final report

Project code: V.EQT.1420

Prepared by: Matthew Kelly
John Thompson

Date published: December 2014

ISBN: 9781740362948

PUBLISHED BY
Meat & Livestock Australia Limited
Locked Bag 991
NORTH SYDNEY NSW 2059

Utilising genetic markers to improve the understanding of the relationship between *Bos indicus* content and consumer eating quality

Meat & Livestock Australia acknowledges the matching funds provided by the Australian Government to support the research and development detailed in this publication.

Executive summary

Background

The MSA prediction model uses easily measured commercial predictors to estimate eating quality. One of the key animal predictors in the MSA model is *Bos indicus* content. In the early stages of implementation of MSA producers filled out a national vendor declaration (NVD) stating *Bos indicus* content. The option to use a prediction based on hump height and carcass weight (BB_Hump) rather than the NVD was then introduced as an option. Over time many producers have opted for this option rather than filing an NVD. In addition to pedigree it is also possible to use SNP genotyping to predict breed composition (BB_Genotype). A series of experiments performed by CRC and MSA provided the opportunity to explore the relationship between BB_Hump, BB_Genotype and *Bos indicus* content and further examine their relationships with eating quality.

Methods

Data from a series of five experiments were used to explore the relationship between *Bos indicus* content predicted from hump height (BB_Hump) and carcass weight and a genomic estimate of *Bos indicus* content (BB_Genotype). Using a number of MSA datasets the usefulness of these estimates of *Bos indicus* content to predict consumer eating quality was also examined.

The CRC III dataset was used to estimate *Bos indicus* content using SNP genotype data. A series of three MSA experiments was used to estimate the relationship between hump height and eating quality in addition to examining the relationship between *Bos indicus* content and eating quality. Lastly, a large set of commercial records on hump height and vendor declared *Bos indicus* content was provided to examine the relationship between hump height and *Bos indicus* content.

Results

The genomic estimate of Brahman content using SNP data was shown to be closely related to Brahman content from pedigree (R^2=98%). Using data from a number of MSA experiments BB_Hump tended to underestimate BB_Genotype at the lower levels of *Bos 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 eating quality. Using an industry dataset from properties with stable breeding programs there was some bias in the current MSA equation used to estimate BB_Hump whereby *Bos indicus* content was underestimated at the lower *Bos indicus* levels. This bias was quantified by calculating the MSA Index using BB_Hump and BB_Genotype estimates. The difference in the MSA Index was found to increase up to 70% BB_Hump and then decreased as it was constrained at 100% *Bos indicus* content. By adjusting the coefficients in the MSA BB_Hump equation this bias

was reduced. It was concluded that BB_Hump was sufficiently accurate to use with the MSA model.

Implications

Using several MSA Data sets the accuracy of predicting eating quality was similar regardless of whether it was estimated from genomics, or from hump height and carcass weight. The relationship between BB_Genotype and BB_Hump was not linear and therefore BB_Hump tended to underestimate *Bos indicus* content at the lower levels. Following a slight adjustment to its coefficients used to calculate Bos indicus content from hump and carcass weight this bias was small across the *Bos indicus* range.

Table of Contents

List of Tables

List of figures

1. Introduction/background

The MSA prediction model uses commercial predictors to estimate eating quality for individual cuts prepared using a number of cooking methods. The predictors include live animal, carcass and value adding traits which can easily be measured or collated at grading (Polkinghorne et al 2008). One of the main animal predictors used in the MSA model is *Bos indicus* content.
A number of studies have reported that *Bos indicus* content impacted on palatability (Shackelford et al 1995, Sherbeck et al 1995, O'Connor et al 1997, Rymill 1997). Many of the meat samples used in the initial development of the MSA model were sourced from the Beef CRC carcasses where *Bos indicus* content was accurately known from pedigree records. The Beef CRC database was supplemented with carcasses sourced from industry herds of known *Bos indicus* content.

When the MSA model was initially implemented in industry, *Bos indicus* content was inputted from the national vendor declaration (NVD) in conjunction with a physical inspection of the cattle by the trained MSA grader. If the NVD stated that the lot had a range in *Bos indicus* phenotypic then the highest *Bos indicus* content was applied to all animals in that lot. Also if the grader felt that the cattle were inaccurately described by the NVD, they could override the stated breed content.

For feedlots with lots of mixed *Bos indicus* content it was apparent that the stress to the animal of drafting mixed lots of *Bos indicus* cattle into like groups was considerable. As management systems at feedlots generally precluded pre-drafting animals into like groups prior to dispatch an alternative method of assessing *Bos indicus* content was required by industry.

Sherbeck et al (1996) showed that the *Bos indicus* content was positively associated with hump height. However using data from animals of known genotype they noted that at any one *Bos indicus* content there was a large range in hump height. In lieu of other indicators of *Bos indicus* content, MSA quantified the relationship between *Bos indicus* content and hump height adjusted for carcass weight and included it as an option in the MSA model. Initially this was included as a check on Belmont Red carcasses, but later it was used by feedlotters who were supplying lots with variable or unknown *Bos indicus* content. Over time the usage of hump height has increased until it is now preferred to NVDs for estimating *Bos indicus* content at grading (MSA, *unpublished data*).

The first task in this project was to develop a genomic algorithm to predict *Bos indicus* content from DNA SNP data using Beef CRC data. If this proved to be an accurate method of quantifying *Bos indicus* content, these algorithms were then used to predict *Bos indicus* content in several historical MSA datasets.

Using these historical MSA datasets, the value of using an estimate of *Bos indicus* content derived from hump and carcass weight in the MSA model to predict palatability could be compared to the accuracy of using *Bos indicus*

content derived from the genomic prediction equation in the MSA model to predict palatability.

As a further check of the hump height/*Bos indicus* function used in the MSA model a large industry data set, comprising 164,726 carcasses from 156 Queensland properties of known *Bos indicus* content was assembled. These properties were known to have stable breeding programs and so the phenotype was accurately defined. The phenotypic estimate of *Bos indicus* content was compared to the estimate predicted by MSA using and hump height and carcass weight. This data set was used to estimate the magnitude of any bias in *Bos indicus* content on the MSA index when *Bos indicus* content was estimated from hump height and carcass weight. The equations initially proposed by MSA were then optimised to minimise the bias.

Overall summary of data sets utlilised in this report

Over time a number of datasets have been generated as part of MSA and associated experiments that can be used to test slightly different aspects of the link between *Bos indicus* content. For this report the estimate of Bos indicus content from hump will be referred to as BB_Hump, whilst the estimate from the DNA SNPs will be referred to as BB_Genotype. Finally if *Bos indicus* content from properties with a stable breeding program was known as BB_Phenotype. The datasets used in this report are summarised in Table 1.

In summary a total of 5 separate experiments were used in this report. The first data set was from the Beef CRC III and it was used to assess the efficacy of predicting *Bos indicus* from genotype and hump height. Subsequently data from three MSA experiments were used to test the relationships between *Bos indicus* content (estimated by either BB_Hump or BB_Genotype) and eating quality. Finally an industry data set of known breeding was used to optimise the equation relating hump height and carcass weight to *Bos indicus* content (BB_Phenotype).

Objectives

- To develop algorithms to estimate *Bos indicus* content from high density SNP chips
- To understand the accuracy of predicting *Bos indicus* content using genetic markers compared to hump height and preliminary analysis of their relationship with consumer eating quality
- More accurate quantification of the impact of *Bos indicus* content on eating quality

Table 1 Summary of the datasets available use in this report

Data set number	Dataset Name	Number	Breed types	Sensory (MQ4 score)	Shear Force	Hump Height	Geno types
1	CRC 3* (genotypes)	15384	Brahman, Composites Crossbreds, *Bos taurus*	-	-	-	Y
2	Long Distance Transport experiment	323	Varying BB content	Y			
3	Senapol evaluation	50	Senapol X Brahman and Brahman	Y		Y	Y
4	Rigor temp experiment	50	Varying BB content	Y			
5	Industry phenotypes	82363	Varying BB content	-		Y	N

* Used to generate breed composition equations

Each of the five datasets used in this study was characterized by different levels of recording and structure. Thus each dataset was used to test individual objectives. Summary of objectives of analysis of each dataset follows

1. Dataset 1, CRC III
    a. Development and validation of BB_Genotype prediction equations
2. Dataset 2 , Long Distance transport experiment
    a. Quantification of the relationship between BB_hump and BB_Genotype
    b. Test the effect of BB_hump and BB_Genotype on consumer eating quality
3. Dataset 3, Senapol evaluation
    a. Quantification of the relationship between BB_hump and BB_Genotype
4. Dataset 4, Rigor temperature experiment
    a. Quantification of the relationship between BB_hump and BB_Genotype
    b. Test the effect of BB_hump and BB_Genotype on consumer eating quality
5. Dataset 5, Industry phenotypes
    a. Estimation of the relationship between BB_hump and vendor declared Brahman content (BB_Phenotype)

2. Estimating Brahman percentage from SNP genotypes using the CRC III dataset (Dataset 1, Table 1)

The first step was to develop a prediction of BB_Genotype and test its efficacy. In order to estimate breed composition from genomic information a large database of genotyped animals with known Brahman content were required. The CRC III dataset with 15,384 genotyped animals with pedigree was used for this purpose. This allowed for the development of the prediction equations using a test data set and their subsequent validation using an independent set of data.

The training data set were randomly selected from the different breeds and the remaining animals used to validate the predictions.

Objective

- Development and validation of BB_Genotype prediction equations

Methods

To develop genomic prediction equations and evaluate their efficacy for prediction of *Bos indicus* content the CRC III database of genotype and breed was used. To build the equations a training set of 5,650 animals and a validation set of 9,734 animals were selected from the total data set. Within the breeds animals were randomly assigned to the training and validation groups (Table 2). The diversity of breeds in the CRC III database meant there was a wide range of breeds and cross bred animals used to test the accuracy and precision of the *Bos indicus* content estimates.

The cattle within this project were genotyped on a number of SNP genotyping platforms which contain different numbers of SNP (from approximately 10,000 to 700,000). A subset of 5,817 markers that were common across all genotyping platforms were selected to be used in the estimation of BB_Genotype.

Table 2 Summary of breed composition of animals used in training and validation of genomic estimates of *Bos indicus* content (Dataset 1, Table 1)

Breed or breed cross	**Breed code**	**Training**	**Validation**	**Total**
Brahman	BBBB	2,000	3,045	5,045
Angus	AAAA	2,000	695	2,695
Charolais	CCCC	400	63	463
Hereford	HHHH	500	244	744
Limousin	LLLL	50	11	61
Murray Grey	MGMG	200	54	254
Shorthorn	SSSS	500	368	868
Angus x Brahman	AABB		40	40
Belmont Red	BRBR		764	764
Belmont Red x Brahman	BRBB		84	84
Brahman x (Charolais x Brahman)	CBBB		20	20
Charolais x Brahman	CCBB		197	197
Drought Master	DMDM		464	464
Hereford x Brahman	HHBB		30	30
Limousin x Brahman	LLBB		244	244
Santa Gertrudis	SGSG		1,563	1,563
Santa Gertrudis x Brahman	SGBB		30	30
Shorthorn x Brahman	SSBB		30	30
Tropical Composite	TCTC		1,788	1,788
	Total	5650	9734	15,384

Analysis Methods

Once the animals were selected for training and validation the program Admixture was used to develop estimates of BB_Genotype from data (Alexander and Lange, 2011; Alexander et al., 2009). This program has been used previously by (Frkonja et al., 2012) to estimate breed composition in beef cattle.

Results and discussion

The Admixture program was used to develop prediction equations for BB_Genotype using 5817 SNP that were common across all Illumina SNP platforms.

Figure 1 shows the estimated *Bos indicus* and *Bos taurus* composition for animals from the breed types used to validate the predictions (ie animals not used to develop the predictions of Brahman content). The genomic estimate of *Bos indicus* content in the various breed groups was consistent with expectation that the predicted closely aligned with the actual *Bos indicus* content, ie the Angus, Hereford and Shorthorn animals showed very low levels of Brahman content, whilst Brahman animals are estimated to have high levels of Brahman content. Cross bred animals such as the Angus – Brahman cross animals (AABB) tended to fall around 50% Brahman and Charolais-Brahman backcross animals fell just below 75%.

A regression of actual *Bos indicus* content against BB_Genotype was also performed and the results are presented in Table 3. The relationship between actual BB% and BB_Genotype was extremely high with a coefficient of determination of 98%. The slope of the relationship between Brahman content from pedigree and from the genomic prediction was 1.1 (slightly higher than the expectation of 1.0) with an intercept of minus 6% which was not significantly (P>0.05) different from zero.

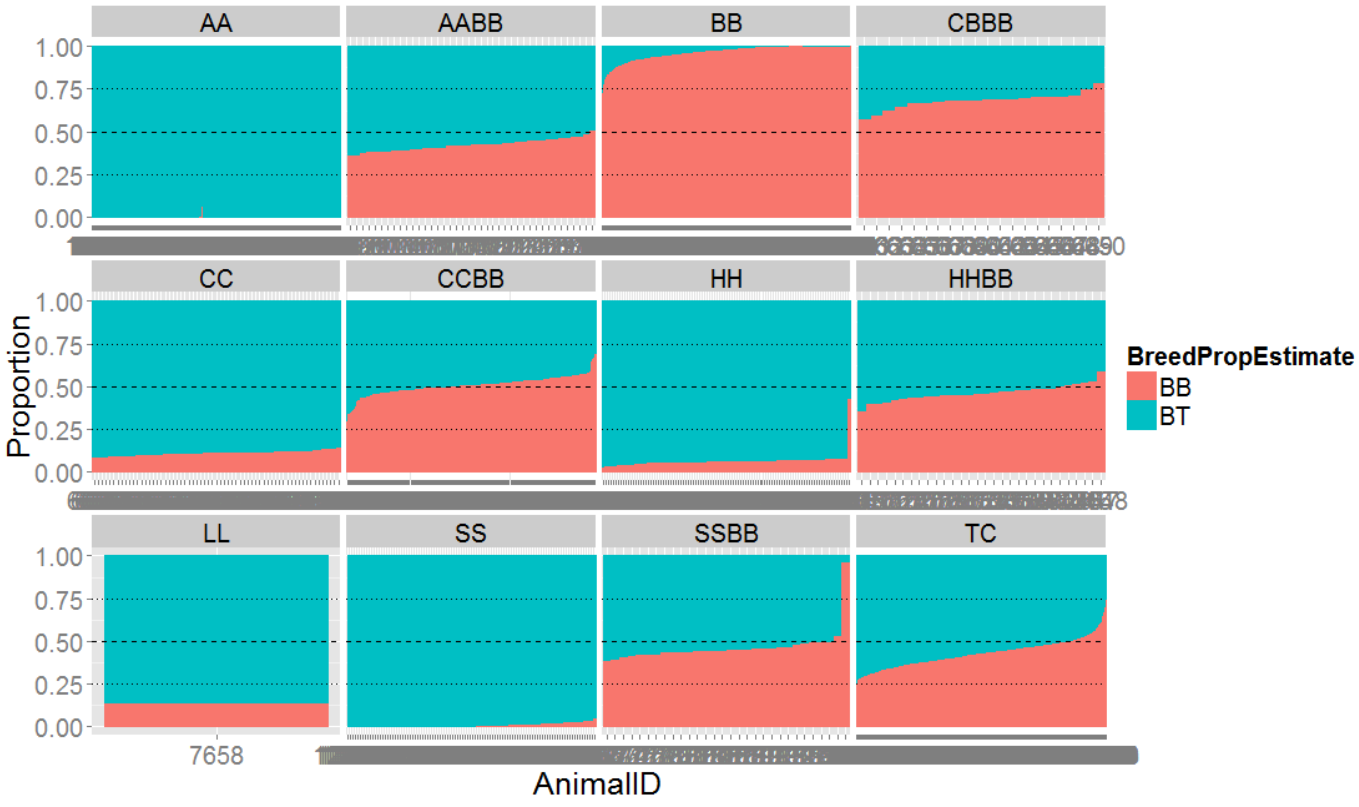


Figure 1 Prediction of proportion of *Bos taurus* and *Bos indicus* for validation animals within 12 breed types) using CRCIII data (Dataset 1, Table 1)

Table 3 Relationship between BB_Genotype and Brahman percentage from pedigree using Beef CRC III data (Dataset 1, Table 1)

Parameter	Value	SE
Intercept	-5.956	0.091
Regression	1.1063783	0.141
R^2	0.9814	
RSD	6.23	

Conclusion

Genomic estimates of BB_Genotype from SNP data were developed using approximately 5,650 cattle from a range of breed types. These genomic predictions were validated using breed composition of an additional 9,734 cattle of known breed composition. Of the animals with known breed composition 8,299 were from breeds with some proportion of Brahman content. The genomic predictions of breed composition were shown to be accurately predicted from genomic SNP data.

3. Comparison of Bos indicus content estimated from both genomics (BB_Genotype) or from hump height and carcass weight (BB_Hump) as predictors of eating quality in the MSA model using Long Distance Transport Dataset (dataset 2, Table 1)

The long distance transport (LDT) data set comprised 343 cattle, over a range of *Bos indicus* content, which had consumer sensory data on the striploin. The data provided an opportunity to estimate *Bos indicus* content by BB_Genotype and BB_Hump and compare their accuracy to predict palatability (MQ4) after adjustment for other MSA inputs.

Objectives

- Quantification of the relationship between BB_hump and BB_Genotype.
- Test the effect of BB_hump and BB_Genotype on consumer eating quality

Methods

Using DNA extracted from frozen blood only 323 of the 343 samples provided DNA profiles which were of sufficient quality to apply the genomic prediction to calculate *Bos indicus* content. In each replicate ca. 88 steers were subjected to four transport treatments. Details of the animals and experimental design are given by Polkinghorne et al (2013).

Bos indicus content was estimated using the MSA equation relating hump heights adjusted for carcass weight (see equation 2, section 5)**.**

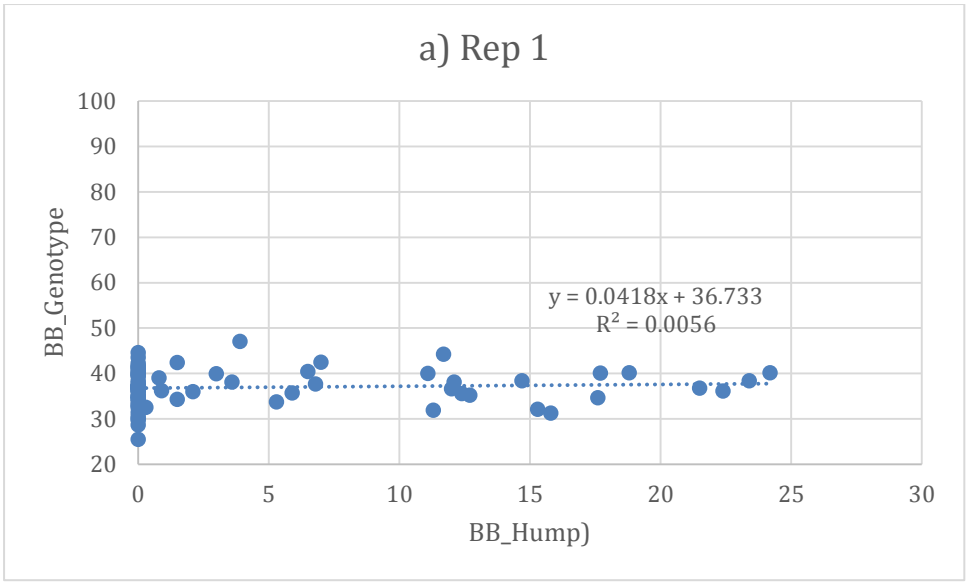
Results and discussion

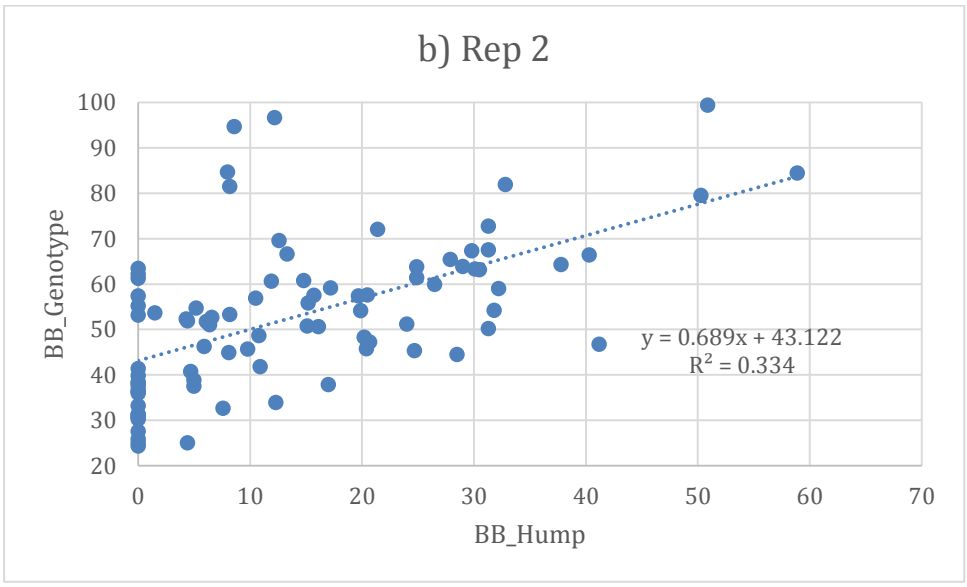
The means and ranges for carcass traits and *Bos indicus* content estimated from both the genomic prediction (BB_Genotype) and the MSA hump height/carcass weight equation (BB_Hump) were presented in Table 4. The four replicates were similar for most carcass traits. Replicate 1 had the lowest *Bos indicus* percentage estimated by both hump height/carcass weight (BB_Hump) and genomic prediction (BB_Genomic). Replicates 2 and 4 had ca. 20% BB_Hump, although BB_Genotype indicated that replicates 2, 3 and 4 all had ca. 50% *Bos indicus* content.

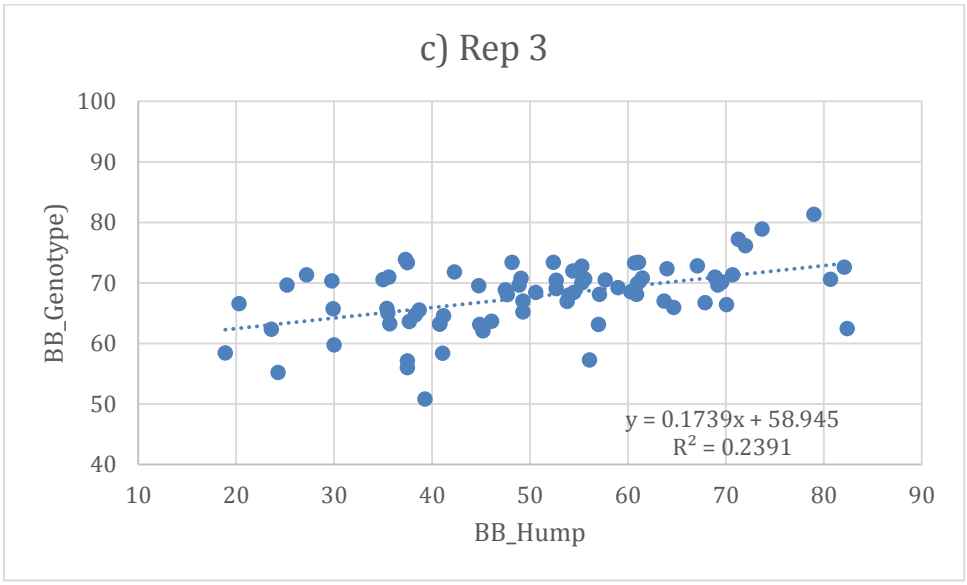
Table 4 Means and ranges for carcass traits from the 4 replicates of the long distance transport experiment (Dataset 2, Table 1)

Input	Rep1		Rep 2		Rep3		Rep4	
Traits	Mean	Range	Mean	Range	Mean	Range	Mean	Range
Number	74		88		77		84	
HSCW	335	293-380	294	255-335	313	243-391	302	262-358
Hump height	73	45-100	81	55-130	122	90-160	86	40-150
Ossification	173	120-200	153	110-350	199	150-350	155	130-230
Marbling	247	150-360	307	200-530	282	150-420	328	220-510
Ribfat	6	2-14	7	1-14	6	3-14	7	3-19
Ultimate pH	5.57	5.40-6.04	5.49	5.32-5.79	5.62	5.42-6.30	5.53	5.43-6.12
Meat colour	3	2-6	3	1.7-5	4	3-6	3	1.7-5
BB_Hump	4	0-24	14	0-59	51	19-82	19	0-79
BB_Genotype	37	25-47	53	24-99	68	51-81	69	11-100

Relationships between *Bos indicus* content estimated using hump/carcass weight and the genomic prediction for the 4 replicates are shown in Figures 2 a, b, c, and d


a) Rep 1
BB_Genotype
BB_Hump)
y = 0.0418x + 36.733
R² = 0.0056


b) Rep 2
BB_Genotype
BB_Hump
y = 0.689x + 43.122
R² = 0.334


c) Rep 3
BB_Genotype)
BB_Hump
y = 0.1739x + 58.945
R² = 0.2391

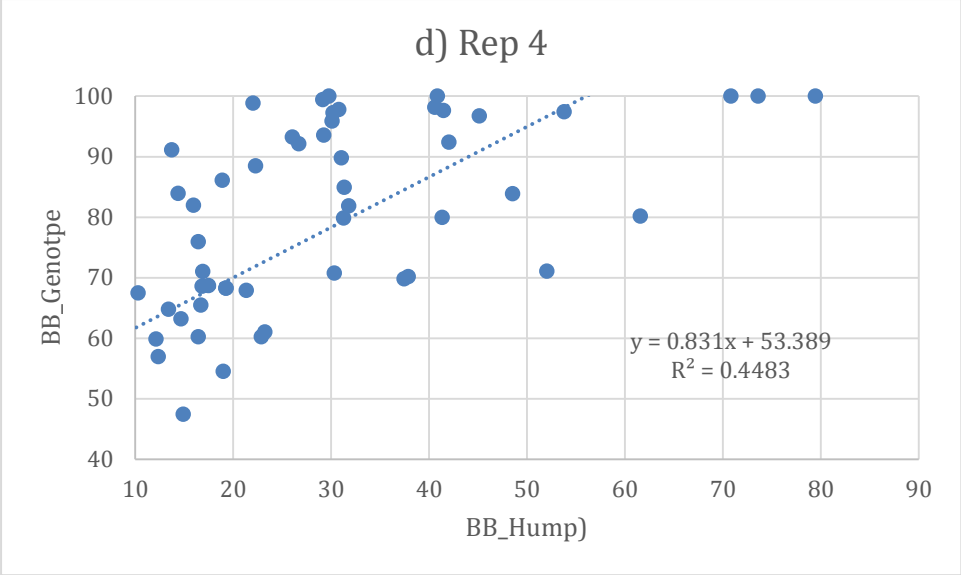


Figure 2 a, b, c and d. Relationships between *Bos indicus* content estimated using hump height/carcass weight and the genomic prediction for replicates 1, 2, 3 and 4 respectively using the long distance transport experiment (Dataset 2, Table 1)

Between replicates the relationship between the two measures of *Bos indicus* content varied widely. Replicate 1, which had the lowest *Bos indicus* content by both measures, had the poorest relationship between the two measurements with BB_Hump only accounting for less than 1% of the variance in BB_Genotype. Relationships were the highest in replicate 4 and intermediate for replicates 2 and 3. If all replicates were pooled then the overall relationship between BB_Genotype and BB_Hump had a coefficient of determination of 40%.

To compare the usefulness of both methods of estimating Bos indicus content on the ability to predict palatability both measures were included in separate models along with other grading inputs to predict palatability. The F ratios of terms in the model are shown in Table 5.

Table 5 F ratios for factors to predict palatability (MQ4) using the MSA model**.** Two model include Model a) BB_Genotype or model b) from BB_Hump along with other carcass traits using the long range transport experiment (Dataset 2, Table 1)

Independent Variable	df	Model a) F ratio	Model b) F ratio
BB_Genotype	1,312	**15.33**	
BB_Hump	1,312		**10.04**
Position	3,312	**13.17**	**16.05**
HGP	1,312	0.18	0.60
HSCW	1,312	2.68	2.40
Ribfat	1,312	2.28	1.76
Oss Score	1,312	1.92	2.49
Mb Score	1,312	**23.62**	**27.04**
pH	1,312	1.08	0.88
RSD		10.60	10.65
R^2		24.5	23.22

Bolded F ratios were significant at P<0.05

MSA models which included either BB_Genotype or BB_Hump were of similar accuracy in predicting palatability. For the same data set both had coefficients of determination of ca. 24% with an RSD of the order of 10.6.

For the LDT dataset the most important factors to predict palatability were *Bos indicus* content (by either BB_Hump or BB_Genotype), position within muscle and marbling score (see Table 5). Whilst terms for ossification score and pH terms were not significant (P>0.05) as expected the coefficients were negative (ie the trend was that higher ossification score and higher pH resulted in less palatable striploin samples). The negative coefficient for rib fat occurred because of its positive correlation with marbling score. By itself the relationship between ribfat and palatability was positive. The trend for a negative relationship between carcass weight and palatability was unusual.
As reported by Polkinghorne et al (2013) the ability of carcass traits to predict palatability in the LDT data set varied between the full data set compared with only those that met the thresholds for MSA (which included low pH <5.7, low meat colour <3, and high ribfat >3mm). These analyses showed that for all carcasses the accuracy increased from 15% to 26% for those that met the quality thresholds. The high proportion of carcasses that failed MSA in this data set (ie ca 40%) provided an opportunity to examine the ability of *Bos indicus* content term to predict palatability in carcasses that failed, or passed, MSA criteria for a variety of reasons.

There were 5 carcasses excluded for low ribfat and only 2 carcasses that had low pH (pH < 5.7) and high meat colour scores (meat colour scores > 3). These carcasses were excluded from the data set and the remaining data sorted into three groups, which included those that passed MSA thresholds (Normal), those that failed because of high pH and high meat colour (DFDpHamc) and finally those that failed because of high meat colour but had low pH (DFDamc).

Table 6 Coefficient of determination and RSD for the MSA Model fitted to the Long Distance Transport Datasets where a) Normal, b) DFDamc c) DFDamcpH (Dataset 2, Table 1)

Data set	Number of	EstBI by genomics		estBI by hump/HSCW	
	Carcasses	R^2	RSD	R^2	RSD
Normal	215	34.6	10.0	34.0	10.1
DFDamc	74	26.2	11.2	26.2	11.2
DFDamcpH	27	41.3	10.92	44.7	10.59

Proportions of variance the MSA model accounted for when fitted to the three data sets are shown in Table 6. The dataset where carcasses met MSA thresholds (ie pH < 5.7 meat colour < 3) accounted for ca. 34% of the variance in MQ4 score and had an RSD of 10, regardless of whether *Bos indicus* content was estimated using BB_Genotype or BB_Hump.

There were 74 carcasses in the sub group which had pH < 5.7 and high meat colour (ie DFDamc). Table 3 showed that this group (DFDamc) accounted for ca. 26% of the variance in palatability. What was of interest was that the regression coefficients for *Bos indicus* content, position and marbling were similar for both the Normal and DFDamc data sets. That is the higher *Bos indicus* content had a lower palatability as did the posterior portion of the striploin. The marbling coefficient showed that palatability increased with increased marbling.

The third data (DFDamcpH) which failed MSA due to high pH and high meat colour only had 27 carcasses and had the highest R^2. It should be noted from Table 6 this group had very low numbers and in the full MSA model few terms were significant. However with these limitations what was of interest were the regression coefficients for the various traits. Even though it was not significant (P>0.05) the slope for *Bos indicus* content input term whether it was estimated by BB_Genotype or BB_Hump was positive. Therefore in the small sample of DFDpHamc carcasses there was a trend (albeit not significant, P>0.05) for higher palatability with high *Bos indicus* content whether measured using genomics or hump height. In other words the normal relationships between input traits and palatability that are seen in most data sets did not appear to apply in the high pH data set.

Conclusion

The LDT data showed that at the lower range in *Bos indicus* content the relationship between estimates using BB_Genotype and BB_Hump was poor. However at the higher *Bos indicus* content there was reasonable agreement between the two methods of estimating *Bos indicus* content.

When used in the MSA model to predict eating quality there was no difference between the two methods of determining *Bos indicus* content. Given the ease and low cost of obtaining hump height and carcass weight this supports this method for use in the MSA model.

The LDT dataset was analysed in three subsets. It was concluded that those carcasses that failed MSA simply because they had high meat colour scores had similar relationships between input variables and palatability compared with those carcasses that eligible for grading. However those carcasses that had a high pH and high meat colour score had very different relationship between the input variables and palatability. This supports exclusion of high pH carcasses from the MSA grading system.

In terms of whether *Bos indicus* content could be adequately predicted from hump height these results showed little difference between MSA models which included a term for BB_Hump or BB_Genotype. Therefore the industry practise of estimating BB_Hump was a suitable alternative to knowing BB_Genotype.

4. Comparison of *Bos indicus* content estimated from both genomics (BB_Genotype) or from hump height and carcass weight (BB_Hump) as predictors of eating quality in the MSA model using data from the rigor temperature experiment (dataset 3, Table 1)

The rigor temperature data set comprised 50 carcasses which were selected at slaughter from a lot of 700 animals. A month before slaughter tail hairs were pulled from all animals which was used to extract DNA, genotype and generate BB_Genotype. Carcasses all had consumer sensory scores on the striploin aged for four different times.

Objectives

- Quantification of the relationship between BB_hump and BB_Genotype
- Test the effect of BB_hump and BB_Genotype on consumer eating quality

Methods

At knocking animals were allocated to three rigor temperature treatments (low rigor temperature, intermediate rigor temperature and high rigor temperature). The different rigor temperatures were achieved using none, moderate and excessive stimulation regimes. Within each carcass the left and right sides were alternatively allocated to two of three hang treatments being achiilles hung (AT), tenderstretch (TX) and super stretch (SS). In addition all rigor temperature cells were balanced with equal numbers of animals from the high and low percentiles for MVP tenderness.

Glycolytic rate was measured in the chiller by MSA. Sides were graded after 18 hours in the chiller. At boning nine primals from each side were collected and held at 1^0C for sample preparation. Sample preparation was undertaken over 4 days. Samples were aged at 1^oC and then frozen down in boxes at the

designated days (ie at 5, 28, 47 or 68 days post-mortem). Only sensory data from the striploin was used in the following analyses.

Results and discussion

Carcasses were typical of domestic bodies processed for the domestic supermarkets trade. Rigor temperature ranged from ranged from 10 to 40^{o}C. Also due to inclusion of animals with divergent MVP tenderness estimates this trait also showed a wide range.

Table 7 Means and range for carcass traits of the 50 carcasses in the rigor temperature experiment. (Dataset 3, Table 1)

Carcass traits	Mean	Min	Max
Carcass weight	226	197	279
Hump	69	40	130
Marbling	287	140	430
Ossification	169	110	380
Ribfat	5	1	20
EMA	66	50	80
Temperature at pH6	29	10.5	39.6
Tenderness MVP	0.21	-0.38	0.70
BB_Genotype	40.0	0	94
BB_Hump	13.0	0	69

The average BB_Genotype content was 40% although individual carcasses ranged from 0 to almost 100%. The average BB_Hump was only 13% and had a slightly smaller range from 0 to 70% (Table 7).
The relationship between the two estimates of *Bos indicus* content are shown in Figure 2. It was clear that BB_Hump underestimated BB_Genotype up until about 50% BI content. Thereafter it increased although it was still an underestimate of the BB_Genotype.

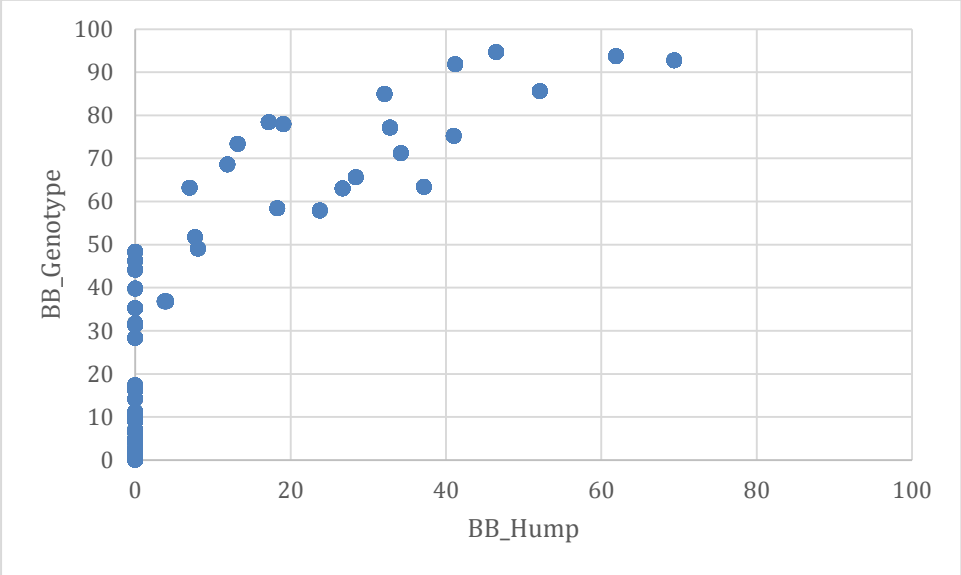


Figure 3 The relationship between *Bos indicus* content estimated using hump height/carcass weight and the genomic prediction in the rigor temperature experiment (Dataset 3, Table 1)

Table 8 F ratios for factors to predict palatability using the MSA model. The two MSA models included *BB_Genotype (Model 1) or BB_Hump (Model 2)* along with other carcass traits used in the MSA model in the rigor temperature experiment. (Dataset 3, Table 1)

MSA traits	Df	F ratio	F ratio
		Model 1	*Model 2*
BB%Genotype	1,281	**18.52**	
BB%Hump	1,281		**12.62**
Position	2,281	**7.19**	**7.09**
Sex	1,281	1.49	1.89
Hang	2,281	**26.32**	**26.13**
Hang*position	4,281	1.74	1.72
HSCW	1,281	0.51	0.65
Ribfat	1,281	0.73	0.57
Oss	1,281	2.11	2.11
Mb	1,281	**26.64**	**24.91**
pH	1,281	3.22	2.80
Days aged	3,281	**15.57**	**16.48**
RSD		10.46	10.55
R^2		39.38	38.16

Table 8 showed the F ratios for the factors used in the MSA model when predicting palatability. Given that BB_Hump underestimated *Bos indicus* content at the lower end of the range.it was surprising that both models accounted for a similar proportion of variance in palatability and had similar RSDs. *Bos indicus* content was important in both models, although BB_Genotype had a slightly higher F ratio than BB_Hump. Other important factors were position, hang, marbling score and days aged. Coefficients for

other input traits aligned with the MSA model, ie ossification score and ultimate pH had a negative effect on palatability.

When adjusted for other terms in the MSA model the regression coefficients for the two estimates of *Bos indicus* content differed slightly. When *Bos indicus* content was estimated by BB_Hump the regression coefficient indicated that an increase in *Bos 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. The relationship between BB_Hump and BB_Genotype was obviously curvilinear (see Figure 3). The non-linear relationship was confirmed when a curvilinear term for *BB_Hump (P<0.054)* was included in model 2 in Table 8. This resulted in a marginal increase in the coefficient of determination to 39.9%. A curvilinear term for BB_Genotype in Model 1 was not significant (P>0.05).

Conclusion

The current MSA equation to predict *Bos indicus* content from hump and carcass weight (BB_Hump) underestimated *Bos indicus* content at the lower levels. However for this data set there was no difference in accuracy to predict palatability using either BB_Hump or BB_Genotype.

5. Comparison of Bos indicus content estimated from both genomics (BB_Genotype) or from hump height and carcass weight (BB_Hump) as predictors of eating quality in the MSA model using data from Senapol Brahman cross and high grade Brahman steers (dataset 4, Table 1)

This data set comprised 50 animals half being Senapol x Brahman first cross and other remainder being high grade Brahman steers. The carcass traits were typical of domestic specifications.

Objectives

- Quantification of the relationship between BB_hump and BB_Genotype
- Test the effect of BB_hump and BB_Genotype on consumer eating quality

Table 9 Means and range for carcass traits of the Senapol x Brahamn cross and Brahman steers (Dataset 4, Table 1)

	Senapol x Brahman			Brahman		
Carcass traits	Mean	Min	Max	Mean	Min	Max
Carcass weight	239	218	284	237	209	270
Hump	88	75	105	138	110	175
Marbling	285	210	380	296	200	390
Ossification	131	100	150	128	110	140
Ribfat	5.5	4	8	7.2	4	13
EMA	68	55	82	64	49	74
Ultimate pH	5.44	5.33	5.56	5.46	5.35	5.53
BB_Genotype	61	54	66	98	91	99
BB_Hump	24	9	37	73	46	100

Results and discussion

The mean carcass traits for the Brahman and Brahman X Senapol steers are shown in Table 9. The mean BB_Genotype was 61% for the Senapol x Brahman steers, although it varied substantially (from 54 to 66%). Interestingly BB_Hump estimated a much lower in Brahman content (average 24%, ranging from 9 to 37%). Given that these animals were at least half Brahman it showed that BB_Hump underestimated actual *Bos indicus* content in both breed groups.

Figure 4 showed the relationship between BB_Genotype and BB_Hump for the Senapol dataset. As expected there was relatively little variation within the two groups for *Bos indicus* content predicted by genomics compared with the relatively large variation for *Bos indicus* content predicted from hump height and carcass weight.

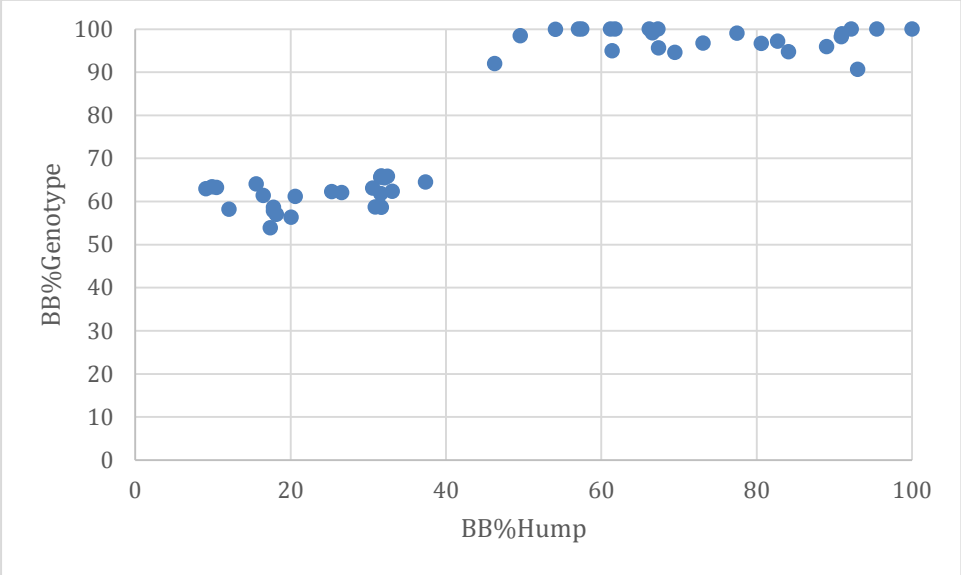


Figure 4 The relationship between *Bos indicus* content estimated using BB_Genotype and BB_Hump for Senapol Brahman cross and Brahman steers (Dataset 4, Table 1)

6. Accuracy of Brahman percentage estimated from hump height assessed using vendor declared Brahman percentage (dataset 5, Table 1)

A processor provided carcass grading records on 82,363 carcasses from 156 vendors. These carcasses were from producers which were considered to run stable breeding programs and therefore the *Bos indicus* content as per their NVD accurately reflected the *Bos indicus* content of their herds. This data set was used as an additional data source for benchmarking the accuracy of hump height based predictions of *Bos indicus* composition.

Objective

- Estimation of the relationship between BB_hump and vendor declared Brahman content

Methods

The grading records from the 156 properties were provided by an processing company. As the number of carcasses varied per lot from 36 to 5350, subsequent analyses were undertaken using lot means (Table 10).

Table 10 Summary of the number of records, BB_Vendor and BB_Hump (n=156, Dataset 5, Table 1)

Parameter	Mean	Stdev	Min	Max
Number of animals/lot	527		36	5350
BB_Vendor	34.3	31.1	0	100
BB_Hump	21.7	19.9	0	83

Table 10 showed that the average BB_Vendor was ca. 13% higher than for BB_Hump. In keeping with the smaller mean, BB_Vendor also had a higher variance and greater ranger than BB_hump.

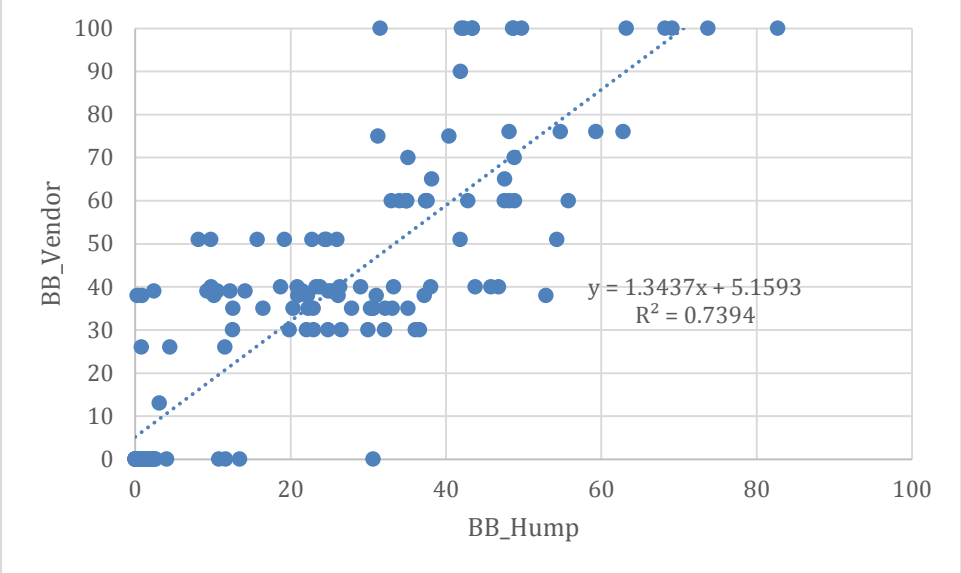


Figure 5 The relationship between BB_Vendor and BB_Hump for lot of cattle from the Industry database (Dataset 7, Table 1)

The relationship between BB_Vendor and BB_Hump using the industry vendor data set was shown in Figure 5.
The equation was

BB_Vendor = 5.2 + 1.3*BB_Hump (equation 1)

Overall this relationship between group means was high with a coefficient of determination of 74%. If the BB_Vendor was assumed to be the best available estimate of *Bos indicus* content, at low levels of BB_Hump the actual *Bos indicus* content was underestimated. The underestimation increased as BB_Hump increased until 70% BB_Hump, when the BB_Vendor was contrained to 100%.

To place the bias into an applied context the difference in the MSA Index was calculated using BB_Hump and BB_Vendor estimates. The MSA Index was calculated for a 300kg steer carcass, no HGP, marbling score 300, ossification score 200, ribfat of 5.6 in 10% increments of BB_Hump.

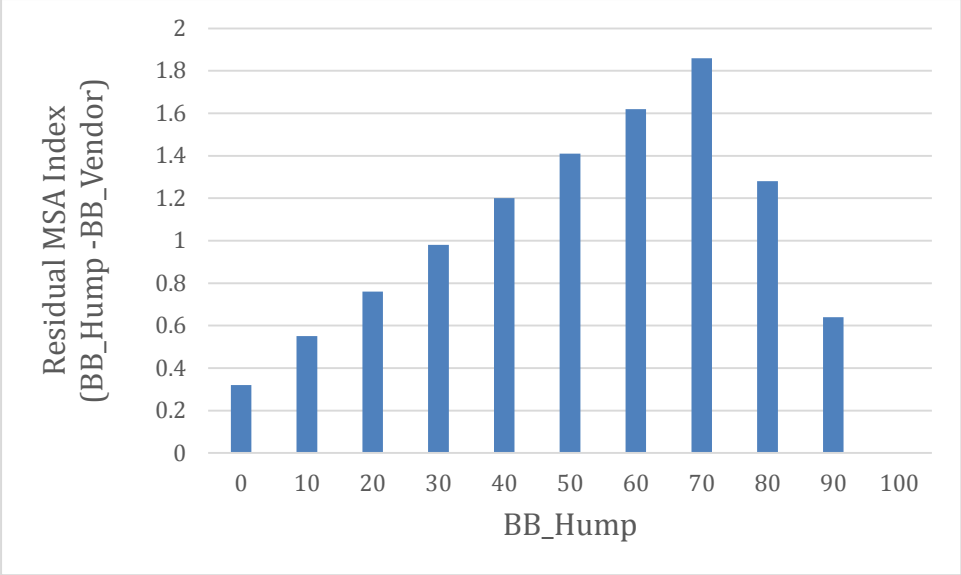


Figure 6 The residual MSA Index (BB_Hump – BB_Vendor) in 10% increments (calculated for a 300kg steer carcass, with no HGP implant, marbling score 300, ossification score 200 and ribfat 6mm) as a function of BB_Hump (Dataset 5, Table 1)

Figure 6 showed that based on the industry vendor data set the use of BB_Hump tended to underestimate vendor *Bos indicus* content resulting in higher MSA index. From Table 10 the average underestimation for the 156 vendors was of the order of 12% in *Bos indicus* content which would translate to an average increase of ca. 1.0 unit in the MSA index from using BB_Hump as opposed to using BB_Vendor. Perhaps of more concern was that the bias was not evenly spread across the range of *Bos indicus* content. As shown in Figure 6 the underestimation in terms of the MSA Index was small at the low BB_Hump rising to a maximum at 70% BB_Hump and then decreasing as the BB_Vendor was constrained to 100%.

The magnitude and the pattern of bias in the MSA index from using BB_Hump as opposed to the actual *Bos indicus* content in the model depends upon the confidence in the BB_Vendor estimates. Certainly the estimates for the current analysis were from a large data set of over 160,000 carcasses. Also the underestimate of the current MSA Hump/Carcass weight equation to predict BB_Genotype was consistent with the trend in the smaller experimental data set (datasets 2,3,5 Table 1), although the actual magnitude of the bias varied between data sets.

General discussion and conclusion

The genomic prediction was able to accurately estimate Brahman composition as assessed with regression on pedigree breed composition. A set of 5800 SNPs that are common across all current bovine Illumina SNP chips was used to develop a prediction equation for BB_Genotype The regression explained approximately 98% of the genetic variation. 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 study by Frkonja et al 2012 the breeds used were much less divergent than *Bos indicus* and *Bos taurus* (Simmental and Red Holstein Friesian) and a much smaller training population was used (495 cattle). Likewise Kuehn et al. (2011) was able to explain between 77% and 92% of the variation in breed composition, in this case working within *Bos taurus* beef breeds. Again in their study the number of animals included in both development and validation were much smaller than in the current study. Given that the *Bos indicus* and *Bos taurus* animals belong to different subspecies and probably diverged from their common ancestor many thousands of years ago the success of the genomics prediction equations was not surprising.

These genomic prediction equations were then used to predict BB_Genotype for individual carcasses from a number of small MSA data sets. The aim was to compare the BB_Genotype estimate with an estimate derived using hump height and carcass weight (BB_Hump). For the four experiments the current function used in the MSA Model based on hump height and carcass weight provided a reasonable estimate of BB_Genotype, although in most cases it was an underestimate of BB_Genotype.

The underestimate of *Bos indicus* content BB_Hump was confirmed using a large industry data set from producers with stable breeding programs. Again the relationship between BB_Vendor and BB_Hump indicated that the use of hump height and carcass weight underestimated actual *Bos indicus* content and hence would inflated palatability estimates from the MSA model. From the large industry data set the average underestimate in *Bos indicus* content using BB_Hump was of the order of 12% which translated to ca. a 1 unit increase in MSA Index.

The current excel Hump/carcass weight function is written as
BB%Hump = MIN(MAX(0,10*(HH/10-HSCW/100),100)) (equation 2)
Where hump height = HH in mm and carcass weight = HSCW in kg

Equation 2 can be simply modified by changing the coefficient 10 to 15. In effect the relationship between BB_Vendor and BB_Hump became
BB_Vendor = 3.8+ 0.99*BB_Hump (equation 3)

Effectively changing the coefficient in equation 2 reduced the average bias in predicting BB_Vendor from BB_Hump to ca. 4% and because the slope was ca. 1 this bias was consistent across the range of *Bos indicus* content.

To place this in an applied context the bias in *Bos indicus* content was estimated in units of the MSA Index. This was demonstrated in Figure 7 where the bias in the MSA Index from using BB_Hump in either the current or modified functions.

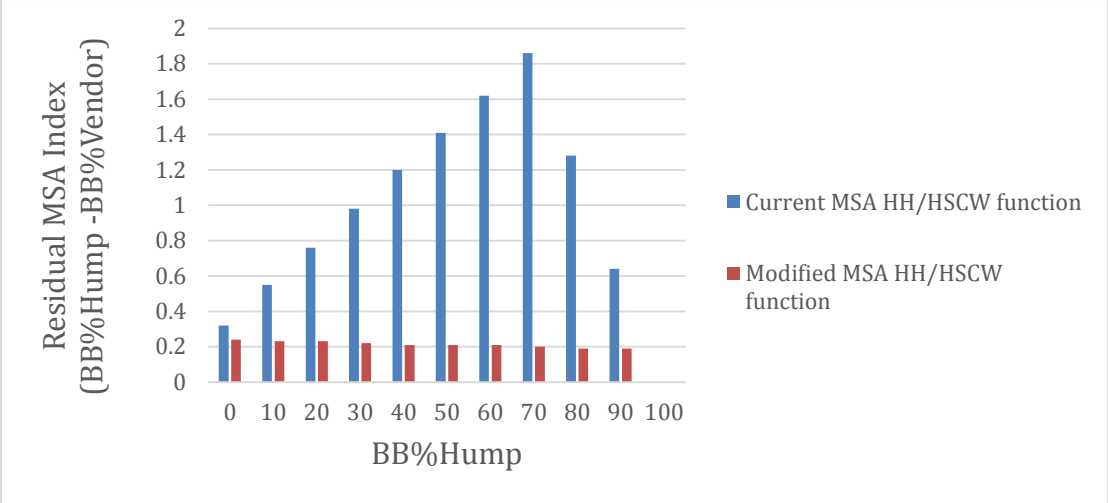


Figure 7 The residual MSA Index (BB_Hump – BB_Vendor) in 10% increments (calculated for a 300kg steer carcass, with no HGP implant, marbling score 300, ossification score 200 and ribfat 6mm) as a function of BB_Hump using the current conversion in the MSA model compared to the modified coefficient.

If there is sufficient confidence in the producer estimates of *Bos indicus* content from the industry dataset it is recommended that the coefficient in equation 2 using to calculate BB_Hump from hump height and carcass weight be changed from 10 to 15. This will effectively minimise the bias and distribute it more evenly across the range of *Bos indicus* content.

7. Implications

The estimation of *Bos indicus* content and its use in the MSA grading system was examined using a number of historical data sets. The results showed that genomics provided a very accurate tool to predict *Bos indicus* content in animals of unknown breed content. Also BB_Hump estimated from hump height sand carcass weight had a similar accuracy at describing palatability as using BB_Genotype when adjusted for the other MSA input traits.
However there was a trend for the current function used in the MSA model used to calculate BB_Hump resulted in an underestimate particularly at the lower *Bos indicus* contents. Using a large industry data sourced from herds *Bos indicus* content it was shown that a slight modification in the equation used to calculate BB_Hump effectively minimized the bias in terms of the MSA Index across the full range of *Bos indicus* content.

8. References

Alexander, D. H., and K. Lange. 2011. BMC bioinformatics 12:246.

Alexander, D. H., J. Novembre, and K. Lange. 2009. Genome research 19:1655-1664.

Frkonja, A., B. Gredler, U. Schnyder, I. Curik, and J. Solkner. 2012. Anim Genet 43:696-703.

Kuehn, L. A., J. W. Keele, G. L. Bennett, T. G. McDaneld, T. P. Smith, W. M. Snelling, T. S. Sonstegard, and R. M. Thallman. 2011. J Anim Sci 89:1742-1750.

O'Connor SF, Tatum JD, Wulf DM, Green RD, Smith GC 1997. Journal of Animal Science 75:1822-1830

Perry, D., P. J. Nicholls, and J. M. Thompson. 1998. J. Anim. Sci 76:87-95.

Polkinghorne R, Thompson JM, Philpott J (2013) Transport duration effects on MSA eating quality. Final Report B.NBP.0722. Meat and Livestock Australia Sydney.

Rymill, S. R. (1997). Master Rural Science thesis, University of New England, Armidale.

Shackelford, S. D., Wheeler, T. L., & Koohmaraie, M. (1995).Journal of Animal Science, 73, 3333–3340.

Sherbeck JA, Tatum JD, Field TG, Morgan JB, Smith GC (1995). Journal of Animal Science, 73, 3613–3620.

Sherbeck, J., J. Tatum, T. Field, J. Morgan, and G. Smith. 1996. J. Anim. Sci 74:304-309.