QTL ANALYSES OF BEEF TASTE PANEL DATA

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SUMMARY

Steaks from a subset of New Zealand (AgResearch) animals from a collaborative QTL trial with the University of Adelaide were evaluated by a Taste Panel in an attempt to identify markers linked to consumer preference for eating qualities of beef. Suggestive QTL were found on several chromosomes; some of these were in regions previously identified as being linked to other objective measures of desirable qualities such as tenderness.

INTRODUCTION

A collaborative study began in 1995 between AgResearch in New Zealand (NZ) and the University of Adelaide in Australia to search for DNA markers linked to production, carcass and beef meat quality traits (Morris *et al.* 2009). The present paper reports on results from a Taste Panel trial. A subset of the animals born in NZ were analysed and we report here a QTL search performed to identify chromosomal regions with linkage to these traits.

MATERIALS AND METHODS

Trial design. The trial design involved dams of two very different *Bos taurus* breeds, Jersey (J) and Limousin (L). In NZ, three first-cross JxL or LxJ bulls were mated with both J and L cows, to produce a total of about 400 female or male back-cross progeny over two successive years. The marker-search involved identifying in the calves sire-derived alleles whose presence was associated with performance in one or more traits ("phenotypes"). The primary traits of interest were carcass composition and measures of beef meat quality. Other simple traits during the growth phase were also recorded, such as live weights and ultrasound measurements. The diet consisted of mainly pasture. At slaughter (28 weekly slaughter groups over 2 years, at 22 to 28 months of age), muscle samples were taken to measure meat quality during the aging process. The results presented here are from Taste Panel assessment of aged cooked steaks taken from the *M. longissimus thoracis et lumborum (M. longissimus)*.

Table 1. Numbers of animals by Breed, Year and Sex (L = Limousin; J = Jersey)

Year of birth	Breed			
	Sex	LJJJ	LJLL	Total
1996	Heifer	66	46	112
	Steer	66	34	100
1997	Heifer	45	30	75
	Steer	57	23	80
Total		234	133	367

A total of 367 steak samples (Table 1) were assessed over the 2 years for 7 subjective measures of eating quality. Steaks had been vacuum-packaged after aging (at 15°C so that aging was completed within 1 week: Morris *et al.* (2006)) and held frozen until assessment. Steaks were thawed to 4ºC and then cooked on a hotplate to an internal endpoint of 75°C, as determined by a temperature probe. Steaks were then cut into sample pieces with outside edges removed, placed

onto a pre-warmed dish (with drainage to prevent samples sitting in juices) and immediately presented to the taste panel. Ten panellists were involved each year, with 9 of the 10 being used in both years. All panellists had at least 4 years' experience at flavour and textural evaluations and they participated in 4 familiarisation sessions prior to the trial, with samples that had been manipulated by processing and cooking techniques to produce a range of attributes. For the experimental samples, all panellists received a portion of the same sample at the same time, with approximately 2 minutes between presentation of samples, and panellists received water and crackers to cleanse the palate between samples.

Each steak was evaluated for seven attributes, using a scale with a range of 0 to 10. The attributes measured are shown with a description in Table 2. There were 64 tasting sessions over the two years and 6 animal samples were tested at each session – animals were randomly assigned to sessions before testing took place and occasionally steaks were not available so there were sessions where only 3 to 5 steaks were tested. Steaks were not repeat-sampled across sessions; animals were represented in only one session.

Table 2. Definition and range with description for the 7 traits assessed by Taste Panel

Attribute	Definition	Score = 0	Score = 10
Softness (SOFT)	Force required to deform/compress the sample, assessed during initial 3-5 bites	Firm	Soft
Initial juiciness (INJU)	Amount of moisture released after 3-5 bites	Dry	Juicy
Tenderness (TEND)	The amount of force required to chew the sample, assessed during initial 3-5 bites	Tough	Tender
Fibre density (FDEN)	Amount of fibres perceived during breakdown of meat, assessed just prior to swallowing; dense/packed = many fibres present (fibrous), loose/large fibres = few fibres present (non fibrous)	Fibrous	Non-fibrous
Cohesiveness (COHE)	The degree to which the chewed sample holds together in a mass, assessed after 7-12 chews; tight/held together = cohesive, loose = non cohesive	Cohesive	Non-cohesive
Sustained juiciness (SUJU)	Amount of moisture still remaining just prior to swallowing	Dry	Juicy
Easy-to-chew/ Succulence (E2CH)	An overall impression of the ease of eating, a culmination of all the attributes (tenderness, fibre density, cohesiveness, juiciness etc)	Not succulent	Succulent

Data analyses. The panellist scores for each of the 7 traits were run through a REML model in GenStat to predict a single value for each trait over panellists, which could then be used as a phenotype for a QTL scan. The REML model was fitted with fixed effects Breed and Slaughter Group (which also accounted for Year and Sex as these animals were slaughtered in 25 (of the 28) same-sex groups). Random effects in the model were Tasting Session within Year, Sire (n = 3), Animal (to account for the repeated scores) and panellist. Predicted values were saved for each of the 7 traits and then run though a Haley-Knott procedure (Knott *et al.* 1996) with SAS, to identify QTL. A total of 284 microsatellites evenly distributed across all the autosomes were used with, on average, 189 informative loci per sire group. Marker positions were taken from the map of Ihara *et al.* (2004). Permutation tests were conducted to determine thresholds for the significance of QTL. The same animals, and their DNA, were part of the experiment with objective measures of beef meat quality described by Morris *et al*. (2009) and Esmailizadeh *et al.* (2011).

Inspection of the trait definitions in Table 2 indicates that these all measure some underlying traits such as tenderness with high scores being desirable. Correlations and Principal Components were calculated and the 1st and 2nd principal components (PC1 and PC2, accounting for 91% of the variation) were also run through the Haley-Knott procedure.

RESULTS

The Haley-Knott runs showed only indications of suggestive QTL; 16 individual QTL for 6 of the 7 traits on 7 autosomes. Correlations between the predicted values from REML for each animal were all positive (Table 3).

Table 3. Correlations of predicted scores

	Softness	Initial juiciness	Tenderness	Cohesiveness	Fibre density	Sustained juiciness
Initial juiciness	0.49					
Tenderness	0.90	0.43				
Cohesiveness	0.82	0.26	0.92			
Fibre density	0.72	0.31	0.82	0.83		
Sustained juiciness	0.55	0.86	0.52	0.35	0.42	
Easy-to-chew	0.88	0.45	0.96	0.91	0.83	0.54

For the 1st and 2nd principal component loadings (plotted in Figure 1), we identified 6 suggestive QTL on 5 autosomes; 3 in total on BTA4, 18 and 29 which were associated with the 1st principal component ('tenderness') and another 3 QTL on BTA4, 8 and 26 associated with the 2nd ('juiciness'). A summary of the QTL results is shown in Table 4 for both the individual traits and the derived principal components.

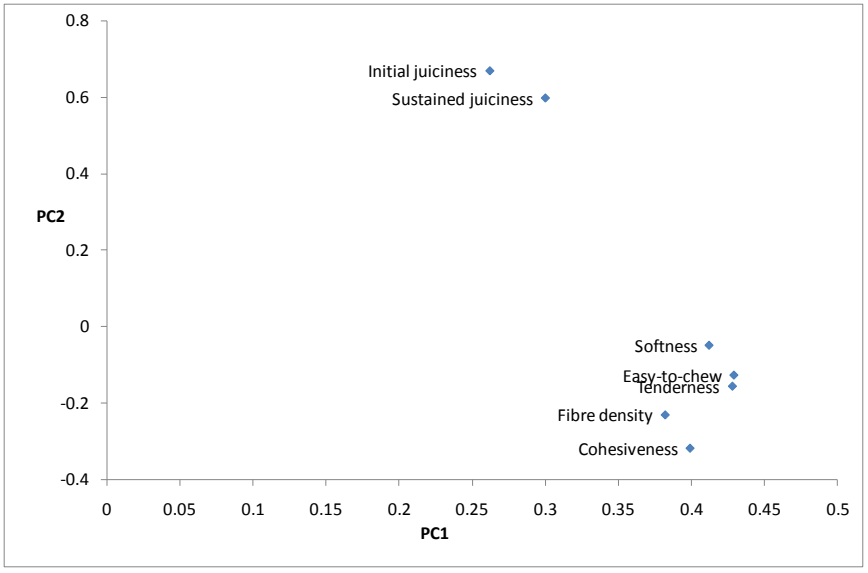

Figure 1: Graph of first 2 principal component loadings

Table 4. Summary of suggestive[1] QTL results by chromosome

Chromosome	Position (M)	Traits (individual)	Traits (principal components)
4	1.01 – 1.08	COHE, E2CH, TEND	PC1, PC2
8	0.26 – 0.34	COHE, SOFT, TEND	-
8	0.55	-	PC2
18	0.56 – 0.69	E2CH, SOFT	PC1
19	0.83	COHE	-
24	0.26	COHE	-
26	0.51	INJU	-
26	0.19	-	PC2
29	0.63 – 0.64	COHE, E2CH, FDEN, SOFT, TEND	PC1

[1] Defined as having less than one false-positive per genome scan (Lander & Kruglyak, 1995)

DISCUSSION

A reliably tender product is one of the most important attributes for maintaining consumer satisfaction with beef steaks. As seen from Figure 1 and Table 3, the 5 traits, excluding the two involving juiciness, are similar measures of 'tenderness'. The QTL for these 5 and PC1 on BTA29 are at the same position as the genome-wide significant QTL identified for shear force on the same muscle at intermediate stages of aging (Esmailizadeh *et al*. 2011). The steaks in this project were taken from exactly the same muscle and aged for as long as the steaks used for the ultimate shear force measure. We did not show any QTL for this measure in Esmailizadeh *et al*. (2011) but Morris *et al*. (2006) did show an association at a SNP on calpain-1 (CAPN1 on BTA29) for ultimate shear force. The calpain proteolytic system has been identified as having a critical role in meat tenderisation. The calpain-1 enzyme is a heterodimer composed of a large catalytic subunit (CAPN1) and a smaller regulatory subunit encoded by the CAPNS1 gene which is a candidate gene for the QTL on BTA18.

Although the QTL on BTA4 identified only 'tenderness' traits, there were suggestive QTL in this region for both principal components, possibly consistent with the shear force QTL reported by Esmailizadeh *et al*. (2011). The same paper reported a region on BTA8 which had a suggestive QTL for glycogen taken from a muscle biopsy and a BTA19 region which also contained a suggestive QTL for cortisol recorded at the same time as the muscle biopsy.

In conclusion, the lack of significant QTL for eating quality of beef was disappointing but this could perhaps be attributed to the subjective appraisal system, or to the power with 367 records. However, a large proportion of these QTL regions have already been reported for objective measures (tenderness), muscle metabolic traits, and blood parameters in this trial.

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