GENOME-WIDE ASSOCIATION STUDY OF CARCASE AND EATING QUALITY TRAITS IN AUSTRALIAN ANGUS BEEF CATTLE

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SUMMARY

Eating quality traits are important determinants of consumer satisfaction and are considered as traits of economic importance for genetic improvement in the Australian beef industry. In this study, the genotypic and phenotypic data of 3,454 Angus cattle were analysed to identify genomic regions that potentially influence carcase traits, especially those related to eating quality. A genome-wide association study revealed 3, 5, 1 and 13 significant SNPs associated with carcase weight (CWT), carcase eye muscle area (EMA), Meat Standards Australia Index (MSA_I) and ossification score (OSS) respectively. They were located across chromosomes 3, 7, 13 and 21 and accounted for 2%, 4%, 6% and 12% of the total genetic variance for CWT, EMA, MSA_I and OSS, respectively. No significant SNPs were evident for MSA marble score (MSA_M). Results of this study may have potential practical application in the design of marker SNP chips and improving the accuracy of genomic prediction for carcase and eating quality traits in Angus beef cattle.

INTRODUCTION

Expectations of eating quality are a primary determinant of purchasing decisions made by consumers of Australian beef products. Consequently, Meat and Livestock Australia (MLA) developed the Meat Standards Australia (MSA) grading system to provide consumers with a level of assurance as to the eating quality of beef products (Watson *et al.* 2008). The current MSA Index, denoted by a single number score, represents a standard national measure that allows beef carcases to be ranked according to predicted eating quality and potential merit (McGilchrist *et al.* 2019). The Index is a weighted average of the predicted eating quality of 39 carcase cuts based on parameters collected by accredited MSA graders and of relevance to consumer preferences for tenderness, juiciness, flavour and overall perceptions of meat products (McGilchrist *et al.* 2019). The moderate heritability reported for MSA Index in both Angus and Brahman breeds (Jeyaruban *et al*. 2017) demonstrates a level of genetic control, suggesting improvements in MSA Index may be possible via selective breeding.

While most beef carcase and eating quality traits demonstrate a level of genetic control, less is known about the structure of these traits at the genomic level. Furthermore, phenotypic information on these traits requires slaughter at ages of maturity that allow market specifications to be met, which means that assessment of genetic merit for these traits is delayed. Genome-wide association study (GWAS) of these traits might therefore have practical application in the design of marker SNP chips as well as improving the accuracy of genomic prediction for these traits, especially of young candidate animals. Several such studies using SNP arrays have been reported for carcase traits in beef cattle breeds (Koohmaraie *et al.* 2006; Saatchi *et al.* 2014; Sudrajad *et al.* 2016).

The objectives of the present study were to investigate the presence of significant genomic regions in association with carcase and eating quality traits in Australian Angus beef cattle, and to quantify the amount of total genetic variation explained by such informative SNPs.

MATERIALS AND METHODS

Phenotypic data used in this study were derived from the performance extracts for Angus Australia as used in the March 2019 Angus BREEDPLAN analysis. Carcase trait records included: hot carcase weight (CWT), eye muscle area (EMA) and ossification score (OSS), the latter being an assessment of physiological maturity and indicative of eating quality (AUS-MEAT 2019). Eating quality traits were represented by two traits of relevance in the MSA grading system: MSA marble score (MSA_M) and MSA Index (MSA_I). Slaughter-based contemporary groups were constructed according to standard BREEDPLAN procedures (Graser *et al.* 2005) with criteria including herd, year, sex and prior performance contemporary group, plus slaughter group and slaughter date. Single animal groups were excluded.

Genomic data for animals with carcase and eating quality phenotypes was supplied by Angus Australia. The reference population for the genotype imputation consisted of 11,226 animals genotyped with a number of 50k arrays (LDMAX_SNPMap, ZM2_SNPMap, GSTP_SNPMap, ZOE-50K). Quality control (QC) was applied where only autosomal SNPs and the SNPs with a call rate higher than a 0.6 GeneCall score were kept. Further QC was undertaken using Plink v1.90b3.42 (Chang *et al.* 2015), filtering out those SNPs with minor allele frequency (MAF) < 0.01, deviation from Hardy Weinberg equilibrium ($P<10^{-6}$), and those SNPs with more than 5% missing genotypes. Only animals that had a valid genotype on more than 95% of SNPs were kept in the analysis. A final data set containing 37,974 SNPs for 3,454 animals was available for GWAS. Although the majority of these animals originated from the Angus Sire Benchmarking Program (Banks 2011), this was not an essential criterion *per se* for this study. Individuals required at least a CWT record and genotypes, within a contemporary group of at least two animals, for inclusion.

GWAS analysis of SNP effects and significance was conducted for each carcase and eating quality trait using the program GCTA (Yang *et al*. 2011) and the following linear regression model:

$$\boldsymbol{y} = \boldsymbol{Xb} + \boldsymbol{Za} + \boldsymbol{e}$$

where $\boldsymbol{y}$ is a vector of phenotypes, $\boldsymbol{b}$ is a vector of fixed effects including contemporary group, linear regression of age and SNP effect, $\boldsymbol{a}$ is a vector of random additive genetic effects and $\boldsymbol{e}$ is a vector of random residual effects. $\boldsymbol{X}$ and $\boldsymbol{Z}$ are incidence matrices relating fixed effects and additive genetic effects to phenotype, respectively. The additive genetic effects were assumed to be normally distributed as: $a \sim N\left(0, \boldsymbol{G}\sigma_a^2\right)$, where $\boldsymbol{G}$ is a genomic relationship matrix based on the 50k SNP genotypes, and σ_a^2 is the additive genetic variance. Significant SNPs were identified using a Bonferroni correction with α=0.05 and –log10 (p)=5.88. Significant SNPs present in the same genomic regions were subjected to joint multivariate regression analysis using GCTA to identify the most informative SNPs for the particular trait.

The variances explained by all SNPs and the heritability were estimated using the restricted maximum likelihood analysis with GTCA including the genomic relationship matrix (GREML). Individual SNP variances were calculated as $2pq\propto^2$, where p and q are allele frequencies and α is SNP effect, once SNPs were confirmed as being in Hardy-Weinberg equilibrium.

RESULTS AND DISCUSSION

Table 1 provides descriptive statistics for the carcase and eating quality traits of the 3,454 animals included in the GWAS.

There were 12 significant SNPs on chromosome 13 associated with OSS after Bonferroni correction (Figure 1). Only one SNP remained significant after multivariate regression analysis, reflecting that all 12 SNPs refer to the same QTL due to high LD between them. A second significant SNP for OSS was

evident on chromosome 21 (Table 2). Similar outcomes were evident in the GWAS results for EMA and CWT, with 5 and 3 significant SNPs on chromosome 7 respectively after Bonferroni correction, and reducing to one significant SNP for each trait after multivariate regression analysis (Table 2).

Table 1. Descriptive statistics for carcase and eating quality traits

Trait	No of Animals	Mean	SD	Minimum	Maximum	Heritability
Carcase traits						
CWT (kg)	3,454	420.24	75.45	167.60	571.50	0.49 ± 0.03
EMA (cm^2)	2,954	89.42	10.89	57.00	128.00	0.47 ± 0.03
OSS (score)	2,704	150.97	17.54	100.00	280.00	0.29 ± 0.04
Eating quality traits						
MSA_M (score)	2,963	500.04	117.17	100.00	1030.00	0.40 ± 0.03
MSA_I (score)	2,658	64.88	1.78	59.15	70.48	0.40 ± 0.04

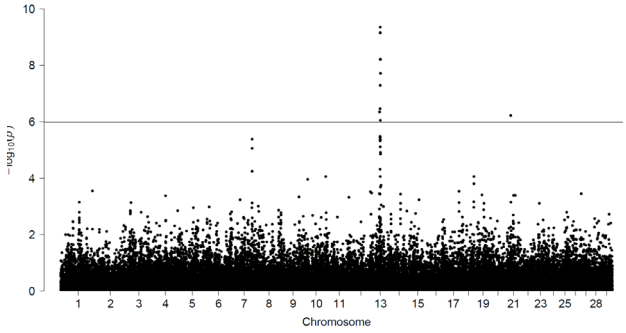

Figure 1. Manhattan plot of -log10 (p) from the Angus cattle GWAS of OSS. The horizontal reference line indicates the genome-wise significance levels (– log10 (p))

In terms of the two eating quality traits, only one SNP remained significant for MSA_I and no significant SNPs remained for MSA_M after Bonferroni correction (Table 2). Manhattan plots for both eating quality traits did suggest that several regions across the genome may warrant further detailed investigation.

Table 2. Significant SNPs and estimates of variance for the carcase and eating quality traits*

Trait	Chr	Mb	P-values	V(G)	%V(snps)
CWT	7	93	1.64E-07	451.1	2
EMA	7	93	3.42E-11	31.10	4
OSS	13	41	4.47E-07	54.04	8
	21	22	7.35E-07	53.21	4
MSA_M	-	-	-	4058.00	-
MSA_I	3	13	1.06E-07	0.74	6

* Chr = Chromosome; Mb = Mega base pairs position; V(G) = total genetic variance =; V(snps) = percentage of total genetic variance explained by significant SNPs.

The variance components and heritability derived for each trait in the current study are similar to those reported by Jeyaruban *et al*. (2017). This is not surprising given the current data extract includes the subset used in the former study. Given the high proportion of base females represented as dams

in this data extract, differences in variance components may reflect differences in how relationships were modelled. The former study used pedigree information whereas the present study used realised relationships via the G matrix.

Sudrajad *et al.* (2016) identified six SNPs distributed across chromosome 4, 6, 27, 10, 9 and 20 as having significant associations with carcase weight, eye muscle area, fat depth and marble score in a commercial population of Hanwoo cattle. In the present study of Australian Angus cattle, the significant SNPs identified for CWT, EMA and MSA_I after Bonferroni correction explained 2%, 4% and 6% of total genetic variance respectively (Table 2). The two significant SNPs identified for OSS (one on each of chromosomes 13 and 21) explained 12% of total genetic variance for the trait. This is a substantial proportion of the genetic variance, encompassing a relatively small number of SNPs.

Chromosome 7 (93Mb position) has been reported previously in association with certain growth and carcase traits in beef cattle. Saatchi *et al.* (2014) reported an association with weight traits and eye muscle area in American Angus, as well as Hereford and a number of other breeds, while Koohmaraie *et al.* (2006) identified the calpastatin gene on chromosome 7 (98 Mb position) in association with meat tenderness. The significant SNPs on chromosome 13 associated with ossification in the present study may perhaps reflect a QTL related to physiological maturity and/or calcium metabolism, given that certain SNPs on chromosome 13 have shown significant associations with lean meat yield and milk yield traits in Holstein Friesian cattle (Doran *et al.* 2014).

CONCLUSIONS

In conclusion, this study identified significant SNPs in the bovine genome associated with eating quality traits for Angus cattle, supported by results from previous studies. Outcomes of the study suggest that significant markers might be added to SNP arrays used for developing Angus-specific SNP panels. Inclusion of these trait-specific markers in genetic evaluation models might also improve the accuracy of prediction of breeding values for such traits.

ACKNOWLEDGMENTS

The authors acknowledge the contributions of Angus Australia and its members who provided access to the data used in this study.

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