ASSOCIATION OF GENOMIC MARKERS (SNP) IN THE *CAPN-1* GENE WITH TENDERNESS IN SOUTH AFRICAN PUREBRED BEEF CATTLE

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I. INTRODUCTION

Research on causative genomic markers affecting meat quality in South African (SA) beef cattle is very limited [1]. Calpain-1 makes the largest contribution to the proteolysis that is responsible for the conversion of muscle to meat and, although several physiologically important single nucleotide polymorphisms (SNPs) are present in the *capn-1* gene (BTA29) [2], these have not been validated for tenderness in purebred SA beef, or whether SNP effects are additive to electrical stimulation. We therefore determined the association of *capn-1* SNPs with physical tenderness measured as WBSF (WBSF) and myofibril fragment length (MFL) to determine their potential use in genomic selection (GS).

II. MATERIALS AND METHODS

South African purebred beef cattle (n=166) were feedlot-finished at the ARC-AP on grain-based diets to a final age of 12 months old with a carcass classification of A2 or A3. Breeds included Angus (n=27), Charolais (n=34), Brahman (n=35), Bonsmara (n=35) and Nguni (n=35), which are commonly used in cross-breeding in SA. The right side of the carcass was electrically stimulated for 120 seconds (ES) at 400 V peak and directly chilled (4°C), while the left side was not electrically stimulated (NS) and chilling was delayed (10°C for 6 hours). Longissimus thoracis et lumborum (loin muscle) samples were vacuum packed and aged at 2 ± 1°C for 3, 9, 14 and 20 days post-mortem. Bulls were genotyped using a Bovine-HD SNP BeadChip (Illumina, USA). The WBSF was determined following oven-broiling to 70°C core temperature, cooling to 18°C and shearing (Universal Instron apparatus Model 4301, England). The MFL were determined for 100 fragments per sample by means of Video Image Analysis. Data were analyzed using PLINK 1.90 and Haploview 4.2, with a simple linear phenotypic association analysis of genotypes with tenderness, using Bonferroni correction.

III. RESULTS AND DISCUSSION

Five SNPs were found to be informative for tenderness in SA beef cattle (Table 1), with between 7 - 20% of the phenotypic variation in tenderness attributed to individual *capn-1* SNPs. A haplotype block was identified that included CAPN1_2 (*capn1-4751*), BovineHD2900013189 and −13190. The predominant associations were found between *capn-1* genotypes and MFL and occurred over the entire ageing period in both NS and ES groups (Table 2), which suggests that the favourable effects of genotypes could be additive to the advantages of electrical stimulation.

Table 1 Informative SNPs in the *capn-1* gene in South African beef cattle genotyped with the Illumina Bovine-HD SNP BeadChip

Chr	Position	Illumina Name	Variant	R^2 values for MFL	R^2 values for WBSF
29	44067968	BovineHD2900013184	rs17871986	0.126 – 0.197	0.076 – 0.115
29	44081056	BovineHD2900013187	rs135658374	0.088 – 0.255	0.090 – 0.101
29	44087629	CAPN1_2 (*capn1-4751*)	rs17872050	0.083 – 0.173	0.067 – 0.080
29	44093671	BovineHD2900013189	rs134827338	0.071 – 0.142	
29	44097970	BovineHD2900013190	rs135736399	0.077 – 0.171	

Indigenous SA beef cattle have the potential to produce tender meat under optimal production and slaughter conditions [3]. Markers in the *capn-1* gene can be used for GS for production of more tender beef more consistently in SA beef breeds, though altered calpain system function [4]. GS should result in significantly improved tenderness (WBSF and/or MFL), as strong associations were evident here.

Table 2. Correlations[#] between *capn-1* genotypes and physical tenderness in South African purebred beef cattle

	Ageing	Treatment	–13184*	–13187	*capn1-4751*	–13189	–13190
MFL	d3	NS		8.8% (P≤0.0119)			
		ES	19.7% (P≤0.0001)	25.5% (P≤0.0001)	17.3% (P≤0.0001)	14.2% (P≤0.0001)	17.1% (P≤0.0001)
	d9	NS	17.1% (P≤0.0001)	15.0% (P≤0.0001)	8.8% (P≤0.0123)	9.1% (P≤0.0087)	8.8% (P≤0.0121)
		ES	13.8% (P≤0.0001)	17.3% (P≤0.0001)	10.8% (P≤0.0018)	8.6% (P≤0.0149)	8.6% (P≤0.0141)
	d14	NS	12.6% (P≤0.0004)	10.6% (P≤0.0021)			
		ES	16.9% (P≤0.0001)	12.3% (P≤0.0004)	8.3% (P≤0.0189)	7.1% (P≤0.0579)	7.7% (P≤0.0339)
	d20	NS					
		ES	12.8% (P≤0.0002)	11.0% (P≤0.0015)	8.5% (P≤0.0162)	8.2% (P≤0.0216)	9.2% (P≤0.0080)
WBSF	d3	NS					
		ES	11.5% (P≤0.0009)	9.8% (P≤0.0048)	6.7% (P≤0.0886)		
	d9	NS					
		ES	7.6% (P≤0.0370)	10.1% (P≤0.0034)			
	d14	NS					
		ES		9.0% (P≤0.0099)	8.0% (P≤0.0242)		
	d20	NS					
		ES					

* BovineHD29000–

[#] Percentage phenotypic variation explained by genotypes of the *cast* SNPs (R^2 expressed as a percentage)

IV. CONCLUSION

To make selection progress, suitable markers need to be identified for the populations in which GS is to be applied. These SNPs in the *capn-1* gene were validated for SA purebred beef, exhibiting several important associations with beef tenderness, including carcasses already electrical stimulated. These data collected with other detailed genotypic and phenotypic observations will be a useful tool for future research to identify other genes (e.g. for growth, development and energy metabolism) and validate their association with SA beef quality for potential use in GS.

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