Contributed paper

MULTIBREED GENOMIC PREDICTION FOR MALE FERTILITY IN TROPICAL BEEF CATTLE

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SUMMARY

Regardless of the mating method (natural or artificial insemination), bull fertility impacts the reproductive outcomes of any breeding herd. There is a need to improve our ability to genetically select fertile bulls, and genomic selection approaches could assist this process. Aiming at this gap in genomic approaches, we collected phenotypes and SNP genotypes on more than 6,000 bulls across six tropically-adapted breeds. Phenotypes related to male fertility were measured during Bull Breeding Soundness Examinations. The genomic correlations of the same trait observed in different breeds were positive for scrotal circumference and sheath score in most breed comparisons but close to zero for percentage normal sperm, suggesting a divergent genetic background for this trait. We confirmed the importance of breeds being part of the reference population while estimating breeding values in an across-breed scenario. Using this dataset, multibreed genomic predictions were obtained with useful accuracies.

INTRODUCTION

Fertility is a key driver of profitability for beef breeding herds in tropical and semi-arid environments. The standardized bull breeding soundness examination (BBSE) involves a general physical examination, a detailed examination of the external and internal genitalia, and a microscopic examination of semen cells (Entwistle and Fordyce 2003). Quantitative traits of the BBSE are heritable (Corbet *et al.* 2013) and can be improved by selection. However, the BBSE is labor intensive resulting in a limited number of animals being tested every year, which hinders the assembly of a reference population. By combining information across breeds, we were able to generate a reference population of reasonable size (>6,000 animals,) and we postulate that the use of multibreed genomic selection approaches could allow the estimation of breeding values with useful accuracy to assist the improvement of commercially relevant male traits.

MATERIALS AND METHODS

Animals and phenotypes. Phenotypic data was sourced on bulls from six different populations varying in number from 535 to 1,093 (Table 1). These were Brahman (BB) and Tropical Composite (TR) from the Beef CRC (Barwick *et al.* 2009), and cattle from four performance recorded breeding herds in Queensland, a Santa Gertrudis (SG), a Droughtmaster (DM), a Belmont Tropical Composite (BT) and an Ultra Black (UB) herd. The observed phenotypes included scrotal circumference (SC, cm), sheath score (Sheath, score 1-5), and the percentage of morphologically normal spermatozoa (PNS, %). The age at which the phenotype was observed varied across the populations; for the CRC cattle, the mean age at SC was around 360 d, and for Sheath and PNS around 700 d. For SG and DM all phenotypes were observed at around 600 d of age, while for UB and BT were around 440 d

and 390 d, respectively.

Genotypes. Most animals were genotyped using a commercial SNP chip with ~50K markers. Genotypes were imputed to ~720K SNP using a reference population that combined Beef CRC and industry cattle genotyped on the higher density platform. Genotypes were first phased using Eagle (Loh *et al.* 2016) and then imputed using Minimac3 (autosomes) or Minimac4 (BTAX) (Das *et al.* 2016). SNP with imputation $r^2 > 0.8$ were kept for further analyses. To visualise the genetic relationship between animals a principal components analyses were calculated using PLINK1.9 (Chang *et al.* 2015).

Table 1. Number of records and descriptive statistics of the observed traits*

	Number of records			Mean (SD) of measurements		
Population**	**SC**	**Sheath**	**PNS**	**SC**	**Sheath**	**PNS**
BB	1,089	1,093	947	21.26 (2.69)	3.79 (0.92)	73.70 (21.95)
TR	985	985	985	26.55 (3.17)	3.12 (1.54)	73.01 (20.59)
SG	918	928	896	34.46 (3.10)	2.95 (0.78)	73.28 (21.57)
DM	568	722	680	33.68 (3.13)	3.14 (0.68)	63.55 (26.28)
UB	836	841	771	33.80 (3.38)	1.78 (0.80)	68.77 (25.30)
BT	527	535	429	28.11 (3.29)	1.64 (0.59)	54.65 (29.70)

* SC scrotal circumference (cm), Sheath score (1-5), PNS percentage of normal sperm (%).
** BB Brahman, TR Tropical Composite, SG Santa Gertrudis, DM Droughtmaster, UB Ultra Black, BT Belmont Tropical Composite.

Statistical analyses. The phenotypes were adjusted using SAS 9.4 (www.sas.com) before the genomic analyses. The model for adjustment included the fixed effects of population (one per farm), year of birth and management group (within farm). The covariates of age and the first two principal components were also used. The genomic relationship matrices (GRM) were constructed following method 1 of VanRaden *et al*. (2008). Univariate, and the GBLUP analyses were run using QXPAK (Perez-Enciso and Misztal 2011).(Porto-Neto *et al.* 2015) The accuracies of the genomic predictions were calculated as the correlation of adjusted phenotypes divided by the square root of heritability and by the method LR (Legarra and Reverter 2019) that compares the predictions based on the whole and partial datasets to estimate accuracies and biases.

RESULTS AND DISCUSSION

The estimates of heritability for SC, Sheath and PNS across-breeds were moderate, with mean heritabilities, estimated using across-breed bivariate models, of 0.45, 0.59, and 0.33, respectively. These were at the lower end of the reported estimates for SC, but similar to values reported in the literature for the other traits (Corbet *et al.* 2013; Fortes *et al.* 2020). The mean genomic correlation between these traits calculated using the same across-breed bivariate analyses were close to zero, apart from a modest 0.11 between SC and Sheath (results not shown in Tables).

Using bivariate models, we also estimated the genomic correlation of the same trait observed in different breeds. The mean correlation estimate for all pair-wise combinations of populations were 0.34, 0.40 and 0.00 for SC, Sheath and PNS, respectively (Table 2). There is very low genomic correlation between all pair-wise combinations for PNS, suggesting different genetic architecture of the trait in the different breeds, except for BB and TR with a moderate -0.30. For SC, the relative lower genomic correlation between BB and the other breeds suggests that this trait is more genetically different when comparing BB to other breeds. The strong genomic correlations between breeds for SC and for Sheath might hint at the presence of common haplotypes affecting the traits

in both populations.

Table 2. Genomic correlation for a given trait in two separate populations*, **

Pop 1	Pop 2	SC	Sheath	PNS
BB	**TR**	0.2694	0.7217	-0.3052
BB	**SG**	0.1248	0.5781	0.0133
BB	**DM**	0.1619	0.5123	0.0289
BB	**UB**	0.1036	0.5498	-0.0191
BB	**BT**	0.0151	0.2347	-0.0124
TR	**SG**	0.5370	0.4773	-0.0017
TR	**DM**	0.6504	0.4785	-0.0024
TR	**UB**	0.5445	0.7920	0.0431
TR	**BT**	0.4803	0.2636	0.1332
SG	**DM**	0.8174	0.0303	-0.0003
SG	**UB**	0.5693	0.7512	-0.0093
SG	**BT**	0.0627	0.0301	0.0209
DM	**UB**	0.2470	0.2925	0.0006
DM	**BT**	0.0263	-0.0051	0.0038
UB	**BT**	0.5031	0.2610	0.0126
	Mean	0.3408	0.3979	-0.0063

* Analyses performed using a bi-population GRM (ie. for the two populations under comparison). ** Traits and populations as described in Table 1.

GEBV accuracy estimates for a breed, when the breed was not represented in the reference, were lower than those when some animals of the breed were included in the reference (comparison between scheme 1 vs 2, Table 3), with the largest impact on BB. This observation was expected given the known relationship between accuracy and genetic distance to the reference population for a given test animal (de Roos *et al.* 2009). Moreover, BB is the most divergent breed among the six populations, even though it was used during the formation of some of the other breeds.

CONCLUSIONS

There are some genomic correlations between the same trait observed in different breeds, implying there exists at least some similarities in the genetic background across breeds; however, this was not observed across all traits. We confirmed that higher accuracies are obtained by including the targeted breed in the reference population. Finally, it was possible to estimate GEBVs with useful accuracies, for fertility-related traits in bulls, in a multibreed scenario. This approach could be further developed in the future, aiming at a broader adoption of the technology by the industry.

ACKNOWLEDGMENTS

This work was supported by the Bull Fertility update project, an initiative from CSIRO, the University of Queensland, and Meat & Livestock Australia. The authors are thankful to the beef producers who took part in this collaborative effort and Meat & Livestock Australia that co-funded the project (L.GEN.1818).

Table 3. Multibreed genomic prediction accuracies calculated using the method LR**

Population	SC	Sheath	PNS	Mean
Scheme #1: From a given population, all records missing in the reference				
BB	0.217	0.217	0.217	0.217
TR	0.479	0.696	0.211	0.462
SG	0.367	0.366	0.233	0.322
DM	0.497	0.358	0.251	0.368
UB	0.381	0.512	0.176	0.356
BT	0.263	0.323	0.227	0.271
Mean	0.367	0.412	0.219	
Scheme #2: From a given population, a random 20% records missing in the reference (mean across five 80/20 cross-validation splits)				
BB	0.513	0.399	0.319	0.410
TR	0.648	0.812	0.402	0.621
SG	0.501	0.412	0.341	0.418
DM	0.593	0.402	0.473	0.489
UB	0.629	0.573	0.406	0.536
BT	0.610	0.343	0.510	0.488
Mean	0.582	0.490	0.408	

* Traits and populations as described in Table 1. ** Legarra, and Reverter (2019)

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