GENOMIC CHARACTERIZATION OF TWO SOUTH AFRICAN BEEF COMPOSITE BREEDS IN COMPARISON TO THEIR BASE BREEDS

P. Sithole[1]*, E. van Marle-Köster[1] & S.F. Lashmar[1,2]

[1] Department of Animal Sciences, University of Pretoria, Pretoria, South Africa
[2] Agricultural Research Council-Animal Production, Irene 0062, South Africa
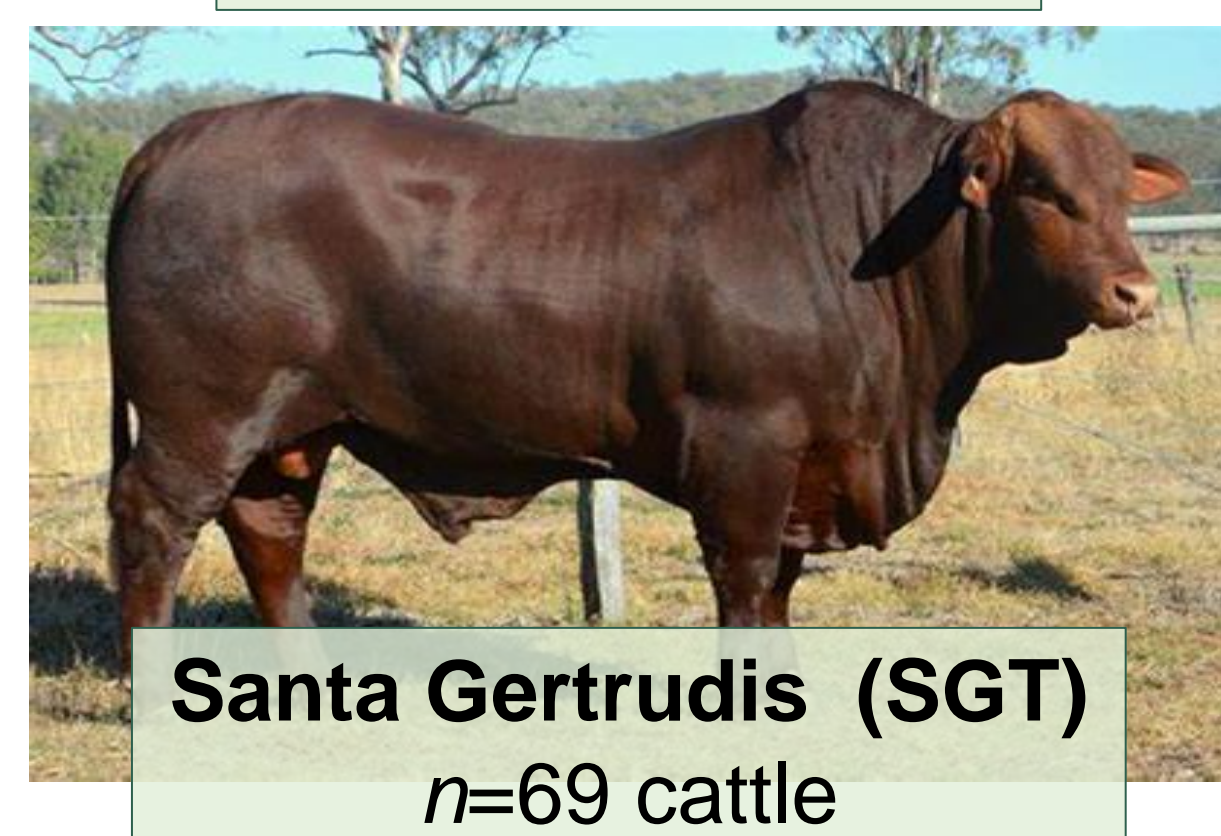* Corresponding author: u21771970@tuks.co.za

INTRODUCTION

❑ **Climate change** poses a significant threat to South African (SA), and global, beef production

❑ The SA beef industry is host to several composite breeds that have **combined adaptive and productive traits**

❑ Because of the Beef Genomics Programme (**BGP**), single nucleotide polymorphism (**SNP**) based genomic data has improved for many beef breeds
→ However, genomic research has focused on the numerically largest and most popular composites (e.g., SA Bonsmara)

❑ Genomic characterization will prove beneficial for breed **conservation, management, and improvement** of composites in the future
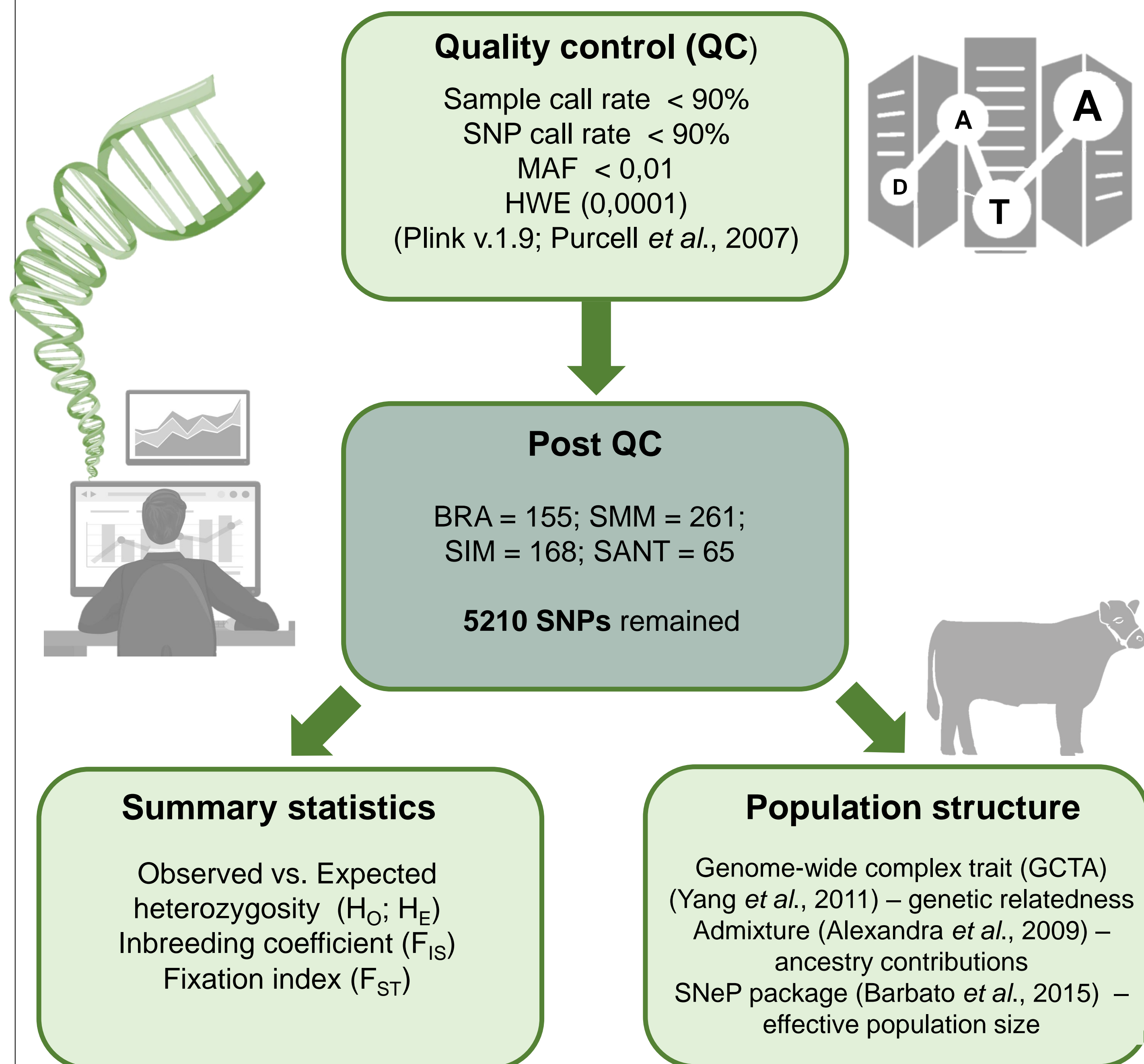
OBJECTIVE

❑ The objective of the study was to utilize genotypic data to characterize the **genetic status** of two SA composite beef breeds in comparison to their base breeds

MATERIALS

Brahman (BRA)
n=182 cattle

Simbra (SIM)
n=172 cattle

Simmentaler (SMM)
n=261 cattle

Santa Gertrudis (SGT)
n=69 cattle

❑ **684 cattle** genotyped
❑ Illumina® Bovine **7K** genotyping panel

METHODS

Quality control (QC)

Sample call rate < 90%
SNP call rate < 90%
MAF < 0,01
HWE (0,0001)
(Plink v.1.9; Purcell *et al.*, 2007)

↓

Post QC

BRA = 155; SMM = 261;
SIM = 168; SANT = 65

5210 SNPs remained

Summary statistics

Observed vs. Expected heterozygosity (H_O; H_E)
Inbreeding coefficient (F_{IS})
Fixation index (F_{ST})

Population structure

Genome-wide complex trait (GCTA)
(Yang *et al.*, 2011) – genetic relatedness
Admixture (Alexandra *et al.*, 2009) – ancestry contributions
SNeP package (Barbato *et al.*, 2015) – effective population size

RESULTS & DISCUSSION

Table 1. Measures of within genetic diversity parameters per population

Population	Average MAF	Average H_E	Average H_O	Average F_{IS}
Brahman	0.182	0.325	0.319	**0.018**
Simmentaler	0.307	0.406	0.408	-0.002
Simbra	**0.332**	0.426	**0.432**	-0.013
Santa Gertrudis	0.322	0.422	0.426	-0.009

❑ The Simbra population displayed the highest levels of genetic diversity, and this may be attributed to its composite nature, a result of the **heterosis effect**
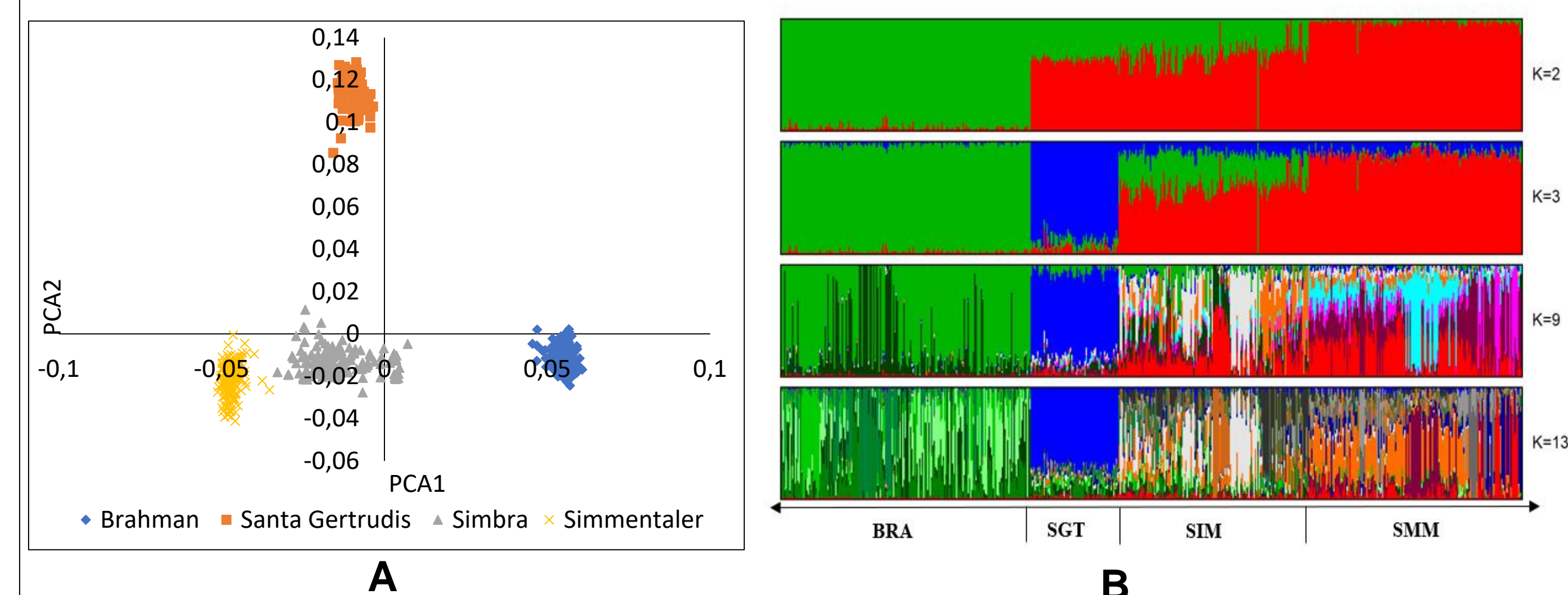
Fig 1. Genetic structure of SA composite breeds and their base breeds, according to principal component analysis (A), and model-based clustering (B)

❑ The Santa Gertrudis appeared as a distinct cluster and from K = 3 to K = 13 it remained **genetically pure**, and this can be attributed to its **unique development** as it did not originate from the SA Brahman breeds

❑ The Simbra breed indicated **subpopulations** when 13 ancestral populations where incorporated (K = 13)
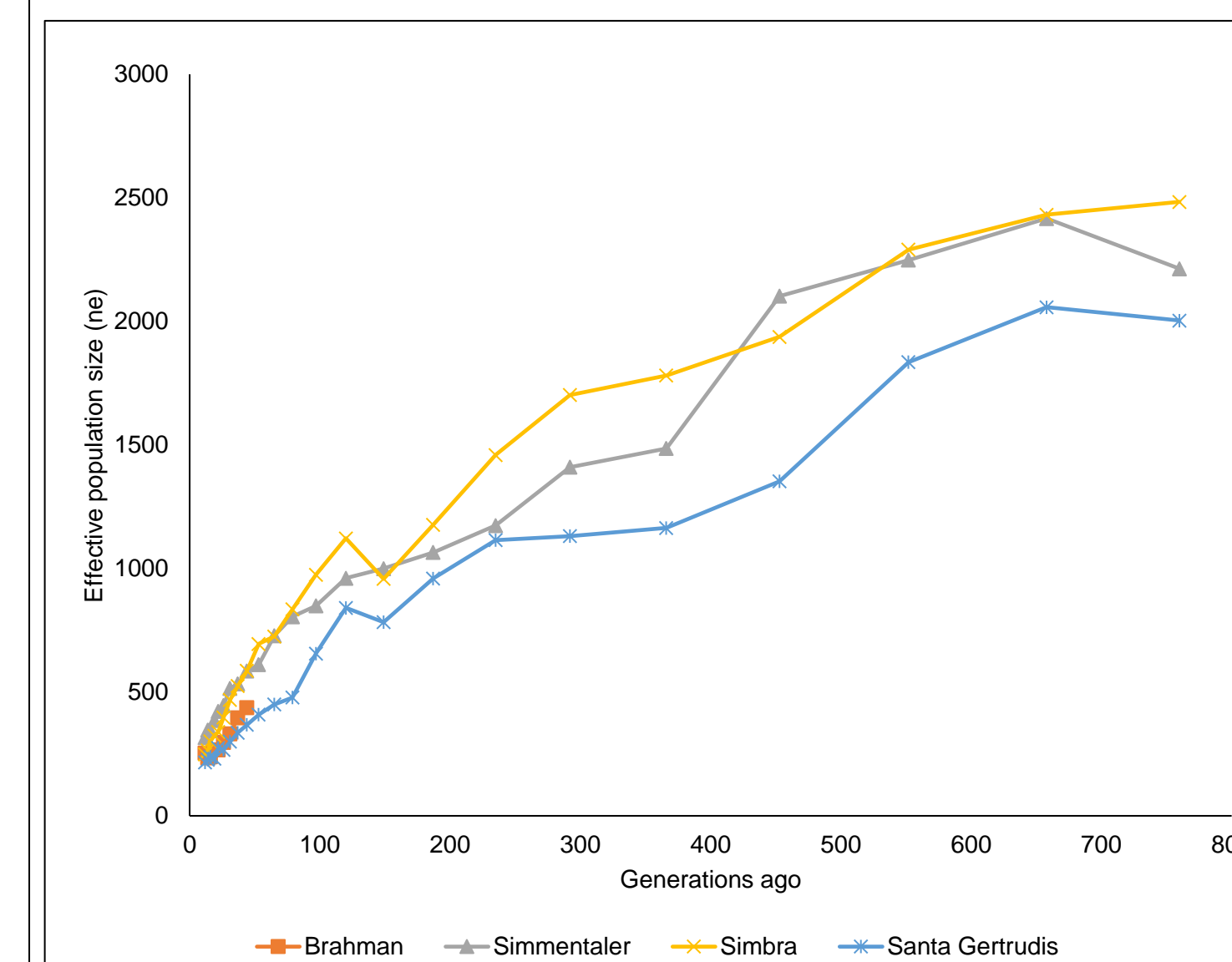
Fig 2. Trends in effective population size over time

❑ There has been a gradual decline in Ne for all populations over the past 800 generations until the recent 12 generations

❑ Expected to be smaller at recent years due to directional **selection**

CONCLUSION

❑ Composite breeds revealed a high genetic diversity - potential for sustainable beef production in both commercial and non-commercial beef production systems

❑ Genomic data for a larger sample size and higher-density SNPs (e.g., whole-genome sequencing) are required for higher-resolution and unbiased comparison

REFERENCES

- Alexander, D.H., Novembre, J. & Lange, K., 2009. Fast model-based estimation of ancestry in unrelated individuals. Genome research, 19(9), 1655-1664

- Barbato, M., Orozco-terWengel, P., Tapio, M. & Bruford, M.W., 2015. SNeP: a tool to estimate trends in recent effective population size trajectories using genome-wide SNP data. Frontiers in genetics, 6, 109.

- Purcell, S., Neale, B., Todd-Brown, K., Thomas, L., Ferreira, M.A., Bender, D., Maller, J., Sklar, P., De Bakker, P.I., Daly, M.J. & Sham, P.C., 2007. PLINK: a tool set for whole-genome association and population-based linkage analyses. The American journal of human genetics, 81(3), 559-575.

- Yang, J., Lee, S.H., Goddard, M.E. & Visscher, P.M., 2011. GCTA: a tool for genome-wide complex trait analysis. The American Journal of Human Genetics, 88(1), 76-82.