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QTL FOR MEAT COLOUR AND pH IN *BOS TAURUS* CATTLE

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SUMMARY

An experimental cattle backcross between the Jersey and Limousin breeds was performed in Australia and New Zealand to map quantitative trait loci (QTL) for diverse production traits. Six crossbred sires and their progeny were genotyped for 253 informative microsatellite markers covering the 29 bovine autosomes. This study reports the results for meat colour and pH recorded on 355 backcross animals in Australia. Results of the genome scan using regression interval mapping revealed evidence for QTL (<5% chromosome-wise level) on BTA10, 18, 19, and 27 for meat colour and BTA2, 3, 5, 6, 11, 12, 13, 16, 24 and 27 for meat pH. A number of detected QTL were mapped to genomic regions likely to contain the 'RN' or 'RYR1' genes, which are known to affect meat quality traits in pigs.

Keywords: beef cattle, meat colour, pH, quantitative trait loci.

INTRODUCTION

Meat colour is the first criterion used to judge meat quality and acceptability (Cornforth, 1994). Beef colour development is a function of ultimate pH (Abril *et al.* 2001). Thus, ultimate pH is the most commonly used trait to assess beef quality and is usually measured at 24 and 48 h *post mortem*. A higher level of acidity (low pH) within the muscle causes the proteins to denature and lose their ability to hold water. Carcasses that have a high pH (above pH 5.70) are rejected under Meat Standards Australia grading and excluded from many meat brands, food service operations and markets because the meat is likely to be tougher. Meat with high ultimate pH will tend also to be darker, more susceptible to bacterial spoilage, and have less flavour (Watanabe *et al*. 1996). Consumers reject dark meat at the retail level, as it is not visually appealing. In Australia, the incidence of dark cutting is almost 10% in beef. This equals a loss for the industry of almost $36 million per year. Genetic improvement of meat quality is difficult when using standard selection methods, but is feasible if the genes responsible for meat quality are identified. Despite increasing economic importance and the number of ongoing QTL experiments, the information concerning meat quality traits in beef cattle is still limited. In order to identify DNA markers for QTL affecting production, carcass and meat quality traits, an international collaboration was established in 1995 between The University of Adelaide (Australia) and AgResearch (New Zealand). This paper reports the results of quantitative trait loci (QTL) analyses for meat colour and pH data recorded in Australia.

MATERIAL AND METHODS

Mapping population. Three-generation resource populations, The University of Adelaide's Davies Gene Mapping and the New Zealand AgResearch Gene Mapping Projects in Australia and New Zealand, respectively, were developed using two phenotypically divergent *Bos taurus* breeds, Jersey

(J) and Limousin (L). Three pairs of first–cross half-brothers were generated, with one of each pair used for mating in Australia and the other used for mating in New Zealand to both pure Jersey and pure Limousin dams creating a total of about 800 backcross progeny. Details on management of the animals are given by Morris *et al.* (2000). This paper reports results from 355 Australian carcasses with meat colour and pH measurements.

Measurement of the traits. Meat colour was assessed on the chilled carcass of the rib eye muscle area (*M.longissimus dorsi*) and scored against the AUS-MEAT Beef Colour reference standards (AUS-MEAT Limited, 1998). AUS-MEAT meat colour scores were 1, 1C, 2, 3, 4, 5, 6 where a high score indicates darker meat. To enable numerical analysis, score 1C was converted to a numerical value of 1.5. pH was recorded in the *M. semitendinosus* and *M. longissimus dorsi* muscles prior to cooking using a WP-80 pH, mV, Temp-meter. pH measurements were taken after four aging treatments (1, 5, 12, 26 days after slaughter) as outlined in an associated paper (Esmailizadeh Koshkoih, *et al*. 2005)**.** pH did not change across the aging treatments, so a simple average was used as the best indicator of ultimate pH of each muscle.

QTL analysis. Sire-derived alleles were determined for a total of 253 informative microsatellite loci (an average 185 loci per sire group) spread across all bovine chromosomes, except for the X and Y. The data were analysed using the least squares approach developed by Knott *et al.* (1996) and implemented in QTL Express (Seaton *et al.,* 2002), a web-based software. Breed of dam, sex and year were included in the model as fixed effects. Positions of microsatellites were taken from the U.S. Meat Animal Research Center map (http://www.marc.usda.gov/genome/genome.html) and are tabulated relative to the centromere of the chromosome. A permutation test (Churchill and Doerge, 1994) was performed with 1000 replicates to determine threshold values.

RESULTS AND DISCUSSION

Across-family analysis of the data revealed four QTL affecting meat pH located on BTA5, 13, 16 and 24. Although the across-family analysis indicated no QTL for meat colour, individual-family analysis identified QTL for meat colour located on BTA10, 18, 19 and 27. Individual-family analysis also indicated QTL for meat pH on BTA2, 3, 5, 6, 11, 12, 13, 16, 24 and 27 (Table 1). The mapping results indicate that the genes controlling pH and meat colour are likely to be different as there was little overlap between QTL for pH and meat colour.

Glycogen content of muscle is an important determinant of the pH decrease *post mortem* and the ultimate pH, and thus, meat colour and tenderness of muscle (Shorthose and Harris 1991). No measures of glycogen or glycolytic potential were obtained in Australia. However, the measures of pH and colour are used as common industry measures of meat quality since they are indirectly correlated with glycogen and glycolytic potential. It is worth noting, consequently, that only the QTL for ultimate pH on BTA5 was observed to be in a similar location for the two different muscle types examined herein, the oxidative *M. longissimus dorsi* and the glycolytic *M. semitendinosus.*

While colour and pH are important meat quality traits, to our knowledge, there is no previous evidence of a QTL affecting meat pH or colour in other mapping experiments in cattle. Comparative mapping will be useful to identify candidate genes for the observed effects of the detected QTL in the

present study. For example, the RN (Rendement Napole) allele is a mutation in the PRKAG3 gene (protein kinase AMP-activated, γ_3 subunit) (Milan *et al.* 2000) well known to affect meat quality traits (pH, glycogen potential, water-holding capacity) in pigs (Ciobanu *et al.* 2001). The RN gene has been mapped to SSC15, which is homeologous to BTA2 and 27. BTA2 harbours QTL for meat pH and BTA27 harbours QTL for both meat colour and pH (Table 2). On the other hand, the gene encoding another subunit of the AMP-activated protein kinase, PRKAG1 (γ_1 subunit), maps to BTA5 at 51-53 cM (http://locus.jouy.inra.fr/cgi-bin/lgbc/ mapping/ common/ gene.operl?BASE =cattle.), where we also detected a muscle pH QTL (37-90 cM).

Table 1. Most likely position, F-statistic values, and allelic effects of detected QTL for meat colour and pH

BTA	Trait	Position[a] (cM)	Sire	QTL effect (S.E.)	F-value	Centromeric marker	Telomeric marker
2	pHst	109	398	0.0323 (0.0106)	9.3**	BMS356	BM2113
3	pHld	46	398	0.0244 (0.0092)	7.0*	BL41	MCM58
3	pHld	73	361	0.0521 (0.0192)	7.3*	HUJ246	BMS2145
5	pHld	37	368	0.0731 (0.0320)	5.2*	OARFCB05	MAF23
5	pHst	90	All three		4.8*	BMS1248	BMS772
6	pHst	87	368	0.0492 (0.0183)	7.2*	BM415	BM8124
10	MC	23	398	0.2799 (0.1038)	7.3*	CSSM38	BMS528
11	pHld	18	398	0.0291 (0.0097)	7.3*	BM827	BMS2131
12	pHld	64	361	0.0500 (0.0179)	7.8*	BMS975	RM113
13	pHld	9	398	0.0303 (0.0090)	11.3**#	TGLA23	BMS1742
13	pHld	67	All three		4.0*	BMS1669	RM327
16	pHst	82	All three		4.2*	BM3509	INRA13
18	MC	43	361	0.3411 (0.1264)	7.3*	BM8151	INRA63
19	MC	1	361	0.3636 (0.1253)	8.4*	BM9202	HEL10
24	pHst	8	All three		4.8*	BM7151	CSSM31
27	MC	63	361	0.3055 (0.1236)	6.1*	INRA134	BM203
27	pHst	0	361	0.0438 (0.0170)	6.6*	BMS2168	BM6526

[a] Position based on the USDA map. * Evidence for QTL significant at the 5 % chromosome-wise level. ** Evidence for QTL significant at the 1 % chromosome-wise level. # QTL significant at the 5 % genome-wise level. BTA= bovine autosome, pHst = ultimate pH of *M. semitendinosus*, pHld= ultimate pH of *M. longissimus dorsi.* MC= Meat colour (score 1-6).

Fuji *et al.* (1991) reported the effects of RYR1 (ryanodine receptor) on pork pH, water holding capacity and colour. This gene maps to BTA18 where we found a QTL for beef colour. Andersson *et al.* (1996) found a QTL on SSC12 affecting pH and pigmentation. SSC12 is homeologous to BTA19 that was found to harbour a QTL for beef colour herein. Rothschild *et al.* (1995) also reported some association of meat colour with regions on SSC4 that is homeologous to BTA3, although there are no obvious candidate genes.

Additional QTL mapping experiments and further analysis must be undertaken for meat quality traits. However, if the genes and pathways controlling meat quality traits in pork are found to control these traits in beef, then identifying molecular markers for selection in cattle should proceed rapidly.

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