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USING MALE PERFORMANCE TO IMPROVE GENOMIC SELECTION FOR FEMALE FERTILITY IN BRAHMAN CATTLE

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SUMMARY

Genomic selection offers the opportunity to improve female fertility in the Northern Australian beef herd. However, genomic predictions for a number of female fertility traits - derived solely from the small number of female fertility records collected thus far - are only of modest accuracy. In this study measures of Brahman male reproduction were used jointly with the female records, increasing the accuracy of genomic predictions for Brahman female fertility. Scrotal circumference measured at 18 months was found to be the most useful to increase accuracies of cow GEBVs for a range of traits upto 22%.

INTRODUCTION

Improving cow fertility has the potential to increase the profitability of Northern Australian beef cattle enterprises. Reducing the age at which heifers reach puberty, and/or increasing the probability of post-partum reconception in subsequent matings can both lead to improved calving rates. Johnston *et al.* (2010) found age at puberty and post-partum anoestrous interval (PPAI, defined as the time from calving to cycle) were moderately to highly heritable in Brahman cows. Early reproduction (measured as the number of calves in the first two opportunities) and lifetime reproduction (number of calves in the first six opportunities) were shown to be lowly heritable in tropical genotypes (Brahman and Tropical Composite) (Johnston *et al.* 2013a). With development of genomic markers, genomic selection could play an important role in genetic improvement. Zhang *et al.* (2013) demonstrated the usefulness of genomic selection for various measures of female fertility; however, accuracies of genomic breeding values, derived from a data set of limited size, were low. Amongst the reproduction traits measured in tropical beef bulls, scrotal circumferences at different ages were found to be highly heritable (Corbet *et al.* 2013) and correlated with female traits (Johnston *et al.* 2013b). This study examines whether the accuracy of genomic breeding values of reproduction traits of Brahman cows could be increased by using scrotal circumference information from their male relatives.

MATERIALS AND METHODS

Animal and measurements. The Brahman bulls and cows used in this study were part of the 'Northern Breeding Project' resource population, bred by the Cooperative Research Centre for Beef Genetic Technologies (Beef CRC) in the tropical regions of Northern Australia (Burrow *et al.* 2003; Barwick *et al.* 2009). A total of 1035 females were phenotyped. The first postpartum anoestrous interval (PPAI) records were observed on the 635 cows that calved at their first opportunity. The cows were progeny of 54 sires (Barwick *et al.* 2009). Age at puberty (AP) was defined as the age when the first c*orpus luteum* (CL) was observed using regular ultrasound scanning. Also, up to 6 calving occurrences were recorded for cows. These observations were used to determine the following fertility traits: 1) PPAI1 - the first PPAI, 2) CR12 - calves born in the

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first two opportunities, 3) WR12 - number of calves weaned in the first two opportunities, 4) LP – lactating-pregnancy status (a binary trait scored as "1" for cows both lactating and pregnant, otherwise "0"), 5) ACR – average calving rate in the first six opportunities and 6) AWR - average weaning rate in the first six opportunities. A comprehensive description of the bull data was provided by Corbet *et al.* (2013). Bulls were born between 2004 and 2010 and were progeny of the cows measured above. Scrotal circumference (SC) measured at ages of 12 (SC12) and 18 months (SC18) of 1142 bulls born from 2004 to 2008 were used in this study.

Genotypes. The SNP genotype data used in this study was a subset of Beef CRC genomic dataset. Details on genotyping, editing and imputation of the Beef CRC genomic data set has been described by Bolormaa *et al.* (2013). Briefly, 49, 821 and 126 cows were genotyped on the Illumina BovineSNP 7K, 50K and 700K SNP platforms (www.illumina.com/agriculture), respectively. The bulls were genotyped with the 50K platform. Genotypes with poor GenCall scores, very low minor allele frequencies and significant deviation from Hardy-Weinberg equilibrium were deleted. Missing genotypes for animals genotyped with the less dense chips were imputed to 700K using BEAGLE (Browning and Browning, 2009). Thus genotypes of 729,068 SNP for 996 Brahman cows and 1118 Brahman bulls were available for subsequent analyses.

Statistical methods. Genetic parameters were estimated for all traits of cows and bulls, with all phenotypic records using pedigree based REML (Wombat, Meyer 2007). Models for all cow traits (Barwick *et al.* 2009, Johnston *et al.* 2009, Johnston *et al.* 2010, Johnston *et al.* 2013a) and for scrotal size of bulls (Corbet *et al.* 2013) were described previously and used in this analysis.
GBLUP Genomic estimated breeding values (GEBVs) for each trait were estimated for animals with genotypes only using Wombat (Meyer 2007). The GBLUP model was as $\mathbf{y = Xb + Zg + e}$, where the phenotype (**y**) is a function of systematic effects (**b**), breeding values (**g**) and residuals (**e**), with incidence matrices (**X, Z**) assigning observations to effects. Covariances among breeding values were modeled with $\mathbf{G}\sigma_g^2$ – where **G** is the genomic relationship matrix (Yang *et al.* 2010) and σ_g^2 the genetic variance – and among residuals with $\mathbf{I}\sigma_e^2$ – where **I** is an identity matrix and σ_e^2 is the residual variance. SNP with very low minor allele frequencies (<0.005) were excluded when calculating **G**

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Cross validation. A 5-fold internal cross-validation procedure was carried out for each female trait. Genotyped cows were divided into 5 approximately equal groups, with 4 subsets used as a training set to predict the 5th subset as the test set. Animals were grouped so that complete paternal half-sib families were in the same subset**.** Cross validation was carried out using univariate and multi-variate analyses with bull scrotal circumferences (SC12 and SC18) as the other trait(s). Each of the cow traits were analysed jointly with either SC12 or SC18 of bulls in bivariate analyses and with both SC12 and SC18 in trivariate analyses.

Accuracy. GEBVs for test animals were correlated with their phenotypes adjusted for systematic effects. Accuracies were calculated as r/h where r is the correlation coefficient between GEBVs and phenotypic values and h is the square root of the heritability of the trait (estimated using all phenotypes). The average of 5 accuracies from the cross validations is presented as the accuracy for genomic prediction of each trait.

RESULTS AND DISCUSSION

The average accuracies and their standard errors of GEBVs for reproduction traits of cows in univariate and bivariate analyses with SC12 or with SC18 of bulls are shown in Table 1. Univariate analyses showed high accuracies of GEBVs for AP and AWR but low values for

PPAI1 and ACR. Accuracies of GEBVs from the bivariate analyses with SC18 were higher than the corresponding univariate values, the highest being for PPAI1 which increased from 0.18 to 0.22. Increases in accuracies of GEBVs were found for those traits with relatively low accuracies from univariate analyses.

However, results from bivariate analyses with SC12 were mixed. Accuracies for AP and PPAI1 were higher than the corresponding univariate results,notable reductions in accuracies were observed for remaining traits. Both SC12 and SC18 were expected to contribute similarly to the accuracies of cow fertility traits as SC12 and SC18 have a genetic correlation of 0.95 (Corbet *et al.* 2013). The genetic correlations between AP or PPAI1 and SC12 were similar to those with SC18, but they were low and not significantly different from zero for others traits with SC12. These mixed accuracies may be related to the low genetic correlations between SC12 and cow traits in genotyped data. Most of the genetic correlation coefficients were associated with large standard errors. These results were in line with results by Johnston *et al.* (2013b). The heritability estimate for SC12 (0.65) was lower than that for SC18 (0.75) (Corbet *et al.* 2013).

Table 1. Accuracies of genomic breeding values (standard errors) of cows in univariate and bivariate analyses with SC12 or with SC18 of bulls.

Trait	Univariate	Bivariate with SC12		Bivariate with SC18		$h^{2\#}$
		Accuracy	Change*	Accuracy	Change*	
AP	0.33 (0.06)	0.38 (0.07)	+16%	0.35 (0.09)	+6%	0.56
PPAI1	0.18 (0.05)	0.19 (0.05)	+6%	0.22 (0.06)	+22%	0.51
CR12	0.25 (0.09)	0.21 (0.11)	-16%	0.28 (0.09)	+12%	0.15
WR12	0.24 (0.07)	0.18 (0.08)	-25%	0.25 (0.07)	+4%	0.21
LP	0.20 (0.05)	0.19 (0.04)	-5%	0.21 (0.05)	+5%	0.39
ACR	0.16 (0.06)	0.10 (0.07)	-37%	0.18 (0.09)	+13%	0.16
AWR	0.39 (0.06)	0.32 (0.05)	-18%	0.40 (0.08)	+3%	0.13

*the percentages of change are based on average accuracies from corresponding univariate analyses. #h^2 from analysis of complete phenotypic data.

Table 2. Average accuracies (standard errors) of GEBV for reproduction traits of cows in trivariate analyses with SC12 and SC18 of bulls.

Trait	Accuracy	Change*
AP	0.37 (0.09)	+12%
PPAI1	0.20 (0.06)	+11%
CR12	0.24 (0.09))	-4%
WR12	0.24 (0.07)	0%
LP	0.21 (0.05)	+5%
ACR	0.13 (0.10)	-19%
AWR	0.33 (0.10)	-15%

*the percentage of changes are based on average accuracies from corresponding univariate analyses.

The average accuracies and their standard errors of GEBVs for cow traits with bull scrotal sizes in the trivariate analyses are shown in Table 2. Change in accuracies from trivariate analyses appeared to be within the ranges observed from bivariate analyses with SC12 and with SC18 (Table 1). Use of both SC12 and SC18 enhanced the accuracies for GEBV of AP and PPAI1 up to 12%. The changes for accuracies of early life time and life time reproduction traits were very small or negative.

These results suggest that the inclusion of scrotal circumference measures from male relatives can enhance the accuracy of GEBVs for female fertility in Northern Australian Brahman cattle. However, their use is limited because the genetic correlations between scrotal measure (SC18) and the female fertility traits ranged from low (0.18) to medium (0.49). More training data is required to increase the accuracies cow GEBVs.

CONCLUSIONS

This study shows that use of reproduction phenotypes and genotypes of bulls can improve the accuracies of genomic selection for traits measured in cows. Incorporating scrotal circumference of bulls can improve accuracies of GEBV for AP and PPAI, up to 22%. Scrotal circumference measured at 18 months was found to be most useful. Results suggest that the use other source of information such as bull fertility measures and increasing quality of phenotypes and records of training population can enhance accuracy of genomic selection.

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