex, sire breed, slaughter age nested within sexes. The model considered partitions the variability in each carcass quality trait into its genetic (sire), maternal, management groups and environmental components. For carcass traits, permanent environment is confounded with the temporary environment because there is only one measurement for each animal, therefore it is called environmental component. Management group was a function of year of birth (1994-97), birth location (Struan or Wandilo) and management (location-year-post-weaning groups) with a total of 16 combinations. Thus, management group is similar to a classic herd/year effect, but includes sex effects as well since male and female calves were managed quite differently post-weaning. Initial analysis showed the majority of the management group variation is variation between years, but pre-weaning location was still important for some traits. Post-weaning location was generally not important and so was not included in the definition of management groups. The advantage of fitting management group as a random effect is being able to estimate covariances between traits.

RESULTS AND DISCUSSION

Breed effects: Sire breed, sex and slaughter age nested within sex were significant for all traits (Table 2). Maternal effects were low for carcass traits. Management group (non-genetic) effects were greatest especially for EMA and IMF.

Predictably, HCWt of South Devon, Belgian Blue and Limousin (as late-maturing breeds) and unexpectedly, Angus were the heaviest on the average (Fig. 1). It also shown that Hereford calves were intermediate and Jersey and Wagyu (as early-maturing breeds) were lighter on the average than others (Fig. 1). With respect to fat traits, roughly three groups were detected. First, carcasses of the Belgian Blue and Limousin had low P8 and IMF, second; carcasses of Hereford and South Devon were intermediate and third; Angus, Jersey and Wagyu had high P8 and IMF. Interesting results observed for Angus crosses in where they exhibited highest P8, IMF as well as HCWt amongst breeds (Fig. 1).

Therefore, it has shown that at the point of slaughter, heavier carcasses tended to have greater EMA and less P8 and IMF than lighter carcasses. Koch *et al.* (1982) and Gregory *et al.* (1994) stated that carcasses of large-framed steers (South Devon, Belgian Blue and Limousin crosses)

Table 2: Estimated mean and standard error of the fixed effects derived from the multi-trait sire model

Effects	HCWt	P8	EMA	IMF
Constant	5.77±0.02	2.72±0.08	4.24±0.03	1.36±0.01
Sex. slage (Heifer-steer)[a]***	0.04±0.03	0.36±0.04	1.20±0.08	1.47±0.13
Sex***				
Sex (Steer)	0.42±0.02	0.56±0.03	0.56±0.08	-0.22±0.12
Sex (Heifer)	-0.41±0.01	-0.29±0.02	-0.13±0.01	-0.29±0.02
Sire breed [a]***				
Jersey	-0.13±0.02	-0.12±0.06	-0.06±0.02	0.23±0.05
Wagyu	-0.10±0.02	-0.06±0.06	0.01±0.02	0.17±0.05
Angus	0.05±0.02	0.15±0.06	0.05±0.02	0.22±0.05
South Devon	0.05±0.02	-0.21±0.06	0.11±0.02	0.04±0.05
Limousin	0.04±0.02	-0.18±0.06	0.15±0.02	-0.15±0.05
Belgian Blue	0.07±0.02	-0.38±0.06	0.21±0.02	-0.22±0.05

[a]Sex. sla. age, slaughter age nested within sex, [b] Management groups include location, year and post-weaning groups combination, ***p<0.001
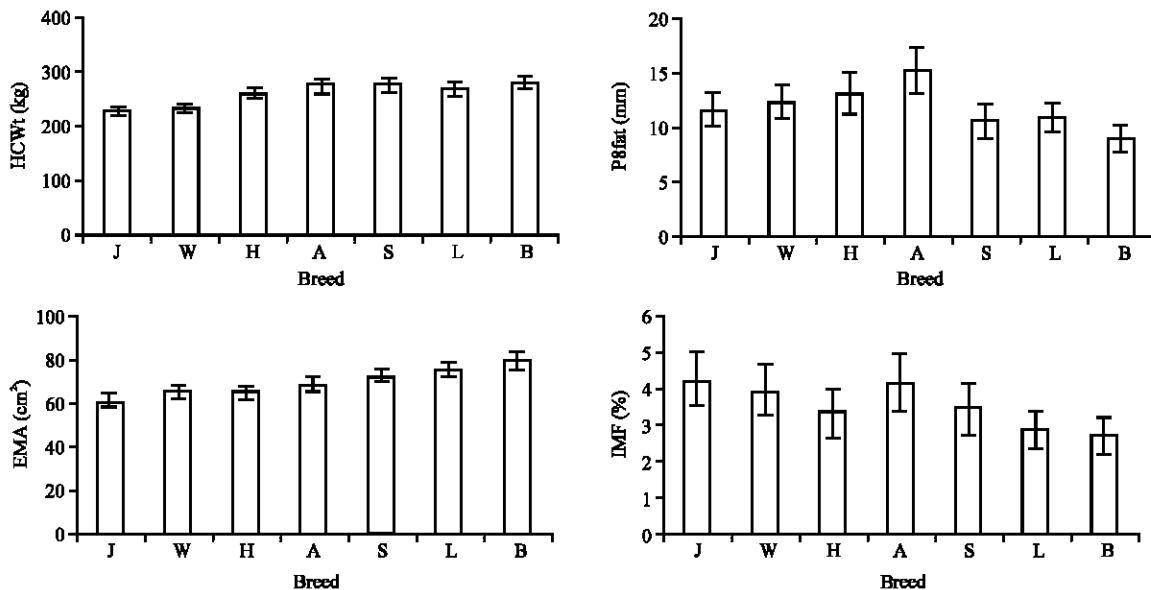

Fig. 1: Median and confidence intervals (CI, 95%) of carcass quality traits for seven sire breeds
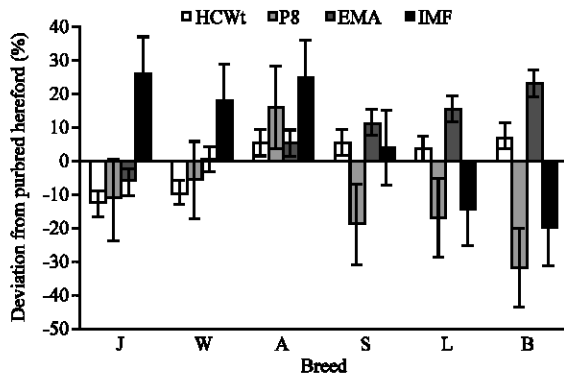
Fig. 2: Deviation of the median of carcass quality traits for six crossbreds from purebred Hereford

Fig. 3: Variance components of carcass traits as the proportion of total variance derived from the sire model

Table 3: Estimated variances (on diagonal) and covariances (off diagonal) components for carcass traits obtained from the multi-trait sire carcass model

Variables	11	12	13	14	21	22	23	24	31	32	33	34	41	42	43	44
HCWt (kg)																
11. Sire	✓															
12. Maternal		✓														
13. Management			✓													
14. Environment[a]				✓												
P8 (mm)																
21. Sire	✓				✓											
22. Maternal		✓				✓										
23. Management			✓				✓									
24. Environment				✓				✓								
EMA (cm²)																
31. Sire	✓				✓				✓							
32. Maternal		✓				✓				✓						
33. Management			✓				✓				✓					
34. Environment				✓				✓				✓				
IMF (%)																
41. Sire	✓				✓				✓				✓			
42. Maternal		✓				✓				✓				✓		
43. Management			✓				✓				✓				✓	
44. Environment				✓				✓				✓				✓

[a]For carcass traits environment component = PE+TE

had less fat at the 12/13th rib interface than carcasses of either smaller medium-framed steers (i.e., Angus, Hereford, Jersey and Wagyu crosses) at any given feeding period. Marshall (1994) indicated that generally, smaller-framed breeds of cattle tend to yield carcasses with higher degrees of marbling on an age-constant basis. This was due to more muscling and less fat in the late-maturing breeds. In the analysis used herein, much of the difference among carcass traits in muscle mass and fat traits may have been due to breed effects.

Comparing deviation of the median of carcass quality traits for six crossbreds from purebred Hereford, Angus cross calves were higher for P8 fat than Hereford. Jersey had highest and Belgian blue lowest IMF deviations from Hereford (Fig. 2). On the contrary, as might be expected, the Belgian blue had the highest and Jersey the lowest EMA deviations from Hereford.
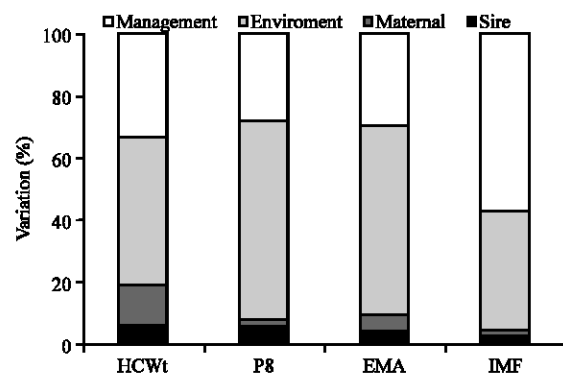
Genetic and non-genetic (co)variance components:
Table 3 presents 40 (co)variance components that were able to be fitted by the multi-trait sire model. Multi-trait models were postulated for sire, maternal, environmental and management effects. Fortunately, in all cases the data support inclusion of all terms. The sire variation represented in Fig. 3 was about 6, 6, 4 and 2% of total variation. The sire component describes 1/4 of the genetic variance. The additive variation ranged from 8 to 26% of all variation of carcass quality traits (Fig. 3). Overall, 81-96% of the total variances in carcass quality traits were non-genetic. In the analysis used herein, environmental variation has been partitioned into between and within (residual) management groups. Management variation was considerable and accounted for about 28-57% of the total variance (Fig. 3). It was largely due to yearly and seasonal variations in pasture availability (e.g., 1995 calves were 50 kg heavier at weaning than the 1994 calves, not reported), age of entry into feedlot and time on feed. Over half of the total variance was residual or error variance for carcass quality traits. Table 4 shows the sire variance components for carcass traits derived from the multivariate model.

Correlations: All phenotypic correlations were positive, although not large. HCWt was lowly correlated with IMF, moderately correlated with P8. The phenotypic correlations between HCWt and EMA was moderate and large (0.61), in agreement with the finding of Lamb *et al.* (1990) and Owens and Gardner (2000) who observed that longissimus muscle area increased as carcass weight increased. P8 was lowly correlated with IMF and moderately correlated with EMA (Table 4). EMA was lowly correlated with IMF.

Table 4: Estimates of heritabilities (h²), phenotypic (r_P) and genetic (r_G) correlations between carcass quality traits derived from the multi-traits sire model

Carcass traits	HCWt	P8	EMA	IMF
HCWt	0.37	0.38	0.61	0.26
P8	-0.12	0.31	0.42	0.13
EMA	0.73	-0.08	0.20	0.23
IMF	-0.40	0.26	-0.43	0.20

Table 5: Estimates of maternal, environmental and management correlations between carcass quality traits derived from the multi-traits sire model

Carcass traits	HCWt	P8	EMA	IMF
HCWt	0.19	0.25	0.46	0.04
P8	0.72	0.03	0.12	0.10
EMA	0.91	0.82	0.08	0.00
IMF	0.84	0.21	0.60	0.05

Maternal effect on diagonal, Environmental correlations above diagonal, Management correlations below diagonal (bold)

The most notable genetic relationship was between HCWt and EMA which are highly genetically correlated (0.72), indicating that selection for higher carcass weight should also lead to greater EMA. The genetic correlation between HCWt and P8 fat depth was low and negative (-0.14). Shanks *et al.* (2001) also found similar correlation on age-constant basis. Based on studies reviewed by Koots *et al.* (1994b), Marshall (1994) and Thonney (2003) there is considerable evidence that the genetic correlation between HCWt and P8 fat depth is positive in British cattle on an age-constant basis. The genetic correlation between HCWt and IMF was (-0.40, Table 4), different to that reported by Koots *et al.* (1994b) for carcass weight and marbling score (0.15). The genetic correlation between two fat depots; P8 and IMF, was not as high (0.18) as expected. It was similar to other reports by American Gregory *et al.* (1994), Ríos-Utrera *et al.* (2005), Japanese Oikawa *et al.* (2000) and Australian Reverter *et al.* (2000) beef cattle breeds. The correlation is positive, but not strong suggesting that it is possible to select within breeds for low P8 fat depth to minimize wastage and high IMF to maximize meat quality, thus causing a change in fat distribution rather than total fatness *per se.* Pitchford *et al.* (2002) with the same data set as that herein with respect to relationships between P8 and IMF implied that there appears to be prospect to select breed combinations that enable IMF to be maximized relative to subcutaneous. One of the challenges in cattle production is to maximise deposition of IMF while minimising deposition of subcutaneous (P8) fat. This is because of the effect of IMF on flavour and juiciness leading to significant premiums paid in some markets, but while some fat cover is important, excessive P8 fat is essentially a waste product with low value and time consuming to remove. EMA was negatively genetically correlated with IMF (-0.43). The genetic correlations between carcass longissimus muscle area and carcass fat thickness was -0.08 (Table 4). The genetic correlations between EMA and P8 fat were -0.08 (Table 4) tend to agree with several studies conducted at a constant age, whereas other studies have reported stronger negative relationships between EMA and P8 fat (Bergen *et al.*, 2006, 2005; Koots *et al.*, 1994b; Marshall, 1994). Moser *et al.* (1998) cited an estimate for the relationship between longissimus muscle area and fat depth, in Brangus seed stock, of

-0.05. This indicates that selecting for a decrease in fat thickness would correspond to selection for an increase in EMA. However, this result was lower than that of reported by Koots *et al.* (1994b). Arnold *et al.* (1991) shown that selection for a decrease in fat thickness was related to larger EMA and a reduction in marbling. Therefore, it is important to take more than one carcass trait into consideration when selecting sires for genetic improvement. This result exhibits a negative genetic relationship (-0.43) between EMA and IMF in agreement with the literature (Koots *et al.*, 1994b; Marshall, 1994; Van der Werf *et al.*, 1998), but Lamb *et al.* (1990) and Shanks *et al.* (2001) found positive values. Studies based on constant quality grade (Brackelsberg *et al.*, 1971; Van Wijk *et al.*, 2005), or weight (Arnold and Bennett, 1991) also reported negative correlations between EMA and marbling score. However, at a fat-constant end point, Gilbert *et al.* (1993) and Wulf *et al.* (1996) found positive correlations. The negative genetic correlation between these traits indicates that high marbling is generally associated with unfavourable genetics for carcass muscularity. However, there still seems an opportunity for within breed selection for high EMA and IMF to simultaneously increase meat production and quality.

Management correlations were very high for most traits (except between P8 and IMF). In general, management group correlations (Table 5) between carcass traits were generally higher than residual correlations. HCWt had the highest management association among carcass traits with EMA (0.91). There was a high positive management correlation (0.82) observed between P8 and EMA (Table 5). The value and direction of the correlation between EMA and IMF for management component (0.60) was different from that in the genetic correlation (-0.43). The management correlation (Table 4) between IMF and P8 was only 0.21, indicating that while positive, it is sufficiently low for there to be substantial opportunity to manage groups of cattle to maximise IMF relative to P8. In addition, there was substantial variation in IMF (Table 2), more than double the between breed variation indicating the importance of management for maximising IMF. That said, it is likely that variation in age at slaughter played a significant role in this. While the management correlation between the fat depots was lower than expected, two

correlations that were higher than expected were between HSCW and fat traits (P8 and IMF) (0.72 and 0.84, respectively) (Table 4).

Heritability (h^2) on diagonal, phenotypic correlations above diagonal, genetic correlations below diagonal. Market specifications in Australia are primarily defined by HSCW and P8 fat depth and the calves were managed to maximise return, so that the majority fell within the specification. Thus, it is perhaps not surprising that the management group correlation between HSCW and fat traits (P8 and IMF) were so high. In addition to IMF, the management variance was also high for HSCW. However, management group accounted for a relatively small proportion of variation in P8 and EMA where environmental variation was substantial indicating less control over these traits.

Koch *et al.* (1995) noticed that slaughter end point can alter the expression of genetic and environmental differences; however, Shanks *et al.* (2001) observed that in general, adjustment to different slaughter end points had minor effects on phenotypic correlations. They also concluded that genetic evaluations of carcass traits conducted on an age-, weight-, or marbling-constant basis produced similar rankings. Amer *et al.* (1994), Bergen *et al.* (2006), Rumph *et al.* (2007), Van Groningen *et al.* (2006), Wilton and Goddard (1996) and Wilton (2003) concluded that when management variables are optimized, economic weights are equivalent regardless of the end point considered. This means that economic weights and selection indexes can be conveniently calculated for age constant end points even though commercial production may use weight or fat depth constant slaughter end points.

Beef cattle grow, develop, mature and fatten at different chronological ages and the differences among individuals are often discussed in terms of physiological maturity (e.g., Block *et al.*, 2001; Berg and Butterfield, 1976). Casas and Cundiff (2006), Santos *et al.* (2008) and Piles *et al.* (2000) suggested that breeds might differ in carcass composition and meat quality at the same market weight due to differences in degree of maturity. Therefore, further investigation seems necessary to determine the effects of maturity or mature size on the correlation between carcass traits.

It should be noted that consistent estimation of genetic parameters requires good data, i.e., sufficient amounts of reliable measurements and good pedigree structure (Meyer and Kirkpatrick, 2004). The wide range of reported estimates seems to indicate that the genetic relationships among carcass traits may vary with the breed or population, or simply may be due to sampling variance because most studies, including this study, have

relatively few observations. Differences in the model used and the use of age- weight- and fat-constant end points may have caused these differences. Therefore, the genetic relationships reported in other studies are hardly extrapolated to the current discussion. Genetic comparisons are only logical if the cattle are treated similarly. Overall, management relationships among carcass traits reported herein were higher than the genetic associations among them. However, estimates of genetic correlations for carcass traits suffered from the small number of records available for these traits and problems associated with a sample of sires that might not have been fully representative of the population for these traits. Hence, estimates involving these traits should hence be regarded with caution and estimation should be repeated when more data for these traits become available.

Heritability: The estimate of heritability for HCWt herein agrees with those from Marshall (1994), who reported an average estimate of 0.41 in a review of earlier study, with estimates ranging from 0.31-0.68. However, compared to Koots *et al.* (1994a), the heritability estimate for carcass traits was higher for HCWt (37 versus 23%) and slightly lower for fat depth (31 versus 44%). The heritability for EMA (0.20) was in agreement with several earlier findings as reported by Marshall (1994) and Shanks *et al.* (2001). However, moderate to high range estimates have been reported by AAABG (2004), Bertrand *et al.* (2001) and Utrera *et al.* (2004). Koots *et al.* (1994a) reported heritability of rib eye area as 42% and Wheeler *et al.* (2001) estimates on longissimus area was 69%, are values significantly higher than the heritability of eye muscle area (20%) reported herein (Table 4). While the site of sampling could be the cause of major differences between studies, the differences may also highlight huge variation in carcass trait estimates as across breeds pooled between *Bos indicus* and *Bos taurus* (Bonilha *et al.*, 2008; Crews *et al.*, 2003; Hoque *et al.*, 2009; Koots *et al.*, 1994a; Riley *et al.*, 2002; Smith *et al.*, 2007; Wheeler *et al.*, 2001) rather than as across breeds pooled between only specific Bos taurus (as herein).

The heritability estimate (Table 4) for P8 (0.31) was similar to those reported by Gregory *et al.* (1995) and Robinson *et al.* (1998). However, it was smaller than some estimates reported by Koots *et al.* (1994a), Marshall (1994), Bertrand *et al.* (2001) and AAABG (2004). For IMF, the heritability estimate (0.20) was generally smaller than marbling score, shown by Koots *et al.* (1994a), Marshall (1994), Bertrand *et al.* (2001) and AAABG (2004). The heritability estimate for IMF in this study agreed favourably with those published for marbling score by Woodward *et al.* (1992) and Robinson *et al.* (1998) who

reported a heritability of 0.23 and 0.15, respectively. Estimates of genetic parameters of marbling are dependent upon the method used to measure the trait, the method of finishing cattle and age and weight at the time of measurement (Ibi *et al.*, 2005).

CONCLUSION

Today in the beef industry, a major goal for beef cattle breeding seems to be to maximize muscle tissue and minimize fat. To this end, any strategies that maximize profit need to balance genetic potential for carcass yield with adverse correlated changes in the quality of the product. Therefore, it is important to take more than one carcass trait into consideration in the analysis of carcass quality when selecting sires for genetic improvement. In general, selection for carcass weight, carcass fatness, longissimus muscle area and marbling could yield genetic progress. Selection for improved carcass quality might be possible without sacrificing lean growth. Improvement can be made in multiple traits that are generally regarded as antagonistic. Results from this study suggest that strategies to increase genetic potential for HCWt, which is the greatest determinant of carcass value at a constant age at slaughter, would increase the genetic potential for EMA but may reduce marbling and tend to slightly increase P8. A slight genetic antagonism may exist between EMA and marbling. This report has partitioned variation in four key production traits into genetic (sire), maternal, management groups and environmental components. In addition, correlations between the traits have been presented. These (co)variances provide tools for those making beef cattle management decisions for maximising number of calves targeting specific markets. It should be clear from this study that there is large variation in all four traits studied. The carcass traits generally had large management variation demonstrating opportunities for managing mobs to target specific markets.

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