

FEASIBILITY OF USING IMAGING CARCASS TRAITS IN GENETIC EVALUATION FOR AUSTRALIAN WAGYU BEEF CATTLE

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SUMMARY

This study estimated genetic parameters for AusMeat and camera image analysis carcass traits. Most carcass traits were moderately to highly heritable. The genetic correlation between AusMeat marble score and the image analysis marbling percentage traits was close to unity, as was the estimate between the two eye muscle area traits. Accuracies of genomic breeding values from single step genomic BLUP (ssGBLUP) were up to 4% higher than those from pedigree based BLUP (PBLUP) evaluations. The highest increase in EBV accuracies from ssGBLUP over those from PBLUP was for animals with a genotype but no phenotype. The use of image carcass traits for selection is feasible for genetic evaluation.

INTRODUCTION

Wagyu is a collective term for Japanese beef cattle breeds (Japanese Black, Japanese Brown, Japanese Shorthorn and Japanese Polled). Australian Wagyu production started in the 1990s. Genetic analysis of Wagyu cattle has been reported in a number of studies, with most from Japan and the USA. As summarized by Oyama (2011), heritability estimates for carcass traits were moderate to high, for instance, 0.23 to 0.78 for carcass weight, 0.28 to 0.61 for rib eye area, 0.24 to 0.50 for fatness and 0.16 to 0.74 for marble score. Recently applied imaging technology for assessing carcass characteristics has the potential to accurately and objectively capture carcass characteristics. Those carcass image analysis traits have been tested in Australian Wagyu cattle on a small scale (Maeda *et al.* 2014). Application of genomic selection in livestock could improve the accuracy of selection and enhance genetic gain. The aims of this study were 1) to estimate genetic parameters for carcass AUSMEAT and image analysis traits Australian Wagyu cattle, in AusMeat and image analysis traits, and 2) to test the accuracies of the Estimated Breeding Values (EBV).

MATERIALS AND METHODS

Phenotypes. Phenotypes were extracted from the Australia Wagyu Association BREEDPLAN database (Aug 2018). Animals used were progeny of 462 sires, with the number of progeny per sire ranging from 1 to 271. Amongst sires whose progeny had carcass records, 168 had only one progeny (3% of total carcass records), 207 sires had more than 5 progeny and 12 sires had more than 100 progeny. The average number of progeny per sire was 12. After editing, 6068 carcass records were used in the analysis. Carcass traits were measured using the AusMeat grading system (AusMeat Limited 2005), including hot carcass weight (CWT, kg), marble score (CMAU, on a scale of 0 to 12), P8 fat (CP8, mm) depth and carcass eye muscle area (CEMA, cm²). Image analysis traits were obtained in two steps, 1) colour images of carcass cross-sections between the 5th and 6th ribs were collected using the digital camera (HK-333, Hayasaka Rikoh, Sapporo Japan, as described by Kuchida *et al.* 2001); 2) images were analysed using the image analysis software, BeefAnalyserII (Hayasaka Rikoh, Sapporo Japan) to generate carcass traits. Details of the processes have been reported previously (Maeda *et al.* 2014). The traits generated by the image analysis software are marbling percentage (CCMP, %), eye muscle area (CCRA, cm²), fineness index or fine marbling particles per cm² (CCFI, count/cm²),

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percentages of coarse fat particles (all > 1 pixel, CCCI; the 5 largest, CCCJ; the 10 largest, CCCK, or the largest one, CCMX, %), number of fat particles (CCNM, count/cm²) and brightness of the eye muscle area (CCLL).

Genotype and genomic relationship matrix. Animals were genotyped for various sizes of Illumina Bovine chips (Illumina Inc., San Diego, CA, USA), ranging from 6K to 800K, with most genotyped with 50K or 150K panels. Genomic data were subjected to quality control (Connors *et al.* 2017) and imputed to 150K using Fimpute 2.2 (Sargolzaei *et al.* 2014). SNP genotypes for 12956 animals were used to calculate the genomic relationship matrix \mathbf{G}_m (VanRaden 2008) 967 bulls and 50,000 markers distributed randomly across 30 chromosomes. Estimation of genomic inbreeding coefficients required accurate estimates of allele frequencies in the base population. Linear model predictions of breeding values were computed by 3 equivalent methods: 1. The numerical relationship matrix \mathbf{H} , that combines the pedigree relationship matrix, \mathbf{A} , and a modified genomic relationship matrix, \mathbf{G} , was used in ssGBLUP analyses. \mathbf{G} was manipulated as, $\mathbf{G} = \lambda \mathbf{G}_m + (1 - \lambda) \mathbf{A}_{22}$, where λ is the fraction of additive genetic variance explained by markers, ranging between 0 and 1.

Statistical Models. Data were analysed using an animal model fitted with fixed effects and covariates to estimate breeding values, genetic variances and heritabilities. For CWT, the fixed effects were contemporary group (defined by herd, original owner, sex, management group and killing dates), and age (days) as linear and quadratic regressors. For other carcass traits linear and quadratic forms of carcass weight (kg) were fitted instead of age. The same model was implemented for each trait in PBLUP and ssGBLUP using Wombat (Meyer 2007). ssGBLUP analyses were performed with the \mathbf{H}^{-1} matrix calculated for four levels of λ : 0.25, 0.50, 0.75 and 0.95 to identify the optimal λ . The prediction accuracies of EBVs were calculated as $Acc = \sqrt{1 - \left(\frac{PEV}{(1+f)\sigma_a^2}\right)}$, where PEV is the prediction error variance of the EBV, f is the inbreeding coefficient and σ_a^2 is the additive genetic variance. The average EBV accuracies were calculated for all animals or subsets of animals in each of PBLUP or ssGBLUP analyses. The EBV accuracies were compared amongst subsets of animals which were identified as animals that were phenotyped, genotyped or both. The comparisons were conducted by firstly, identifying the highest average EBV accuracy from the 4 ssGBLUP analyses for each trait. The difference between this accuracy and the PBLUP accuracy was obtained for this subset of animals.

Bivariate analyses were performed for pairs of marbling traits (CCMP, CCFI or CCCI vs CMAU) and eye muscle area traits (CCRA vs CEMA).

RESULTS AND DISCUSSION

Trait summary. The average slaughter age was 1003 days and the average carcass weight was 419 kg with an AusMeat marble score of 7.2 and an eye muscle area of 66 cm² (Table 1). Image carcass traits showed the same eye muscle area with higher variation. An average of 27% of the eye muscle was intramuscular fat (CCMP), 7.3% was coarse fat flecks (CCCI) and 2.7 was fine fat particles per cm² of rib eye area (CCFI).

Variance and genetic parameters. Heritability estimates for most traits were moderate, with relatively low standard errors (Table 2). Heritability estimates for AusMeat traits ranged from 0.42 for CEMA to 0.60 for CWT. This is in line with estimates reported previously. For image analysis traits, CCMP, CCFI and CCRA were moderately heritable and those estimates tended to be significantly different from zero. The heritability estimates for coarseness (CCCI, CCCJ, CCCK) were moderate but with large standard errors. The brightness of eye muscle (CCLL) was also moderately heritable. The relative proportion of the largest marbling particle (CCMX) had low heritability which was not significantly different from zero. The current estimates were similar to those by Maeda *et al.* (2014), but with lower standard errors. Heritabilities from ssGBLUP (not shown) for different λ values varied. The estimates at a λ of 0.25 were the highest and were higher than those estimated from PBLUP.

EBV Accuracies from different analyses. The EBV accuracies from PBLUP and ssGBLUP at 4 levels of λ : 0.25, 0.50, 0.75 and 0.95, are shown in Table 3. The highest EBV accuracies from ssGBLUP were higher than those from PBLUP. Accuracy increases ranged from 0.02 for CCMP to 0.04 for CCMX. The maximum eye muscle area (CEMA or CCRA) EBV accuracies from ssGBLUP were the same or slightly lower than those from PBLUP. The highest ssGBLUP EBV accuracies were found at a λ of 0.95 and mostly for the fatness traits. The highest ssGBLUP EBV accuracy for CCLL was identified at a λ of 0.25, which was slightly lower than that from PBLUP (-0.02).

The highest increase in EBV accuracies was 0.04 and found in the subset of genotyped animals, either with (0.03) or without (0.04) phenotypes. For non-genotyped animals, the maximum EBV accuracies from ssGBLUP were almost identical to those from PBLUP (with an average increase of 0.01).

Table 1. Descriptive statistics for carcass traits of Australian Wagyu cattle

Trait	Count					Trait			
	Animal	Sire	Dam	cg	Genotype	Mean	Std	Min	Max
CWT	6068	462	4007	1543	1380	418.7	54.28	256	580
CMAU	5634	422	3744	1296	1368	7.23	1.77	2	12
CP8	3496	242	2169	851	1100	22.04	8.34	4	46
CEMA	3374	305	2374	993	1116	65.83	23.17	41	128
CCMP	2109	281	1867	587	727	27.02	7.31	9	49
CCRA	1849	250	1700	386	750	65.92	26.51	0	129
CCFI	1942	263	1743	515	692	2.70	0.60	0	4
CCCI	1838	247	1689	383	750	7.26	5.52	0	42
CCCJ	608	88	601	113	45	4.66	3.02	0	25
CCCK	608	88	601	113	45	5.68	3.42	0	26
CCLL	1113	156	1001	246	656	79.57	10.89	0	118
CCMX	1766	233	1633	371	728	2.47	2.19	0	24
CCNM	608	88	601	113	45	1099.10	688.95	49	4389

Table 2. Variance components and heritability for carcass traits of Australian Wagyu cattle

Trait	$\sigma_a^2 \pm se$	$\sigma_e^2 \pm se$	$h^2 \pm se$
CWT	832.64±105.65	552.49±72.55	0.60±0.06
CMAU	1.01±0.15	1.38±0.11	0.42±0.05
CP8	17.95±3.09	17.6±2.11	0.51±0.07
CEMA	32.09±6.45	23.32±4.44	0.58±0.09
CCMP	11.97±3.66	20.98±2.94	0.36±0.10
CCRA	36.04±9.31	38.50±7.25	0.48±0.11
CCFI	0.10±0.03	0.16±0.02	0.39±0.11
CCCI	1.39±0.71	8.92±0.67	0.14±0.07
CCCJ	1.97±1.61	4.48±1.43	0.30±0.24
CCCK	2.57±1.95	5.27±1.73	0.33±0.24
CCLL	24.14±9.23	32.98±7.07	0.42±0.14
CCMX	0.11±0.16	3.65±0.20	0.03±0.04

Bivariate analyses. The genetic correlations between eye muscle area (CCRA vs CEMA) and marbling traits (CMAU vs CCMP) were close to unity (not shown). Genetic correlations among the three measures of fat particle coarseness (CCCI, CCCJ and CCCK) were high and positive, suggesting they were measurements of the same trait. The fat fineness index (CCFI) was negatively correlated with the coarseness measures CCCJ and CCCK, but not with CCCI.

Beef 1

Phenotypically, the two measurements of marbling were highly correlated, but were on different scales. An increase of one unit of AusMeat marble score (CMAU) is equivalent to a 3.5% increase in marbling percentage (CCMP). Two eye muscle area measures were almost identical (1.0 cm² of CEAM is equivalent to 0.99 cm² of CCRA). All coarseness indices represent essentially the same marbling trait, being similarly correlated to the marbling percentage (CCMP) trait. The regression of CCMP on CCFI showed that increasing fine fat particle per cm² of eye-muscle area by 1.0 increases CCMP by 9.8%.

Table 3. Accuracies of EBVs from PBLUP (Ped) analyses and ssGBLUP analyses with 4 levels of λ , 0.25, 0.50, 0.75 and 0.95 (H25, H50, H75 and H95)

Trait	Ped	H25	H50	H75	H95	Increment
CWT	0.53	0.53	0.53	0.55	0.56	0.03
CMAU	0.50	0.50	0.50	0.51	0.52	0.03
CP8	0.48	0.48	0.48	0.49	0.51	0.03
CEMA	0.49	0.48	0.47	0.46	0.47	0.00
CCMP	0.44	0.44	0.43	0.44	0.45	0.02
CCRA	0.45	0.45	0.44	0.44	0.44	0.00
CCFI	0.42	0.41	0.40	0.41	0.42	0.00
CCCI	0.36	0.37	0.32	0.39	0.41	0.05
CCCJ	0.29	0.27	0.27	0.29	0.31	0.02
CCCK	0.30	0.28	0.27	0.29	0.31	0.02
CCLL	0.42	0.40	0.36	0.36	0.37	-0.02
CCMX	0.22	0.21	0.21	0.23	0.26	0.04

CONCLUSIONS

Most of the AusMeat and image analysis carcass traits were moderately to highly heritable with moderate standard errors. The genetic correlation between AusMeat marble score and the image analysis marbling percentage was close to unity. A similarly high genetic correlation was estimated between the eye muscle area traits. Image analysis of carcass characters is feasible for use during selection in Australian Wagyu cattle. Accuracies of genomic breeding values at optimal levels of λ could be increased by 4% across traits. For traits from reasonably sized datasets, an increase of 6% in EBV accuracies could be achievable.

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REFERENCES

- AusMeat Limited. (2005) Handbook of Australian Meat. 7th ed. (AusMeat: Brisbane).
- Connors N.K., Cook J., Girard C.J., Tier B., Gore K.P., Johnston D.J. and Ferdosi M.H. (2017) *Proc. Assoc. Advmt. Anim. Breed. Genet.* **22**:317.
- Kuchida K., Suzuki M. and Miyoshi S. (2001) *Anim. Sci. J.* **72**:J224.
- Maeda S., Grose J., Kato K. and Kuchida K. (2014) *Anim. Prod. Sci.* **54**:557.
- Meyer K. (2007) *Journal of Zhejiang University. Science. B* **8**:815.
- Oyama K. (2011) *Anim. Sci. J.* **82**:367.
- Sargolzaei M., Chesnais J.P. and Schenkel F.S. (2014) *BMC Genomics*, **15**:478.
- VanRaden P.M. (2008) *J. Dairy Sci.* **91**: 4414.0.