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The economics of breeding to improve eating quality of beef using tenderness marker panels

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Abstract

The economics of including tenderness markers within MSA was examined in a series of simulation analyses based on a commercial data set of cattle with MVPs for tenderness. In this study the relationships for the 39 muscles individual muscles in the MSA model between MVPs and consumer palatability scores (MQ4) were estimated from data from three experiments. Premiums for the different grades was based on willingness to pay (WTP) data from consumers. The combination of MQ4 for each muscle, yield and WTP data allowed the calculation of carcass value for each carcass in a commercial case study herd with and without gene markers. A large range in individual carcass values differences (up to $150/head) was observed with and without the gene marker tests.

It was found that little marginal benefit obtained from harvesting cuts based on improved estimates of eating quality using the genetic markers. Assuming a cost of $20/head to undertake the gene test a population would need to have a tenderness MVP which was 0.26, 0.61 or 0.50 lower than the current average MVP to cover the cost of testing in scenarios which assumed the full MSA premiums for all graded cuts, half the premiums and then only harvesting the four sweet cuts (striploin, tenderloin, cube roll and rump). The current scenario of a threshold (3 star of better) premium for quality showed little benefit in using gene markers.

Selection of sires with improved MVPs could increase the carcass value of the progeny. It was estimated that selection of elite sires from within the example dataset could increase the carcass value by $11.3, $19.2, 23.9 and $29.1 with 30%, 10% 5% and 1% of sires selected respectively. Thus one round of selection would generally not cover the cost of testing individual progeny with current prices unless an elite sire from the top 5% or better was used. Using either the 56 SNP panel or individual SNPs the response to selection was predicted to plateau after 3 to 4 generations suggesting that if the technology was to be adopted for MSA an investment in research funds to continually update and revalidate genomic EBVs for tenderness is required. The results were discussed in terms of future research programs which would be needed to support incorporation of gene markers into MSA.

Executive summary

Meat Standards Australia (MSA) is an eating quality assurance program underpinned by a large body of consumer tests (Watson et al., 2008). The MSA grading system is unique in the world in that it assigns a palatability score to every cut/cook combination. To achieve this it uses empirical prediction equations to estimate eating quality from commercial inputs collected at grading. Previous MLA research has shown that individual gene markers (i.e. T1, T2, T3 and T4) and MVP predictions impacted on beef palatability (i.e. MQ4 score) for a range of muscles(Cafe et al., 2010b; Greenwood et al., 2013; Thompson, 2011; Weaber and Lusk, 2010; White et al., 2005). However the pathway to application and its use in genetic improvement is unclear. The first step in incorporating these results in MSA pathways is to examine the potential returns for using MVP predictions for harvesting and in selection of superior sires.

Existing data sets were used to estimate the effect of the tenderness gene markers on palatability across the musculature of the carcass. These estimates were used to calculate the expected effect of the tenderness gene markers on the MSA Index for the 39 muscles in the MSA model. In addition the economic impact of the tenderness gene marker will be estimated for an enterprise where cuts were simply harvested from a population. The economic impact of selection for tenderness gene markers in open and closed breeding systems was also be evaluated.

The cost of currently testing the SNP for the tenderness genes is currently of the order of $40/head. The fixed costs of testing are of the order of $7/head so it would be unlikely that a commercial service would be offered at less than $20/head. It was found that harvesting cuts based on the tenderness MVP without selection was unlikely to increase returns unless the average of the group had substantially lower MVPs than the across breed base (MVP at least 0.26 below). Selection of sires with improved MVPs could increase the carcass value of future progeny. It was estimated that selection of elite sire from within the example dataset could increase the carcass value by $11.3, $19.2, 23.9 and $29.1 with 30%, 10% 5% and 1$ of sires selected respectively. Therefore it is only with a high selection differential (greater than 5%) that one generation of testing would be likely to cover the cost testing.

Prior to any implementation better estimates of the relationship between tenderness MVP and MQ4 for the 39 muscles in the MSA model are required. It is suggested that increased consumer testing is required to cover the full musculature or a better means of predicting the regression coefficients for individual muscles as a function of MQ4 be developed. To this end a more strategic approach may be to invest in experiments to better understand the relationship with ageing rate and the mechanisms by which gene markers influence palatability.

Using either the current 4 markers or the 56 SNP panel it was predicted that response to selection based on the tenderness MVP would plateau as the genes became fixed in the population after 3 to 4 generations of selection. To avoid this better genomic functions need to be estimated using the full number of available SNPs. It is suggested that the current BIN resource be used to develop genomic predictions that are focused on using current sires.

In conclusion it is unlikely that producers could benefit from harvesting cuts based on MVPs, however this depends where the base for the MVP is set. Currently it is set at the mean of MVPs across all breeds. Therefore breeds with lower than average MVP would be penalized if they tested and reported MVPs on their animals. It was clear from the modeling exercises that selection for a tenderness MVP would lead to short to medium term improvements in MQ4 of selected animals. If the tenderness MVP is to be an input in the MSA model there are limited ways to defray the relatively high per animal testing costs. At $20/head the testing costs were of the order of 0.10$/kg carcass weight, whereas this would be effectively reduced by increasing carcass weight. Alternatively if used within a closed supply chain where product is marketed under a brand it may not be necessary to test individual progeny, rather the assumption is that a higher frequency of favourable tenderness SNPs will further promote the brand in terms of consumer satisfaction.

Given the finite lifespan of the current MVP which is based largely on the 4 tenderness SNPs (it was predicted that response to selection would plateau in 3 to 4 generations) it was suggested that the current beef information nucleus projects be harnessed to provide prediction equations using new closely spaced markers.

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1. Background

The tenderness gene markers are located within the calpain/calpastatin genes and variants lead to different activity levels of the calpain and calpastatin genes (Barendse, 2002; Cafe et al., 2010a; Fortes et al., 2013; Robinson et al., 2012, Greenwood et al., 2013). These genes are largely responsible for protein turnover in the body of the live animal. After slaughter their activity carries over from the live animal to the carcass where they are largely responsible for proteolysis in the carcass. These changes in the post-mortem muscle are ultimately seen as changes in tenderness that occur with the post-mortem ageing of meat (Koohmaraie and Geesink, 2006). Initially four markers were promoted to the Australian beef industry as a star system which was simply a summation of the number of copies of favourable SNPs in an individual animal. More recently Pfizer Animal Genetics released a molecular value prediction (MVP) for tenderness based on a 56 SNP panel (which included the four tenderness genes), along with other SNPs which impact to varying degrees on tenderness. The tenderness MVP function has been calibrated using shear force data so the more negative the tenderness MVP the more tender the meat.

The Meat Standards Australia (MSA) grading system has been developed to use commercial input traits to predict the palatability of individual beef cuts cooked using a variety of cooking methods (e.g. Polkinghorne et al., 2008a; Polkinghorne et al., 2008b; Thompson, 2002). The MSA model grades individual cuts of beef from the carcass into one of four grades being unsatisfactory (2 star), good everyday (3 star), better than everyday (4 star) and premium (5 star). The benefits arising from implementation of MSA to the Australian beef industry are considerable (Griffith et al., 2009, 2012), particularly given that currently industry adoption of the different grades is only in the most rudimentary form with often no distinction between 3, 4 and 5 star grades (i.e. all graded cuts are bulked and sold as MSA graded when they reach the 3 star threshold). The consumers willingness to pay (WTP) responses reported by Lyford et al., (2010) clearly showed that consumers were willing to pay more for better quality beef. Therefore even though the current use of MSA has generated substantial premiums for all participants in the supply chain (Griffith et al., 2009, Griffith and Thompson 2012), the use of all three grades at retail where the

higher quality grades commanded a premium would give a clearer price signal for producers to implement new technology such as the gene markers for tenderness.

The tenderness gene markers are currently marketed to the beef industry via the seedstock industry. Whilst improvements in the seedstock area will be eventually passed on to the commercial sector, progress will generally be slow, particularly for a trait such as tenderness where it may be difficult to identify a clear benefit for the commercial sector. It is unlikely that producers will invest in technology to improve tenderness unless they are paid for it. Uptake would be increased dramatically if a 'pull' effect was created whereby improvements in tenderness could be easily identified and producers paid directly for this improvement. The MSA grading scheme, where producers are rewarded for eating quality, could provide that 'pull' effect.

In addition to use by the seedstock industry tenderness markers may also have a role as a management tool for either drafting animals prior to sale or carcasses after slaughter into different quality groups. Groups of animals or carcasses which carried the favourable tenderness SNPs would attract a higher MSA grade and therefore a premium at slaughter. An additional benefit from the improved prediction accuracy of the MSA model would be a more consistent product being offered within any of the grades.

A recent US study by Weaber and Lusk (2010) showed how using the tenderness gene markers in sire and dam selection strategies resulted in changes in consumer demand which increased profitability by up to $10 per carcass per year. However the extrapolation of their results to Australian production systems which use the MSA grading scheme was not straight forward.

In their study,Weaber and Lusk (2010) assumed that improvements in the eating quality of the striploin were equally reflected across the musculature of the carcass. In contrast the results from Greenwood et al (2013) indicated the tenderness MVP interacted with cut, with those muscles that had the faster ageing rate showing the larger gene marker effect. Given the MSA model shows that different muscles have a wide range in palatability and may interact with gene markers it was perhaps too simplistic to assume that changes in one muscle such as the striploin would be reflected over all muscles in the carcass.

In our report the limited experimental data available on the relationship of the tenderness MVP on palatability for individual muscles was used to extrapolate to all muscles in the carcass. As changes in palatability were assumed to be related to changes in value, it was possible to convert palatability to value. This provided the basis to model the impact of the gene marker technology under a number of different management and breeding scenarios on both palatability and dollar value.

The evaluation undertaken in this report uses a template described in Appendix 1 to evaluate the impact of gene technologies on both eating quality and value to the Australian beef industry. The impact of the gene marker technology was extrapolated from several muscles to the full musculature. The template then used the MSA model to estimate the effects of the gene marker technology on the 39 MSA cuts. This allowed the impact of the technology on the MSA index to be estimated. The impact of the gene marker technology on carcass value assumed a range of harvesting options (ie, what MSA cuts were being collected) and the pricing premiums. Finally changes in carcass value were modeled using several breeding scenarios which placed selection pressure on the tenderness SNPs.

1.1 Project objectives

The project used existing data sets to estimate the effect of the tenderness gene markers on palatability across the musculature of the carcass. These estimates were then used to calculate the expected effect of the tenderness gene markers on the MSA Index. The economic impact of the tenderness gene markers was also estimated for an range of management and breeding options.

2. Methodology

The evaluation of the tenderness gene markers involved the following steps

1. Collation of current data sets on the relationship between the tenderness MVP and palatability for specific muscles and extrapolation to the 39 muscles in the MSA model.
2. Development of prediction equations to allow carcass yield and cut distribution in a domestic beef population to be estimated
3. Estimation of the effect of the tenderness MVP on the MSA Index

4. Estimation of the economic impact of the tenderness MVPs on carcass value
    a. Applying both a threshold effect for all MSA graded product and different price premiums for the different quality grades
    b. Only harvesting high value cuts from the carcass
    c. Assuming that MSA operates only a threshold effect where the same premium is paid for 3 star or better grades
    d. Response in value following a selection of elite bulls for one set of progeny
    e. Response to selection based on current tenderness MVP (which contains 56 SNP markers)
    f. Response to selection based on hypothetical new MVP based on with markers linked to all genes across the genome genomic breeding value.

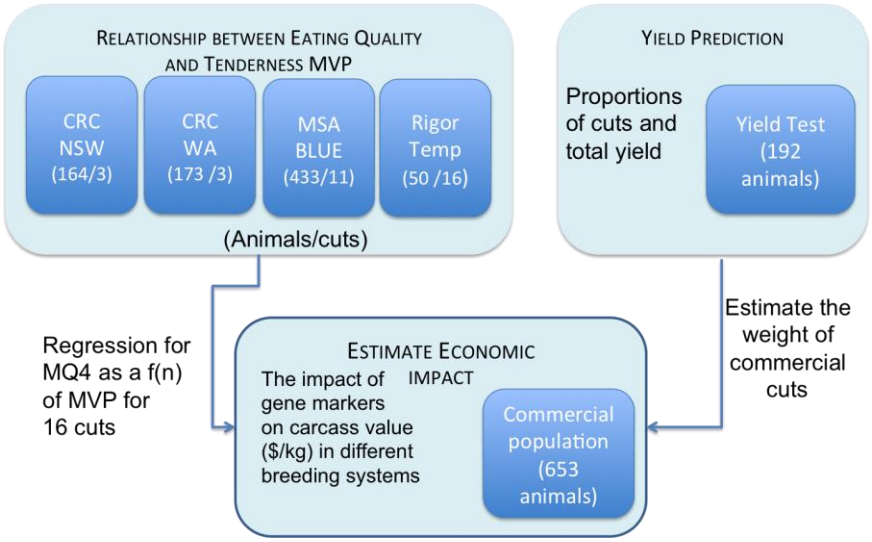

Figure 1 Overview of datasets and processes used to determine carcass value

2.1 Collation of data on the relationship between palatability and the tenderness MVP for specific muscles

As an initial step published and unpublished data sets on the gene markers effects on palatability were collated to estimate the relationship between tenderness MVP and palatability for specific muscles. This included four experimental datasets from three experiments outlined in Figure 1. These experiments each used different

populations of cattle, had a different range of cuts, cooking methods and aging times. Where there was more than one estimate for particular muscles the mean of the different estimates was used. Estimates of the regressions for the tenderness MVP as a function of MQ4 score for the 16 cuts were regressed against ageing rate and this relationship used to estimate the regression coefficients for the remaining 23 cuts. A prediction equation for cut yield was then developed from a separate data set to estimate the yield of trimmed primal from domestic weight carcasses.

The estimates of both the effect of the tenderness MVP on palatability and the predictions of eating quality and cut yield were then applied to the results of a commercial dataset of 653 animals. Each of the data sets and their results in terms of the estimates of the tenderness MVP for a range of muscles are detailed below.

2.1.1 The CRC data set

This data was part of a large Beef CRC study on the mechanisms by which tenderness gene markers impact of the metabolic system of the animal and ultimately beef tenderness. The screening of animals, experimental design, data and results has been described in detail (Cafe et al., 2010a; Cafe et al., 2010b; Robinson et al., 2012, Greenwood et al., 2013). Thus, only a brief description was provided here.

Two concurrent experiments were conducted, one at the NSW Agricultural Research and Advisory Station, Glen Innes, NSW and one at the WA Department of Agriculture and Food Vasse Research Station near Busselton, WA. For the NSW site, 1090 animals were tested for the four tenderness SNPs prior to weaning and based on those results 164 weaners were selected for the experiment. For WA, 574 animals were tested for the tenderness SNPs prior to weaning of which 173 were selected for the experiment. Given the distribution of SNPs the selection of animals was on the basis of favourable or unfavourable SNPs for calpastatin and calpain3, with as balanced a range as possible for calpain1 (both the 316 and 4751 variants).

At both sites the cattle were grown out from weaning on pasture and then finished in a domestic feedlot prior to slaughter at domestic weights. At feedlot entry cattle were allocated to HGP or control treatments. The NSW cattle were fed a concentrate ration for 117 days, whilst the WA cattle were fed for 80 days. At slaughter one side from each carcass was tenderstretched whilst the other was

normally hung. Sides were MSA graded and at boning the striploin, rump and oyster blade primal collected for subsequent sensory testing. These primals were aged for seven days and then the *mm. longissimus dorsi (STR045), gluteus medius (RMP131)* and *supraspinatus (OYS036)* dissected, trimmed of all epimysium and fat and cut into steaks for sensory testing.

The MSA consumer testing protocol has been described by Watson et al., (2008). Briefly, untrained consumers scored each sample for tenderness, juiciness, liking of flavor, and overall liking. These scores were then weighted and combined into a meat quality score (MQ4). The number of animals and cuts that were available for analysis from the NSW and WA experiments to estimate the regression of tenderness MVP on MQ4 score are shown in Figure 1.

The regressions of MQ4 as a function of the tenderness MVP for the three muscles were reported taken by Greenwood *et al.,* (2013). The data was adjusted for sex (where appropriate), HGP treatment and slaughter date and slaughter group. For each site (ie NSW and WA) the MVP regression coefficients presented by Greenwood et al (2013) for the STR045 (both Achilles hung and tenderstretched), RMP131 and OYS036 and presented in Table 1. All estimates were negative and whilst the tenderstretch effect was not significant, there was a significant difference between muscles.

Table 1 Regression coefficients for the tenderness MVP as a function of the MQ4 score for the Striploin (both Achilles hung AT and tenderstretched TS), rump and oyster blade (Greenwood et al 2013)

Cut	Hang	NSW	WA
STR045	AT	-16.17 (5.342)	-12.49 (5.231)
STR045	TS	-8.01 (5.340)	-9.58 (5.221)
RMP131	AT	-13.87 (5.174)	-4.88 (5.270)
OYS036	AT	-3.17 (4.684)	-5.70 (4.525)

2.1.2 The MSA BLUE data base

The MSA BLUE data base comprised all sensory and animal records for samples which had been sensory tested using the MSA consumer protocol. As part of the data collection protocol DNA samples were specified for all carcasses, however

when it came to retrieve the DNA samples it was found that many had either been misplaced, lost or never stored.

The MSA BLUE data set and the analysis was described in detail by Thompson (2011). Only a brief overview of the methodology will be reported here. In total there were 3,537 samples from 38 different muscles and 6 different cooking methods which were derived from 433 animals which had DNA samples available. The DNA profiles were run by Pfizer Animal Genetics and the tenderness MVP calculated.

Not all cells in the muscle/cooking method matrix were filled. When the data was tabulated according to muscle and cooking method it was apparent that the only muscles with sufficient numbers for analysis were the BLD096, CUB045, EYE075, OUT005, RMP005, RMP131, RMP231, STR045, TDR062 and TOP073. For these cuts there were only sufficient samples from the GRL and RST cooking methods. In a further attempt to increase the numbers in different analyses, portions of the same muscle were combined and the model adjusted for cut. This assumed that the mechanism by which SNPs were expressed were similar within muscle. Effectively this allowed the data for STR045 to be grouped with CUB045, the RMP131 grouped with RMP231 and finally the OUT005 grouped with RMP005. The number of animals and cuts which were finally available from the BLUE DATA BASE to estimate the regression of tenderness MVP on MQ4 are shown in Figure 1.

For analysis, the MSA model was fitted so the effect of the tenderness MVPs was estimated after adjustment for all other inputs in the MSA model. Terms included in the MSA adjustment comprised sex, HGP status, *Bos indicus* content, hang, cook method, cut (where portions of the same muscle were included in the analysis), marble score, ossification score X carcass weight interaction, ultimate pH (both linear and curvilinear effects) and days aged (also as linear and curvilinear effects) along with tenderness MVP. Estimates for the regression coefficients of palatability (MQ4) as a function of the tenderness MVP from the MSA BLUE database analyses are listed in Table 2. All estimates of the regression coefficients were negative with the exception of EYE075 which was positive (but had a very large standard error).

Table 2 The regression coefficients for the tenderness MVP as a function of MQ4 score for 8 muscles in the report by Thompson (2011)

Cut	Regression coefficient	Se
STR045/CUB045	-7.0	(3.2)
RMP131/231	-6.8	(4.7)
OUT005/RMP005	-15.6	(6.1)
BLD096	-5.8	(4.7)
TOP073	-9.2	(4.6)
TDR062	-0.4	(5.6)
OYS036	-1.2	(5.6)
EYE075	11.7	(9.0)

2.1.3 The MSA rigor temperature experiment

This data set was part of a larger MSA experiment which examined the interaction between rigor temperature, hang method and ageing of different muscles in the carcass (R Polkinghorne and JM Thompson, *unpublished data*). Given the exceptional co-operation of the feedlot and abattoir there was an opportunity to overlay a gene marker treatments across all treatments.

A domestic feedlot identified ca. 700 head (ie 2 pens) of cattle that were scheduled for slaughter after 60 days on feed. As part of second weighing tail hair samples were collected from ca. 700 animals, DNA extracted, genotyping performed and the tenderness MVP estimated. Prior to slaughter the tenderness MVPs were used to sort animals into low and high percentiles for the tenderness MVP which allowed animals for the rigor temperature experiment to be selected and allocated to treatments at the knocking box. This procedure of balancing each treatment for extremes in tenderness MVP values allowed gene marker status to be overlaid across the other experimental treatments. The experimental design involved allocating 100 sides from 50 carcasses to placed in 10 different hang and stimulation treatments. The number of animals and cuts that were available to estimate the regression of tenderness MVP on MQ4 scores are shown in Figure 1.

From the two pens of ca. 700 animals only 653 of the animals that were delivered for slaughter could be matched with the NLIS tags for tenderness MVPs. At slaughter the population of 653 carcasses were MSA graded. A total of 9 primals from each of the 100 sides were collected and prepared for consumer panels. The 9 primals were

dissected into 16 MSA cuts (TDR062, CUB045, SPN081, STR045, OYS036, RMP005, RMP131, RMP231, RMP087, TOP001, TOP033, TOP073, EYE075, OUT005, KNU066, KNU099) with samples aged for 5, 26 and 47 days for all cuts (the STR045 and CUB045 were large enough to age samples to 68 days).

Data analyses was done on individual cuts and used a mixed model which contained fixed effects for hang (AT, TX and SS), muscle position, with covariates for days aged (both linear and curvilinear), temperature at pH6 and tenderness MVP. Interactions between days aged x hang and days aged x position were also included in the model. Interactions between tenderness MVP and both hang and days aged were tested and found non-significant ($P<0.05$). The regression coefficients for the tenderness MVP as a function of palatability (MQ4) for the 16 muscles from the Rigor Temperature experiment analyses are listed in Table 3. As shown in Table 3 the regression coefficients for MVP as a function of MQ4 score were all negative. Estimates for individual muscles were significantly different and estimates ranged from -10.46 for RMP087 to -0.63 for the TOP001.

Table 3 The regression coefficients and standard errors for the tenderness MVP as a function of MQ4 score for 16 muscles in the Rigor temperature experiment (Polkinghorne and Thompson unpublished data)

Primal	MSA Cut	Regression coefficient	SE
Spinalis	CUB081	-6.08	(2.83)
Tenderloin	TDR062	-8.78	(1.69)
Cube roll	CUB045	-7.60	(3.04)
Striploin	STA045	-11.56	(1.85)
Oyster blade	OYS036	-3.98	(2.50)
Rump	RMP131	-4.77	(2.92)
Rump	RMP231	-9.99	(2.96)
Rump	RMP005	-1.88	(2.93)
Rump	RMP087	-7.24	(2.78)
Knuckle	KNU066	-6.44	(2.51)
Knuckle	KNU099	-3.01	(2.75)
Outside flat	OUT005	-5.51	(1.60)
Eye round	EYE075	-6.87	(1.72)
Topside	TOP001	-4.37	(2.38)
Topside	TOP033	-3.17	(2.59)
Topside	TOP073	-6.35	(1.48)

2.2 Estimation of the tenderness MVP regression for individual muscles as a function of MQ4 score

Where possible the data from the three experiments with estimates of tenderness gene marker effects were pooled to provide the most robust estimate to use in the modeling exercise. By relating these estimates to ageing rate in the MSA model the regression coefficients for tenderness MVP as a function of MQ4 were extrapolated to all 39 MSA cuts.

2.2.1 Calculation of the MSA index for carcasses with and without the tenderness markers

The MSA Index is a weighted average of all 39 MSA cuts in the carcass. Using the 653 carcasses from the commercial population which had been MSA graded and had tenderness MVPs available, the MSA model was used to predict the MQ4 for each cut/cook combination. The impact of the tenderness gene markers was estimated by multiplying the regression coefficients for the 39 muscles in Table 6 by the animal tenderness MVP. This adjustment was then added or subtracted to the MQ4 score estimated by the MSA model. The MVP regression coefficients for the 39 muscles were all negative (see Table 6) and therefore multiplying by a negative MVP resulted in an increase in the MQ4 for all 39 muscles for that animal. Therefore for an animal with a negative tenderness MVP the adjustment increased the MQ4 scores and hence the MSA Index. Conversely a positive animal tenderness MVP resulted in a decrease in the MQ4 score for each muscle and so the MSA Index decreased.

2.3 Estimation of carcass yield

To calculate the economic impact of the tenderness gene markers the change in MQ4 score had to be converted to dollars which required an estimate of cut weight. This was obtained using a regression equation to predict the yield of saleable cuts. The estimated yield of saleable was then multiplied by the proportional distribution of cuts to estimate cut weight.

As part of a previous experiment with the same supply chain a commercial yield trial had been undertaken in 2009 using 192 sides. These carcasses had been MSA

graded and the left side yielded to produce trimmed wholesale cuts, lean trim at 65 and 95% CL, fat trim and bone.

The yield protocol involved boning sides into trimmed retail cuts and weighing all trim (both CL90 and CL65),fat and bone in the side. The weights of all cuts, trim, fat and bone were summed and checked against the initial side weight. Recoveries averaged 96% and ranged from 92 to 100%. The trimmed retail cuts and their proportions were expressed as a proportion of the total boned product.

Table 4 Regression coefficients used to predict yield of trimmed cuts and chemical lean using MSA inputs traits in 192 domestic carcasses

Terms	Regression coefficient
Intercept	0.6690774662
Hot carcass wt	0.0000721106
Eye muscle area	0.00046092
Hump	0.0000772166
P8	0.0000743693
RSD	0.0169
R^2(%)	5.58

Regression equations using MSA carcass traits (Hot carcass weight, P8, eye muscle area and hump height) were estimated to predict yield of trimmed cuts and lean trim (both CL65 and 95%). In addition the mean distribution of trimmed cuts as a proportion of total trimmed cuts plus lean trim was calculated (Table 5).

The accuracy of the prediction equations and the regression coefficients for the input traits are shown in Table 4. The resultant regression equation accounted for less than 6% of the variance in the proportional yield of trimmed cuts. This was low but not unexpected as the carcasses underwent very little trimming with the proportion of fat trim being ca. 5%. This equation was applied to the commercial data set (the 653 carcasses with tenderness MVPs) to predict the weight of retail trimmed cuts plus trim. Cut weights were then predicted for this population using the proportions in Table 5.

The 3 star $/kg assumed for the different cuts are also shown in Table 5. This base price was varied using different premiums for the different MSA grades.

Table 5 Primal cut and trim portion weights as proportions of total boned product, along with 3 star prices ($/kg) used to value cuts.

Primal	MSA cut name	Proportion of total trimmed product	3 star cut values ($/kg)
Oyster blade	OYS036	0.020	6.00
Bolar Blade	BLD096	0.020	4.40
Chuck tender	CTR085	0.012	3.40
Chuck	CHK078	0.053	7.00
Brisket	BRI056	0.071	4.00
Striploin	STR045	0.050	12.00
Cube roll	CUB045	0.025	16.00
Foreshin	Foreshin	0.006	5.00
Topside	TOP073	0.046	5.50
Knuckle	KNU099	0.050	7.70
Outside	OUT005	0.031	4.30
Eye round	EYE075	0.016	4.80
Hindshin	Hindshin	0.010	5.00
Rump	RMP131	0.026	7.50
Tenderloin	TDR062	0.019	21.00
Flank steak	TFL051	0.006	7.00
CL 90		0.266	3.50
CL65		0.275	2.25
Fat and bone			0.20

2.4 Calculation of the economic value of carcasses with and without the tenderness MVPS.

The economic impact of tenderness MVPs was modeled using the commercial population of 653 animals which had tenderness MVPs measured. The methodology used in was outlined in Appendix 1.

To assess the impact of the tenderness MVPs several assumptions regarding the cuts and their value and the price premiums for eating quality to be applied have to be made. Commercially the Australian beef industry is still along way from fully utilizing all 39 MSA cuts. In practice traditional primals are harvested and although these primal may contain several MSA cuts the quality of the largest muscle is generally used to assign an MQ4 to that primal. An example would be the topside primal which comprises 3 MSA cuts being the TOP001, TOP033 and TOP073. Clearly the largest muscle is TOP073 and so this is generally used to denote the eating quality of this primal.

Finally there was the question as to what price premiums should be applied to eating quality. The best evidence of the likely premiums to apply to the different MSA grades was the study of Lyford et al. (2010) where exit surveys on the consumers willingness to pay (WTP) for eating quality was collected on almost 7,000 consumers from 4 countries as they exited the MSA consumer tests. Given the consumers from the different countries valued the grades using different units the results were expressed as a ratio of what they expected to pay for 3 star product. These results showed that with the possible exception of the Japanese, consumers tended to pay ca. 2, 1.5 and 0.5 for 5, 4 and 2 star quality relative to the price they would pay for 3 star product. Not unexpectedly the analysis by Lyford et al. (2010) showed the Japanese would pay up to 3 times the 3 star price for the 5 star grade. Interestingly there was little difference between countries in the price for 2 and 4 star grades.

Therefore the following analyses investigated several scenarios. The first scenario assumed MSA price premiums which were 2, 1.5 1.0 and 0.5 for 5, 4, 3 and 2 star product and the second scenario assumed premiums (and discounts) that were half this, ie 1.5, 1.25 1.0 and 0.75 for 5, 4, 3 and 2 star respectively.

The third scenario was one where only the sweet cuts were harvested as MSA graded cuts, viz the striploin, cube roll, rump and tenderloin.

The final scenario was one that reflects current usage whereby a premium was obtained if the cut achieved a threshold of 3 star or greater. From Table 1f reported by Griffith and Thompson (2012) the average premium for achieving 3 star threshold across 9 cuts in the carcass was ca. 5%. This premium was then run across all cuts in the carcass with and without taking into account gene marker status.

2.5 Description of methods used to estimate response to selection

A series of simulation studies was performed to examine the following scenarios (1) the economic impact of a single year of sire selection on the current MVP (2) The impact of selection on the four calpain/ calpastatin markers (3) selection on the current 56 Marker MVP and (4) selection on an EBV for MQ4 with a variance similar to the current MVP variance but no limitation on the number of markers. In each simulation only sire selection was performed and it was assumed that sires were selected with varying selection intensities.

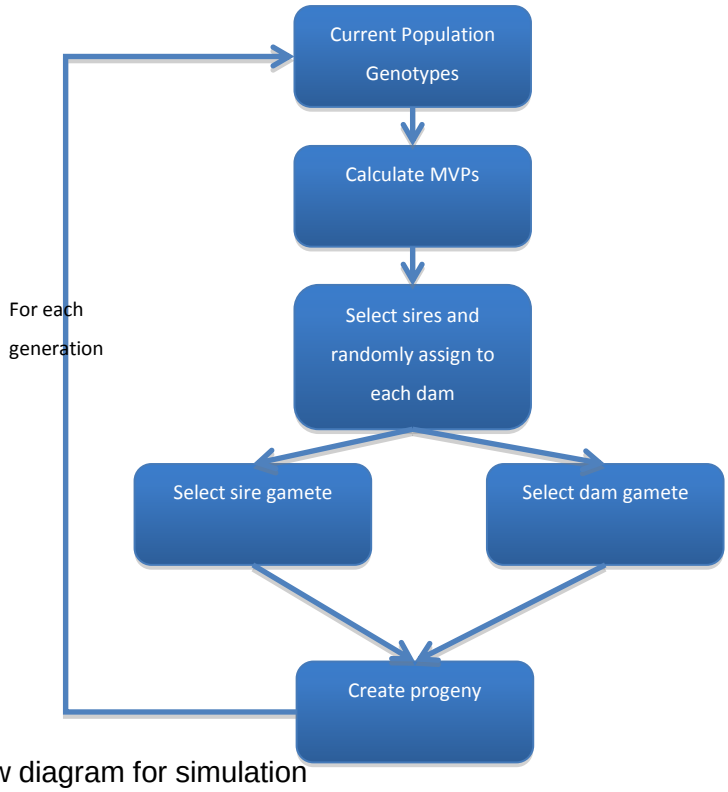

Figure 2 Basic flow diagram for simulation

A similar method was followed in each simulation. The outline is presented in **Figure 2**. The simulations all started with the commercial case study population of 653 animals. As all animals had been measured for the tenderness MVP this allowed the top proportion of animals to be selected to be sires in the subsequent generation. These sires were then evenly allocated at random to mate with all animals in the population. The progeny of these mating were then simulated slightly differently in each simulation. In simulation (1) only one set of progeny were generated as half way in between the sires and dam MVPs, (2) only four markers (ie 2 calpain markers plus calpain 3 and calpastatin) were used, in simulation (3) 56 markers were simulated and used in generation of progeny. In simulation (4) a genomic MVP was generated using a normal distribution. These methods are described in more detail below.

2.5.1 Estimation of the response from selection of elite bulls and use over animals with range of MVPS similar to commercial dataset

Progeny of a single year of sire selection was simulated as the average of the current MVPs in the commercial dataset and those of sires from the top 50%,

20%,10% and 5% of animals. These MVPs were then used in place of the current MVPs and the change in value estimated. The change in value was estimated using the previously described economic model.

To simulate progeny from sires from sires selected from the MVPs of the current commercial dataset were adjusted as follows;

$$mvp_{progi(i)} = \frac{(mvp_i + mvp_{sire(p)})}{2}$$

mvp_i is the MVP of individual (i) in the commercial population, $mvp_{sire(p)}$ is the average MVP of sires selected from the *p*th percentile and $mvp_{progi(i)}$ is the predicted progeny from this mating

The economic value of $mvp_{progi(i)}$ was estimated by substituting the $mvp_{progi(i)}$ for the MVP of mvp_i in the equations previously developed. This is the predictor of the economic value of this progeny given that MVP is independent of other traits used in estimating MQ4.

2.5.2 Estimation of the response to selection each generation using 4 calpain/calpastatin markers (MVP4)

Within the current marker panel four markers (calpain and calpastatin) account for approximately 50% of the variance (r^2) in MVP as estimated by regression. These markers were the original genes found to be associated with changes in beef tenderness.

Thus the rate of genetic improvement will continually decrease as these markers moving towards fixation (where there is no variation in the population). To evaluate the response to selection on the four tenderness markers a simulation study was performed using the test results from the commercial population as a base. From this population individuals were selected to be the sires and dams of future progeny. These future progeny were then used in 10 repeated rounds of progeny. Each year animals from the top 5% of MVP were used as sires of the next generation.

The description of simulation of progeny based on the four markers is described in detail below. The correlations between the markers within each gene necessitated a slightly more complicated simulation strategy than that applied in (Weaber and Lusk, 2010). This correlation between markers was handled by simulating haplotypes with matching relationships between markers as estimated from the correlations between genotypes in commercial population.

2.5.3 Estimation of the response to selection each generation using a 56 SNP MVPS (MVP56)

A simulation similar to that performed by Weaber and Lusk (2010) was used to model selection on the current 56 marker panel for MVPs (MVP56). In this simulation the commercial population was used as a base. Similarly to the previous studies MVPs were calculated and the highest ranking animals were selected as sires to be used across the whole current generation as progeny. Individual marker alleles were selected at random from each sire and dam to combine into new progeny genotypes. MVPs were then calculated for each of these progeny genotypes and the process started again.

2.5.4 Estimation of the response to selection each generation using a polygenic marker model for MVPS (MVPEBV)

This involved developing a hypothetical polygenic panel which explained a similar percentage of variance in MQ4. Advances in genotyping technology and previous research have shown that it would be possible to develop such a test given appropriate genotypic and phenotypic resources. The study of (Reverter et al., 2003) has shown that consumer eating quality is a heritable trait for two muscles (*m. longissimus dorsi* and *semitendinosis*). This could provide the basis for developing such a test to be incorporated in MSA and genetic evaluation programs.

The response to selection on MVP was estimated each generation using a simulation process.

- MVPs were simulated for an initial population (N=1000) assuming that the MVP followed a normal distribution (N(0.24,0.22)).
- For each generation
    - The top 5% of animals were chosen as sires and mated randomly to the population.
    - MVP of the progeny was calculated as follows

$$mvp_{prog} = \frac{(mvp_{dam} + mvp_{sire})}{2} + 0.5 \times N(0, 0.22)$$

- Average carcass value was calculated using spreadsheet model by adjusting the mean value of the commercial population to match average MVP in year of study

3. Results and discussion

3.1 Estimation of the tenderness MVP effect across the musculature of the carcass

Tables 1, 2 and 3 show the individual muscle regression coefficients for palatability (MQ4) as a function of the tenderness MVPs .The CRC experiment showed a trend for lower tenderness MVP regression coefficients for tenderstretched compared with Achilles hung striploins, although from the standard errors the differences were not significant (P>0.05, Table 1). In the Rigor Temperature experiment the interaction between hang and gene marker status was tested and out of the 16 muscles there were five muscles that did show a significant (P<0.05) hang and tenderness MVP interaction. However in four of those cases the interaction was due to the superstretch treatment which would not apply in practice. Overall it was concluded that for the data that was available commercial hang treatments did not have a substantial effect on the magnitude of the MVP coefficients for muscle.

As discussed previously the tenderness markers are located within the calpain/calpastatin genes which control protein degradation in the live animal and subsequently ageing rate in the carcass. In the Rigor Temperature experiment the interaction between days aged and tenderness MVP was only significant (P<0.05) for one muscle (TDR062) out of the 16. This was an interesting result and suggested that if that muscle was disregarded, for the remaining 15 muscles the magnitude of the tenderness MVP effect was on the intercept and effectively the same differences were evident from 5 to 47 days and for the CUB045 and STR045 up to 68 days ageing. From these results it was concluded that the tenderness MVPs regression coefficients used in this study operated across all ageing times.

Both the CRC and the Rigor Temperature experiments used designs where extremes in gene marker status were selected to provide divergent groups. This had

the effect of over-estimating the significance of the gene marker effects. On the other hand it had the effect of providing much more accurate estimates of the regression coefficients for tenderness MVP as a function of the MQ4 score. Whilst the distributions in the CRC and Rigor temperature experiments were not normal, the distributions in the MSA BLUE data base were approximately normal.

The CRC study sampled all sensory samples at only one ageing time. In contrast the sensory data from the Rigor temperature experiment were sampled at a number of different ageing times. If tenderness MVPs for individual muscles were related to ageing rate then this should be evident between the muscles in the Rigor Temperature experiment. A series of univariate analyses which included fixed effects for hang, position, interaction of hang and position with days aged as a covariate (both linear and curvilinear) were undertaken for individual muscles. Ageing rate at 5 days of age was calculated from the first derivative of the linear and curvilinear effects of days aged and ageing rate estimated at 5 days. The regression coefficients for the tenderness MVP were plotted against days aged (the relationships are not shown in this report). Whilst this relationship was negative (ie as expected lower regression coefficients for individual muscles were associated with higher ageing rates), surprisingly the relationship was very weak only accounting for 10.3% of the variance. Given the poor relationship it was possible that factors other than proteolysis impacted on ageing rate in the Rigor Temperature experiment. To test the strength of the relationship between proteolysis and the tenderness MVP would require further research.

Frozen samples from these muscles exist at UNE it is suggested that further work be undertaken to measure the appearance of titin or desmin breakdown products in these muscles and this data be related to animal MVP values for individual muscles. The appearance of these breakdown products is another measurement of proteolysis. It may be that the relationship between proteolysis products and the tenderness MVP was strong enough to use this as a predictor in the future.

To provide estimates of regression coefficients for tenderness MVP as a function of the MQ4 score to be used in the modeling exercise the regression coefficients from the three experiments (Tables 1, 2 and 3) were averaged. The exception was the positive regression coefficient of 11.70 for the EYE075 which was excluded from the estimates. This extremely high value appeared to be an aberration given all the other

estimates were negative. It should be noted that the coefficient for the EYE075 had a standard error of 9.0 so the estimate was not significantly from zero.

The MSA model uses ageing rates for individual muscles which have been estimated on samples from many experiments. Therefore although there was only a weak relationship between ageing rate and tenderness MVP in the Rigor Temperature experiment it was considered that the ageing estimates from the MSA model may be more robust. The resultant graph for the MSA ageing rates as a function of the averaged tenderness MVPs showed a moderate relationship (see Figure 2), with an R^2 of ca. 31%. It should be noted that ageing rates in the MSA model were generally averaged across the different muscles in the same primal. Whilst this would have been necessary to have sufficient numbers in estimating ageing rates it may not reflect the biology as proximity of muscles in the carcass may not necessarily reflect their metabolic and structural properties.

The relationship shown in Figure 3 was then used to estimate regression coefficients for MQ4 as a function of tenderness MVP for all 39 muscles in the MSA model. These coefficients are shown in Table 6.

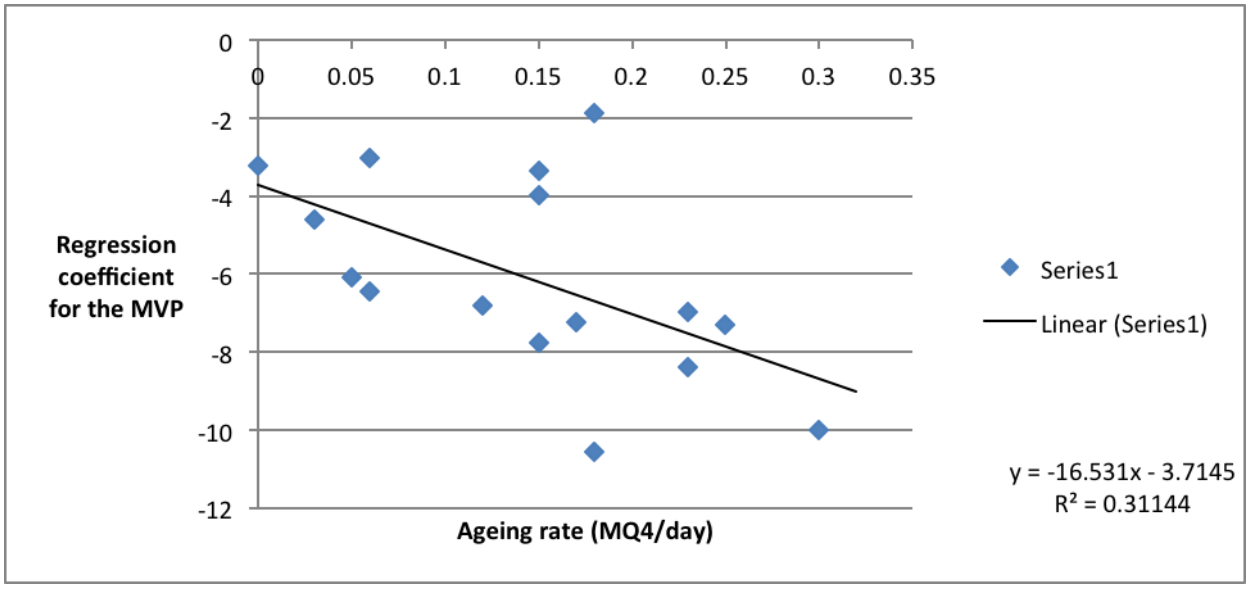

Figure 3 The plot for the MVP regression coefficients (averaged across the 3 experiments) as a function of muscle ageing rate (as specified by the MSA model).

Table 6 The ageing rates for individual muscles from the MSA model along with predicted regression coefficients for the relationships between MQ4 score and tenderness MVP using the equation from Figure 3

MSA Cut	MSA ageing rate	Predicted reg coeff for MVP	MSA Cut	MSA ageing rate	Predicted reg coeff for MVP
CUB081	0.05	-4.54	OUT005	0.18	-6.69
TDR034	0.03	-4.21	OUT029	0.07	-4.87
TDR062	0.03	-4.21	EYE075	0.12	-5.70
TDG062	0.03	-4.21	TOP001	0.15	-6.19
CUB045	0.25	-7.85	TOP033	0.15	-6.19
STA045	0.30	-8.67	TOP073	0.15	-6.19
STP045	0.32	-9.00	CHK068	0.09	-5.20
OYS036	0.00	-3.71	CHK074	0.09	-5.20
BLD095	0.05	-4.54	CHK078	0.09	-5.20
BLD096	0.05	-4.54	CHK081	0.09	-5.20
CTR085	0.05	-4.54	CHK082	0.09	-5.20
RMP131	0.23	-7.52	TFL051	0.08	-5.04
RMP231	0.23	-7.52	TFL052	0.08	-5.04
RMP005	0.18	-6.69	TFL064	0.08	-5.04
RMP032	0.17	-6.52	RIB041	0.00	-3.71
RMP087	0.17	-6.52	BRI056	0.00	-3.71
KNU066	0.06	-4.71	BRI057	0.00	-3.71
KNU098	0.06	-4.71	FQshin	0.00	-3.71
KNU099	0.06	-4.71	HQshin	0.00	-3.71
KNU100	0.06	-4.71	INT037	0.00	-3.71

In concordance with many other studies a clear relationship between MVP and consumer eating quality was found for most muscles across from the three experiments examined. This was related to the aging rates from the MSA model to develop predictions of the effect of MVPs across 39 muscles. The estimates of the regression between tenderness MVP and consumer eating quality MQ4 scores ranged from -3.7 to -6.69.

3.2 The commercial population with the tenderness MVPS and MSA predictions

A commercial population of 653 carcasses which had been measured for the tenderness MVP was used to estimate the economic impact of the gene markers. These animals were the commercial population from which the 50 animals in the rigor temperature experiment were selected.

The carcass traits for this population of carcasses were described in Table 7. The mean carcass weight was typical of domestic carcasses with a low P8 fat depth and

small eye muscle area. As expected ossification and marbling scores were also low. The variation in carcass yield % was very low which in part reflected the low levels of trim undertaken on these domestic bodies, but also reflected the low accuracy of the yield prediction equation.

The mean tenderness MVP of the commercial population was 0.24 with a standard deviation of 0.22 and minimum and maximum values of -0.38 and 0.81 respectively. The frequency distribution for the tenderness MVP was shown in Figure 4 and appeared normal. The commercial population comprised Brahman cross animals which overall had a visual phenotype of approximately 60% *Bos indicus* content. As the units of the tenderness MVP are kg shear force a positive mean tenderness MVP was in line with expectations from a *Bos indicus* cross herd.

Table 7 Summary statistics for carcass traits for the 653 animals in the commercial population

Trait	Mean	Standard deviation	Min	Max
HSCW (kg)	227	16	177	294
P8 (mm)	8.7	4.2	2.0	28.0
Hump (mm)	75	20	40	155
EMA (cm^2)	61	6.77	41	86
Ossification score	154	19.70	100	350
MSA marbling score	272	96	100	840
pH (units)	5.57	0.06	5.40	6.05
LoinTemperature (^oC)	6.1	0.44	1.60	8.60
Yield (proportion)	0.7188	0.0040	0.7100	0.7312
Tenderness MVP (kg)	0.24	0.22	-0.38	0.81

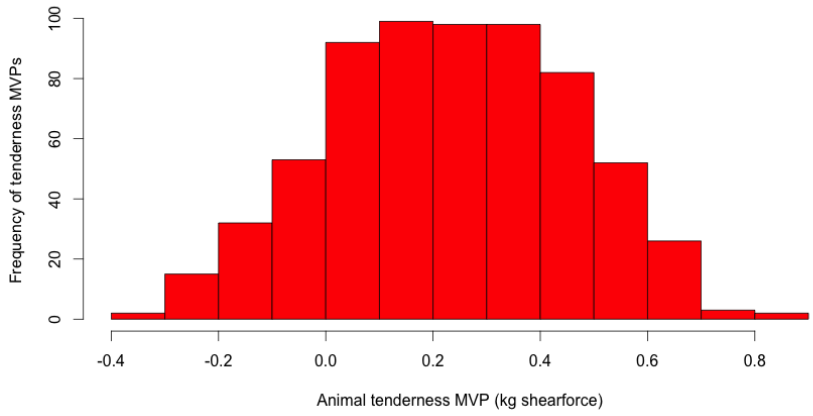

Figure 4 The frequency distribution of tenderness MVP for the 653 animals from the commercial population.

Table 8 Correlation coefficients between carcass traits, yield and tenderness MVP for the 653 animals from the commercial population

	HSCW	P8	Hump	EMA	OSS	MSAMB	PH	RFT	MVPTend
HSCW	1.00								
P8	0.09	1.00							
Hump	-0.08	0.06	1.00						
EMA	0.42	-0.15	-0.07	1.00					
OSS	0.00	0.21	0.08	-0.04	1.00				
MSAMB	0.08	0.19	-0.2	0.01	0.12	1.00			
PH	0.02	0.01	0.01	0.04	0.06	-0.04	1.00		
RFT	0.12	0.7	0.05	-0.21	0.15	0.25	-0.04	1.00	
MVPTend	-0.17	0.06	0.53	-0.15	0.09	-0.19	0.05	0.02	1.00
% Yield	0.58	-0.14	0.30	0.89	-0.01	-0.05	0.04	-0.16	0.03

The correlation matrix between carcass traits, predicted yield % and tenderness MVPs are shown in Table 8. As expected predicted carcass yield % was positively correlated with HSCW, eye muscle area and to a lesser extent hump height and negatively associated with ribfat as these were the predictors used in the yield prediction equation. The tenderness MVP was positively correlated with hump height (r=0.53, Table 8). As the units of the MVP are shear force then this aligned with a greater hump height having a higher tenderness MVP and consequently tougher meat. Other carcass traits were generally poorly correlated with tenderness MVP.

3.3 The effect of the tenderness MVP on the MSA Index of a commercial population

The MSA Index is a weighted average of the MQ4 scores for the 39 muscles in the MSA model (Thompson et al., 2012).The MSA Index is currently being introduced as a feedback tool for producers to assess changes in the quality of their carcasses. This section demonstrated the magnitude of the gene marker effect on the MSA Index. The effect on the MSA Index for animals with and without the tenderness MVP for the commercial population was shown in Figures 4 and 5.

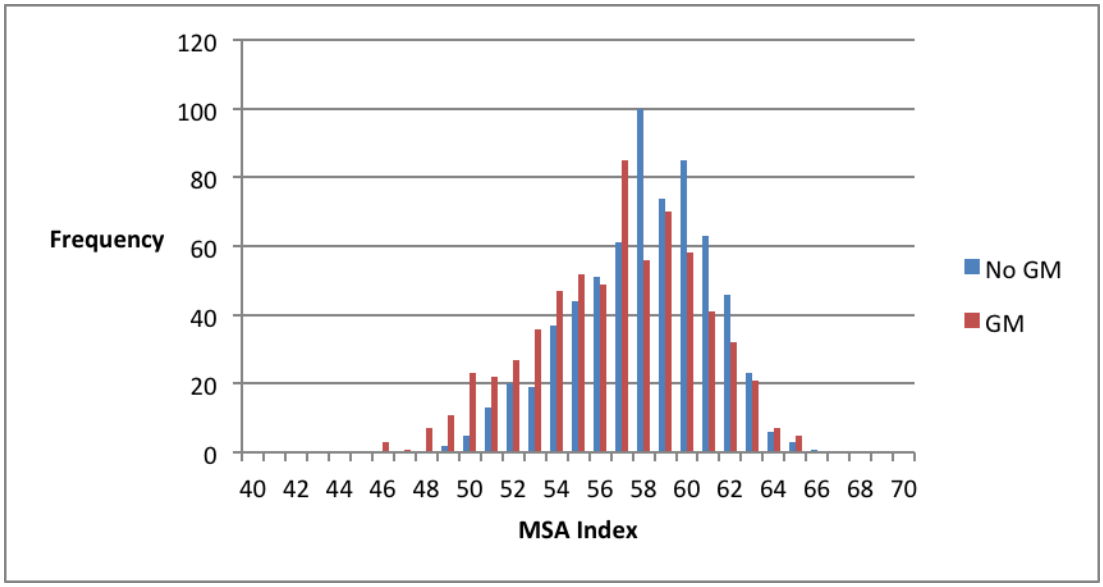

Figure 5 The frequency distribution for the MSA Index calculated for the commercial population of carcasses where the effect of the tenderness MVP has been estimated and carcasses where no effect was assumed.

Table 9 The MSA index calculated for the commercial population of cattle assuming no tenderness gene markers (No GM) and tenderness gene markers (GM).

Treatment	Mean	Stdev	Minimum	Maximum
No GM	57.49	3.09	48.44	65.23
GM	56.27	3.76	45.43	64.57

The average MSA index was lower in the commercial population following the adjustment for tenderness MVPs (Table 9). The decrease of 1.2 units (from 57.5 to 56.3) reflected that these commercial animals had a lower average MVP than used to set the population mean for MVP. The population mean MVP is based on a mix *of Bos indicus* and *Bos taurus cattle* thus the it would be expected that a group of cattle with a high Brahman content such as the commercial population examined in this study would have a lower MVP and thus MQ4 adjusted for MVP than the population average.

By plotting the difference in the MSA Index calculated with and without adjustment for the tenderness gene markers against the animal MVP it was possible to quantify the change in the MSA Index as a function of the change in the animal tenderness MVP (Figure 6). Although the regression coefficients of the tenderness MVP varied for the different muscles they were applied to all carcasses and so the change in the MSA Index as a function of the animal MVP was a perfect negative linear relationship. That is an increase of 0.1 units in the animals tenderness MVP resulted

in a decrease in the MSA Index of 0.51 units. Conversely a decrease of 0.1 units in the animals tenderness MVP resulted in an increase of 0.51 MSA Index units.

As can be seen from Table 9 adjusting the MQ4 values for the tenderness MVP increased the variance in the MSA Index. As the adjustments for individual muscles varied across the musculature (ie faster ageing muscles showing a larger effect for the tenderness markers) this increase in variance was to be expected.

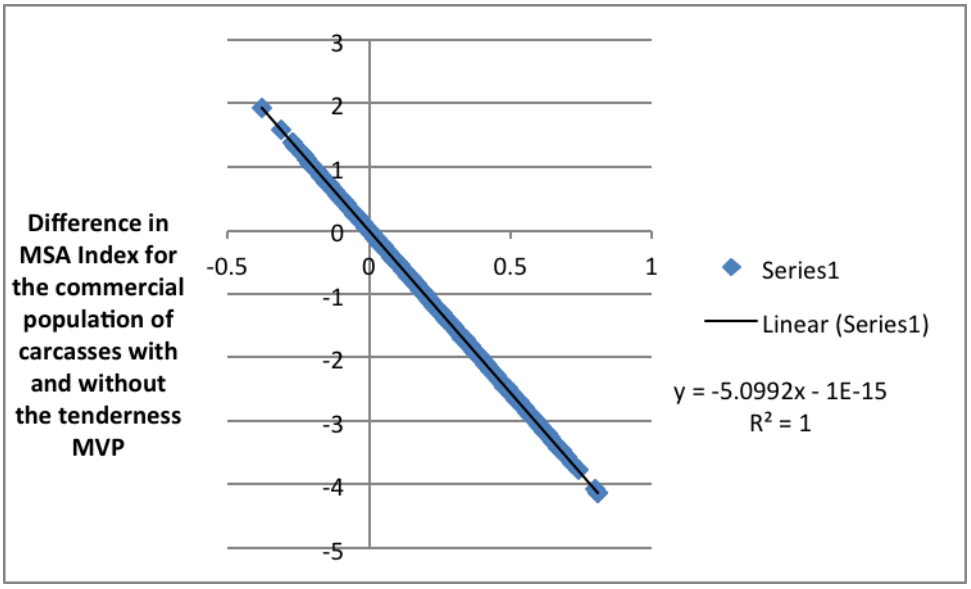

Figure 6 The relationship between the change in MSA index as a function of the MVP for tenderness

3.4 The economic impact of the tenderness MVP when harvesting cuts from carcasses

Before assessing the value of using the tenderness MVP as a breeding tool a first step was to examine the economic impact of using the variation in the tenderness MVPs within a population to harvest higher eating quality cuts. The price assumptions based on traditional cut pricing are laid out in Table 5. The effect of pricing the cuts in the commercial population using these premiums was calculated and summed across the carcass. Chemical lean both 90 and 65 CL and fat trim and bone were priced at the same rate in all carcasses.

The first scenario used the base prices in Table 5 and applied the quality premiums/discounts reported by Lyford et al. (2010) of 0.5 1.0, 1.5 and 2.0 for 2, 3 4

and 5 star, respectively. In the commercial population the average price of carcasses which were normally hung and had no gene marker premiums or discounts applied was $3.64/kg. If the premiums and discounts associated with the tenderness MVP were applied the average price decreased to $3.56/kg. Given the mean tenderness MVP for the population was 0.24 the $0.08/kg decrease in the average value by taking account of the changes in eating quality due to gene markers was expected. If the carcasses were tenderstretched the average carcass value increased, but there was still a decrease in the average carcass value from $4.14/kg to $4.02/kg by taking account of gene markers.

It was of interest to examine the relationship between the changes in carcass value as a function of the tenderness MVP which was shown in Figure 7 for normally hung carcasses.

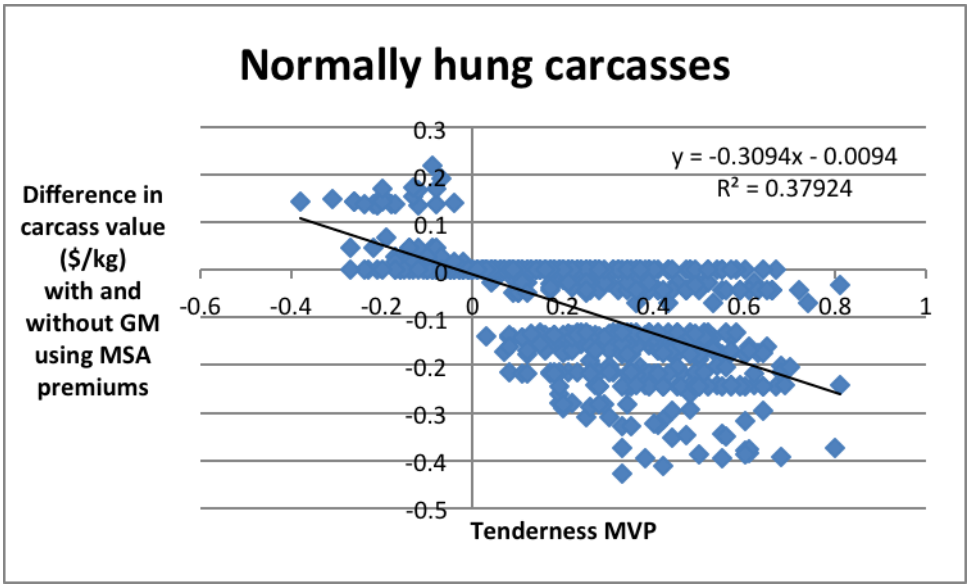

Figure 7 The difference in carcass value ($/kg) with and without using the tenderness gene markers and assuming the MSA premiums from Lyford et al (2010)

Whereas the relationship between the change in the MSA Index from applying the tenderness gene markers and the tenderness MVP was a perfect linear relationship (Figure 6), there was considerable variation about the relationship between the change in carcass value and the tenderness MVP in Figure 7. This was due to changes in the MQ4 of specific cuts not always being reflected in a change of price. Given that the grades were categorical (eg, 3 star goes from 46 to 64 MQ4 units and 4 star from 64 to 76 MQ4 units) there was a range of MQ4 scores over which price

did not change. Therefore even though there was a lot more noise about the relationship the linear function in Figure 7 it showed that on average a 1 unit decrease in the tenderness MVP resulted in a $0.31/kg increase in value.

The impact of tenderness gene markers on the difference in carcass value will vary according to the premiums that are paid for eating quality. Figure 8 showed that if the premiums were halved the rate of change in carcass value due to the tenderness MVP also halved. In Figure 8 the premiums were reduced to 0.75, 1.25 and 1.5 for 2, 4 and 5 star, respectively a 1 unit decrease in the tenderness MVP only resulted in an increase of $0.15/kg in carcass value.

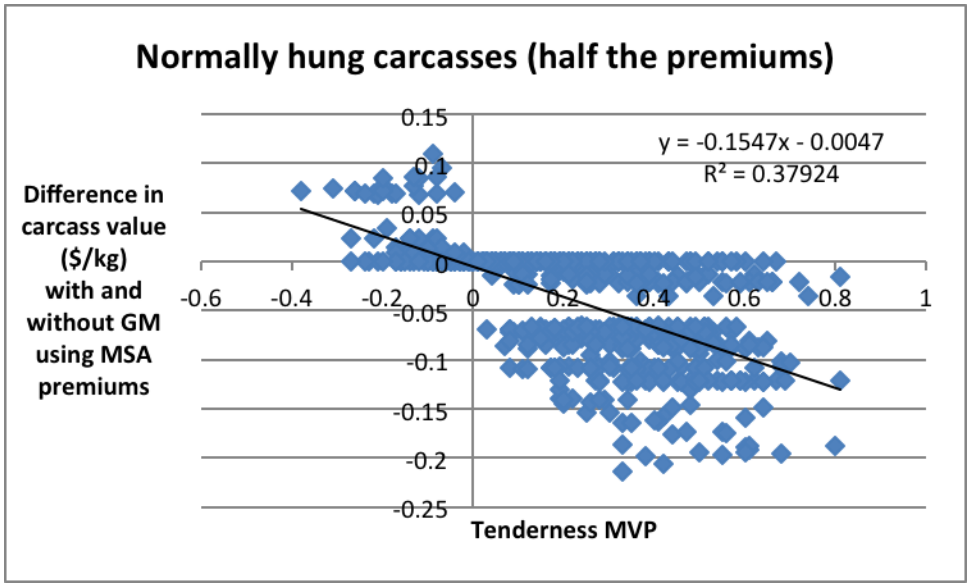

Figure 8 The difference in carcass value ($/kg) with and without using the tenderness gene markers and assuming half the MSA premiums from Lyford et al (2010)

Currently most wholesalers are only harvesting a selection of the cuts and marketing them as MSA. To model this only the sweet cuts (ie STR045, CUB045, TDR062 and RMP131) were harvested and the premiums from Lyford et al 2010 applied. The relationship for the difference in carcass value in $/kg with and without gene markers when only the sweet cuts were harvested was shown in Figure 9.

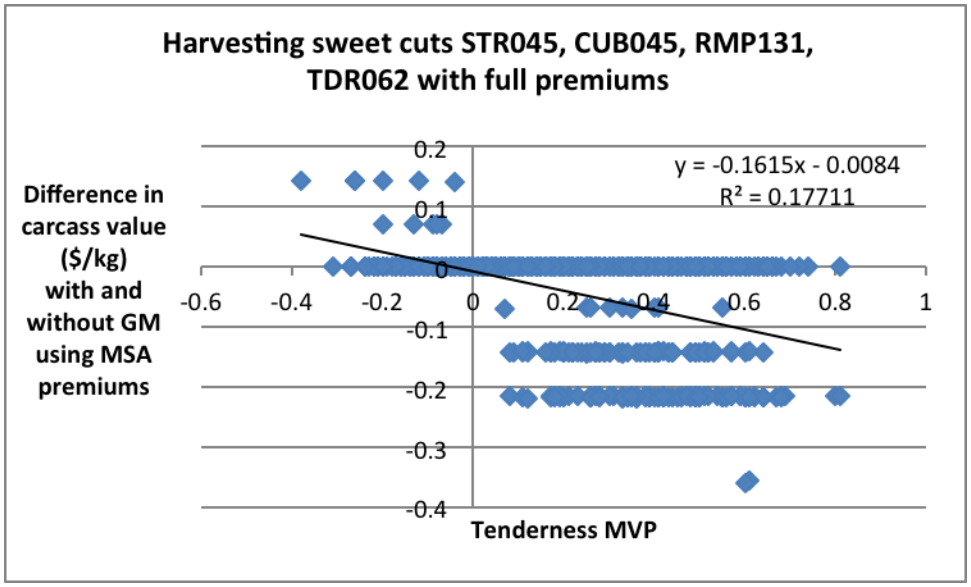

Figure 9 The difference in carcass value ($/kg) with and without using the tenderness gene markers when only the sweet cuts (striploin, cube roll, rump and tenderloin) were harvested and assuming the MSA premiums from Lyford et al. (2010)

Figure 9 showed that only harvesting sweet cuts decreased the strength of the relationship between the difference in carcass value ($/kg) and tenderness MVP decreased from an $R^2$of 38% to 18%. Similarly the slope of the relationship also decreased indicating that the lower number of cuts resulted in less value being realized by adjustment for gene markers. Figure 9 showed that only harvesting a selected number of cuts resulted in many more carcasses not changing value, hence the lower accuracy of the relationship.

The final scenario was one whereby the difference in carcass value with and without adjustment for gene markers was calculated applying a 5% premium for those cuts which achieved 3 star or better palatability. This was set up to model the current scenario where the MSA grading premium is applied as a threshold to cuts that achieve 3 star or better. No premium is applied if cuts change from 3 to 4 or 4 to 5 star. The effect of using MSA as a threshold grade is shown in Figure 10. Given that the mean tenderness MVP was positive the average carcass decreased in palatability and received a small discount. There were only very few carcasses that showed a deviation from this. Hence the relationship between the difference in carcass value with the tenderness MVP whilst still positive was very weak.

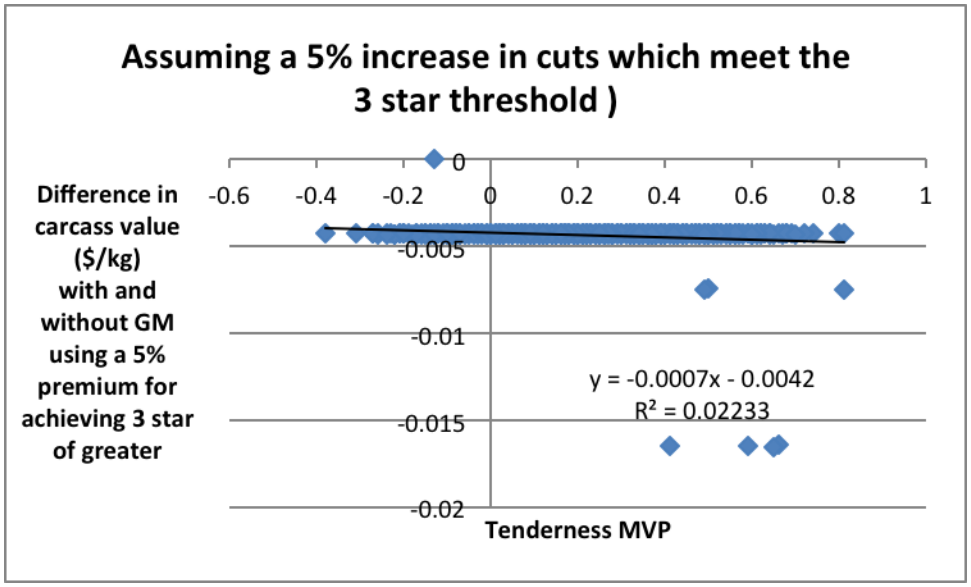

Figure 10 The difference in carcass value ($/kg) with and without using the tenderness gene markers when a 5% price premium was applied to all cuts that achieved 3 star or better palatability. The premium of 5% was calculated from Griffiths and Thompson (2012)

Obviously for the tenderness gene markers to be implemented via the MSA grading scheme and to be of value to the Australian beef industry there has to be a substantial premium paid for eating quality to off-set the cost of DNA testing every animal. The value of gene markers is eroded accordingly if the premiums for the different quality grades are reduced. Even if the premiums are there the value of using tenderness gene markers to identify better cuts and then simply harvesting these cuts from a population of cattle will depend upon where the population average tenderness MVP sits relative to Australian beef population. For populations that have a high *Bos indicus* content (and therefore a positive tenderness MVP) the value of DNA testing is unlikely to be recouped unless the mean tenderness MVP for the group is substantially less than the Australian population.

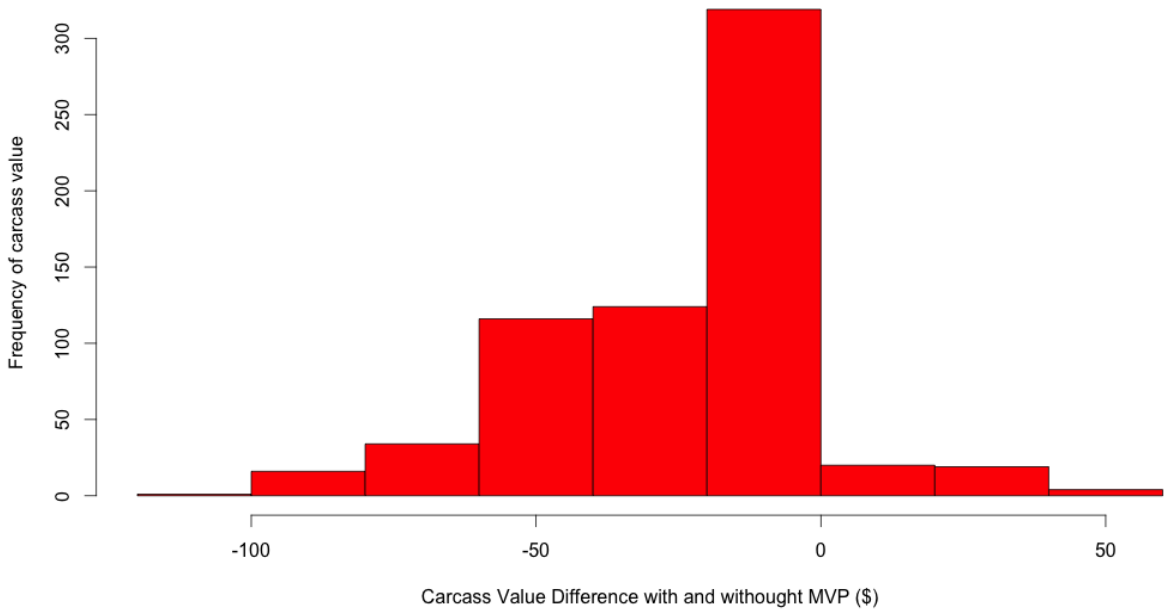

Figure 11 Frequency histogram of difference in carcass value with and without adjustment for tenderness MVP. Large differences in carcass value existed between carcass value with and without MVP (**Figure 1**). The difference in individual carcasses of including or excluding the tenderness MVPs was up to $150.

The cost of testing for gene markers which is currently at ca. $40/head would suggest that it is too high for a producer to recoup the cost of testing. The fixed costs of chemicals and reagents in gene testing are of the order of $7 to 10/sample (E Piper *personal communication*). If a profit margin was added it would likely that the cost of the test would be of the order of $20/sample, or for the commercial population in Table 7 it would be $0.09/kg carcass weight. By solving the equations in Figures 7, 8 and 9 it was estimated that a decrease 0.26, 0.61 and 0.50 in the tenderness MVP was required to cover the fixed cost of gene testing in scenarios which assumed the full MSA premiums for all graded cuts, half these premiums for all graded cuts and then only harvesting the sweet cuts and assuming the full MSA premiums for those cuts.

Given the relatively high testing costs the benefits of using the tenderness gene markers as a tool to identify and harvest high quality carcasses are likely to be limited. the next stage of the report will focus on using the tenderness MVP as a breeding tool.

3.5 Estimation of the response from selection of elite bulls and use over animals with range of MVPS similar to commercial dataset

The selection of sires based on MVP has potential to increase the value of carcasses in a value based marketing system. Table 10 presents the results of selecting sires from different percentiles of the commercial population used in this study for mating across females. The response per carcass was increased by just over $20 per carcass if sires from the top 5 and 1% percentiles were used. Thus a single sire selection was unlikely to change value enough to justify testing of all progeny from that sire at current testing cost and the simulated market premiums unless it had an MVP which was -0.5 less than the mean of the breeding herd.

Table 10 Response to selection of a superior sire for a single round of progeny

Sire			Average progeny value		Change in value*	
Percentile threshold	Selection differential MVP	Expected Progeny MVP	($/head)	($/kg)	($/head)	($/kg)
50	-0.089	0.150	815.88	3.59	10.5	0.046
30	-0.130	0.110	819.65	3.60	13.2	0.058
20	-0.157	0.083	822.42	3.62	16.9	0.074
10	-0.196	0.043	826.03	3.63	19.9	0.087
5	-0.231	0.009	829.05	3.65	25.3	0.112
1	-0.298	-0.059	834.52	3.67	0.0	0.000
99	-0.003	0.237	809.17	3.56	0.0	0.000

*represents the change in value relative to no selection (~99 of animals selected)

3.5.1 Estimation of the response to selection each generation using a 4 marker panel (MVP4) consisting of calpain and calpastatin SNPS

The four markers within the 56 marker panel are amongst the widely tested genes in the beef cattle. These genes have been tested in a wide variety of breeds and production systems. Hence the first step in this series of simulation studies was to evaluate the impact of selecting only upon markers within these major genes. Selection on the MVP4 lead to an increase in the MSA Index (**Figure**). There was less difference between the sires selected at 10% or 5% levels than would be expected from a standard normal distribution (0.07 and 0.09) in compared to the expectation (0.048 and 0.099) from the normal distribution due to the finite population and small numbers . Thus there was less difference between the 5% and 10% sire selection strategies. When selecting top 5% or 10% of sire MQ4 was reaching a plateau after around six generations of selection whilst it took longer (~8) generations with a lower selection intensity.

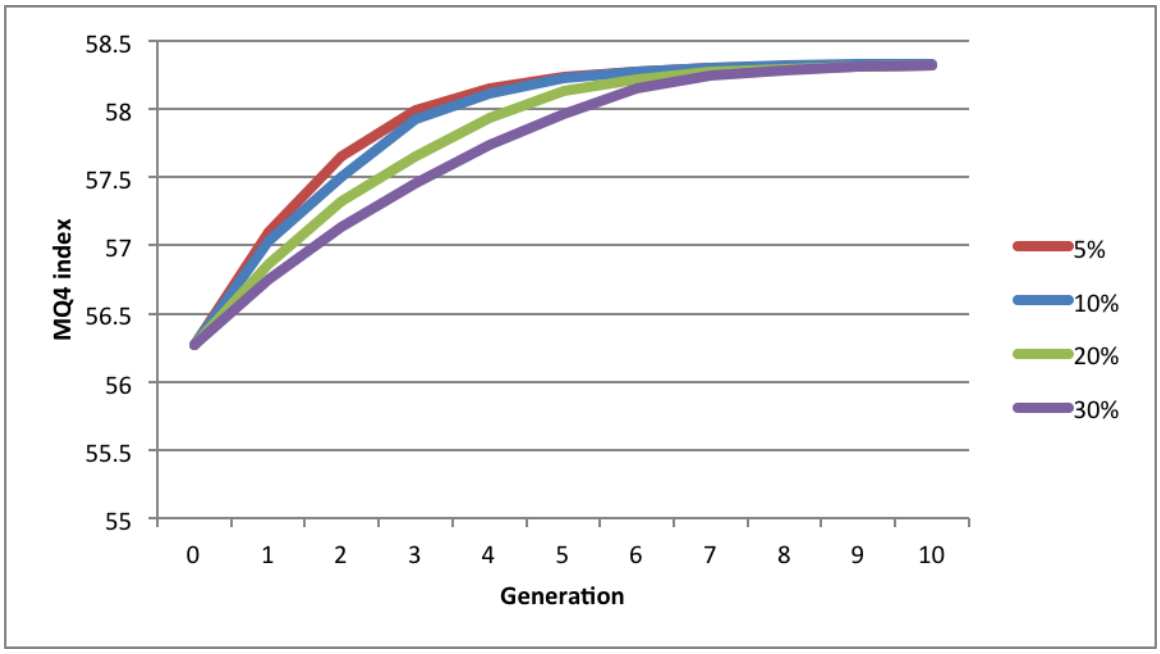

Figure 12 Relationship between weighted carcass MQ4 and generation of selection on 4 calpain/calpastatin markers with top 5% to 30% of sires selected each generation

Similar patterns were observed when predicting change in carcass value (**Figure**). The changes in carcass value were slightly higher when predicted using regression than using the discrete pricing function where MQ4 of each individual cut and its price estimated.

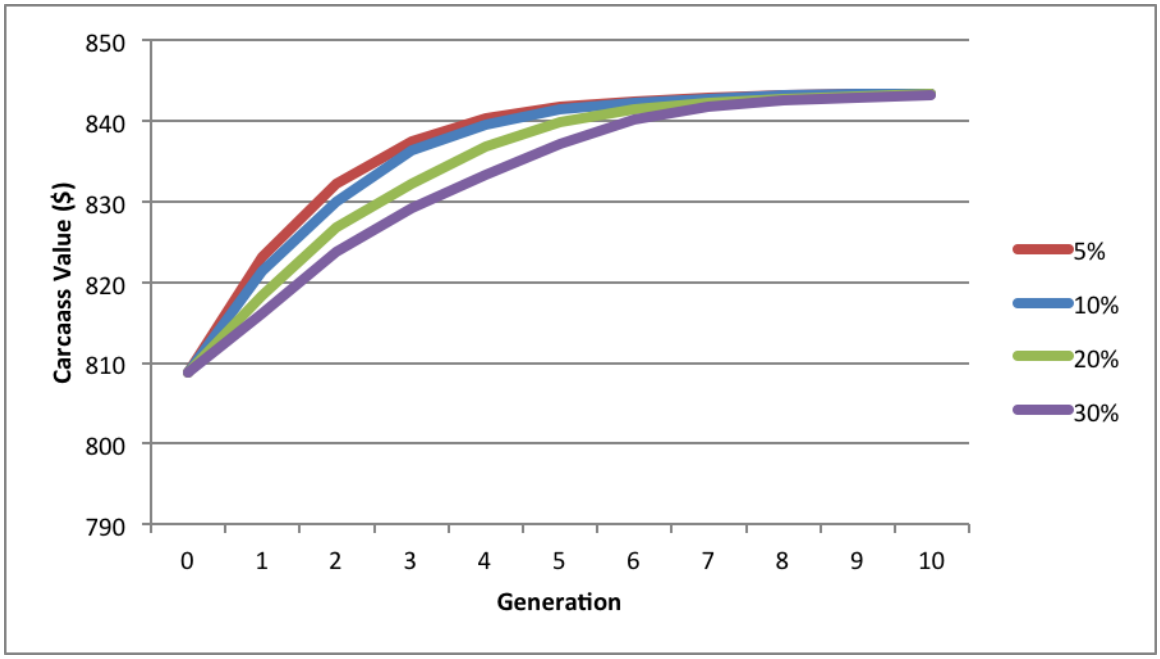

Figure 13 Relationship between estimated carcass value and generation of selection on 4 calpain/calpastatinmarkers with top 5% to 30% of sires selected each generation

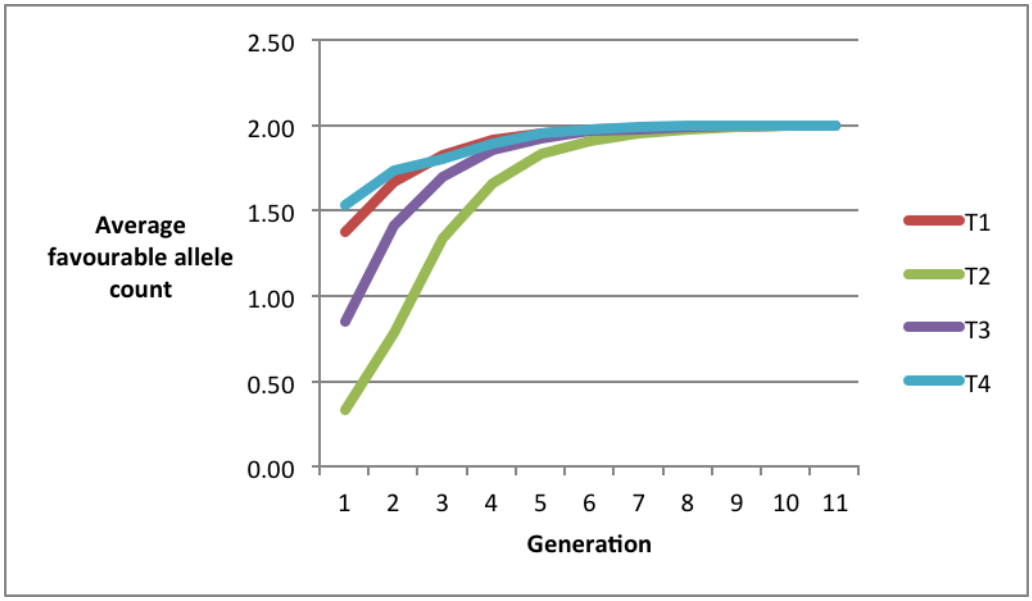

Figure 14 Average count of favourable alleles and generation of selection on 4 calpain/calpastatinmarkers with top 5% of sires selected each generation

Figure and Table 11 show the progression of the individual markers towards fixation. Markers T1,T3 and T4 approach fixation after 3-4 generations. The final marker T2 took approximately 2 extra generations to reach fixation. Although benefit could be derived from selection upon these markers the lifespan of selection would be short to moderate depending upon the selection intensity. This lead us to consider utilizing an increased numbers of markers and gene effects.

Table 11 Selection on MVP4, change in average favourable allele count, predicted MVP carcass value and MQ4 (top 5% selected as sires)

	Average favourable allele count						
Generation	T1	T2	T3	T4	MVP*	Carcass Value	MSA Index *
0	1.37	0.33	0.85	1.53	0.24	808.87	56.27
1	1.67	0.78	1.41	1.73	0.07	823.19	57.10
2	1.83	1.33	1.70	1.81	-0.04	832.30	57.66
3	1.91	1.66	1.85	1.89	-0.10	837.56	57.99
4	1.96	1.83	1.92	1.96	-0.13	840.34	58.16
5	1.98	1.91	1.96	1.98	-0.15	841.79	58.24
6	1.98	1.95	1.98	1.99	-0.16	842.50	58.28
7	1.99	1.97	1.99	2.00	-0.16	842.84	58.30
8	1.99	1.99	1.99	2.00	-0.16	843.22	58.32
9	2.00	1.99	1.99	2.00	-0.16	843.38	58.32
10	2.00	2.00	2.00	2.00	-0.17	843.38	58.33

*MVP and MQ4 were predicted based on regression

3.5.2 Estimation of the response to selection each generation using a polygenic marker model for MVPS (MVPEBV)

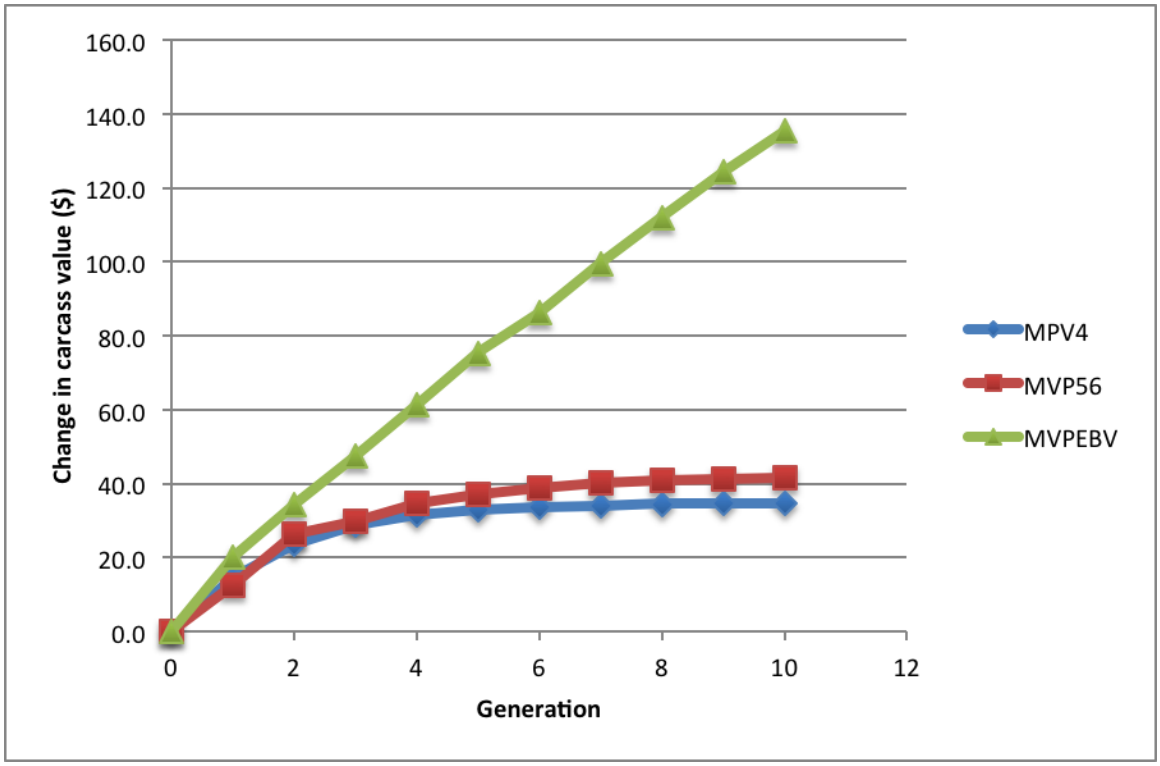

Figure 15 Response to selection on MVP with either 4 marker panel, selection within current best bulls in the population and assuming infinitesimal model (MVP4 is selection on the 4 calpain/calpastatin markers only).

Figure 15 and Table 12 show the response per generation to sire selection on MVP in the three simulations. If only the best sires within the current generation are considered or selection is only on the MVP4 response asymptotes at approximately $844, after 3-4 generations. The increase in the number of markers leads to an increase in the final MVP and carcass value. MVP56 leading to an additional $7 at equilibrium. Meuwissen et al. (1991) proposed using dense panels of markers for predicting breeding values based on all QTL across the genome. Subsequently this technology has been successfully applied in the dairy industry to reduce progeny testing cost and generation interval (Schaeffer, 2006). In beef cattle the success of this technology has been less successful however, within the Angus breed it has been used to select across a wide range of traits including (Garrick, 2011; Saatchi et al., 2011). Development of a genomic selection test was simulated based on the

amount of variation explained by the current MVP56. The only difference under this model was that it was assumed that there was an unlimited number of genes segregating that influence MQ4, which is a standard assumption development of breeding values (simulation and genetic evaluations).

Table 12 Comparison of the different selection strategies including carcass value and average MVP each generation (with selection on top 5% of sires)

	Carcass Value ($)			MVP		
Generation	MVP4	MVP56	MVPebv	MVP4	MVP56	MVPebv
0	808.87	808.87	808.87	0.240	0.240	0.240
1	823.19	821.28	829.03	0.076	0.092	0.010
2	832.30	835.19	843.03	-0.033	-0.068	-0.160
3	837.56	838.56	856.35	-0.098	-0.111	-0.310
4	840.34	843.49	870.06	-0.131	-0.165	-0.450
5	841.79	846.06	884.18	-0.148	-0.200	-0.590
6	842.50	847.85	895.15	-0.155	-0.221	-0.720
7	842.84	849.18	908.46	-0.159	-0.238	-0.860
8	843.22	849.75	920.89	-0.162	-0.246	-1.000
9	843.38	850.14	933.10	-0.163	-0.254	-1.130
10	843.38	850.49	944.23	-0.164	-0.257	-1.270

4. Implications

The effects of markers within calpain and calpastatin genes have been demonstrated to impact on tenderness across diverse range of cattle across a range of experiments (Cafe et al., 2010a; Cafe et al., 2010b; Greenwood et al., 2013; Johnston and Graser, 2010; Robinson et al., 2012; White et al., 2005). It has been shown that these relationships act through changing the ageing rate of muscles (Koohmaraie and Geesink, 2006). Based on this principle the effects of the tenderness MVP was extended across the musculature of the carcass. However the

size of these experiments lead to the standard errors around some of these estimates being quite large. Thus we recommend that this relationship should be explored further with additional experimentation. In addition an opportunity exists to examine proteolysis rates utilizing samples from the Rigor Temperature experiment and use these estimates to better understand the relationship between MVP and aging rate. This would increase our confidence in the extrapolation of the MVP effects in muscles which have not been evaluated.

Given the relatively high testing costs the benefits of using the tenderness gene markers as a tool to identify and harvest high quality carcasses are likely to be limited. It was found that the population would need to have a mean tenderness MVP which was 0.26, 0.61 and 0.50 lower than the current average MVP to cover the cost of testing in scenarios which assumed the full MSA premiums for all graded cuts, half these premiums for all graded cuts and then only harvesting the sweet cuts and assuming the full MSA premiums for those cuts. A herd having MVPs this different would not be achieved without a breeding program that selected upon MVP. The results for simulated breeding programs were examined using simulation based upon the commercial herd.

In the current dataset MVP was independent or lowly correlated with all other traits except hump height. This would probably be expected as there are differences in eating quality and *Bos indicus* content/hump height. Additionally the allele frequencies of the favourable alleles for tenderness and thus eating quality were lower in *Bos indicus* animals. The current model estimates suggest that the effects of individual muscle regression for tenderness MVP and hump height do not interact, fitting the effect of hump height decreased the effect of MVP in most muscles and increased it in three muscles. However given the adjustment was based on 50 animals over a narrow range of *Bos indicus* content the relationship was quite unstable. Thus it is suggested that this assumption is tested in subsequent experiments with a wider range of *Bos indicus* content.

In our study the use of gene markers within the MSA systems was evaluated at three levels. (1) the impact of using MVP as a harvesting tool and simply sorting a current population based on their MVPs, (2) one round of selection of sires with elite MVPs for tenderness (2) incorporation of MVPs into a selection program for multiple generations.

Whilst there was substantial variation in the carcass value and MQ4 (**Figure**), without any selection on MVP it was found that simply testing individual carcasses for their MVP and harvesting cuts would be unlikely to be beneficial. Given the variation in tenderness MVP within a herd any gains from identifying higher value carcasses based on MVP was offset by reductions in the value of the remaining carcasses. This assumes that the group of animals with MVPs is around the average, if animals were lower than average MVP then increasing carcass value could potentially be captured if the animals were lower than average. This relationship is shown in Table 10, if the average MVP was than 0.25 lower the average carcass value was $22 higher.

Selection of sires with improved MVPs could increase the carcass value. It was estimated that selection of elite sire from within the example dataset could increase the carcass value by $11.3, $19.2, 23.9 and $29.1 with 30%, 10% 5% and 1$ of sires selected respectively. Thus one round of selection would generally not cover the cost of testing individual progeny with current prices unless an elite sire from the top 5% was used. However, increases in volume and cheaper genotyping platforms may make this feasible.

There are very few studies that examine the economics of including beef tenderness in selection programs. (Weaber and Lusk, 2010) examined the economics of including MVPs in a breeding program as a predictor of Warner-Bratzler shear force. In their study selection on MVPs resulted in an increased profitability of ca. $10per animal per year. This was quite similar to the return estimated from a single round of sire selection in this study at the same selection intensity ($11.30)although both studies used substantially different underlying models. The model proposed by (Weaber and Lusk, 2010) had very simplistic extrapolations of changes in value across muscles which were based on results from striploin on tenderness across the remaining cuts in comparison to the approach used in the current study were eating quality of each muscle was estimated from the aging rate links between valued muscles. The model proposed in our study was more simplistic in an handling of the price point, just using estimates from MSA willingness to pay extended to star thresholds previously determined, whereas (Weaber and Lusk, 2010) valued changes value based on demand shifts contingent on changes in tenderness and its relationship with willingness to pay. The simulation was performed on a change per

year rather than per generation as in this study. However the results from our study could be converted to the steady state response in genetic merit by simply dividing by the generation interval.

5. Recommendations

If it was assumed that if the current MSA model was set for a tenderness MVP of zero then under this scenario there would be little incentive for a producer with a mean lot tenderness MVP of -0.2 to test and harvest cuts assuming a fixed cost of $20/animal for testing. It may be an industry decision to modify the base in the MSA model so that the base eating quality prediction was equivalent to an MVP of 0.2. This modification would make it profitable for producers with a mean MVP of 0 or less to cover the cost of genomic testing to harvest cuts.

Therefore if gene markers are to be incorporated into the MSA model the setting of the base for the MSA model is an industry decision that must be addressed. In addition there will be infrastructure costs to set up a system to align test results with the NLIS number at slaughter. Therefore whereas the animal testing costs are likely to be an ongoing cost that will have to be borne by producers the infrastructure costs are likely to be an industry investment and have not been considered as part of the operating costs.

This project proposed a general framework for estimating the economic impacts of technologies that change MSA (**Figure**). It is proposed that this framework could be used to assess the impact of other factors within the MSA model. Examples of other factors that could be investigated using a similar framework include new feed additives or HGPs such as Zilmax and ractopamine or the value of enhancement technologies ,to improve palatability of specific cuts.

Prior to any incorporation of gene markers in the MSA model better estimates of the relationship between tenderness MVP and MQ4 for the 39 muscles in the MSA model are required. It is therefore suggested that a series of additional consumer tests are required to add to the current data set for 16 muscles and to also extend these estimates to the remaining 23 muscles. Whilst the use of sensory to provide empirical estimates of the regression coefficients for individual cuts is feasible it is expensive and a more strategic approach may be to invest in research which

provides a better understanding of the why muscles differ in their response to differences in gene marker status. In the longer term this may be a cheaper approach to allow estimation of the MQ4/tenderness MVP relationship for individual muscles.

The results of this study showed that using the current 56SNP panel the response to selection for the tenderness MVP would plateau in 3 to 4 generations. To avoid this plateau better genomic functions need to be estimated. It is suggested that the current BIN resource be used to develop genomic predictions that are focused on using current sires. In addition any future animals which are consumer tested as part of the MSA R&D program should also be tested for gene marker status. Preferably this should include both the Pfizer test but also store a DNA sample for developing new genomic prediction function. This will incur a cost of pulling a tail hair from individual animals and submitting this for genomic testing prior to slaughter. As discussed previously the future cost of genomic testing will likely be of the order of $20/test and unlikely to be less than $15/sample. Given this cost is likely to be a barrier to industry adoption in the short to medium term the only alternative to lower the sample testing cost would be to incorporate the genomic testing for the tenderness MVP with genomic tests for other production traits or other genomic tests such as the polled gene, parentage testing or tests for deleterious genes.

In conclusion it is unlikely that producers could benefit from harvesting cuts based on MVPs, however this depends where the base for the MVP is set. Currently it is set at the mean of MVPs across all breeds. Therefore breeds with lower than average MVP would be penalized if they tested and reported MVPs on their animals. It was clear from the modeling exercises that selection for a tenderness MVP would lead to short to medium term improvements in MQ4 of selected animals. If the tenderness MVP is to be an input in the MSA model there are limited ways to defray the relatively high per animal testing costs. At $20/head the testing costs were of the order of 0.10$/kg carcass weight, whereas this would be effectively reduced by increasing carcass weight. Alternatively if used within a closed supply chain where product is marketed under a brand it may not be necessary to test individual progeny, rather the assumption is that a higher frequency of favourable tenderness SNPs will further promote the brand in terms of consumer satisfaction.

Given the finite lifespan of the current MVP which is based largely on the 4 tenderness SNPs (it was predicted that response to selection would plateau in 3 to 4 generations) it was suggested that the current beef information nucleus projects be harnessed to provide prediction equations using new closely spaced markers.

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7. APPENDIX 1 A template for evaluating the economic impact of new technologies on the MSA grading scheme

The Meat Standards Australia (MSA) grading system uses commercial input traits to predict the palatability of individual beef cuts cooked using a variety of cooking methods (e.g. Thompson 2002, Polkinghorne *et al.* 2008). Outputs of the MSA model are palatability score (MQ4) for 39 MSA cuts for up to four different cooking method which allows individual cuts to be allocated to one of four palatability grades. These four grades have been generated by the consumers classifying taste panel samples as unsatisfactory (2 star), good everyday (3 star), better than everyday (4 star) and premium (5 star). More recently an MSA Index, which is a weighted average of the 39 MSA cuts, has been developed as a feedback tool for producers to monitor changes in palatability.

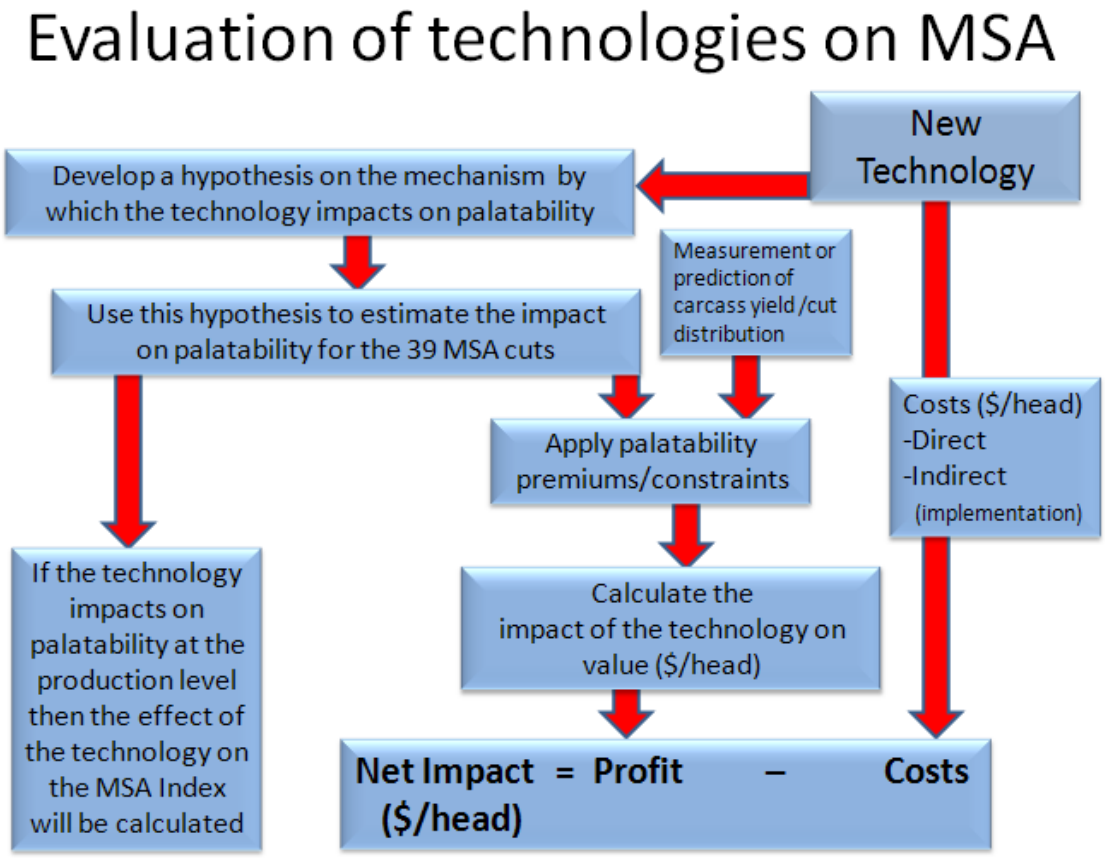

Figure 16 A diagrammatic representation of how the impact of new technologies on MSA can be evaluated

A template for evaluation of new technologies has been developed for MSA and is shown in Figure 16. To undertake any impact analysis there either needs to be experimental data on the magnitude of the technology on palatability, or a working hypothesis as to the mechanism by which the technology works. This hypothesis may operate by effecting changes in one or a combination of proteolysis, sarcomere length, connective tissue (both the amount and solubility) or intramuscular fat content. In reality the impact of the technology on palatability will most likely be a combination of experimental data and a working hypothesis on the mechanism. As experimental data will generally only include a limited number of muscles these effects need to be extended over the total 39 MSA cuts in the MSA model.

The technology impact on the palatability of individual muscles may simply be additive to the current MQ4 scores or it may operate by modifying or extending the impact of some of the inputs of the MSA model. Examples of this would be the tenderness gene markers which are thought to operate via their effect on proteolysis. Experimental data suggested that whilst the effect of the tenderness gene markers differed between the muscles (presumably due to the ageing rate of that muscle) when viewed within a muscle there was no interaction with ageing rate. It was conceivable that whilst ageing rates of individual muscles vary across the carcass the impact of tenderness gene markers may alter the rate at which these enzymes degrade elements of muscle structure post-mortem and effectively was constant over all ageing periods.

Other technologies such as tenderstretch operate via physical stretching or contraction the muscle fibres which presumably operates directly on palatability after rigor and on the subsequent ageing rates of the muscles. On the other hand the mechanism by which hormonal growth promotants impact on palatability suggests that the effects differ according to the ageing rate of the muscle and that they do not interact with ageing rate within muscles.

It may be that new hypotheses are generated for inputs that already exist within the MSA model and the approach in Figure 13A used to test the cost/benefit of new experiments to further refine additional effects. An example of this could be that whilst in the current model simply has the *Bos indicus* effect resulting in a differential effect on palatability of muscles there is some evidence that it should also interact with ageing rate. Using the template in Figure 13 the cost of confirming this and

developing estimates of differential ageing rate for the model against the potential benefits for industry could be estimated.

If the new technology effects palatability by manipulation at the production end of the supply chain the effect on the MSA index can be calculated. It should be stressed that the MSA Index is a feedback tool for producers and will not necessarily related to price and so should not be confused with an economic analysis.

To allow economic analyses to be undertaken an estimate of the effect of the technology on palatability and also carcass yield and distribution of tissue is required. For some technologies yield differences may already be available whilst in most cases the yield of cuts will have to be estimated. Currently many of the 39 MSA cuts are not harvested and used by industry therefore the yield of cuts should reflect current boning practices. At a commercial level cuts are seldom broken down to their individual muscles so there will have to be some summarization made in the cuts that are used in the economic analyses. In many commercial boning rooms only the sweet cuts (striploin, cube roll, rump and fillet) may be collected and sold as graded cuts and hence the economic analysis would be restricted to these cuts with all other cut being sold at commodity prices (ie 3 star).

The price premiums for the different quality grades are an important component of any economic analyses. Whilst in many cases the quality grades for 3 star and above are sold for a flat price. There are a number of examples of companies developing premiums for 4 and sometimes 5 star product but in most cases these premiums are still developing and would be expected to increase rapidly in the near future. In lieu of real data on price premiums the willingness to pay (WTP) data from Lyford et al (2010) is useful. In their study they analysed data from an exit survey conducted using almost 7,000 consumers from Australia, US, Japan and the Irish Republic. Based on steaks that had been prepared using different cooking methods after the sensory panels were completed consumers were asked to mark what they would pay for steaks they had rated as unsatisfactory (2 star), good every day (3 star), better than every day (4 star) and premium (5 star). Given that the different nationalities had used different units to value cuts all data was expressed as a proportion of 3 star grade. For the Australian, US and Irish consumers the premium for 5 and 4 star product was ca. 2.0 and 1.5 respectively. All nationalities valued 2 star at 0.5 the value of 3 star. Not surprisingly the Japanese consumers tended to

value quality more than other nationalities with 5 star product being valued at 3.0 times the 3 star product. The premiums to value quality may be set by industry but in lieu of good data the weightings of Lyford et al (2010) could be used to generate premiums for quality. The quality premiums in conjunction with estimates of the commercial cuts will allow the carcass to be valued. Trim, fat and bone would be valued at a standard rate.

The cost of the technologies will involve some estimate of the per animal cost for applying the technology. There may also be implementation costs if additional data handling and verification schemes are required to ensure that carcasses are accurately described when presented for grading.

The final step is to calculate a profit function on a per animal basis where net profit from a technology is simply the additional value of the carcass minus the costs.

The template provided here can be used to undertake an analysis of a range of different technologies that impact on palatability. If analyses are conducted in a rigorous manner using the best estimates of the impact of the technology on palatability and then converting these to value and finally net impact the template will provide a means to rank the different technologies on their potential benefits to the beef industry. There is also the opportunity to undertake sensitivity analyses to guide investment in future research programs.

8. APPENDIX 2 Detailed description of simulation process

- Relationship between markers (T1-T4) and MVP estimated using regression
- For each generation
    - MVP was estimated given the values of markers (T1-T4)
    - Top sires were selected
    - Most likely haplotypes estimated for each animal using em algorithm in haplotype.em. (Sinnwell and Schaid, 2013)
    - All animals were assumed to be dams
        - Mated to randomly selected sires
    - New sire and dam haplotypes were simulated for each progeny as follows
        - A reference haplotype was selected at random from parental haplotypes
        - Select Haplotype 1 if N(0,1)<0.5 and 2 if N(0,1)>=0.5
        - For markers j =2-4 the alternate haplotype was selected if N(0,1)>N_density($r^2_{j-1,j}$,0,1)
    - Average carcass value was calculated using spreadsheet model by adjusting the mean value of ACC animals to match average MVP in year of study

Table 13 Correlations between genotypes used in simulations

	T1	T2	T3	T4
T1	1			
T2	0.01	1		
T3	0.16	0.29	1	
T4	0.19	0.02	0.09	1

9. APPENDIX 3 Full simulation results

Table 14 Impact of changing tenderness MVP on carcass value (both as $/head and $/kg) independent of other MSA effects (Note base is commercial herd which has a higher MVP than average)

Change in		Average carcass value		Change in value	
MVP	MQ4	($/head)	($/kg)	($/head)	($/kg)
0	56.270	808.9	3.56	0.00	0.00
-0.1	56.780	816.7	3.59	7.85	0.03
-0.25	57.544	830.6	3.65	21.72	0.10
-0.5	58.819	850.7	3.74	41.83	0.18
-0.75	60.094	875.8	3.85	66.98	0.29
-1	61.369	899.3	3.96	90.48	0.40
-1.25	62.644	922.0	4.06	113.17	0.50
-1.5	63.919	943.4	4.15	134.55	0.59
-1.75	65.193	966.2	4.25	157.30	0.69
-2	66.468	986.5	4.34	177.68	0.78
-2.5	69.018	1025.2	4.51	216.31	0.95
-3	71.567	1060.5	4.67	251.63	1.11

Table 15 Detailed simulation results for all scenarios examined included four marker MVP, 56 marker panel and estimated breeding values

Generation	Scenario	Selection proportion	Change in MVP	MVP	MQ4	Carcass Value (%)	Carcass Value ($/kg)	Change in Carcass value ($)	Change in Carcass value ($/kg)
0	MVP4	5%	0.00	0.24	56.27	808.87	3.56	-41.28	-0.18
1	MVP4	5%	-0.16	0.08	57.10	823.19	3.62	-26.96	-0.12
2	MVP4	5%	-0.27	-0.03	57.66	832.30	3.66	-17.84	-0.08
3	MVP4	5%	-0.34	-0.10	57.99	837.56	3.68	-12.58	-0.06
4	MVP4	5%	-0.37	-0.13	58.16	840.34	3.70	-9.81	-0.04
5	MVP4	5%	-0.39	-0.15	58.24	841.79	3.70	-8.36	-0.04
6	MVP4	5%	-0.39	-0.15	58.28	842.50	3.71	-7.64	-0.03
7	MVP4	5%	-0.40	-0.16	58.30	842.84	3.71	-7.30	-0.03
8	MVP4	5%	-0.40	-0.16	58.32	843.22	3.71	-6.93	-0.03
9	MVP4	5%	-0.40	-0.16	58.32	843.38	3.71	-6.76	-0.03
10	MVP4	5%	-0.40	-0.16	58.33	843.38	3.71	-6.76	-0.03
0	MVP56	5%	0.00	0.24	56.27	808.87	3.56	-124.23	-0.55
1	MVP56	5%	-0.15	0.09	57.03	821.28	3.61	-111.81	-0.49
2	MVP56	5%	-0.31	-0.07	57.84	835.19	3.67	-97.90	-0.43
3	MVP56	5%	-0.35	-0.11	58.06	838.56	3.69	-94.54	-0.42
4	MVP56	5%	-0.40	-0.17	58.33	843.49	3.71	-89.61	-0.39
5	MVP56	5%	-0.44	-0.20	58.51	846.06	3.72	-87.03	-0.38
6	MVP56	5%	-0.46	-0.22	58.62	847.85	3.73	-85.25	-0.38
7	MVP56	5%	-0.48	-0.24	58.71	849.18	3.73	-83.92	-0.37
8	MVP56	5%	-0.49	-0.25	58.75	849.75	3.74	-83.35	-0.37
9	MVP56	5%	-0.49	-0.25	58.79	850.14	3.74	-82.95	-0.37
10	MVP56	5%	-0.50	-0.26	58.80	850.49	3.74	-82.61	-0.36
0	MVPebv	5%	0.00	0.24	56.27	808.87	3.56	-124.23	-0.55
1	MVPebv	5%	-0.23	0.01	57.44	829.03	3.65	-104.06	-0.46
2	MVPebv	5%	-0.40	-0.16	58.31	843.03	3.71	-90.06	-0.40
3	MVPebv	5%	-0.55	-0.31	59.07	856.35	3.77	-76.75	-0.34
4	MVPebv	5%	-0.69	-0.45	59.79	870.06	3.83	-63.03	-0.28
5	MVPebv	5%	-0.83	-0.59	60.50	884.18	3.89	-48.92	-0.22
6	MVPebv	5%	-0.96	-0.72	61.16	895.15	3.94	-37.95	-0.17
7	MVPebv	5%	-1.10	-0.86	61.88	908.46	4.00	-24.63	-0.11
8	MVPebv	5%	-1.24	-1.00	62.59	920.89	4.05	-12.21	-0.05
9	MVPebv	5%	-1.37	-1.13	63.26	933.10	4.10	0.00	0.00
10	MVPebv	5%	-1.51	-1.27	63.97	944.23	4.15	11.13	0.05
0	MVP4	10%	0.00	0.24	56.27	808.87	3.56	-124.23	-0.55
1	MVP4	10%	-0.15	0.09	57.03	821.47	3.61	-111.63	-0.49
2	MVP4	10%	-0.24	0.00	57.51	829.95	3.65	-103.15	-0.45
3	MVP4	10%	-0.32	-0.08	57.92	836.46	3.68	-96.63	-0.43
4	MVP4	10%	-0.36	-0.12	58.11	839.56	3.69	-93.53	-0.41
5	MVP4	10%	-0.38	-0.14	58.22	841.43	3.70	-91.67	-0.40
6	MVP4	10%	-0.39	-0.15	58.27	842.35	3.70	-90.75	-0.40
7	MVP4	10%	-0.40	-0.16	58.30	842.70	3.71	-90.39	-0.40
8	MVP4	10%	-0.40	-0.16	58.32	843.22	3.71	-89.88	-0.40
9	MVP4	10%	-0.40	-0.16	58.33	843.38	3.71	-89.71	-0.40

10	MVP4	10%	-0.40	-0.16	58.33	843.38	3.71	-89.71	-0.40
0	MVP4	20%	0.00	0.24	56.27	808.87	3.56	-124.23	-0.55
1	MVP4	20%	-0.12	0.12	56.87	818.40	3.60	-114.70	-0.51
2	MVP4	20%	-0.21	0.03	57.32	826.77	3.64	-106.32	-0.47
3	MVP4	20%	-0.27	-0.03	57.66	832.26	3.66	-100.84	-0.44
4	MVP4	20%	-0.33	-0.09	57.94	836.83	3.68	-96.27	-0.42
5	MVP4	20%	-0.37	-0.13	58.13	839.88	3.69	-93.22	-0.41
6	MVP4	20%	-0.38	-0.14	58.22	841.49	3.70	-91.60	-0.40
7	MVP4	20%	-0.39	-0.15	58.27	842.35	3.70	-90.75	-0.40
8	MVP4	20%	-0.40	-0.16	58.30	842.69	3.71	-90.41	-0.40
9	MVP4	20%	-0.40	-0.16	58.32	843.07	3.71	-90.02	-0.40
10	MVP4	20%	-0.40	-0.16	58.32	843.38	3.71	-89.71	-0.40
0	MVP4	30%	0.00	0.24	56.27	808.87	3.56	-124.23	-0.55
1	MVP4	30%	-0.09	0.15	56.75	816.24	3.59	-116.86	-0.51
2	MVP4	30%	-0.17	0.07	57.14	823.75	3.62	-109.34	-0.48
3	MVP4	30%	-0.23	0.01	57.46	829.19	3.65	-103.91	-0.46
4	MVP4	30%	-0.29	-0.05	57.73	833.42	3.67	-99.68	-0.44
5	MVP4	30%	-0.33	-0.09	57.96	837.23	3.68	-95.86	-0.42
6	MVP4	30%	-0.37	-0.13	58.15	840.12	3.69	-92.98	-0.41
7	MVP4	30%	-0.39	-0.15	58.24	841.76	3.70	-91.33	-0.40
8	MVP4	30%	-0.40	-0.16	58.29	842.50	3.71	-90.59	-0.40
9	MVP4	30%	-0.40	-0.16	58.31	842.91	3.71	-90.19	-0.40
10	MVP4	30%	-0.40	-0.16	58.32	843.22	3.71	-89.88	-0.40