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USING GENOMIC AND PHENOTYPIC DATA TO CHARACTERISE THE GENETIC STRUCTURE OF BRAHMAN CATTLE POPULATIONS IN SOUTHERN AFRICA

W.M.S.P. Weerasinghe and B.J. Crook

Agricultural Business Research Institute, UNE, Armidale, NSW, 2350 Australia

SUMMARY

Knowledge of the genetic structure of cattle breed populations is an important consideration in genetic evaluations. This study used both genomic and phenotypic data to characterise the structure of the Brahman cattle population distributed over three countries in Southern Africa. Principal component analysis based on the genomic relationship matrix demonstrated two sub-populations, with the first principal component explaining 32% of the variation. Subsequent review of both groups showed differences in coat colour as the main source of differentiation, this being red coloured Brahmans and those that were white or grey in colour. Unsupervised analysis using ADMIXTURE with two populations revealed a unique signal in the red Brahman. Variance components and heritability estimates for 200-day weight were similar in the red, white and grey populations and the genetic correlation between the red and white types was 0.88. However, genetic correlations involving the grey type were considerably lower (0.25 with red, 0.58 with white) reflecting the limited comparisons of the grey type with either the white or red type in the same herds and contemporary groups.

INTRODUCTION

Development of the American Brahman commenced in the late 19th century with the importation of several *Bos indicus* breeds from India, followed by subsequent imports of *Bos indicus* types (such as Nellore, Guzerat, Gir and Indu-Brasil) from India and Brazil, and some infusion of local *Bos taurus* genetics (Utsunomiya *et al.* 2019). Live animal exports to Southern Africa commenced in the 1950s, with American genetics increasingly utilised via semen and embryos, and more recently from Australia and Brazil. Combined with the trade in Brahman genetics between countries in Southern Africa, this has led to the Brahman breed contributing significantly to commercial beef production in that region. The Brahman Cattle Breeders' Society of South Africa have utilised the BREEDPLAN genetic evaluation service provided by the Agricultural Business Research Institute (ABRI) since 2002, this being extended to include the Brahman Cattle Breeders' Society of Namibia in 2004 and the Brahman Breeders Society of Zimbabwe in 2021. Pedigree and performance data are combined for evaluation, with over 711,000 animals represented in a multi-trait analysis of phenotypes associated with birth (gestation length and birth weight), post-birth growth (weaning, yearling, final and mature cow weight), fertility (scrotal size and female days-to-calving), ultra-sound scan traits and net feed intake results. The genotyping of seedstock Brahman cattle represents a more recent development in Southern Africa, with a goal towards incorporating genomic data in the genetic evaluation. The objective of this study was to describe the genetic structure of the Brahman cattle population distributed across South Africa, Namibia and Zimbabwe and to investigate data structure relative to the genomic structure of the population including genetic analysis of 200-day weight.

MATERIALS AND METHODS

Genomic analysis. Genotypes were available on Brahman populations in South Africa (n=1,204), Namibia (n=749) and Zimbabwe (n=73), with SNP densities of 54K (n=1,434) and 140K (n=592). The markers located on autosomal chromosomes were considered. Quality control (QC) of genomic data was conducted using PLINK software (Chang *et al.* 2015). Individual SNPs were

removed at a minor allele frequency of <0.01, a call rate <90% and a deviation from Hardy–Weinberg equilibrium of $p<1E^{-6}$, with individual genotypes being excluded if the call rate for all loci was <85%. This resulted in a dataset of 1,746 individuals. Genotypes were imputed to the highest density represented using FImpute v3 (Sargolzaei *et al.* 2014), giving 86,110 SNPs for the genetic studies. Principal component analysis (PCA) was carried out on the genomic relationship matrix (VanRaden 2008) to investigate the population structure and genomic variability within the Brahman population. The PCA highlighted two sub-groups, with review of each suggesting recorded coat colour as the main point of differentiation: between red coloured cattle (RE, n=256) distributed across all 3 countries and those recorded as white (WH, n=299) in Namibia or grey (GR, n=786) in South Africa. An unsupervised model-based clustering approach using ADMIXTURE 1.3 (Alexander *et al.* 2009) was used to explore the population structure and infer genomic admixture levels in the RE, WH and GR clusters. A cluster of animals of unrecorded colour (n=405), many from Namibia, was also included. The expected number of subgroups (*K*) was varied from 2 to 4.

Genetic analysis. For animals recorded as RE, WH or GR, their 200-day weights (200D) were extracted from the November 2022 BREEDPLAN evaluation for Southern African Brahman. Phenotypes were pre-adjusted for age at weighing and age of dam as outlined by Graser *et al.* (2005). Contemporary group was defined as herd of origin, sex, year of birth, birth number (single vs twin), birth type (natural vs ET), breeder-defined management group and weigh date. Extracted records were pruned to remove single-animal contemporary groups and those comprising ET calves. The final data set contained 138,764 records for 200D representing RE (34,103), WH (24,486) and GR (80,175) animals. Weight records for RE, WH and GR animals were defined as different traits in a multivariate analysis including additive genetic, maternal genetic (uncorrelated), maternal permanent environment and residual components within trait and a direct genetic correlation only between traits. Contemporary group was fitted as a fixed effect. Six generations of pedigree were included, giving 215,947 animals in the analysis. A genotype file and associated map file were included in the analysis, with 51% of genotyped animals having a 200D record. The GIBBSF90 program in the BLUPF90 family of software (Misztal *et al*. 2018) was used, with 50,000 rounds, a burn-in of 5,000 and every 20th round stored. (Co)variance components were obtained from posterior means using the POSTGIBBSF90 program and a burn-in of 20,000.

RESULTS AND DISCUSSION

The first and second principal components of the PCA explained 31.7% and 5.3% of total variation in the genomic data, with PC3-5 accounting for an additional 3.7%, 2.4% and 2.2% respectively. PC1 reflects a clear stratification in the genotyped population, with RE animals separated as a distinct genomic sub-type compared to WH and GR animals (Figure 1). WH and GR animals show considerable overlap, suggesting they are colour variants of more closely related types. The admixture proportions from the unsupervised analyses with *K*=2, 3 and 4 are shown in Figure 2. Based on the simplest model of *K*=2, the differentiation of RE as a distinct sub-type in the PCA reflects a significant difference in breed composition compared to WH and GR. Subsequent analyses with *K*=3 and *K*=4 were informative yet did not add considerably beyond the simplest model suggesting the predominant breed content of RE is a minor component of the WH and GR. With *K*=4, however, a breed fraction of larger representation in the WH than in the GR was evident. Based on the estimated breed allele frequencies, (i) a low frequency of mis-recorded colour codes seems evident and (ii) the unknown cohort appears to represent all 3 colour types with WH as the primary colour. One limitation of unsupervised model-based clustering is that breed allele frequencies are not explicitly specified, meaning that estimated breed allele frequencies may be biased by familiar relationships among the sample (Gobena *et al.* 2018). The genomic diversity evident in the Brahman population of Southern Africa is reflective of the heterogeneous ancestry of the breed. Although the Brahman breed societies of Southern Africa record all coat colour types

among their registered cattle populations, as do their American and Australian counterparts, the results of this study describe the red Brahman as a genomically distinct sub-type within the breed.

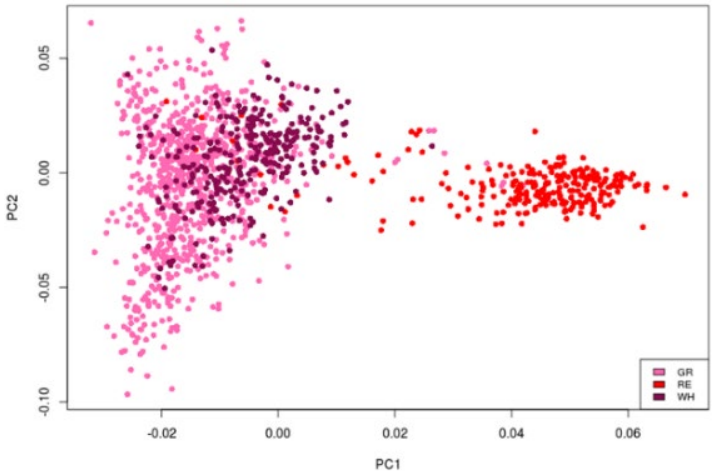

Figure 1. Plot of PC1 vs PC2 for Grey (GR), Red (RE) and White (WH) coloured Brahman

The summary statistics and variance component estimates for 200D in the RE, WH and GR are given in Table 1. The direct and maternal genetic heritability estimates are similar across the 3 types and the ratio of maternal permanent environment to phenotypic variance was 0.08 in each instance. These heritability estimates fall within the range of estimates reported for Brahman cattle in Brazil (de Oliveira Bessa *et al*. 2021), Australia (Davis 1993) and South Africa (Pico *et al.* 2004).

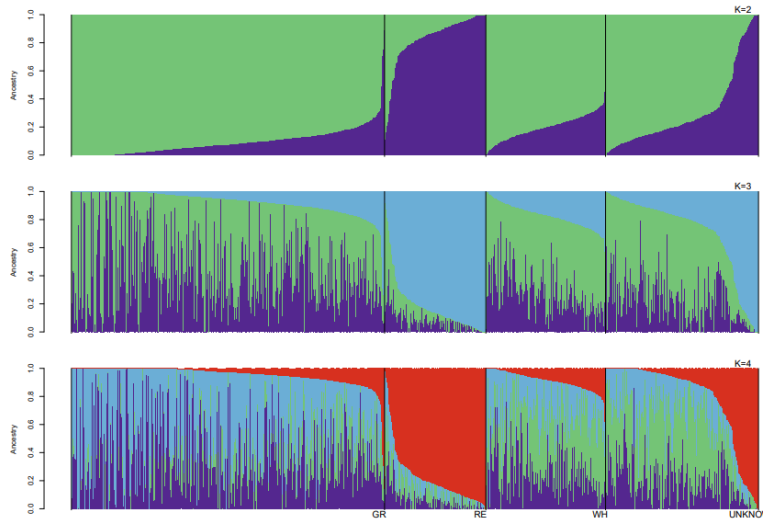

Figure 2. Estimation of admixture proportions of Grey (GR), Red (RE), White (WH) and unknown coat colour, unsupervised with K=2 (top) to K=4

These results suggest a similar mode of genetic expression for 200D in each colour group without the need for type-specific variance components. In the current study however, the genetic correlation for 200D between coat colour types was inconsistent: 0.88 for RE-WH, 0.25 for RE-GR and 0.58 for WH-GR, with high posterior density intervals (95%) of 0.85-0.90, 0.17-0.36 and 0.50-0.65 respectively. A plausible explanation is the lack of comparative data involving grey animals. Only 19 of the 18,441 contemporary groups recorded for 200D contained all 3 colour types, accounting for 320 animals in total. Of those groups comprising 2 colour types (44,003 animals in 3,013 groups), the predominantly contained red and white animals only. Most 200D records (71%) were in contemporary groups representing a single coat colour. Lower genetic correlations involving grey animals reflected limited linkage in the data available for estimation of covariance components.

Table 1. Performance statistics (mean and standard deviation, SD), variance components and heritability estimates for 200-day weight, according to coat colour. Additive genetic variance (V_A), total phenotypic variance (V_P), direct heritability (h^2_D) and maternal genetic heritability (h^2_M). All units in kilograms

Colour	Mean	SD	V_A	V_P	h^2_D	h^2_M
Red	199.8	37.7	85.72±7.01	451.37±4.55	0.19±0.02	0.08±0.01
White	203.4	34.6	75.57±5.50	412.74±4.55	0.18±0.02	0.08±0.01
Grey	206.1	36.4	80.69±5.72	480.93±3.26	0.17±0.02	0.07±0.01

CONCLUSION

Results of the genomic analysis indicate the red Brahman as a distinct sub-type within the wider Brahman population of Southern Africa, though genetic analysis suggests all 3 colour types show a similar genetic expression of 200-day weight. Data structure does, however, indicate limited linkage between the grey Brahman and the other colour types, reflecting a preference of grey Brahman breeders for grey cattle only. Genetic evaluation of the breed in Southern Africa will benefit from increasing representation of all 3 colour types in the reference population.

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