

## **GENOMIC PREDICTION OF CONSUMER SATISFACTION TRAITS OF AUSTRALIAN BEEF**

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### **SUMMARY**

Consumer satisfaction has become a key focus for beef producers as eating quality traits such as tenderness and flavour dictate purchasing choices and, ultimately, the price consumers are willing to pay. Due to the difficulty in measuring eating quality traits and the inability to predict those traits prior to slaughter, beef producers opt to select for correlated traits and indirectly select for eating quality. Genotyping of animals offers the opportunity for the selection of cattle with superior eating quality directly for both breeding and market allocation. The aim of this study was to determine the accuracy of genomic prediction along with heritabilities for eating quality traits; tenderness, juiciness, flavour and overall liking as well as the overarching consumer satisfaction trait known as MQ4 in a 10-fold cross validation. Phenotypes from 1,701 cattle recorded in eating quality trials held across Australia were collected for the 5 eating quality traits. Those same cattle were genotyped using varying Illumina SNP arrays between 50k and 100k density and then imputed up to high density 700k using a reference set of 4,506 cattle representing most breeds and crossbreds composites of the Australian beef herds. A linear mixed model was used with cohort, days aged, carcass weight, principal components 1-4 and heterozygosity fit in the model. Heritabilities ranged from 0.21 to 0.32 between juiciness and tenderness respectively, while tenderness and MQ4 had the highest accuracy of 0.27 from the cross validation and juiciness and flavour having the lowest accuracies of 0.23. While accuracies observed in this study were low, moderate heritabilities indicate selection for eating quality traits is feasible.

### **INTRODUCTION**

Beef eating quality has been identified as the leading factor in Australian consumer purchasing habits (Bonny *et al.* 2018). This has led to an increased emphasis on the selection for eating quality traits such as tenderness, juiciness, flavour and overall liking in beef herds for both domestic and export beef herds (Watson *et al.* 2008a). Consumer derived eating quality traits are expensive to test so large-scale measurement is not viable. Processors currently rely on the Meat Standards Australia (MSA) model to predict consumer satisfaction based on objective carcass measurements such as intramuscular fat (IMF), ossification (physiological maturity), paying producers based on meeting phenotype thresholds. This results in producers having to rely on selection of related traits such as IMF content which is known to increase tenderness through muscle fibre dispersion as well as impacting flavour due to modified fatty acid profiles. Genomic analysis offers opportunities to select for eating quality traits prior to slaughter with the possibility of the implementation of genomic estimated breeding values (GEBVs) in commercial Australian beef herds. The aim of this study is to examine the heritability and accuracy of genomic prediction for beef eating quality traits within the diverse Australian cattle herd using Genomic Best Linear Unbiased Prediction (GBLUP)

## MATERIALS AND METHODS

**Phenotypes.** The Striploin muscle (*longissimus lumborum*) was collected and consumed by Australian consumers from 1,701 genotyped Australian cattle between 1997 and 2019. The animals were from 65 cohorts and encompass a diverse breed profile to represent the Australian beef herds. Breeds represented in this research covered tropical *Bos indicus* (261 Brahman), *Bos taurus* (285 Angus, 274 Hereford, 38 Shorthorn), composite breeds (100 Belmont Red and 83 Santa Gertrudis), dairy *Bos taurus* (72 Holstein, 23 Jersey), 121 crossbred cattle and 444 cattle with unidentified breed profiles. The study used steers (n=1319), heifers (n=345) and bulls (n=37) however breed and sex were found to be completely confounded with cohort. Carcase weight ranged from 50.6kg to 576kg, averaging 261.4kg. Steak samples were grilled to protocol as described in Watson *et al.* (2008). Steak samples from each animal were consumed by ten consumers for tenderness, juiciness, flavour and overall liking on a sliding bar scale from poor to excellent. Scores were clipped by removing the top and bottom two scores with the remaining six averaged. Consumers were given seven samples during the sitting with the first sample (link) being removed from analysis (Watson *et al.* 2008b). The four eating quality traits are then used to calculate a singular satisfaction score known as Meat Quality 4 (MQ4) which is based of weightings to reflect Australian consumers preferences;  $MQ4 = 0.3 \times \text{tenderness} + 0.1 \times \text{juiciness} + 0.3 \times \text{flavour} + 0.3 \times \text{overall liking}$  (Thompson *et al.* 2010). Animal phenotypic data included cohort, days aged (post slaughter proteolysis period), and carcase weight.

**Genotypes.** The genotypes for the 1,701 animals were obtained using five different Single Nucleotide Polymorphism (SNP) chips (Illumina BovineSNP50 Genotyping Beadchip v1, v2, GeneSeek Genomic Profiler (GGP) Bovine 50K, GGP Bovine 100K and the TropBeef chip). SNP densities ranged between 50k and 100k with the TropBeef SNP chip having approximately 19k overlap with those used for *bos taurus*. Cleaning of genotypes removed any SNP with missing rates >0.1, minor allele frequencies (MAF) <0.01 and those departing from Hardy-Weinberg equilibrium at  $p < 1 \times 10^{-8}$ . All genotypes were imputed to high density 709,068 SNP with findhap4 (VanRaden *et al.*, 2013) utilising a reference set of 4,506 individuals of which were originally genotyped with Illumina HD array. This reference set spans most breeds, composites and crossbreds in Australia and was adequately suited for the imputation of this dataset. The first four principal components from a genomic relationship matrix (GRM) based on GCTA (Yang *et al.*, 2011) explained around 25% of the genetic variance and were used to represent the breed proportion effect in the model. The proportion of heterozygous loci for animals were calculated from the imputed genotypes to be used in the model.

**Analysis.** A univariate mixed linear model based on GBLUP approach was performed using airemlf90 from the BLUPf90 family of programs (Aguilar *et al.*, 2018) for each of the five eating quality traits to obtain estimates of fixed effects along with heritability of the trait:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{e} \quad (1)$$

Where  $\mathbf{y}$  is the phenotype,  $\mathbf{b}$  is the estimated fixed effect of group and effect of covariates; days aged, carcase weight, principal components 1-4 and heterozygosity,  $\mathbf{u}$  is the vector estimated genomic breeding values (GEBV) of animals,  $\mathbf{e}$  is the residual term.  $\mathbf{X}$  and  $\mathbf{Z}$  are incidence matrices relating to observations to effects fitted in the model. It was assumed that  $v(\mathbf{u}) = G\sigma^2$  where  $G$  was the genomic relationship matrix based on VanRaden (2008) and  $\sigma^2$  is the additive genetic variance.

Animals were randomly assigned into ten groups of equal size. A 10-fold cross validation was performed by removing the phenotypes of each fold allowing the information from the approximately 1,530 animals to estimate breeding value for the remaining 170 animals with deleted phenotypes. Correlations between the EBV and adjusted phenotypes for each group were calculated and averaged across the ten folds to calculate accuracies based on the trait heritability.

## RESULTS AND DISCUSSION

Estimated heritabilities were moderate for all five traits (0.21-0.32; Table 1) with tenderness having the highest observed heritability. Heritabilities were similar to other studies for both Australian and international herds suggesting the potential for selection for eating quality traits directly in commercial herds (O'Connor *et al.* 1997; Johnston *et al.* 2003). Johnston *et al.* (2003) reported heritabilities for temperate *Bos Taurus* and tropical *Bos indicus* separately and found that tropically adapted cattle had higher heritabilities (0.2 – 0.32) across all traits while temperate breeds had markedly lower heritabilities (0.05 – 0.15) for all traits. The current study reports heritabilities from commercial herds in Australia which resembles mixed breed profiles of temperate, tropical and composite animals. Re-estimation of heritabilities of eating quality traits for different breeds may benefit the industry in the future as many commercial herds still have singular classes of cattle to reflect the market and climate.

Accuracies were low with tenderness and MQ4 having the highest accuracy of 0.27, while juiciness and flavour had the lowest accuracies of 0.23. This dispersal of accuracies is reflected in Forutan *et al.* (2023) who used the same data set to examine four separate strategies for prediction through a BayesR model. Observed accuracies were between 0.2 and 0.5 for tenderness with Strategies 2,3 and 4 outperforming the GBLUP model used in this study with juiciness repeatedly having the lowest accuracies of >0.3 (Forutan *et al.* 2023). Miller *et al.* (2014) used GBLUP method for the prediction of breeding values for mechanical tenderness (shear force) in a Canadian beef herd consisting of *Bos Taurus* breeds (predominantly European breeds) and found correlations of 0.1 to 0.5 between GEBV's and adjusted phenotypes but they observed a lower heritability of 0.19 for shear force tenderness. However, due to the correlation between mechanical tenderness and panel tenderness being approximately -0.72 it is expected that studies utilising shear force as a phenotype would differ in heritability estimates than that of panel derived tenderness (Destefanis *et al.*, 2008). There is valid argument as to utilising shear force over consumer tenderness scores due to most consumers being able to only differentiate changes of around 1kg of force rather than the minute increments detectable by machine. Zwambang *et al.* (2013) examined the heritability of beef tenderness (shear force) at differing aging points and found that the heritability of beef tenderness reduced from 0.19 to 0.05 when comparing the same beef at 7 and 21 days aged suggesting that genetic variance is reduced by longer days aging. However, the study examined only *Bos Taurus* breeds (predominantly European breeds) and did not need to consider the declined aging potential of *Bos indicus* breeds due to their altered enzyme production. The increased heritabilities in this study may be owed to the diverse breed profile of the data set.

**Table 1. Means ( $\pm$  SD), heritabilities ( $\pm$  SE) and accuracy of GBLUP prediction of phenotype ( $\pm$  SE) for tenderness, juiciness, flavour, overall liking and MQ4**

Trait	Mean	$h^2$	Accuracy
Tender	57.35 $\pm$ 16.5	0.317 $\pm$ 0.07	0.27 $\pm$ 0.04
Juiciness	57.72 $\pm$ 14.18	0.213 $\pm$ 0.07	0.23 $\pm$ 0.03
Flavour	59.11 $\pm$ 12.24	0.268 $\pm$ 0.07	0.23 $\pm$ 0.03
Overall liking	58.34 $\pm$ 14.19	0.272 $\pm$ 0.07	0.25 $\pm$ 0.04
MQ4	57.81 $\pm$ 13.76	0.301 $\pm$ 0.07	0.27 $\pm$ 0.04

The current study was hindered by the confounding nature of cohort, where both sex and identified breed were completely confounded by the group ID. Other difficulties identified in this research was the lack of uniformity of phenotypes when utilising a large number of datasets where

the effects being observed differ. This was evident when age (days) was available for a proportion of the cattle in this study but not for others. While this could have been addressed in the same way that the MSA model utilises ossification as an indication of physiological age or maturity, it was decided that only effects that can be measured or predetermined prior to slaughter be used. Carcase weight as an effect in this study could be interpreted in multiple ways as the effect of size or maturity due to the large range in recorded weight. For simplicity however, it was used as an indication of size alone however further manipulation on the way carcase weight could be fitted will be examined in further research. Although breed was confounded with cohort, there were a large proportion of animals unidentified, or misidentified when examining a plot of the first two principal components. Principal components were fitted to rectify the lack of breed information for a proportion of the dataset by also giving an indication of breed proportion. Even though it is likely that breed would still be confounded with group due to the nature of these projects not assessing breed effect, a reliable identification of breed or cross for all animals would have been of value in assessment.

## CONCLUSION

Economically important traits such as tenderness and consumer satisfaction can be predicted and selected for through GBLUP models in diverse beef herds. However, improvements to the model and data structure with increased consistency of phenotype records, reduced data collection periods and a controlled breed profile may strengthen the low accuracies observed in this study. Genomic prediction of eating quality traits is a financially viable option for both commercial and seed stock breeding herds.

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