MULTI-BREED GENOMIC ESTIMATED BREEDING VALUES PREDICT LIVEWEIGHT PRODUCTION IN NORTH AUSTRALIAN BEEF CATTLE

B.J. Hayes¹, G. Fordyce¹, E. Dodd¹, S. Speight² and K. McCosker¹

¹ University of Queensland, Queensland Alliance for Agriculture and Food Innovation, Centre for Animal Science, Brisbane, QLD, 4000 Australia
² Black Box Co Mareeba, QLD, 4880 Australia

SUMMARY

Lifetime productivity of cows is a major driver of profitability of beef enterprises. One of the key components of lifetime productivity is liveweight production, the sum of the weight of cow's calves at weaning and its own annual liveweight change. Here multibreed genomic estimated breeding values (GEBV) for weight at 600 days, body condition score, heifer puberty, pregnant or not 4 months after calving (P4M), temperament, tick score, buffalo fly lesion score, teat score and udder score are assessed for their association with liveweight production that was recorded in two independent populations. GEBV for weight, heifer puberty and P4M were significant predictors of liveweight production in Brahmans. In tropical composites GEBV for weight, P4M, temperament and teat score were significant predictors of liveweight production. Results suggest selecting for GEBV for these traits will improve liveweight production.

INTRODUCTION

Lifetime productivity of beef cows is a key trait driving profitability of beef enterprises, however this trait has only rarely been measured due to the expense and long time frame required. Many predictors of lifetime productivity have been suggested, including heifer age at puberty (Johnston *et al.* 2013) and longevity (Martinez *et al.* 2005). Liveweight production, which combines weight of calves weaned and cow weight change, has also been suggested (Fordyce *et al.* 2023). Note that liveweight production is an imperfect measure of lifetime productivity, for example it does not account for feed eaten. Multi-breed genomic estimated breeding values for northern Australian beef cattle have been developed utilising a large reference population of commercial cattle from 60 properties across northern Australia (Hayes *et al.* 2023). The GEBV include weight at approximately 600 days, body condition score, heifer puberty (from an ultrasound scan assessing the presence or absence of a corpus luteum at approximately 600 days), pregnant or not 4 months after calving, temperament, tick score, buffalo fly lesion score, teat score and udder score. To assess if using these GEBV might be useful in selecting for improved lifetime productivity, we regressed GEBV simultaneously on liveweight production in a population independent of the reference.

MATERIALS AND METHODS

Animals, phenotypes and genotypes. The reference set for calculating GEBV was described in Hayes *et al.* (2023). Recently, 6,000 additional records have been added to that reference. Briefly, the reference set includes 34,292 heifers from sixty beef cattle herds, including crossbred and purebreds from at least 14 breeds, i.e. Angus, Belmont Red, Brahman, Charolais, Droughtmaster, Hereford, Limousin, Murray Grey, Santa Gertrudis, Shorthorn, Wagyu, Boran, Senepol and Tuli. Traits measured on the heifers included live weight, hip height and body condition score (BCS) at an average of 600 days, and a heifer puberty trait. The heifer puberty trait was cycling or not cycling by an average of 600 days assessed by the presence or absence of corpus luteum using ovary scanning. Tick scores (0-5), buffalo fly lesion scores (1-5), temperament (docility) scores (1-5) and teat and udder scores (1-5) were also recorded on some animals (Table 1) following BREEDPLAN guidelines for these traits (Table 1). Pregnant or not 4 months after calving (McCosker *et al.* 2023)

was derived from foetal aging. All heifers were genotyped with the 35k or 50k TropBeef SNP array by Neogen, Australasia, or the Weatherbys 50k array. SNPs were removed if more than 10% of the genotypes were missing for that SNP. If an individual genotype had a GC score less than 0.6, it was set to missing and recovered by imputation. Genotypes were imputed up to 709,768 SNPs (bovine high-density (HD) array) using the findhap software (VanRaden *et al.* 2013) and a panel of 4,506 cattle from relevant breeds and crossbreds that were genotyped with the Bovine HD array. The accuracy of imputation was at least 93% for all breeds/crossbreds (Hayes *et al.* 2023).

Statistical models. To predict genomic estimated breeding values (GEBV), the model was $y=1_n\mu+Xf+Zu+\epsilon$, where y is the vector of trait records; μ is the population mean, and 1_n is a vector of 1s; f is the vector of fixed effects including contemporary group, the herd+birth year+paddock year of recording (2015, 2016, 2017, 2018, 2019, and 2020), a linear covariate of the average marker heterozygosity (to capture heterosis effects); X is a design matrix that relates fixed effects to records; u is the vector of random genetic effects $\sim N(0,G\sigma_g^2)$ with G being the genomic relationship matrix between all the heifers and σ_g^2 the genetic variance captured by the SNPs, with G constructed according to Yang et al. (2010); G is a design matrix that relates records to animals; G is a vector of random deviations G is a vector of random deviations G in G is an identity matrix and G the error variance. There were at least 25 animals in each contemporary group. Variance components and heritabilities were estimated with G (Yang et al. 2010). Note this is the NOBREED model of Hayes G al. (2023).

Effect of GEBV on liveweight production. GEBV for all traits were predicted for a completely independent dataset; the Beef CRC groups of 894 and 1,088 Brahman and Tropical composite cattle (Johnstone *et al.* 2013). The 50k genotypes of these animals were imputed to 709,768 SNP using a large reference set, then multiplied by the SNP prediction equations from backsolving the system of equations above (Hayes *et al.* (2023). The accuracy of the GEBV were assessed by correlating the GEBV with phenotypes for these cattle for the most closely related trait they were measured for and dividing by the square root of heritability for these traits. Liveweight production for each cow was calculated following Fordyce *et al.* (2023) as the sum of the weight of its calf at weaning and its own annual liveweight change. The GEBV for all traits were regressed on liveweight production simultaneously. As producers receiving GBV also receive which quintiles their animals are in (based on all animals in the reference set), for heifer puberty and P4mM we also plotted actual age at puberty and percentage pregnant in the validation sets for the group of animals in each predicted quintile. Quintiles are always 1 =worst 20% for a trait to 5 = best 20% for a trait.

RESULTS AND DISCUSSION

Heritability of fertility traits was moderate (heifer puberty) to low (P4M; Table 1). Heritability estimates were fairly consistent with previous estimates (Johnston *et al.* 2003; Johnston *et al.* 2009; Johnston *et al.* 2013; Porto-Neto *et al.* 2104; Bunter and Johnston 2013).

Table 1. Number of records, heritabilities and standard errors for GEBV traits

Trait	Number	Heritability
Weight	31,673	0.33 ± 0.01
Hip height	30,903	0.44 ± 0.01
Body condition score	32,104	0.23 ± 0.01
Heifer Puberty	34,292	0.22 ± 0.01
Pregnant 4 months after calving	14,419	0.10 ± 0.01
Temperament	5,650	0.31 ± 0.03
Tick score	5,307	0.32 ± 0.03
Buffalo fly lesion score	13,203	0.11 ± 0.02
Teat score	4,044	0.34 ± 0.04
Udder score	4,044	0.25 ± 0.03

In the validation set, there was a good association between heifer puberty GEBV quintile and age at puberty. Animals in the 5th quintile reached puberty approximately eighty days before the 1st quintile, Figure 1. For P4M, 30% more animals in quintile 5 were pregnant than in the 1st quintile.

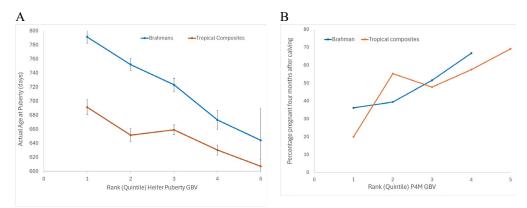


Figure 1. A. Average age at puberty for animals in the validation set by their GEBV quintile for heifer puberty (5=20% most likely to be pubertal at 600 days, 1=20% least likely to be pubertal at 600 days). B. Percentage of animals pregnant for animals by GEBV quintile (5=20% of animals most likely to be pregnant within 4 months of calving, 1=20% of animals lease likely to be pregnant within 4 months of calving.

Accuracies of GEBV were moderate for most traits (Table 2). The lowest accuracy was for tick score in Brahman. This was because there was very limited variation for this trait in the validation set. The standard errors on the correlations are 0.03 so accuracy for all traits, except tick score in Brahmans, is significantly greater than zero. The accuracies are encouraging given there is likely to be considerable genetic distance between the reference set and validation, given the time that has elapsed since the Beef CRC recording was conducted (20 years), and the difference in traits definition between GEBV reference and CRC validation.

Table 2. Accuracy of GEBV in the Brahman and Tropical Composite Beef CRC validation set

GEBV trait	Beef CRC trait	Accuracy	
		Brahman	Trop Comp
600 day weight	600 day weight	0.24	0.32
Hip height	Hip height	0.57	0.53
Body condition score	Body condition score	0.15	0.36
Heifer puberty	Age at corpus luteum	0.39	0.25
P4M	Post partum anoestrus interval	0.11	0.35
Docility	Flight time	0.30	0.24
Tick score	Tick score	-0.07	0.17
Fly lesion score	Fly lesion score	0.16	0.50
Teat score	Back teat score calving	0.14	0.13
	Front teat score calving	0.12	0.25
Udder score	Udder score calving	0.28	0.29

The GEBVs that had a significant effect on liveweight production were for Brahmans, weight, heifer puberty and P4M, and weight, P4M, temperament and teat score GEBV for tropical composites.

Table 3. Regression of GEBV on liveweight production in Brahman and Tropical composite cattle. Significance of effects, effect estimates (for significant effects)

Trait	P-values		Estimates (kg)	
	Tropical composites	Brahmans	Tropical composites	Brahmans
Weight	< 0.001	0.04	0.5	0.1
Height	0.76	0.07		
BCS	0.14	0.25		
Heifer puberty	0.99	< 0.001		27.2
P4M	0.02	0.01	31.9	80.5
Temperament	0.04	0.08	-12.7	
Tick	0.30	0.88		
Fly	0.77	0.55		
Teat	0.04	0.35	-34.2	
Udder	0.77	0.79		

Effects were mostly in the expected direction, for example better P4M (closer to one) was associated with increased liveweight production in both breed types, and larger (potentially bottle) teats were associated with decreased liveweight production in tropical composites. It should be again noted that these observed regression coefficients where for a population a few decades old, it would be useful to repeat this exercise in a population of more modern cattle.

CONCLUSION

GEBV for weight, heifer puberty and P4M are significant predictors of liveweight production in Brahmans. In tropical composites GEBV for weight, P4M, temperament and teat score are significant predictors of liveweight production. Variation in heifer puberty in tropical composites is much less than in Brahmans, which may explain why this trait is not significant for tropical composites. These results suggest selecting for GEBV for these traits will improve liveweight production. With some (considerable) extension (for example inclusion of the effect of heterozygosity estimated from the model, some measure of feed intake, economics of production), this index could also predict future profit potential of females (eg Dunne *et al.* 2020).

ACKNOWLEDGEMENTS

Funding for this project was generously provided by the Meat and Livestock Australia donor company, project numbers P.P.S.H 1420 and P.PSH.P0833. We would also like to gratefully acknowledge Brian Burns and Nick Corbet, as well as the Beef CRC.

REFERENCES

Bunter K.L.. and Johnston D.J. (2013) Anim. Prod. Sci. 54: 50.

Dunne F.L., Berry D.P., Kelleher M.M., et al. (2020) J. Anim. Sci. 98: skaa334.

Fordyce G., Barnes T.S., McGowan M.R., et al. (2023) Anim. Prod. Sci. 63: 395.

Hayes B.J., Copley J., Dodd, E., et al. (2023). Genet. Sel. Evol. 55: 71.

Johnston D.J., Reverter A., Burrow H.M., et al. (2003) Aust. J. Agri. Res. 54: 107.

Johnston D.J., Corbet N.J., Barwick S.A., et al. (2013). Anim. Prod. Sci. 54: 74.

Johnston D.J., Barwick S.A., Corbet N.J., et al. (2009) Anim. Prod. Sci. 49: 399.

Martinez G.E., Koch R.M., Cundiff L.V., et al. (2004) J. Anim. Sci. 82: 1912.

Porto-Neto L.R., Reverter A., Prayaga K.C., et al. (2014) PLoS ONE 9: e113284.

VanRaden P.M., Null D.J., Sargolzaei M., et al. Cole J.B., et al. (2013) J. Dairy Sci. 96: 668.

Yang J., Lee S.H., Goddard M.E., et al. (2011). Am. J. Hum. Genet. 88: 76.