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# Accuracies of Genomic Prediction in Beef Cattle

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### Summary and Implications

The objective of this study was to derive and evaluate the accuracies of molecular breeding values (MBV) for economically relevant traits for commercial implementation in several beef cattle breeds. We developed MBV for Hereford, Red Angus and Simmental breeds. Accuracies of MBV ranged from 0.18 to 0.45 in Hereford, 0.37 to 0.85 in Red Angus, and from 0.29 to 0.65 in Simmental using within breed genomic predictions. Single breed genomic predictions had no utility when applied to other breeds. However, the accuracies of MBV improved for some breeds when predictions were derived using multi-breed reference populations. These results have now been implemented as routine predictions for breeders of American Hereford, American Red Angus and American Simmental beef cattle. Similar findings will soon be extended to other breeds.

### Introduction

Assays can be used to genotype cattle for more than 50,000 single nucleotide polymorphisms (SNP). The resulting SNP markers can be used to produce molecular breeding values (MBV) for selection candidates that do not necessarily have phenotypes. Selection using MBV could reduce generation intervals and increase genetic progress.

### Materials and Methods

A total of 1,081 Hereford, 1,274 Red Angus and 2,703 Simmental animals were genotyped with the BovineSNP50 assay. De-regressed estimated breeding values (DEBV) were used as observations in a weighted Bayesian analysis to estimate marker effects for MBV calculation. Bivariate animal models were used for each trait to estimate the genetic correlation between DEBV and MBV as a measurement of their average accuracy. Such accuracies of MBV were evaluated using single or multi-breed reference populations.

### Results and Discussion

Table 1 presents the accuracies of MBV using within-breed, across-breed and multi-breed genomic predictions. Poor accuracies were obtained from across-breed genomic predictions. Using multi-breed reference population, accuracies of MBV for some traits in some breeds improved (e.g. 5% increase for Red Angus, on average). The MBV show promise for routine use by beef cattle breeders to predict genetic merit of their animals at a young age.

### Acknowledgments

We are indebted to the respective Breed Associations and to numerous beef cattle breeders and AI companies that provided DNA. We gratefully acknowledge support from the National Beef Cattle Evaluation Consortium.

**Table 1. The accuracies<sup>1</sup> of MBV for economically relevant traits in several beef cattle breeds.**

Trait	Hereford using Hereford	Simmental using Simmental	Red Angus using Red Angus	Red Angus using Hereford <sup>2</sup>	Red Angus using Multi-breed <sup>3</sup>
Birth weight	0.45	0.65	0.66	0.31	0.75
Calving ease direct	0.40	0.45	0.59	0.32	0.60
Calving ease maternal	0.18	0.32	0.37	-0.12	0.32
Carcass weight	-	0.59	0.62	-	0.75
Fat thickness	0.45	0.29	0.85	0.00	0.90
Marbling	0.33	0.63	0.77	-0.10	0.85
Rib eye muscle area	0.42	0.59	0.71	0.03	0.75
Weaning weight direct	0.32	0.52	0.55	0.22	0.67
Weaning weight maternal	0.26	0.34	0.54	-	0.51
Yield grade	-	0.62	0.81	-	0.83
Yearling weight	0.32	0.45	0.57	0.22	0.69

<sup>1</sup>Accuracies generally calculated as genetic correlation between DEBV and MBV. <sup>2</sup>Accuracies of this comparison calculated as the simple correlation between DEBV and MBV. <sup>3</sup>Using information of several beef cattle breeds mainly Simmental (including Red Angus).