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GENETIC AND PHENOTYPIC CHARACTERIZATION OF MSA INDEX AND ITS ASSOCIATION WITH CARCASE AND MEAT QUALITY TRAITS IN ANGUS AND BRAHMAN CATTLE

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SUMMARY

MSA Index (MSA_I) predicts overall eating quality of a carcase from predictions of tenderness, juiciness, flavour and overall liking based on extensive consumer taste panel studies. Prices paid by processors for MSA graded meat are consistently higher than non-MSA graded cattle. There is significant industry pressure to determine the level of genetic control for MSA_I. This study used data from Angus (ANGS) and Brahman (BRAH) BIN cattle to estimate genetic parameters for MSA_I and their genetic and phenotypic relationships with key carcase and meat quality traits. Heritabilities for MSA_I were 0.50±0.09 and 0.49±0.16 in ANGS and BRAH cattle, respectively. In ANGS, genetic correlations between MSA_I and carcase weight (CWT), carcase rump fat (CP8), ossification score (OSS), MSA marble score (MSA_M), shear force (SF) and meat colour L (Col_L) were 0.41±0.12, 0.02±0.15, -0.22±0.18, 0.96±0.02, -0.33±0.19 and 0.40±0.16, respectively and in BRAH, were 0.12±0.21, 0.19±0.24, -0.51±0.20, 0.94±0.05, -0.18±0.25 and 0.46±0.21. Similar trends were observed in the correlations between MSA_I and carcase and meat quality traits in both breeds. This study showed that MSA_I has a very high genetic association with MSA_M and, to a lesser extent, OSS in both breeds. Selecting for higher MSA_M and lower OSS will genetically improve MSA_I of carcases of ANGS and BRAH cattle, and the addition of MSA_I as an additional trait in the evaluation would contribute almost no additional information about meat quality or value.

INTRODUCTION

Eating quality is important if the beef industry in Australia is to remain competitive in the world and domestic markets. Eating quality refers to the compositional quality and the palatability of meat, and in the 1990s, consistency of beef eating quality was identified as a key issue for marketing Australian beef (Bindon 2001). Beef consumers were unsure of how to identify beef of acceptable quality and this led to a decline in domestic beef consumption (Polkinghorne *et al.* 2008). Furthermore, concerns with the fat content of beef, and associated health implications, and a decline in understanding of beef cuts, cooking methods and an inability to predict quality from product appearance also impacted on demand for beef products on the domestic market. Meat and Livestock Australia (MLA) developed the Meat Standards Australia (MSA) grading system to provide consumers with assurance of eating quality (Watson *et al.* 2008). MSA eating quality scores are a combination of consumer assessed tenderness, juiciness, flavour and overall liking of meat products. Initially, the grading system assigned an eating quality score to specific muscle portions cooked by defined methods (Watson *et al.* 2008). Subsequently, a single number and standard national measure called the MSA Index (MSA_I) was developed to predict overall eating quality of a whole carcase (Thompson 2014).

The MSA model predicts the eating quality of 39 cuts in a carcase using measurements collected by accredited MSA graders (MSA Index, Meat and Livestock Australia, 2014). MSA_I is a weighted average of these scores for the 39 MSA cuts for the most common corresponding cooking method, ranging from 30 to 80 and expressed to 2 decimal places, to represent the

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[1] AGBU is a joint venture of the NSW Department of Primary Industries and University of New England

predicted eating quality of a whole carcase. The MSA_I is independent of any processing inputs and is calculated using only attributes influenced by pre-slaughter factors. It is a benchmark which can be used across all processors, geographic regions and over time, and reflects the impact on eating quality of management, environmental and genetic differences between cattle at the point of slaughter (MSA Index, Meat and Livestock Australia, 2014). Currently, over 40 processors are grading MSA beef, with prices received for MSA graded g cattle being consistently higher than non-MSA cattle (Southern Beef Technology services, 2015). There has been a recent request from industry to examine genetic and non-genetic influences on MSA_I and genetic relationships between MSA_I and key carcase and meat quality traits. This study aimed to estimate these in temperate and tropical breeds.

MATERIALS AND METHODS

Carcase and meat quality data used for this study were recorded as part of the Angus (ANGS) Sire Benchmarking Program and Brahman (BRAH) beef information nucleus (BIN) project up to June 2016. ANGS steers were grain fed with a ration containing an energy level of 12MJ/kg for 300 days and Brahman steers were finished on pasture. ANGS and BRAH steers were killed at mean age of 794 and 963 days, respectively. Hot carcase weight and hot P8 fat depth were recorded before the carcase entered the chiller. Carcases were dressed according to AUSMEAT standard specifications (AUS-MEAT 2005) while limiting the subcutaneous trimming to not influence the fat depth measurement at the P8 or 12/13th rib measurements sites. Carcase weight (CWT), rump P8 fat (CP8), MSA marble scores (MSA_M), and ossification scores (OSS) were measured by MSA certified graders. Samples were collected from the *Longissimus dorsi* and transported to a laboratory where meat colour was recorded as Minolta l (COL_L) and shear force (SF) was measured as described by Perry et al. (2001). MSA_I was calculated as the weighted average of the predicted eating quality scores using the empirical modelling described by Thompson (2014). Inputs to this calculation included hormone growth promotant status, milk fed vealer status, sale yard status, sex, *Bos indicus* content, hump height, CWT, OSS, 12/13th rib fat and MSA_M. The number of records and descriptive statistics for all traits are given in Table 1. The number of sires with progeny recorded differed across the six traits, ranging from 83 to 123 for ANGS and 72 to 80 for BRAH.

For each trait, records that were more than three standard deviations from the mean were removed as outliers. A univariate linear animal model was used to estimate genetic parameters for carcase and meat quality traits in both breeds:

$$Y_{ik} = cg_i + \beta_1 \text{ age/weight}_k + \beta_2 (\text{age/weight}_k)^2 + a_k + e_{ik}$$

Where Y_{ik} is the trait of interest of animal k in a fixed contemporary group i (cg_i), age/weight is age or weight of animal k, β_1, and β_2 are regression coefficients for linear and quadratic effects of age or weight of animal (included in models based on significant level), a_k is the random additive genetic effect of animal k and e_{ijk} is the random error associated with this prediction. Contemporary groups for all traits were defined based on protocols for carcase traits in the BREEDPLAN evaluation (Graser *et al.* 2005). Genetic variances, variance ratios and genetic correlations were estimated by restricted maximum likelihood (REML) using univariate and bivariate animal models, with three generations of pedigree, using WOMBAT (Meyer 2007).

RESULTS AND DISCUSSION

Raw means by trait and breed are presented in Table 1. Design of this study will not allow direct comparison of breeds. This is because BRAH and ANGS were subjected to different finishing regimes, slaughtered at different abattoirs, at different ages and graded by different graders at different quartering sites.

Table 1. Number of records and the descriptive statistics for carcase and meat quality data

Trait	Angus[1]					Brahman				
	No.	Mean	SD	Min	Max	No.	Mean	SD	Min	Max
Carcase traits										
CWT (kg)	1394	460.1	37.1	334.0	568.0	898	314.4	24.1	227.0	382.0
CP8 (mm)	1383	23.1	6.1	10.0	41.0	891	12.0	4.0	2.0	24.0
OSS (score)	1383	154.8	110.0	110.0	200.0	894	138.6	13.7	110.0	190.0
Meat quality traits										
MSA_I (score)	1349	65.1	1.7	60.0	69.9	629	53.7	1.7	49.5	58.5
MSA_M (score)	1382	515.2	115.6	160.0	880.0	886	267.2	67.5	120.0	490.0
SF (kg)	737	3.8	0.6	2.0	5.7	881	4.5	0.8	2.8	7.5
Col_L (score)	1384	42.7	2.8	35.7	50.3	891	38.3	2.6	30.5	46.2

[1] Design of this study will not allow direct comparison of breeds.

Estimated heritabilities for MSA_I and genetic and phenotypic correlations with carcase and meat quality traits are given in Table 2. Heritabilities were similar for MSA_I in both breeds (0.50 in ANGS and 0.49 in BRAH). Heritabilities for carcase and meat quality traits were moderate to high for both breeds. For ANGS, estimated heritability for MSA_M agreed with the value of 0.48 reported by Barwick *et al.* (2009) for ANGS crosses. However, estimates for CWT and CP8 in ANGS were higher than the values reported for temperate breeds by Reverter *et al.* (2003) and the estimates for meat quality traits were also higher than the values reported for temperate breeds by Johnston *et al.* (2003). Except for OSS, heritability estimates for carcase and meat quality traits in BRAH were higher than the estimates reported by Wolcott *et al.* (2009). Both ANGS and BRAH steers used in this study were killed at a higher age than those in the previous studies and this led to higher means and variations (SD) for carcase and meat quality traits in the two breeds.

The genetic correlation between MSA_I and carcase and meat quality traits was variable in sign and magnitude, but was in the same direction for both breeds. For ANGS, MSA_I had a moderately positive genetic correlation with CWT (0.41), a low or no correlation with CP8 (0.02) and a moderately negative correlation with OSS (-0.22). For meat quality traits in ANGS, MSA_I had a highly positive genetic correlation with MSA_M (0.96), a moderately positive genetic correlation with Col_L (0.40) and a moderately negative correlation with SF (-0.33).

Table 2. Heritabilities (h^2) and genetic correlations (r_g) between MSA Index and carcase and meat quality traits (standard error in parenthesis)

Type	Traits						
	MSA_I	CWT	CP8	OSS	MSA_M	SF	COL_L
				Angus			
h^2	0.50 (0.09)	0.66 (0.10)	0.48 (0.19)	0.22 (0.07)	0.48 (0.09)	0.43 (0.14)	0.31 (0.08)
r_g		0.41 (0.12)	0.02 (0.15)	-0.22 (0.18)	0.96 (0.02)	-0.33 (0.19)	0.40 (0.16)
				Brahman			
h^2	0.49 (0.16)	0.59 (0.14)	0.36 (0.11)	0.36 (0.11)	0.37 (0.11)	0.38 (0.12)	0.44 (0.12)
r_g		0.12 (0.21)	0.19 (0.24)	-0.51 (0.20)	0.94 (0.05)	-0.18 (0.25)	0.46 (0.21)

In BRAH, MSA_I had a low positive genetic correlation with CWT (0.12), a low positive correlation with CP8 (0.19) and a moderately negative correlation with OSS (-0.51). For meat quality traits, MSA_I had a positive genetic correlation with MSA_M (0.94), a moderately positive genetic correlation with Col_L (0.46) and a moderately negative correlation with SF (-0.18).

The high positive genetic correlations between MSA_I and MSA_M, along with moderately negative correlations with OSS in both breeds, suggests that selection primarily for higher marbling and lower OSS will improve the MSA_I of carcases in ANGS and BRAH cattle. Currently, marble scores are included in the BREEDPLAN evaluation of these two breeds and, therefore, the genetic evaluation of meat quality is being adequately addressed in the BREEDPLAN evaluation of these two breeds.

CONCLUSIONS

MSA-Index measured in Angus and Brahman steers were moderately heritable and had very similar genetic correlations with carcase and meat quality traits in both breeds. The very high genetic correlations with MSA_M and moderate to high negative genetic correlations with OSS indicate that improving those two traits will improve the MSA_I in both breeds. Marble Score included in BREEDPLAN evaluation is, therefore, expected to underpin the genetic of meat quality as assessed by MSA_I in Angus and Brahman cattle. Further evaluation of OSS, with more data, is required before being included in the BREEDPLAN evaluation.

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