

Estimating the economic value of using a panel of tenderness markers to select for improved consumer palatability scores

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ABSTRACT: Simulation studies were used to examine the economics of including tenderness genomic predictions within the Meat Standards Australia beef grading scheme (MSA). In this study the relationships between consumer palatability scores (MQ4) for 39 muscles individual cuts and genomic predictions of tenderness (MVPs) were estimated. A large range in individual carcass values differences (up to \$150/head) was observed. However, little benefit could be obtained from gene markers from simply harvesting cuts based on improved estimates of eating quality. Selection of sires with improved MVPs could increase the carcass value of the progeny. It was estimated that selection of elite sire from within the example dataset could increase the carcass value by \$12.5 in the first generation with 5% sires selected as parents. Using genomic prediction in a breeding program led to an increase in carcass value of \$41.6 per carcass but plateaued after 4-5 generations.

Keywords: genetics; meat quality; tenderness MVP

Introduction

The Meat Standards Australia (MSA) beef 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 (Polkinghorne et al 2008a, b; Thompson, 2002). The MSA model grades 39 individual cuts of beef from the carcass into one of four grades; unsatisfactory (2 star), good everyday (3 star), better than everyday (4 star), and premium (5 star).

Commercially, the MSA system is not being used to its full potential, as most graded meat is sold at the same price, i.e. graded 3 star or better. Despite this constraint, MSA in its current usage has generated substantial premiums for all participants in the supply chain (Griffith et al., 2009, 2012).

An exit survey conducted as part of consumer taste panels showed that consumers were willing to pay (WTP) more for better quality beef (Lyford et al. 2010). Therefore, use of all three quality 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.

A number of genetic markers have been identified within the calpain/calpastatin genes that are associated with different activity levels of the calpain and calpastatin genes (Barendse, 2002; Cafe et al., 2010; Fortes et al., 2013;

Robinson et al., 2012). These genes are largely responsible for regulating the rate of protein turnover in the body of the live animal. After slaughter, their activity carries over to the carcass, where they are largely responsible for post-mortem proteolysis. These changes in post-mortem muscle are ultimately seen as changes in tenderness that occur with ageing of meat (Koochmaraie 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 SNP alleles 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 tenderness to varying degrees. The tenderness MVP function has been calibrated using shear force data, so a negative tenderness MVP indicates more tender meat. Combinations of the various tenderness SNPs, either individually (Robinson et al 2012) or in the form of an MVP for tenderness (Greenwood et al 2013), have been shown to impact both shear force and consumer taste panel results.

Previous simulations have shown that using the tenderness gene markers in sire and dam selection strategies result in changes in consumer demand, which in turn could increase profitability by up to \$10 per carcass per year (Weaber and Lusk, 2010). However, extrapolation of their results to Australian production systems that 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, results from Robinson et al. (2012) and Greenwood et al. (2013) showed that the impact of the tenderness markers, either individually as SNPs or as an MVP, interacted with cut, with those muscles that had the faster ageing rate showing larger gene marker effects. Given the MSA model shows that different muscles have a wide range in palatability and may interact with the effects of the gene markers, it was simplistic to assume that the same magnitude of change in one muscle such as the striploin, would be reflected across all muscles in the carcass. Thus, this study estimated the impact of selection on the tenderness MVP on carcass value assessed by summing the effect on the 39 muscles in the MSA model.

Materials and Methods

There were three key steps in estimating the carcass value changes obtained in carcasses over a range of

MVP values. Firstly, the relationship between palatability and the tenderness MVP was regressed against the ageing rate of individual muscles. This included four experimental datasets from three experiments (Greenwood et al. 2013; Polkinghorne et al 2008a, b; Thompson, 2002). These experiments each had a slightly different range of cuts, cooking methods and aging times. When there was more than one estimate for particular muscles, the mean of the 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 used in the MSA model and this relationship was used to estimate the regression coefficients for the remaining 23 cuts.

A separate data set of 190 carcasses was used to predict % carcass yield from carcass measurements of hot carcass weight, eye muscle area and fatness. This data was also used to estimate the distribution of trimmed retail cuts across the carcass musculature. By applying this equation, the weight of trimmed primals could be estimated for individual carcasses

Results for willingness to pay were obtained from Lyford et al. (2010), who showed that consumers were willing to pay ca. 2, 1.5 and 0.5 times as much for 5, 4 and 2 star quality relative to the price they would pay for 3 star product. This was applied to the base carcass price of \$3.64/kg.

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.

The simulation process was similar to that described by Weaber and Lusk (2010). Animals from the commercial population were chosen to be sires and dams of the next generation. Sires were chosen from the top animals on MVP, depending on the modeled selection intensity (5%, 10%, 20% and 30%). These selected animals were then randomly assigned to females randomly selected from the population to form the next generation of animals. For each marker of each sire and dam combination, one allele was randomly selected from each parent. The MVP was then calculated for each new progeny to form the parents of the next generation. This process was repeated 10 times to form the ten generations of simulation. The MVPs of the animals in each generation were then used in the MSA economic model described earlier to estimate carcass price for each simulated animal. Changes in value were then assessed as differences from generation zero.

After discussions with several commercial laboratories, the cost of the MVP laboratory procedure was assumed to be of the order of \$20/sample. Relative to today's costs, this estimate assumes increased efficiency with increased throughput and also increased competition between laboratories.

Results and Discussion

Selection of sires based on MVP has the potential to increase the value of carcasses in a value based marketing system. Table 1 shows the estimated change in carcass value for 10 generations of selection, using the top 5% of animals as sires on MVP. Over 10 generation of selection, carcass value was increased by \$41.6. The response to the first generation was the largest (\$12.5) and the response decreased as underlying markers reached fixation. If only the best sires within the current generation were considered, or selection was based solely on the 4 individual SNPs, the average carcass value asymptoted at approximately \$844, after 3-4 generations.

Table 1. Comparison of the different selection strategies based on carcass value for MVP or on 4 Calpain/Calpastatin markers each generation (with selection of the top 5% of sires)

Generation	Average carcass value MVP	4 Calpain / Calpastatin SNPs
0	808.87	808.87
1	821.28	823.19
2	835.19	832.30
3	838.56	837.56
4	843.49	840.34
5	846.06	841.79
6	847.85	842.50
7	849.18	842.84
8	849.75	843.22
9	850.14	843.38
10	850.49	843.38

Whilst there was substantial variation in the carcass value based on MQ4 of individual cuts estimated from the MSA model with and without MVPs (Figure 1), it was found that in the test population of 653 carcasses, simply testing individual carcasses for their MVP and harvesting cuts was unlikely to cover the cost of the genomic test. As the gains in value made by selecting the best animals on MVP were lost by downgrading the remaining animals. In fact the MQ4 and carcass value was estimated to be lower than before inclusion of MVP in the model. Additionally the base is set at the average of all animals thus many producers would be discounted on average if the current base for the MSA model and MVP were retained at the current level. 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. Although this is not important for selection to improve eating quality, if MVPs are estimated for the purposed of value based marketing it would effect the way premiums and discounts are applied.

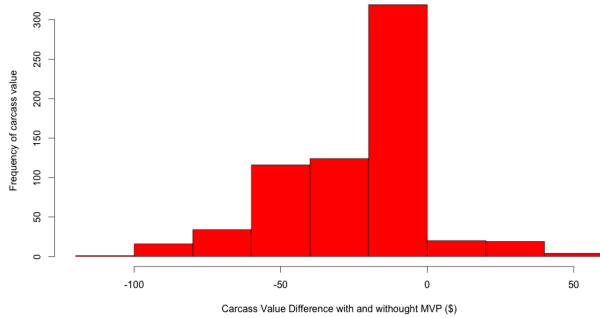


Figure 1 Frequency distribution of difference in carcass value carcass value based on eating quality score (MQ4) for animals estimated from the MSA model with and without adjustment for genetic markers.

Few studies have examined 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. \$10 per 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 (\$12.50). This was despite the two studies being based on vastly different underlying assumptions. The model proposed by Weaber and Lusk (2010) had extrapolated 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, where eating quality of each muscle was estimated from the aging rate links between valued muscles. On the other hand Weaber and Lusk (2010) valued changes value based on demand shifts contingent on changes in tenderness and its relationship with willingness to pay

Conclusions

The value of selecting on MVP was estimated to be approximately \$40 of increased carcass value per animal after 4 generations. As a subset of markers in the calpain/capastatin system are driving most of this change in the MVP and thus tenderness the rate of improvement reaches a plateau rather quickly, as these markers reach fixation. Under value based marking selection on MVP could increase carcass value substantially.

Acknowledgements

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Literature cited

- Barendse, W. 2002. DNA markers for meat tenderness. WO Patent 2,002,064,820.
- Cafe, L., B. McIntyre, D. Robinson, G. Geesink, W. Barendse, and P. Greenwood. 2010. *J. Anim. Sci* 88:3047-3058.
- Fortes, M. R. S., K. Kemper, S. Sasazaki, A. Reverter, J. E. Pryce, W. Barendse, R. J. Bunch, R. McCulloch, B. E. Harrison, S. Bolormaa, Y. D. Zhang, R. J. Hawken, M. E. Goddard, and S. A. Lehnert. 2013. *Anim Genet* 44:636-647.
- Greenwood, P., L. Café, B. McIntyre, G. Geesink, J. Thompson, R. Polkinghorne, D. Pethick, and D. Robinson. 2013. *J. Anim. Sci* 91:5912-5925.
- Griffith, G., H. Rodgers, J. Thompson, and C. Dart. 2009. *Australasian Agribusiness Review* 17:94-114.
- Griffith, G., H. Rodgers, J. Thompson, and C. Dart. 2012. *Australasian Agribusiness Review* 20:11-38.
- Koohmaraie, M., and G. H. Geesink. 2006. *Meat Science* 74:34-43.
- Lyford, C., J. Thompson, R. Polkinghorne, M. Miller, T. Nishimura, K. Neath, P. Allen, and E. Belasco. 2010. *Australasian Agribusiness Review* 18:1-17.
- Polkinghorne, R., J. Philpott, A. Gee, A. Doljanin, and J. Innes. 2008a. *Anim. Prod. Sci.* 48:1451-1458.
- Polkinghorne, R., J. Thompson, R. Watson, A. Gee, and M. Porter. 2008b. *Anim. Prod. Sci.* 48:1351-1359.
- Robinson, D. L., L. M. Cafe, B. L. McIntyre, G. H. Geesink, W. Barendse, D. W. Pethwick, J. M. Thompson, R. Polkinghorne, and P. L. Greenwood. 2012. *J. Anim. Sci* 90:2850-2860.
- Thompson, J. 2002. *Meat Science* 62:295-308.
- Weaber, R. L., and J. L. Lusk. 2010. *American Journal of Agricultural Economics* 92:1456-1471.