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TRANSLATING MULTIBREED GENOMIC PREDICTION OF BULL FERTILITY TRAITS INTO ON-FARM SELECTION OF BULLS

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SUMMARY

Genomically enhanced estimated breeding values (GEBV) have been used by many protein-producing industries for several years. However, its use to improve herd fertility has been limited in beef cattle, especially in Northern Australia. The recording of fertility-related traits like those measured in a bull breeding soundness examination (BBSE) following a standard protocol offers an opportunity for improving those traits via genomic selection strategies. Here we describe analyses performed using a multibreed dataset comprising around 8,000 bulls of six tropical breed types and with BBSE data. The heritability estimates varied from low (0.168) for the percentage of proximal droplets to high (0.547) for the sheath score. The GEBV were unbiased and not over-dispersed. The overall accuracies of the GEBV varied from moderate (0.321, proximal droplet, %) to high (0.549, scrotal circumference, cm). These accuracies varied depending on the population. The phenotypic differences between animal quartiles ranked by the GEBV demonstrated the usefulness of those estimates. For example, 25kg of body weight and 2.5 cm in scrotal circumference were observed between quartiles one and four, demonstrating the value of those GEBV.

INTRODUCTION

The use of genomically enhanced estimated breeding values (GEBV) has been implemented in several animal production systems aiming at genetically improving a diverse range of traits. In cattle, the dairy industry leads the adoption by far, possibly followed by some of the Angus breed programs. In tropical cattle, there is limited adoption of the technology, especially when considering hard-to-measure traits like fertility. The use of the standardized bull breeding soundness examination (BBSE) (Entwistle and Fordyce 2003), known to have heritable components (Corbet *et al.* 2013), creates an opportunity to explore its use for genetic evaluation in a multibreed scenario. It might be hard to collect enough records within a single breed to build a breed-specific reference population. Therefore, the multibreed option becomes attractive. Here we tested the feasibility of a multibreed reference population for bull traits and evaluated if the accuracies obtained could be translated into a useful selection tool for on-farm selection of groups of bulls.

MATERIALS AND METHODS

We assembled a reference dataset of genotypes and trait observations on 6,063 bulls (Porto-Neto *et al.* 2023) which has now grown to more than 8,000. These comprise six tropical breed types, Brahman (n=1,817), Santa Gertrudis (n=1,314), Droughtmaster (n=1,008), Ultra-Black/Brangus (n=1,286) and different tropical composite populations (n=2,663) to which a BBSE was recorded. Here we present results for body weight (WT), scrotal circumference (SC), sheath score (SHEATH, 1 - tight to 9 - pendulous), percentage of normal sperm (PNS) and percentage of the most common sperm cell defect, proximal droplets (PD). Table 1 presents the number of records and descriptive statistics of the traits.

Most animals were genotyped using a commercial SNP array with around 50K markers. Genotypes were imputed to ~700K SNP using a reference population that encompassed Beef CRC, and industry cattle genotyped using the high-density Illumina array (BovineHD). Imputation was

performed in two steps; first, genotypes were phased using Eagle software (Loh *et al.* 2016) and then imputed using either Minimac3 or 4 (Das *et al.* 2016).

The genomic analyses were performed with pre-adjusted phenotypes. The model for adjustment ran in SAS 9.4 (www.sas.com) included the fixed effects of the population (one per farm), year of birth and management group (within the farm). Additionally, it also fitted the covariates of age at measurement and the first two principal components derived from the genomic relationship matrix constructed following Van Raden's method 1 (VanRaden 2008). Univariate GBLUP models were run using QXPAK (Perez-Enciso and Misztal 2011). The accuracies of the GEBV were calculated as their correlation with adjusted phenotypes divided by the square root of the heritability and the LD method (Legarra and Reverter 2019), both following a five-fold cross validation where a random 20% of the traits data were set to missing. To evaluate the phenotypic potential of those GEBV, we ranked the animals using the GEBV, then calculated the average phenotypic difference between the quartile 1 to 4 (referred as Q1-Q4).

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

Trait	N	Mean	SD	Min	Max
WT, Kg	7,730	383.05	93.82	109.50	810.00
SC, score	7,869	30.93	4.29	15.50	52.50
SHEATH, score	7,749	3.13	1.67	1.00	9.00
PNS, %	7,240	62.34	27.37	0.00	100.00
PD, %	7,214	13.13	19.78	0.00	96.00

* WT – body weight, SC – scrotal circumference, SHEATH – sheath score, PNS – the percentage of normal sperm, PD – the percentage of proximal droplets in sperm cells, N – number of observations, SD – standard deviation, Min – minimum value, Max – maximum value observed.

RESULTS AND DISCUSSION

Using our assembled multibreed reference population, we estimated the heritabilities varying from 0.168 (PD) and 0.547 (SHEATH) (Table 2). The moderate to high heritability estimates agreed with previously estimated values for those traits (Corbet *et al.* 2013), giving us confidence the dataset is sound and the traits amenable to improvement via selection.

The GEBV were unbiased and, with the possible exception of SHEATH, not over-dispersed (Table 2). Additionally, using a five-fold cross-validation approach, we obtained reasonably high accuracies (ACC LR, 0.321 to 0.549). The accuracies within populations varied (result not shown), in line with previous analyses using a partial dataset (Porto Neto *et al.* 2021).

Aiming to translate the observed accuracies into phenotypic differences between the validation bulls, we first ranked the bulls by their GEBV, split them into quartiles, and then observed their adjusted trait record (Table 2, Q1-Q4) within their quartile groups. The accuracy of 0.549 for SC translated into a 2.59 cm difference in scrotal size between to top and bottom quartile of bulls. Similarly, the Q1-Q4 analyses for PNS resulted in a 9.49% difference in sperm cells that passed the morphology test. These analyses resulted in group means with large SD and variation within breed types (result not shown). Nonetheless, the translation of the observed accuracies into phenotypic differences was encouraging and demonstrated the potential for using such a tool for on-farm selection of a group of bulls.

Table 2. Results summary. Heritability estimates for observed traits, bias, dispersion, accuracies of estimated breeding values, and the phenotypic difference between animal quartiles ranked by GEBV *

Trait	h2	Bias Mean (SE)	Dispersion Mean (SE)	ACC LR	ACC Trad	Q1-Q4
WT, Kg	0.310	-0.058 (0.365)	-0.042 (0.032)	0.531	0.460	25.14
SC, score	0.436	0.007 (0.027)	-0.001 (0.026)	0.549	0.565	2.59
SHEATH, score	0.547	-0.009 (0.008)	0.165 (0.020)	0.472	0.525	0.67
PNS, %	0.270	-0.112 (0.175)	0.089 (0.033)	0.365	0.300	9.49
PD, %	0.168	0.038 (0.073)	0.043 (0.028)	0.321	0.339	5.19

* WT – body weight, SC – scrotal circumference, SHEATH – sheath score, PNS – the percentage of normal sperm, PD – the percentage of proximal droplets in sperm cells, h2 – heritability estimated, SE – standard error, ACC LR – estimated accuracy of GEBV calculated using the method LR, ACC Trad – estimated accuracy of GEBV calculated using the correlation method, Q1-Q4 – the phenotypic difference between animal quartiles ranked by GEBV, where Q1 is the quartile of animals with highest GEBV and Q4 the quartile with lowest GEBV.

CONCLUSIONS

This study shows that it is feasible to assemble a multibreed reference population for fertility-related traits of tropical bulls. The reasonable to high heritability estimates confirm the quality of the dataset and encourage its adoption in selection breeding programs. The GEBV were mostly unbiased, and although variation within cattle type and population existed, the accuracies of GEBV could be translated into a useful tool for on-farm selection.

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