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THE IMPACT OF GENETIC MARKERS FOR TENDERNESS ON STEER CARCASS AND FEEDLOT EXIT AND HEIFER PUBERTY TRAITS IN BRAHMAN CATTLE

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SUMMARY

Four genetic markers (T1, T2, T3 and T4) have been shown to have a significant effect on tenderness (measured as shear force) in Brahman cattle. This study examined the relationship between tenderness markers and steer (N = 940) feedlot exit and carcass, and heifer (N = 973) puberty traits. For most traits assessed, tenderness markers had no significant effects. Differences in T1 genotype, however, significantly ($P < 0.05$) affected P8 fat depth measured in steers at the end of finishing and/or on the carcass, as did T3 and T4. Regression coefficients for these relationships were consistently negative, showing that steers with more copies of the favourable alleles were leaner. When protocols were applied to combat false discovery in multiple testing analyses, the relationship between T3 genotype and feedlot exit P8 fat depth remained significant. T1 also influenced age at puberty in Brahman heifers, with the trait significantly reduced (regression coefficient = -14.54) for animals which had more copies of the favourable allele. The exploitation of tenderness markers in Brahman cattle will need to be undertaken with an awareness of the impact of selection for these markers on other production and puberty traits.

INTRODUCTION

Tenderness is the key factor influencing consumer satisfaction reported for cooked beef products (Egan *et al.* 2001). As tenderness can only be measured on slaughter stock late in the production cycle, and measurement is time consuming and expensive, it has been among the first traits in beef cattle to be targeted for genetic marker analyses. The recently released SmartGENE for Beef report (Johnston and Graser 2008) showed that genetic markers for tenderness explained a significant amount of variation for the trait (measured as kg shear force) in Brahman cattle. If genetic marker results are to be incorporated into the multi-trait BREEDPLAN evaluation, there is a need to determine whether there is any association between marker genotypes and other important carcass and production traits. This study aimed to examine the relationship between tenderness marker genotypes and steer finishing and meat quality, and heifer puberty traits, to determine the degree to which selection based on tenderness markers may impact these key productivity traits.

MATERIALS AND METHODS

Animals. The experiment involved Brahman steers and heifers representing 53 sires. The cattle were bred on 5 co-operating properties in Queensland and the Northern Territory with calving taking place over 4 years from 1999 to 2003. After weaning, steers (N = 853) were relocated to one of five backgrounding properties, where they were grown out to feedlot entry, at a mean target group liveweight of 400kg. Steers were implanted with a hormonal growth promotant (COMPUDOSE®) at an average age of 10 months, with implants replaced, according to manufacturer recommendations, until feedlot exit. Steers were slaughtered after an average of 119 days in the feedlot (Wolcott, *et al.* 2009). After weaning, heifers (N = 907) were transported to one of 3 locations which characterized the range of beef production systems in northern Australia.

*AGBU is a joint venture of NSW Department of Primary Industries and University of New England

Heifers were mated for the first time at approximately 27 months. At each location, heifers of the same year of birth were managed as a single contemporary group (defined as a cohort). See Johnston *et al.* (2009) and Barwick, *et al.* (2009) for a complete description of heifer and steer allocation and management respectively.

Measurements. Eleven feedlot exit and 11 carcass traits (described by Barwick *et al.* 2009 and Wolcott *et al.* 2009 respectively) were analyzed. Feedlot exit measurements included liveweight, growth rate from feedlot entry to feedlot exit, feed intake and efficiency, hip height and condition score, and ultrasound scanned measurements of P8 fat depth (P8X), rib fat depth (RIBX), and eye muscle area (EMAX). Blood samples were collected at feedlot exit for insulin like growth factor I (IGFX) analysis. Carcass measurements included carcass weight, hot P8 fat depth (HP8), cold P8 (CP8) and rib fat depth, eye muscle area, retail beef yield as well as Meat Standards Australia grading of hump height (HUMP), USDA marbling score (MS) and ossification score. At slaughter, right sides were hung by the Achilles tendon. Sides were chilled overnight, and at approximately 24 hours post mortem, a 15cm sample of the *M. Longissimus thoracis et lumborum* (LD) muscle was collected caudal to the $12/13^{th}$ rib, and frozen for later shear force (SF) measurements. Samples were thawed, cooked in a water bath (70^0C for 60min) and chilled overnight, prior to SF measurement. A second sub-sample of the LD was used to measure percent intramuscular fat (CIMF) using a near infra-red spectrophotometry method. See Perry *et al.* (2001) for a complete description of methodologies regarding meat sample preparation and trait measurement.

Heifer puberty traits are described by Johnston *et al.* (2009). Briefly, prior to the onset of puberty (at a cohort mean liveweight of 200kg), a regime of ultrasound scanning at approximately monthly intervals was initiated to identify the presence of the first corpus luteum (CL), which, when identified, was interpreted as signaling the onset of puberty. When the first CL was observed, measurements of age (AGECL), liveweight, P8 fat depth, and condition score were recorded. Binary scores were also generated to identify heifers which had a CL identified at any time prior to the start of joining (CLPRIOR), and of these animals, a subset were identified as displaying a CL at the scanning closest to joining (CLJOIN).

Data for four tenderness markers (T1, T2, T3 and T4) were analysed for this experiment. Marker genotypes were generated by Catapult Genetics®, and reported as expressing 0, 1 or 2 copies of the favourable allele for each marker. See Johnston and Graser (2008) for details of phenotypic and tenderness marker data.

Statistical analysis. The significance and effect of tenderness markers on feedlot exit, carcass and heifer puberty traits were analyzed by individually including marker genotype (0, 1 or 2) in models for each trait, containing significant fixed effects, and with sire fitted as random, using PROC GLM in SAS (SAS Institute Inc.: Cary, NC). Wolcott *et al.* (2009), Barwick *et al.* (2009) and Johnston *et al.* (2009) provided details of fixed effect modeling for carcass and meat quality, steer feedlot exit, and heifer puberty traits respectively. Marker genotype was fitted as a continuous variable. Significance levels were re-estimated applying the principles described by Benjamini and Hochberg (1995) to account for the potential errors associated with multiple testing, and accepting a 5% false discovery rate. For each marker, animals with missing genotypes were excluded from the analysis.

RESULTS AND DISCUSSION

Table 1 presents the number of animals analysed for each marker, and the genotype frequencies for tenderness markers. Genotype frequencies did not differ significantly for steers and heifers (Johnston and Graser, 2008) and the results presented in Table 1 are therefore pooled across sexes. T2 was virtually fixed at the unfavourable homozygous genotype, with the

favourable allele occurring in only 3.6% of animals. For T3, the favourable allele was also present at a low frequency (15.9%), though it was only the T2 allele frequency which deviated significantly from the expectations of Hardy-Weinberg equilibrium ($P < 0.001$).

Table 1. Number of animals (pooled across sexes) displaying 0, 1 or 2 copies of the favourable allele for GeneSTAR tenderness markers T1 – T4

Genotype	T1	T2	T3	T4
0	203	1277	1248	554
1	831	76	463	845
2	726	11	49	361

Table 2 presents significant regression coefficients, their standard errors, number of observations analysed, and significance levels for the relationship between marker genotypes and steer feedlot exit and carcass traits, and heifer puberty measurements. For the majority of traits measured, there was no significant ($P > 0.05$) effect of the markers. There was, however, a significant effect of the T1, T3 and T4 markers on fat depth or fat related traits in steers carcass and feedlot exit measurements. The regression coefficients of T1, T3 and T4 marker genotypes for fat depths (HP8 and P8X) were consistently negative, showing that steers which had more copies of the favourable tenderness alleles were significantly leaner. The consistency of the direction of the effect across markers and fat measurements provides some confidence that the effect is real. The T4 marker also had a significant and negative relationship with HUMP, which was positively genetically related to both SF and P8 fat depth for these animals ($r_g = 0.19$ and 0.31 respectively, see Wolcott *et al*. 2009). The significant relationship between T4 and IGFX in steers is also likely to reflect a strong positive genetic correlation between IGF-I measured at feedlot exit and shear force ($r_g = 0.59$), as reported by Wolcott *et al*. (2009).

Table 2. Number of observations (N), means and standard deviations (SD), regression coefficients (b) and standard errors (SE), and P-values describing significant relationships between tenderness markers (T1 – T4) and steer feedlot exit and carcass, and heifer puberty traits in Brahman cattle

Marker	Trait	Units	N	Mean	SD	b	S.E.	P - value
Steer carcass and feedlot exit traits								
T1	HP8	mm	853	13.6	4.0	-0.49	0.22	0.0260
T3	P8X	mm	787	11.9	3.4	-0.71	0.22	0.0014*
T3	CIMF	%	708	2.2	0.8	0.11	0.05	0.0359
T3	MS	Score	842	264.8	64.3	-9.10	4.27	0.0334
T4	HUMP	mm	786	166.8	34.8	-4.45	1.81	0.0144
T4	IGFX	ng/ml	636	584.2	132.9	16.35	6.96	0.0192
T4	HP8	mm	855	13.6	4.0	-0.48	0.21	0.0242
Heifer puberty traits								
T1	AGECL	Days	907	746.5	141.7	-14.54	5.85	0.0130
T1	CLPRIOR	1=yes, 0=no	885	0.43	0.49	0.049	0.02	0.0221

* Relationship maintained significance under multiple testing protocols at $P < 0.0018$.

The significant relationship between the T3 marker and marbling measurements is difficult to interpret, though differences in numbers of measurements available for CIMF and MS may have

contributed to the results. Genetically CIMF and MS are highly correlated (r_g = 0.95), though at the phenotypic level the relationship was weaker (r_p = 0.50) (Wolcott *et al.* 2009). That CIMF and MS should have regression coefficients in opposite directions is likely to reflect the marginal significance levels of T3 genotype as predictors of the traits (P = 0.036 and 0.033 for CIMF and MS respectively). These results must therefore be considered with the caveat that further testing would be desirable, before conclusions are drawn.

The significant relationships between T1 genotype, and AGECL and CLPRIOR, suggested that heifers with more copies of the favourable T1 allele, were more likely to reached puberty earlier (b = -14.54), and display a CL prior to joining (b = 0.049). Results presented by Johnston *et al*. (2009) suggested that there was little evidence of genetic antagonism between tenderness and heifer puberty traits, with genetic correlations between shear force and AGECL and CLPRIOR of -0.16 and 0.11 respectively. The directions of these correlations were in contrast to the regression coefficients presented for the current study, but must be considered in association with the report of Johnston and Graser (2008) which demonstrated marginal significance (P = 0.068) of T1 genotype as a predictor of tenderness in the Brahman cattle used for this experiment.

Applying the multiple testing principles of Benjamini and Hochberg (1995), the regression of T3 genotype on P8X was significant at a re-estimated threshold of 0.0018, while P-values for the remaining relationships did not meet these more stringent requirements. This suggests that the effect of improved T3 genotype on fatness in BRAH steers at feedlot exit was real, and that this effect must be considered when Brahman breeders select animals based on the T3 marker.

CONCLUSIONS

Genetic markers have been shown to be significantly related to tenderness in Brahman cattle. This study has demonstrated that, for most of the feedlot exit, carcass and heifer puberty traits examined, tenderness marker genotype had no significant effect on phenotypic performance. For some fat depth and marbling traits measured in steers, and age at puberty in heifers, however, there was a significant (P < 0.05) association with T1, T3 or T4 markers. This suggests that if BREEDPLAN is to incorporate tenderness marker results into the Brahman multi-trait evaluation, provision will need to be made for their relationship with steer fatness and marbling, and heifer age at puberty. More generally, as the technology develops and larger panels of markers are released, it will be important to estimate the relationships of these markers with other traits, before they are incorporated into the BREEDPLAN multi-trait evaluation. Future work in this area will expand the markers tested to include those for marbling and feed efficiency, as well as fitting combinations of markers to test for possible epistatic effects.

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