USING HUMP HEIGHT TO ESTIMATE BOS INDICUS CONTENT IN THE MSA BEEF GRADING MODEL WHICH PREDICTS EATING QUALITY

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SUMMARY

Bos indicus content is a key predictor of beef eating quality under Meat Standards Australia (MSA) quality grading scheme. Initially a phenotypic estimate of the proportion of *B. indicus* was used in the MSA model although more recently this has been estimated from hump height and carcass weight. The Admixture software was used to develop an estimate of *B. indicus* content using genomic information. It was demonstrated that *B. indicus* content could be accurately estimated from SNP genotype data (BB_genotype). This knowledge was used to examine the accuracy of estimating *B. indicus* content from hump height (BB_hump). The estimation of *B. indicus* content using BB_hump was found to provide a moderate accuracy of estimating *B. indicus* percentage. However, this difference in accuracy did not translate into substantial differences in the prediction of eating quality under the MSA model.

INTRODUCTION

The Meat Standards Australia (MSA) beef grading model uses commercial inputs at grading to predict beef eating quality. The MSA prediction of eating quality is based on a series of equations for individual cuts for up to five different cooking methods. The MSA model inputs include the following traits, estimated *Bos indicus* content (estBI%), whether the animal was treated with hormonal growth promotants (HGP), sex (female or steer), carcass characteristics (carcass suspension method, carcass weight, marbling and ossification scores, ribfat, and ultimate pH), and value adding effects (cooking method and days aged). One of the key animal predictors in the MSA model is estBI% (Thompson 2002, Watson *et al.* 2008). The impact of estBI% on eating quality was estimated by Watson *et al.* (2008) to be between three and 13 MQ4 score units for the different cuts in the carcase. For the MSA model development, estBI% was derived largely from pedigreed animals, or from herds of known *B. indicus* content.

When the MSA model was initially implemented nationally in 2000, estBI% was determined from the national vendor declaration (NVD) in conjunction with a physical inspection of the cattle by a trained MSA grader. Mixed lots of cattle were graded to the highest estBI% in the lot. This often necessitated redrafting mixed lots into like groups at the abattoir, which generally increased stress on the animals prior to slaughter. Hump height adjusted for carcass weight was proposed as an alternative method of assessing estBI% (Sherbeck *et al.* 1996) and this was included in the MSA model. Over time, the usage of hump height adjusted for carcass weight has increased until it is now preferred to NVDs for assessing estBI% at grading (MSA, *unpublished data*).

Given that the regression coefficients for the effect of estBI% on eating quality were largely generated from animals of known genotype it was timely to confirm the accuracy of using hump height adjusted for carcass weight compared with using animal phenotype to predict eating quality. A series of experiments performed by CRC and MSA provided the opportunity to explore relationships between estBI% estimated from hump and carcass weight (BB_Hump), genomics

(BB_Genotype) and BI% from known phenotype. It was also possible to compare the relative accuracy of BB_Hump and BB_Genotype as predictors of eating quality in the MSA model.

MATERIALS AND METHODS

A series of datasets were used to investigate different objectives. The first objective was to develop a estimate of *B. indicus* content from genomic SNP panels and then test this estimate using independent data. The second objective was to evaluate the relationship between estimated B. indicus content (estBI%) predicted from hump height and carcass weight (BB_Hump) and estBI% from genomic information (BB_Genotype). Finally, the accuracy of using either BB_Hump, or BB_Genotype along with other MSA input traits to predict eating quality, was assessed.

Development of BB_Genotype estimate. To develop an estimate of *B. indicus* content (BB_genotype) and evaluate its efficacy for prediction of BI content, the CRC III genotype and phenotype databases were used. To build the estimate, a training set of 5,650 animals and a validation set of 9,734 animals were selected from the total data set. Within breeds, animals were randomly assigned to training and validation groups. The diversity of breeds in the CRC III database meant there was a wide range of breeds and crossbred animals used to test the accuracy and precision of the *Bos indicus* content estimates. A subset of 5,817 markers that were common across all Illumina 10k, HD50k and 700k genotyping platforms were selected in the prediction equation for BB_Genotype.

Admixture software was used to develop estimates of BB_Genotype from SNP data (Alexander *et al.* 2009, Alexander and Lange 2011). The animals selected as training animals were coded as either *Bos taurus* (BT) or *Bos indicus* (BI) and the supervised option was used. The animals set coded as BT included Angus (n=2,000), Murray Grey (n=200), Shorthorn (n=500), Hereford (n=500), Limousin (n=50) and Charolais (n=400). There were 2,000 Brahmans used in the analysis as the BI reference. This program has been used previously (Porto Neto *et al.* 2014) to estimate breed composition in beef cattle.

The relationship between BB_Hump and BB_Genotype. This relationship was assessed using three data sets. Firstly, the CRC II data which comprised 1,012 animals that had been slaughtered and MSA graded. Secondly, the long distance transport (LDT) data set (Polkinghorne *et al.* 2013) which comprised 343 cattle, and lastly, 50 animals from a Rigor Temperature Experiment (RTE) (J Thompson, unpublished data). A simple linear regression was used to estimate the relationship between BB_Hump and BB_Genotype.

Prediction of eating quality using either BB_Hump or BB_Genotype in the MSA model. The LDT and RTE data sets had consumer eating quality on striploin samples. For both data sets regression models to predict eating quality (MQ4 score), included MSA input traits (carcass weight, marbling and ossification scores, ribfat and ultimate pH) along with terms for either BB_Hump or BB_Genotype. A multiple regression was used to assess the relationship between BB_Hump and BB_Genotype following adjustment for components routinely considered in the MSA eating quality prediction model.

RESULTS AND DISCUSSION

The genomic estimate of Brahman content using SNP data was shown to be closely related to Brahman content from pedigree (R^2=98%). This was slightly higher than the estimate of Frkonja *et al.* (2012) who was able to explain approximately 94% of the breed composition. However, in the earlier study, the breeds comprised Simmental and Red Holstein Friesian which were much less divergent than in the current data set. In addition, the study by Frkonja *et al.* used a much smaller training data set (495 cattle). Likewise, Kuehn *et al.* (2011) was able to explain between 77% and 92% of the variation in breed composition within *Bos taurus* beef breeds.

Table 1. The coefficient of determination (R^2), residual standard deviation (RSD), intercept and slope for the relationship between BB_Genotype and BB_Hump for three data sets.

Data set	Range BB_Genotype	R^2	RSD	Intercept	Slope
CRC II	40-100%	0.44	25.3	0.08 (2.07)	0.84 (0.02)
RTE	0-100	0.70	17.8	22.2 (3.06)	1.43 (0.14)
LDT	0-100	0.40	15.5	44.8 (1.21)	0.56 (0.04)

To examine the relationship between hump height and *B. indicus* content three data sets were used (Table 1). Within all three data sets there was a positive relationship between BB_Genotype and BB_Hump, the coefficient of determination ranging from 40 to 70%. The residual standard deviation indicated that the error in predicting BB_Genotype from BB_Hump was similar for the two RTE and LDT datasets, but larger for the CRC II dataset. The slopes of the different regressions indicated that BB_Genotype was under or overestimated in the different data sets. Thus, there may be scope to adjust the equation used to predict *BB%* from BB_Hump in order to reduce bias.

Table 2. F ratios for input traits used to predict palatability (MQ4) using data from the rigor temperature (RTE) and the long distance transport (LDT) experiments.

MSA traits	F Ratio			
	RTE		LDT	
	Model 1	Model 2	Model 1	Model 2
BB_Genotype	18.52	-	15.33	-
BB_Hump	-	12.62	-	10.04
Steak Position	7.19	7.09	13.17	16.05
Sex	1.49	1.89	-	-
Hang	26.32	26.13	-	-
Hang*position	1.74	1.72	-	-
HSCW	0.51	0.65	2.68	2.4
Ribfat	0.73	0.57	2.28	1.76
Ossification	2.11	2.11	1.92	2.49
Marbling	26.64	24.91	23.62	27.04
Ultimate pH	3.22	2.8	1.08	0.88
Days aged	15.57	16.48	-	-
HGP	-	-	0.18	0.6
Residual standard deviation	10.46	10.55	10.6	10.65
R^2	39.38	38.16	24.50	23.22

Model 1 includes BB_Genotype and Model 2 includes BB_Hump. Degrees of freedom (DF) for Rigor temperature 1,281 for all terms except position (2,281), hang (2,281), position* hang (4281) and days aged (3281)

DF for LDT was 1312 for all terms except position (2,212)

When adjusted for other terms in the MSA model the regression coefficients for the two estimates of *B. indicus* content differed slightly. When *B. indicus* content was estimated by BB_Hump the regression coefficient indicated that an increase in *B. indicus* content from 0 to 100% resulted in a decrease of 14 MQ4 units in palatability. By contrast when BB_Genotype was used the decrease was only 9 MQ4 units.

Using two MSA datasets the accuracy of predicting eating quality (MQ4) was similar regardless of whether it was estimated using BB_Genotype, or BB_Hump (Table 2). The use in isolation of BB_Genotype or BB_Hump had a large effect on the total F ratio (data not shown). However, there was little difference in the overall percentage of variation explained when using either BB_Hump or BB_Genotype to adjust for BB% under the MSA model. The coefficient of determination dropped by approximately 1% in both cases. In both experiments, the F ratios were slightly higher when estBI% was predicted from BB_Genotype compared with using BB_Hump. As the variation explained using all the MSA inputs did not change substantially, the variation that should have been due to BB% under the BB_Hump term was partitioned across other terms in the model. In the case of LDT this variation was picked up by marbling score possibly due to the correlation between marbling score and BB% in this data set. In RTE it was less clear which individual terms accounted for the difference in using BB_Genotype or BB_Hump.

IMPLICATIONS

Using data from a number of MSA experiments, BB_Hump predicted BB_Genotype with reasonable accuracy, although in the different data sets there was a tendency to either over or underestimate BB_Genotype. This could be corrected by adjusting the formula used to convert hump height to BB_hump, or by using a genomic estimate of *B. indicus* content. When used in a regression model with other MSA inputs, both BB_Hump and BB_Genotype were similar in their ability to predict consumer eating quality.

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