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Accuracy of genomic selection in predicting carcass traits in meat sheep

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SUMMARY

Australia's red meat supply chains are shifting from supplier-driven production to consumer-driven demand. The ability of the red meat supply and demand chain to allocate animals to end-users will be determined by the increase in phenotype prediction accuracy (for allocation of animals to specific slaughter cohorts or consumer markets) and the increase in breeding value accuracy (genome-assisted selection of breeding animals).

The aim of this study was to determine the accuracy of predicting phenotype for the following carcass and growth traits: hot carcass weight (HCWT, kg), cold eye-muscle area (CEMA, cm^2) and intramuscular fat percentage (IMF). The three statistical models were used: 1) fixed effects only, 2) fixed effects and additive genetic polygenic effects (pedigree) and 3) fixed effects, pedigree and genotypic data (50 K single nucleotide polymorphisms [SNPs]). The fixed effects models included management group, breed, gender, birth and rear type, season and age. Variance components and heritability were estimated using ASReml (Gilmour *et al.* 2002). We used the BayesB model (Meuwissen *et al.* 2001) with a strong Bayesian prior for proportion of SNPs included in the model and set at 1%. Cross validation (Kohavi 1995) was performed for 8 replicates using training data, which included 75% of the data, and validation data, which comprised the remaining 25%. Three scenarios were tested for prediction accuracy by choosing training and test sets either randomly, across sire families or across breeds. We calculated correlations between predicted and observed phenotypes. The accuracy of predicting breeding value can be approximated from our results by taking the incremental variance explained due to fitting SNP data as a proportion of the variance not explained by fixed effects multiplied by trait heritability.

Table 1. Accuracy of predicted and observed phenotypes for carcass weight, eye muscle area and intramuscular fat

Trait	Model	Random	Across sire	Across breed
HCWT	Fixed effects	0.69	0.66	0.60
	Fixed + Poly G	0.71	0.72	0.60
	Fixed + Poly G + SNP	0.74	0.74	0.64
CEMA	Fixed effects	0.51	0.54	0.52
	Fixed + Poly G	0.60	0.62	0.51
	Fixed + Poly G + SNP	0.77	0.70	0.60
IMF	Fixed effects	0.57	0.42	0.39
	Fixed + Poly G	0.57	0.44	0.40
	Fixed + Poly G + SNP	0.58	0.44	0.39

Table 1 shows that accuracy was higher when predicting within random subsets than across sire families, and lowest when predicting across breeds. The derived accuracy of predicting breeding values was 0.45, 0.72 and 0.32 for HCWT, CEMA and IMF, respectively, but these values were reduced when predicting across sire or breed. The use of genomic data would increase the accuracy of both phenotypic prediction and genomic selection.

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