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ACCURACY OF GENOMIC PREDICTIONS FOR BEEF EATING QUALITY TRAITS

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SUMMARY

Eating quality is the primary factor influencing consumer purchasing decisions for beef products. Consumer-derived sensory eating quality traits capture the actual eating experience and are directly aligned with consumer expectations. Accurate genomic prediction of these traits can enable selective breeding, allowing for continuous genetic improvement and consistent consumer satisfaction. In this study we used an international dataset from Australia, the USA and Ireland to estimate genetic parameters for five meat eating quality traits and to evaluate the accuracy of genomic estimated breeding values under different cross-validation scenarios. Heritability estimates ranged from 0.19 to 0.31 for Australia, 0.07 to 0.20 for the USA, 0.09 to 0.17 for Ireland, and 0.14 to 0.22 for the combined dataset. Prediction accuracies for all traits were moderate when using the Australia-only reference population but increased to high accuracies when international data were included. This highlights the value of incorporating international data into the reference population, creating a larger and more diverse dataset, and ultimately improving prediction accuracies.

INTRODUCTION

Eating quality is a key driver of beef purchasing decisions, as it directly influences consumer satisfaction and perceived value for money. Factors such as tenderness, flavour, juiciness, and overall liking play a crucial role in shaping consumer preferences and purchasing behaviours. Meat Standards Australia (MSA) has developed an index to grade beef carcasses based on their expected eating quality, using chemical and physical characteristics of the meat (Watson *et al.* 2008). The MSA index incorporates carcass traits such as marbling, ossification and hang method to predict the expected satisfaction grade of individual beef cuts. These factors, along with the proposed cooking method, are considered to influence the eating quality of the meat. Consumer-derived sensory eating quality traits, on the other hand, reflect the actual eating experience and align more closely with consumer expectations. These traits are typically assessed through structured sensory evaluation protocols, often involving trained consumer panels or large-scale untrained consumer testing, where key attributes of consumer satisfaction are quantified using standardized scoring systems.

Despite their importance, sensory eating quality traits are costly and difficult to measure, and direct assessments on selection candidates are not feasible as they require animal slaughter. Consequently, genetic improvement for these traits in cattle breeding programs is hindered by the scarcity of direct phenotypic data. Genomic selection offers an opportunity to provide accurate estimates of genetic merit for eating quality traits, enabling more efficient genetic improvement. Genomic selection incorporates the genomic relationship between animals in a reference set, comprising both genotyped and phenotyped individuals, and those in a target set with only genotypes to predict the genetic merit of the latter (Meuwissen *et al.* 2001). However, the accuracy of genomic estimated breeding values remains a key factor in determining the overall effectiveness of breeding strategies.

This study aimed to estimate genetic parameters and evaluate the accuracy of genomic prediction for consumer-derived eating quality traits using an international dataset from Australia, the USA,

and Ireland. By comparing different reference sets, we assessed the potential benefits of multi-country data for enhancing the reliability of genomic evaluations in the Australian population.

MATERIALS AND METHODS

Data. Striploin muscle samples were grilled and evaluated by 10 consumers following the MSA consumer testing protocols (Watson *et al.* 2008). Each consumer assessed the samples for tenderness (TENDER), juiciness (JUICY), flavour (FLAVOR) and overall liking (OVERALL), scoring them on a scale from 0 to 100. A meat quality score (MQ4) was then calculated for each sample based on the optimum linear discriminating function developed by Watson *et al.* (2008). To minimise the impact of extreme values, the highest and lowest two scores for each sample were excluded, and the remaining six were averaged. After quality control, the final dataset comprised 3,526 records from Australia (AUS), 3,197 from the USA, and 1,297 from Ireland (IRE) for analysis. The genotypes were obtained using a variety of different medium density panels and were then imputed up to 700K separately for each country using appropriate reference sets. In total, there were 4,928, 3,230 and 1,312 genotyped animals 4072 available from AUS, USA and IRE, respectively.

Statistical model. A mixed linear univariate animal model was fitted separately for each of the 5 meat eating quality traits from each country using BLUPF90+ (Misztal *et al.* 2014):

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{e}$$

where **y** is the vector of phenotypes; **b** includes the estimates of fixed cross-classified contemporary group, sex and hormonal growth promotant effects, and covariates of days aged after slaughter, carcass weight, first 4 principal components and heterosis; **u** is the vector of genomic estimated breeding value (GEBV) of animals; and **e** is the residual term. **X** and **Z** are incident matrices relating observations to fixed and random effects, respectively. It was assumed that $v(u) = G\sigma_a^2$ where G was the genomic relationship matrix based on VanRaden (2008) and σ_a^2 is the additive genetic variance. The full dataset was used to estimate variance components and heritabilities for each trait within each country. Additionally, to estimate variance components and heritabilities across all three countries, all records for each eating quality trait were combined into a single dataset. A fixed cross-classified country effect was added to account for differences between countries.

Cross-validation. To assess the genomic evaluation accuracies for AUS animals, three 5-fold cross validation strategies were implemented. In the first strategy (RANKED1), AUS animals were sorted based on the first principal component (PC1) and assigned into one of five groups of approximately equal size to maintain a balanced genetic representation in each group. In the second strategy (RANKED2), AUS animals were sorted based on PC1 and divided into five groups of approximately equal size. The top 20% of animals were placed in the first group, the next 20% in the second group, and so on. This approach created more distinct genetic clusters within the validation sets. In the third strategy (RANDOM), animals were randomly assigned into five groups of approximately equal size, without considering any genetic or temporal structure. In each iteration, one group's phenotypes were masked while the remaining four were used to estimate GEBVs. Accuracy was evaluated using LR method (Legarra and Reverter 2018) by comparing GEBVs from whole-data models with those from partial-data cross-validations. Accuracies were averaged across the five validation groups, and the standard error was calculated as STD/√5. The predictive ability of the model for AUS animals was assessed using two reference sets, one with only AUS animal and another that included animals from USA and IRE in addition to AUS cohort (AUS_USA_IRE).

RESULTS AND DISCUSSION

Variance components and heritabilities. Table 1 presents the estimates of variance components and heritabilities (± standard errors) for the five meat quality traits, obtained from a single-trait GBLUP model. Among all countries, TENDER exhibited the highest additive genetic variance, resulting in the highest heritability estimates across the five traits. Heritabilities were

generally highest in AUS compared to USA and IRE, with the largest difference observed for TENDER. The lowest heritabilities were found for JUICY in AUS and IRE, and for FLAVOR in the USA. When combining data from all three countries (AUS_USA_IRE), the heritability estimates were intermediate, falling between the individual within-country estimates. Forutan *et al.* (2025) applied the BayesR approach using the same dataset and obtained similar estimates for variance components and heritabilities. Our results indicate that the additive genetic component makes a significant contribution to the variability of meat eating quality traits, suggesting that genetic improvement through selective breeding is feasible.

Table 1. Variance components and heritabilities (± SE) for five meat quality traits estimated for each country separately (AUS, USA, IRE) and for the combined dataset (AUS_USA_IRE)

Trait	Variances	AUS	USA	IRE	AUS_USA_IRE
TENDER	σ_a^2	56.47 ± 8.91	28.18 ± 5.99	21.24 ± 9.53	34.62 ± 3.97
	σ_e^2	124.48 ± 7.15	111.74 ± 5.36	109.69 ± 8.92	121.78 ± 3.50
	h^2	0.31 ± 0.05	0.20 ± 0.04	0.16 ± 0.07	0.22 ± 0.02
JUICY	σ_a^2	26.92 ± 6.49	22.47 ± 5.93	10.53 ± 7.64	20.33 ± 3.15
	σ_e^2	117.57 ± 5.72	124.32 ± 5.60	101.66 ± 7.58	120.38 ± 3.10
	h^2	0.19 ± 0.04	0.15 ± 0.04	0.09 ± 0.07	0.14 ± 0.02
FLAVOR	σ_a^2	22.63 ± 4.95	7.65 ± 3.50	16.00 ± 7.22	13.99 ± 2.27
	σ_e^2	84.59 ± 4.27	95.21 ± 3.75	85.03 ± 6.80	90.94 ± 2.28
	h^2	0.21 ± 0.04	0.07 ± 0.03	0.16 ± 0.07	0.13 ± 0.02
OVERALL	σ_a^2	34.74 ± 6.32	13.67 ± 4.25	17.59 ± 7.95	21.06 ± 2.82
	σ_e^2	97.15 ± 5.24	101.86 ± 4.26	92.82 ± 7.47	101.15 ± 2.68
	h^2	0.26 ± 0.04	0.12 ± 0.04	0.16 ± 0.07	0.17 ± 0.02
MQ4	σ_a^2	34.99 ± 6.07	15.16 ± 3.85	16.75 ± 7.26	34.62 ± 3.97
	σ_e^2	89.89 ± 4.97	82.10 ± 3.65	83.85 ± 6.79	121.78 ± 3.50
	h^2	0.28 ± 0.05	0.16 ± 0.04	0.17 ± 0.07	0.22 ± 0.02

Accuracy of GEBVs. Figure 1 illustrates accuracy, slope and bias obtained from the 5-fold cross-validations for the five meat quality traits, using AUS-only or AUS_USA_IRE reference populations. For the AUS-only reference, JUICY had the highest prediction accuracy (0.69) among all traits and across all validation strategies, while the other four traits had similar accuracies, ranging from 0.62 to 0.65. Among the different validation strategies, RANKED2 consistently produced the lowest prediction accuracies for all traits (0.44 – 0.51), whereas the other strategies yielded similar results, with accuracies ranging from 0.62 to 0.69. Adding international data from USA and IRE to the reference population improved the prediction accuracies for all traits and across all validation strategies, highlighting the value of a larger and more diverse reference population. The prediction accuracies followed a similar trend to the AUS-only reference, with RANKED2 producing the lowest accuracies, ranging between 0.59 and 0.66, and the other two strategies achieving similar accuracies, ranging between 0.83 and 0.89. Considering the RANDOM validation strategy, the accuracies from the AUS_USA_IRE reference population showed notable improvements compared to the AUS-only reference, increasing by 0.21 for TENDER (from 0.62 to 0.83), by 0.20 for JUICY (from 0.69 to 0.89), by 0.25 for FLAVOR (from 0.64 to 0.89), by 0.23 for OVERALL (from 0.64 to 0.87), and by 0.23 for MQ4 (from 0.63 to 0.86). These findings underscore the benefits of incorporating international data to enhance prediction accuracies for beef eating quality traits in Australia.

The lower accuracy in RANKED2 is expected, as animals from one breed were used to predict the genetic merit of a different breed, representing the lower bound of prediction accuracy. In

contrast, RANKED1, which split animals from different breeds between reference and validation sets, improved accuracy by better capturing within-breed variation. The poor performance of RANKED2 highlights that due to significant breed diversity in commercial populations, genetic merit predictions from one breed background cannot accurately translate to another.

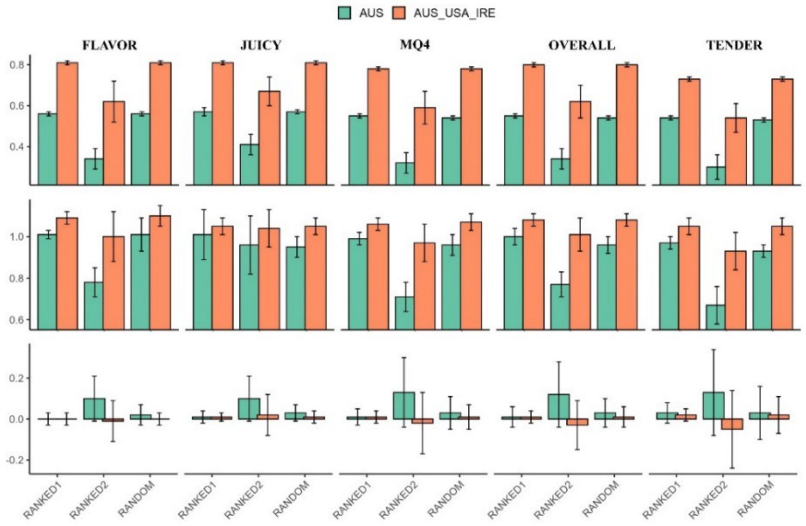

Figure 1. Accuracy (top), slope (middle) and bias (bottom) for five eating quality traits across different cross-validation scenarios, using AUS-only or AUS_USA_IRE reference sets

CONCLUSION

This study highlights the importance of a diverse reference population for genomic prediction of eating quality traits in commercial beef cattle. Incorporating international data improves the accuracy of genetic merit predictions by creating a larger reference with greater breed diversity.

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