

**Genomic Breeding values from Across Breed Prediction in Practice:  
Accuracy of Beef-CRC Genomic Breeding Values in Australian Angus and Australian Brahman beef cattle**

**V. Boerner, D.J. Johnston and B. Tier**

Animal Genetics and Breeding Unit(AGBU<sup>1</sup>), University of New England, Armidale, NSW, Australia

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**ABSTRACT:** Genomic selection in the Australian beef cattle sector is challenged by the variety of small breeds and a low number of phenotyped and genotyped individuals in each breed. The Beef Cooperative Research Center (Beef CRC) derived prediction equations (PE) on mixed-breed and pure-breed training sets. This paper presents the accuracy of the resulting genomically estimated breeding values (GEBV) assessed by their genetic correlation to their phenotypic target trait recorded in the seed-stock cattle populations of Australian Angus and Brahman. Accuracies of the majority of GEBVs was between 0.1 and 0.4, and were highest when the PE of the pooled across-breed training population were used. The difference in accuracies from using pure-breed PEs were small. Results were generally low compared to accuracies estimated within breeds, but in line with those derived in other across-breed populations. Thus prediction equations derived by the Beef CRC can contribute to the implementation of genomic selection in Australian beef cattle breeding.

**Keywords:** beef cattle, genomic selection, across-breed prediction

### Introduction

Genomic selection (GS) in the Australian beef cattle sector is challenged by the variety of small breeds and a number of genotyped individuals in each breed which is generally not sufficient to calculate accurate within-breed genomically estimated breeding values (GEBV)(Johnston et al., 2012). A possible approach to make GS feasible for small breeds with a low number of genotypes and phenotypes is the derivation of equations which allow prediction of GEBVs across breeds (Goddard and Hayes, 2007). The across-breed prediction approach was followed by the Australian Beef Cooperative Research Center (www.beefcrc.com, Beef CRC), which derived prediction equations (PE) on a pooled training population of genotyped individuals from eight different cattle breeds as well as on different across-breed and pure-breed subset of this pooled set (Bolormaa et al., 2013). The aim of this work was to determine the accuracies of GEBVs calculated from several different Beef CRC PEs applied to independent samples of genotyped individuals of Australian Angus and Brahman beef cattle.

### Materials and Methods

**Genomically estimated breeding values.** PEs were derived within the Beef CRC on genotypes obtained from a 800K Illumina HD Bovine SNP Chip (www.illumina.com) using various methods and different sets of individuals. For a detailed description of the derivation see Bolormaa et al. (2013). In short, the PEs used in this study

were derived in a GBLUP approach on a pooled set of individuals (ALL), originating from Australian populations of Angus, Murray Grey, Shorthorn, Hereford, Brahman, Belmont Red, Santa Gertrudis, Tropical Composite, and F1 crosses of Brahman with Limousin, Charolais, Angus, Shorthorn and Hereford. GBLUP PEs were also derived on subsets of Angus only (ANGUS), Bos Taurus only (Angus, Murray Grey, Hereford, Shorthorn) (BOSTAURUS) and Brahman only (BRAHMAN). PEs from these four sets were supplied to the authors for the following traits: post-weaning live weight (g.WW), live weight at feedlot entry (g.YW), live weight at feedlot exit (g.FW), ultrasound scan eye muscle area (g.SEMA), ultrasound scan rib fat (g.SRIB), carcass rib fat (g.CRIB), scan P8 fat (g.SP8), carcass P8 fat (g.CP8), carcass intra-muscular fat (g.CIMF) and carcass weight (g.CWT). GEBVs were calculated by applying these PEs to genotypes of two sets of animals within each breed: highly used sires and current generation animals where non of the individuals were used to derive the PEs. The specific number of sires/current generation animals was 383/1199 for Angus and 108/302 for Brahman. The genotypes of all these individuals were obtained from the Illumina 50K Bead Chip and were imputed to 800K.

### Compilation of phenotypic target trait data.

Phenotypic and pedigree data were obtained from databases of Angus Australia and Australian Brahman Breeders' Association. All phenotypic data were adjusted for systematic effects as described in Graser et al. (2005). Traits included in the analysis were 200 day weight (p.WW), 400 day weight (p.YW), 600 day weight (p.FW), bull ultrasound scan eye muscle area (p.BEMA), heifer ultrasound scan eye muscle area (p.HEMA), bull ultrasound scan rib fat (p.BRIB), heifer ultrasound scan rib fat (p.HRIB), carcass rib fat (p.CRIB), carcass P8 fat (p.CP8), carcass intra-muscular fat (p.CIMF) and carcass weight (p.CWT). Although only proxies for carcass target traits, live animal ultrasound scan traits were included in the analysis because of data availability.

**Accuracy estimation.** The GEBV accuracies were obtained as genetic correlations from a series of bi-variate REML analysis of GEBVs, modelled as traits, together with their phenotype target traits. The general linear model was  $y = Xb + Z_d u_d + Z_m u_m + Z_p p + e$ , where  $y$ ,  $b$ ,  $u_d$ ,  $u_m$ ,  $p$  and  $e$  are vectors of phenotypic observations and fixed, random direct additive genetic, random maternal additive genetic, random maternal environmental and random residual effects, respectively, and  $X$ ,  $Z_d$ ,  $Z_m$  and  $Z_p$  are incidence matrices relating the effects to their phenotypic observations. The observations were assumed to follow the distribution  $N(Xb, Z_d A Z_d' \sigma_a^2 + 2Z_d A Z_m' \sigma_{am} + Z_m A Z_m' \sigma_m^2 +$

$Z_p Z_p' \sigma_p^2 + I \sigma_e^2$ ), where A is the numerator relationship matrix, and I is an identity matrix.  $\sigma_a^2$  is the variance of the direct additive genetic effect,  $\sigma_{am}$  is the covariance between the direct additive genetic effect and the maternal additive genetic effect,  $\sigma_m^2$  is the variance of the maternal additive genetic effect,  $\sigma_p^2$  is the variance of the maternal permanent environmental effect and  $\sigma_e^2$  is the variance of the residual effect. The model was reduced by p and  $u_m$  for all GEBVs and all phenotypic traits except p.WW, p.YW and p.FW. Across phenotypic traits, contemporary group was the only fixed effect, and for GEBVs no fixed effect was fitted except the mean.

## Results

**Phenotypic observations.** Table 1 summarises the number of phenotypic observations and the number of phenotyped individuals also used to derive the prediction equations (note that non of the individuals with GEBVs was used to derive the prediction equations). For both breeds, the number of growth and live animal body composition trait records exceeded those of the difficult and expensive-to-measure carcase traits by far.

**Table 1: Number of Phenotypic observations and number of phenotyped individuals used to derive the prediction equations**

trait	Angus		Brahman	
	N <sup>1</sup>	n <sup>2</sup>	N	n <sup>3</sup>
p.WW	120928	73	145558	0
p.YW	81428	39	67115	0
p.FW	114170	54	70955	0
p.BEMA	88265	0	6655	0
p.HEMA	101221	250	4494	0
p.BRIB	88256	0	6097	0
p.HRIB	101360	289	4018	0
p.BP8	88087	0	6292	0
p.HP8	101530	289	4184	0
p.CRIB	1203	573	1486	0
p.CP8	2183	0	1575	0
p.CIMF	2822	0	1584	0
p.CWT	3839	0	1753	0

1: number of phenotypic observations, 2: number of Angus individuals with a phenotypic record in this data set which have also been used for deriving ANGUS, BOSTAURUS and ALL prediction equation, 3: number of Brahman individuals with a phenotypic record in this data set which have also been used for deriving BRAHMAN and ALL prediction equation, note that non of the individuals with GEBVs was used to derive the Beef-CRC prediction equations

**Accuracies of Australian Angus GEBVs.** Table 2 summarises the genetic correlation( $r_g$ ) between GEBVs and phenotypic traits for Australian Angus. The highest  $r_g$  of 0.53 was found for p.CRIB:g.CRIB derived from BOSTAURUS PE (note that the data set for this trait was not independent), the lowest of -0.01 for p.BP8:g.SP8 derived from BRAHMAN PE, but the majority were <0.2. Across traits ALL PE and BOSTAURUS PE had highest  $r_g$ s

followed by ANGUS and BRAHMAN PE, where the ALL PE results almost mirror those from ANGUS and BOSTAURUS PE. Especially for live animal scan traits and carcase traits BRAHMAN PE was inferior, whereas for growth traits (except p.FW:g.FW) differences between  $r_g$ s of different PEs were small.

**Table 2: Correlation(standard error) between direct additive genetic components of the phenotypic trait and the GEBV for Australian Angus**

trait1	trait2	All <sup>1</sup>	Angus <sup>2</sup>	BosTaur <sup>3</sup>	Brahman <sup>4</sup>
p.WW	g.WW	.09(.06)	.07(.05)	.10(.06)	.11(.06)
p.YW	g.YW	.08(.06)	.09(.06)	.09(.06)	.14(.06)
p.FWD	g.FW	.19(.05)	.18(.05)	.21(.05)	.11(.06)
p.BEMA	g.SEMA	.16(.06)	.18(.06)	.16(.06)	.01(.06)
p.HEMA	g.SEMA	.15(.05)	.10(.05)	.13(.05)	.09(.06)
p.BRIB	g.SRIB	.26(.06)	.25(.06)	.25(.05)	.09(.06)
p.HRIB	g.SRIB	.20(.05)	.19(.05)	.20(.05)	.05(.05)
p.BP8	g.SP8	.25(.06)	.27(.06)	.25(.06)	-.01(.06)
p.HP8	g.SP8	.21(.05)	.23(.05)	.21(.05)	.02(.05)
p.CRIB	g.CRIB	.51(.21)	.36(.17)	.53(.21)	.12(.35)
p.CRIB	g.SRIB	.17(.17)	.20(.22)	.20(.16)	.24(.37)
p.CP8	g.CP8	.36(.20)	.27(.17)	.34(.19)	.12(.23)
p.CP8	g.SP8	.25(.19)	.11(.18)	.18(.17)	.16(.24)
p.CIMF	g.CIMF	.33(.12)	.29(.12)	.36(.13)	.00(.17)
p.CWT	g.CWT	.25(.15)	.30(.12)	.25(.14)	-.00(.17)

1: ALL prediction equation, 2: ANGUS prediction equation, 3: BOSTAURUS prediction equation, 4: BRAHMAN prediction equation

**Accuracies of Australian Brahman GEBVs.** Table 3 summarises the results for Australian Brahman, which varied across traits and PEs from one(p.CWT:g.CWT) to -0.50(p.CIMF:g.CIMF). However, negative  $r_g$ s were almost exclusively found in ANGUS and BOSTAURUS PE, whereas BRAHMAN and ALL PE had only a single negative  $r_g$ (p.BEMA:g.SEMA). Moreover, results from ALL PE almost mirror those from BRAHMAN PE, whereas ANGUS and BOSTAURUS PEs yielded much smaller absolute  $r_g$ s which were often of opposite sign, but this was not the case for the early in life growth traits (p.WW and p.YW).

**Table 3: Correlation(standard error) between direct additive genetic components of the phenotypic trait and the GEBV for Australian Brahman**

trait1	trait2	All <sup>1</sup>	Angus <sup>2</sup>	BosTaur <sup>3</sup>	Brahman <sup>4</sup>
p.WW	g.WW	.27(.10)	.07(.11)	.15(.10)	.23(.09)
p.YW	g.YW	.19(.10)	.14(.11)	.14(.11)	.20(.09)
p.FW	g.FW	.20(.09)	-.17(.11)	-.07(.10)	.20(.10)
p.BEMA	g.SEMA	-.08(.22)	.19(.26)	-.24(.26)	-.17(.23)
p.HEMA	g.SEMA	-.04(.24)	-.23(.26)	-.10(.27)	-.06(.26)
p.BRIB	g.SRIB	.45(.17)	-.08(.23)	.01(.22)	.41(.17)
p.HRIB	g.SRIB	.18(.22)	-.29(.26)	-.14(.25)	.19(.23)
p.BP8	g.SP8	.34(.20)	-.08(.21)	-.16(.21)	.24(.20)
p.HP8	g.SP8	.32(.21)	.20(.23)	-.09(.23)	.30(.21)
p.CRIB	g.CRIB	.70(.20)	.10(.46)	.44(.43)	.65(.21)
p.CRIB	g.SRIB	.96(.26)	-.49(.46)	-.17(.45)	.92(.33)
p.CP8	g.CP8	.57(.19)	.46(.30)	.44(.34)	.34(.24)
p.CP8	g.SP8	.68(.33)	.66(.32)	.54(.34)	-.01(.47)
p.CIMF	g.CIMF	.56(.27)	-.50(.37)	-.20(.41)	.36(.25)
p.CWT	g.CWT	1.00(.13)	.44(.42)	.50(.31)	.89(.16)

1: ALL prediction equation, 2: ANGUS prediction equation, 3: BOSTAURUS prediction equation, 4: BRAHMAN prediction equation

### Discussion

Compared with results published in other studies,  $r_{gs}$  for Australian Angus presented here are generally at the lower end of the range of accuracies estimated within breed (Boerner and Johnston, 2013; Kachman et al., 2013). Beef CRC PEs were derived across indicine and taurine breeds, but studies on beef cattle across-breed predictions are limited (Kachman et al., 2013; Weber et al., 2012).  $r_{gs}$  of p.CIMF:g.CIMF and p.WW:g.WW given here were in the range of Weber et al. (2012), but  $r_g$  of p.YW:g.YW was  $\sim 0.1$ , compared to 0.3 and 0.45 in both the latter citations. However, with regard to our results for carcass traits, it must be kept in mind that the independence of the Angus

data set is not fulfilled. Differences between  $r_{gs}$  as functions of applied PEs were minor except between BRAHMAN PE and the other three PEs. For differences between ANGUS and BOSTAURUS PE this might result from a Bos Taurus training set which consisted of almost 50 % Angus individuals (Bolormaa et al., 2013). But the addition of indicine breeds to the training set, which were about 60 % of the ALL PE training set, had small positive effects on the GEBV accuracy for almost all traits. In contrast, the BRAHMAN PE performed worst in Angus for the majority of traits. However, given the  $r_g$  standard errors,  $r_g$  differences within traits across PEs were generally not statistically significant. For Brahman, the only pure-breed Bos Indicus cattle in the training population, ALL PE yielded highest  $r_{gs}$  for the majority of traits, followed by BRAHMAN PE, where some  $r_{gs}$  were very high (e.g. g.CWT, g.SRIB, g.CRIB). The poor performance of BOSTAURUS and ANGUS PE is in line with the poor performance of BRAHMAN PE in Angus, reflecting the need of having all predicted breeds in the training population. However, with regard to the large standard errors results from ALL and BRAHMAN PE are not significantly different.

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