AIT Research

Estimating the Frequency of Genomic Polymorphisms associated with Meat Quality in Irish Beef Cattle

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Introduction

The calpain (CAPN) and calpastatin (CAST) genes play significant roles in meat tenderness (Casas *et al.,* 2005). Identification and estimation of the frequency of DNA mutations involved in meat tenderness would not only maximise beef potential and product revenue but also result in more efficient production systems, increased producer profitability and improved experience for the consumer.

The current objectives were to estimate Minor Allele Frequency (MAF) and deviation from Hardy Weinberg Equilibrium (HWE) for six DNA mutations in *CAPN* and *CAST* in Irish beef cattle.

Table 1 Information for the SNPs included in this investigation (n=6).

Gene Name	Variant Name	Chromosome : Location	Amino Acid	Consequence	SIFT Score*
Calpastatin	Calpastain 282	7:96119510	--	Intron variant	--
	Calpastatin 2870	7:96165472	--	3 prime UTR variant	--
	Calpastain 2959	7:96165561	--	3 prime UTR variant	--
Calpain 1	Calpain1 316	29:43405875	A/G	Missense variant	0.53
	Calpain1 530	29:43422455	V/I	Missense variant	0.1
	Calpain1 4751	29:43424442	--	Intron variant	--

**Variants with scores 0.05-0.1 are predicted to be tolerated (benign).*

Methods

Genotypes for the six SNPs from 120,000 beef cows were obtained from the Irish Cattle Breeding Federation (ICBF). Genotype quality control and data filtering were performed on all data prior to this analysis. Animal and SNP call rates were all ≥0.9. Bonferroni correction of the significance levels was undertaken to account for multiple testing.

Genotypes included Calpastain_282, Calpastain_2870, Calpastain_2959, Calpain1_316, Calpain1_530 and Calpain1_4751 and analysis was carried out within breed - (Aberdeen Angus (AA), Belgian Blue (BB), Charolais (CH), Limousine (LM), Hereford (HE) and Simmental (SI)).

Findings

MAF for CAST_282 ranged from 0.36 to 0.47, CAST_2870 from 0.34 to 0.50 and CAST_2959 from 0.17 to 0.28.
MAF for CAPN1_316 ranged from 0.09 to 0.21, CAPN1_530 from 0.14 to 0.39, CAPN1_4751 from 0.19 to 0.45.

Table 2 MAFs across six breeds.

	AA	BB	CH	HE	LM	*SI*
CAST_282	0.41	0.47	0.40	0.36	0.41	0.45
CAST_2870	0.40	0.46	0.39	0.37	0.34	0.50
CAST_2959	0.17	0.19	0.20	0.19	0.28	0.22
CAPN1_316	0.20	0.21	0.15	0.19	0.17	0.09
CAPN1_530	0.19	0.26	0.39	0.30	0.14	0.39
CAPN1_4751	0.30	0.33	0.39	0.45	0.19	0.39

Deviations from HWE (P<0.01) were observed for four variants across three of the cattle breeds (Table 3). Following adjustment for multiple testing all observed HWE deviations remained significant (adjP<0.05).

Table 3 HWE results across breed*.

	AA	BB	CH	HE	LM	SI
CAST_282	1.00	1.00	1.00	1.00	1.00	P<0.05
CAST_2870	1.00	1.00	1.00	1.00	1.00	1.00
CAST_2959	1.00	1.00	1.00	1.00	1.00	1.00
CAPN1_316	1.00	1.00	1.00	P<0.05	1.00	P<0.05
CAPN1_530	1.00	1.00	1.00	1.00	P<0.05	1.00
CAPN1_4751	1.00	1.00	1.00	1.00	1.00	1.00

**P values were corrected for multiple testing by Bonferroni.*

Discussion and Conclusion

The above results suggest that genomic polymorphisms associated with meat tenderness are segregating, indicating their potential for inclusion in genome-enabled cattle breeding programmes. Ongoing work includes estimating the effects of polymorphisms in *CAPN* and *CAST* on a panel of production traits using the same sample of 120,000 beef cattle.

References

Casas, E., White, S. N., Riley, D. G., Smith, T. P. L., Brennemant, R. A., Olson, T. A., … Chase, C. C. (2005). Assessment of single nucleotide polymorphisms in genes residing on chromosomes 14 and 29 for association with carcass composition traits in Bos indicus cattle. Journal of Animal Science, 83(1), 13–19