BREED COMPOSITION EFFECTS AND GENETIC PARAMETERS FOR PRODUCTIVITY OF TROPICAL BEEF CATTLE

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SUMMARY

The ability of beef cattle to remain productive in tropical environments is largely determined by heat tolerance and tick resistance. In Australia, crossbreeding and composite breeding with *Bos indicus* cattle have been used to introduce these traits into *Bos taurus* breed backgrounds. We examined SNP genotyping data and phenotypes for six production traits from a Tropical Composite herd in Central Queensland to test whether the *Bos indicus* ancestry (Indicus) percentage was able to explain the performance of beef cattle in tropical Australia. Tick count and coat length were significantly linked to Indicus percentage, while live weight, body condition, rectal temperature and scrotal circumference were not influenced by the Indicus content of the genome.

INTRODUCTION

Tropical Composites and the Brahman breed are the main types of cattle across Northern Australia. The term "Tropical Composite" generally refers, to minimally stable crossbred herds of European ancestry (*Bos taurus*) with varying degree of crosses with *Bos indicus* influenced cattle (Porto-Neto *et al.*, 2014). These types of cattle have been chosen for their adaptation or tolerance to challenges in tropical environments (Barwick *et al.*, 2009; Prayaga *et al.*, 2009).

The complex ancestry of the cattle *per se* does not limit the potential genetic improvement of those herds, but when combined with extensive herd management practices, and lack of relationship (pedigree) information, the intricacy of breed ancestry does add another layer of complexity to derive accurate estimates of genetic merit. In recent years, advanced analytical tools have been developed to better explore genotypes derived from single nucleotide polymorphisms (SNP) arrays. These new methods facilitate broader adoption of genomic technology as it, for instance, gives an alternative approach around the lack of pedigree, and allows the estimation of breed ancestry.

Here we analysed a Tropical Composite herd genotyped for around 50,000 SNP (Harrison *et al.*, 2012), with multiple observations for six phenotypes. We used the molecular data to study the population structure, estimate heritabilities, genomic correlations, breed composition, and to test the effect of ancestry on observed phenotypes.

MATERIALS AND METHODS

We targeted a Tropical Composite commercial population (TXX, n = 877) from central Queensland (Harrison *et al.*, 2012), and, for some analyses, used a set of animals as genotypic references representing ancestral breeds of the targeted population. These included Charolais (CHA, n = 90), Senepol (SEN, n = 69), Belmont Red (BEL, n = 73), and Brahman (BRM, n = 90) (Barwick *et al.*, 2009; Porto-Neto *et al.*, 2013). Most animals were genotyped using the BovineSNP50 v1 (Illumina Inc., San Diego, CA), the remaining animals were genotyped using more recent platforms (e.g. BovineSNP50 v2 or BovineHD). Standard quality control was applied to genotypes. If the analyses required samples that were genotyped using different arrays, only SNP that were in common across all platforms were kept for analyses.

Animals were phenotyped between 2 to 4 times across two years. Most animals were phenotyped around yearling age. The observed phenotypes were transformed tick counts (Tick, log2 of average tick counts), coat score (Coat, average coat score), condition score (Cond, average body condition

score), rectal temperature (Temp, average rectal temperature), scrotal circumference (SC, single observation) and live weight (WT, average weight).

To assist the visualization of the populations substructure we ran principal components analysis (PCA) using PLINK 1.9 (Chang *et al.*, 2015), and estimated the ancestral proporti ons of *Bos taurus* and *Bos indicus* using Admixture software (Alexander *et al.*, 2009), as previously described (Porto-Neto *et al.*, 2014). A hexa-variate analysis was run to estimate heritabilities and genomic correlations between phenotypes fitting a precomputed genomic relationship matrix (VanRaden, 2008) in Qxpak v5 (Perez-Enciso and Misztal, 2011). Finally, we tested the effect of ancestral proportions on the observed phenotypes using SAS (SAS Inst., Cary, NC). The statistical model included the covariates of estimated percentage of *Bos indicus* and age at observation for each measurement, and the fixed effects of sex, breed type, management group, and operator (tick counts). For WT, after some exploratory analyses, an additional interaction between percent *Bos indicus* and sex was fitted.

RESULTS AND DISCUSSION

After quality control, around 760 animals (TXX) with genotypes (n = 49,573) and phenotypes were available for analysis, apart from SC which had a reduced number of observations (Table 1). There was large variation in phenotypes within the analysed population.

Table 1. Summary statistics of observed phenotypes

Phenotype	N	Mean	Std. Dev.	Min.	Max.
Tick	758	3.58	1.76	0.00	6.89
Coat	760	3.67	0.92	1.00	8.00
Cond	760	6.33	1.38	3.00	10.00
Temp	757	39.64	0.49	38.30	41.80
SC	248	28.41	3.70	17.50	38.00
WT	760	294.39	73.79	126.50	562.00
Indicus	761	24.48	7.64	5.02	60.45

Transformed tick counts (Tick), Coat score (Coat), Condition score (Cond), Rectal temperature (Temp), Scrotal circumference (SC), Weight (WT), and SNP-based percent estimate of *Bos indicus* ancestry (Indicus).

To explore and visualize potential population substructures we ran PCA analysis using additional cattle samples representing the breeds used during the formation of the targeted population (Figure 1). The majority of the animals appear to have varying proportions of three main ancestral breeds, Charolais, Senepol and Belmont Red with only a minor component of BRM. Moreover, a number of individuals seem to represent pure ancestral breeds, as they cluster together with the reference pure-breed clusters, these were seen with CHA, SEN and BEL clusters.

Using a genomic relationship matrix in the hexa-variate analyses we estimated the heritabilities and genomic correlation between phenotypes (Table 2). Heritability estimates varied from 0.391 (Temp) to 0.492 (Coat). It is worth noting that a known major gene variant affecting coat type that is derived from SEN cattle (Littlejohn *et al.*, 2014) segregates in this population and greatly influences the coat type. For Tick, the heritability (0.466) agrees with previous analyses using the same and one other population (Harrison *et al.*, 2012; Prayaga *et al.*, 2009), but is higher than other reports (Porto Neto *et al.*, 2011). For the other phenotypes, most estimates agreed with those

previously reported for another sample of Tropical Composite cattle, maybe with the exception of Temp (higher here), and WT (lower here) (Porto-Neto *et al.*, 2014; Prayaga *et al.*, 2009).
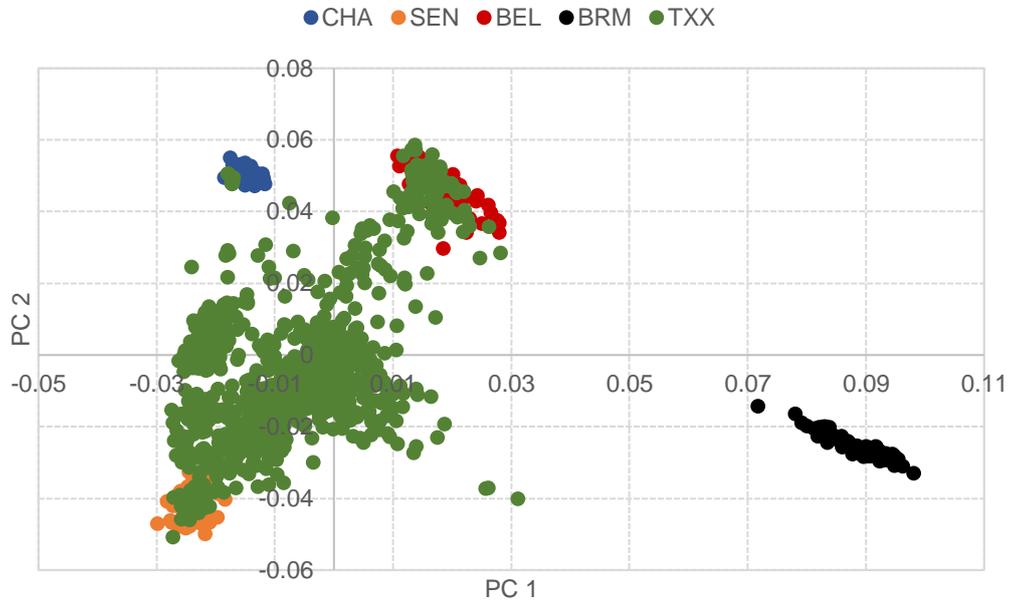

Figure 1. Principal Components Analyses using SNP genome-wide distributed (n = 33,620) including Charolais (CHA), Senepol (SEN), Belmont Red (BEL), Brahman (BRM) and Tropical Composite (TXX).

The estimated genomic correlations, in general, were not strong. Nevertheless, we detected positive correlations varying from 0.402 to 0.612 between Cond, SC and WT, which are different from some previously reported negative genetic and phenotypic correlations between Cond and WT (Porto-Neto *et al.*, 2014). The positive correlation between Tick and Coat (0.207) has the same direction of effect, but differs in magnitude from that previously reported (0.49) in a mixed breed analysis (Prayaga *et al.*, 2009).

Table 2. Estimated heritabilities (diagonal), and genomic correlations (off-diagonal) derived from hexa-variate analyses for observed traits

	Tick	Coat	Cond	Temp	SC	WT
Tick	**0.466**	0.207	-0.140	0.037	-0.143	-0.073
Coat	0.207	**0.492**	-0.066	0.065	-0.052	-0.105
Cond	-0.140	-0.066	**0.346**	0.061	0.402	0.612
Temp	0.037	0.065	0.061	**0.391**	-0.115	-0.014
SC	-0.143	-0.052	0.402	-0.115	**0.395**	0.516
WT	-0.073	-0.105	0.612	-0.014	0.516	**0.429**

Transformed tick counts (Tick), Coat score (Coat), Condition score (Cond), Rectal temperature (Temp), Scrotal circumference (SC) and Weight (WT).

The average percentage of *Bos indicus* ancestry (Table 1) of the population was low (24.48, ranging from 5.02 to 60.45, with only 47 animals > 35.0), confirming the suggestive conclusion from the PCA analyses (Figure 1) of little influence of Brahman cattle within this herd. The effect of Indicus percentage was significant only for Tick (-0.053 ± 0.010; p-value < 0.0001) and Coat (-0.024 ± 0.005; p-value < 0.0001). Both trait values were negatively affected by Indicus percentage, supporting the common knowledge that higher the Indicus content is, the lower is the tick load and the shorter the coat length. We confirm the effect on Coat, but could not detect the previously observed effect of Indicus on Temp, Cond and WT (Porto-Neto et al., 2014). This could perhaps be explained by the much lower Brahman influence within the tested herd, and the additional complexity in dealing with different breed compositions and levels of crossbreeding. An alternative model where the Indicus covariate was nested within breed type resulted in the main effect of breed becoming non-significant except for WT (p-value < 0.05). In addition to the already observed significant effect of Indicus for Tick and Coat, this alternative model estimated significant Indicus effect for some breeds in SC and WT.

The moderate to high heritabilities of all six traits measured in this herd clearly advocate for a genetic approach to tropical beef productivity. The need for Bos Indicus-derived adaptation genes is particularly evident for the tick count and coat length traits, confirming the rationale for using Brahman cattle for their tick resistance and heat tolerance traits in Australian beef breeding. More detailed genomics studies may be able to identify the exact alleles which confer the Bos indicus-derived tick resistance and heat tolerance traits in breeding programs. This will enable the maintenance of tropically adapted *Bos taurus* beef breeds with minimal Brahman influence.

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