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ASSESSING THE GENETIC DIVERSITY OF AUSTRALIAN GOATS

P. Alexandri[1], T. Atkinson[2], D.J. Brown[1], K. Gore[1], K. Smith[3], S.F. Walkom[1] and T. Granleese[3]

[1] Animal Genetics Breeding Unit[*], University of New England, Armidale, NSW, 2351
Australia
[2] NSW Department of Primary Industries and Regional Development, Dubbo, NSW, 2830
Australia
[3] Western Local Land Services, Dubbo, NSW, 2830 Australia
[4] NSW Department of Primary Industries and Regional Development, Grafton, NSW, 2460
Australia

SUMMARY

Assessing genetic diversity and population structure of Australian goats is the first step towards establishing a genomic reference population to enable a multibreed genetic evaluation. This study explored the genetic structure of Australian goat breeds, focusing mostly on Rangeland, Boer, and Kalahari Red goats. Results revealed clear genetic distinctions between Boer, Rangeland, dairy, and fibre breeds. Rangeland goats exhibited multiple ancestries but formed distinct groups, suggesting they are a separate breed. Australian Boer goats clustered with global Boer populations, while Australian Kalahari Red goats were genetically similar to Boers, indicating little differentiation. The results highlight the genetic makeup of Australia's diverse goat population and lay the groundwork to facilitate multibreed genetic evaluations, ultimately improving breeding strategies and accelerating genetic progress across Australian goat breeds.

INTRODUCTION

Currently little is known about the genetic structure of Australian goat breeds. Goats were first brought to Australia by European settlers with the first goats arriving onboard the first fleet (January 1788). Since then, multiple introductions have been recorded. Goats adapted to the arid conditions of the Australian environment and expanded through most of the continent without human management, resulting in a population of feral goats of unknown genetic composition, commonly referred to as Rangeland goats (Kijas *et al.* 2013). The Australian Rangeland goat population plays a crucial role in supporting the country's goat meat industry, an export sector valued at $235 million annually, but the majority of goat meat is sourced from harvesting operations that collect goats in a semi-feral state. Within the Measured Goats project (Granleese *et al.* 2023), Rangeland goats along with Boer and Kalahari breeds will be used to establish a genomic reference population to assess the genetic structure and diversity of Australian meat goat breeds and estimate heterosis effects to be used for updating the KIDPLAN genetic evaluation. Therefore, this study aimed to deliver an initial characterisation of the genetic structure of Australian goat breeds, focusing on understanding their population structure, and between breed relationships.

MATERIALS AND METHODS

The Measured Goats project (Granleese *et al.* 2023) provided genotype data from 2,588 goats selected within the project and genotyped with a 70K goat specific panel (https://neogenaustralasia.com.au/ggp-goat-70k/). Genotyped animals of known breed came predominantly from Boer and Rangeland breeds but individuals from Kalahari Red, Australian

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Contender and Savanna breeds were also included. To better represent the genetic diversity of the Australian goat population, previously published genotype data from Kijas *et al.* (2013) were also included. This dataset comprises 183 genotypes from Australian Boer, Angora, Cashmere, and Rangeland goats. Additionally, the Goat ADAPTmap Project (Stella *et al.* 2018) provided genotypes from a broad range of goat breeds worldwide, enabling the study of goat diversity on a global scale. The original ADAPTmap dataset includes 4,653 animals from 169 populations across 35 countries, spanning Europe, West Asia, North America, South America, and Oceania (Colli *et al.* 2018). Initial analysis showed only distant relationships between a big number of international goat breeds and the Australian goat population. Therefore, for the purpose of this study, only genotypes from breeds present in Australia were considered.

To merge genotypes, SNP profiles from each of the above data sets were mapped to the latest goat genome assembly (ARS1.2, Brickhart *et al.* 2017). This step was crucial, given some of the data came from the first version of the Illumina goat 50K SNP chip (Tosser-Klopp *et al.* 2014).

Table 1. Number of unrelated individual goat genotypes (N) available after quality control per breed and country or continent. Study indicates previously published genotypes or data generated within this study

Breed	N	Country / Continent	Source of genotype data
Anglo Nubian	4	Australia	Measured Goats Project
Australian Brown	2	Australia	
Boer	14	Australia	
British Alpine	5	Australia	
Contender	13	Australia	
Kalahari Red	4	Australia	
Pygmy	2	Australia	
Rangeland	334	Australia	
Savanna Goats	4	Australia	
Boer	2	USA	
Alpine	87	Europe	Colli *et al.* (2018)
Boer	5	Australia	
Boer	84	Worldwide	
Cashmere	7	Australia	
Nubian	41	Worldwide	
Rangeland	33	Australia	
Saanen	81	Worldwide	
Toggenburg	13	Africa	
Angora	3	Australia	Kijas *et al.* (2013)
Boer	5	Australia	
Cashmere	3	Australia	
Cashmere	2	New Zealand	
Rangeland	6	Australia	
Total	754		

Genotype quality control was applied to exclude SNPs on sex chromosomes and unmapped locations, SNPs with minor allele frequency (MAF) lower than 0.05 and a genotyping rate lower than 90%. Individuals with more than 10% missing SNPs were also excluded.

To avoid bias in the analysis due to closely related animals, individual genotypes were selected within breed to maximise genetic distance. A genomic relationship matrix using all available genotypes was constructed based on the approach described by Yang *et al.* (2011) and only individuals with an average genomic relationship below 0.2 were retained for the analysis.

The genetic distance between individuals of different breeds was estimated using the VCF2Dis software (https://github.com/BGI-shenzhen/VCF2Dis). The results were used to construct a Neighbor-Joining (NJ) phylogenetic tree with FastMe2.0 (Lefort *et al.* 2015), which was visualised using the iTOL program (Letunic and Bork 2024).

RESULTS AND DISCUSSION

The final genotypes dataset after quality control and genomic relationship filtering included 754 unrelated individuals from 16 breeds (Table1) genotyped in 27,876 SNPs. Number of animals, breed, country and data origin are detailed in Table 1.

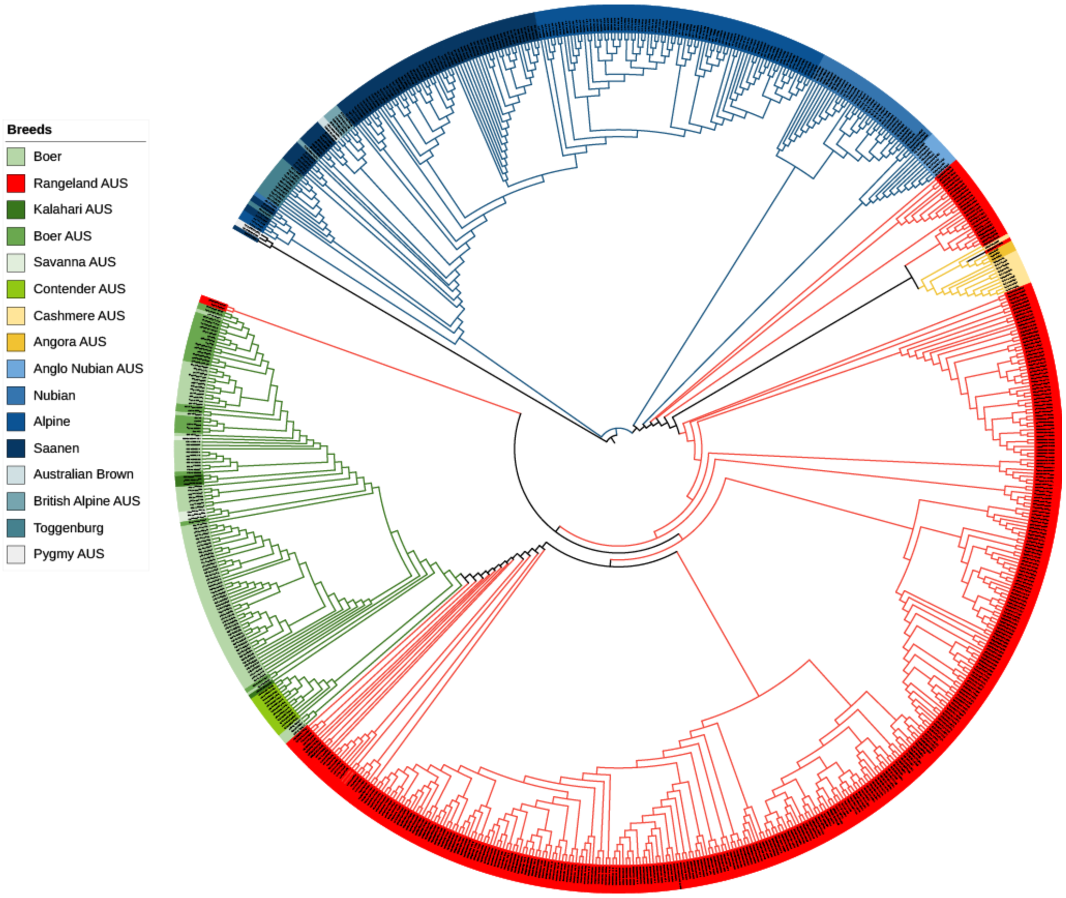

Figure 1. Phylogenetic relationships between breeds presented on Table 1 using 27,876 SNPs

Phylogenetic analysis showed the relationship between each breed as well as between individuals within each breed. The 754 individuals were grouped into 17 branches representing different breeds and within breed populations (Figure 1). The main branches included Boer, Rangeland, Australian fibre breeds (Angora and Cashmere) and Australian and worldwide dairy breeds indicating a clear genetic division existing between Boer, fibre and dairy breeds as well as some Rangeland populations. A closer look within the Rangeland individuals reveals several well defined groups. These groups indicate the existence of a separate Rangeland breed but also the diverse origin of the Rangeland goat population as several individuals appear to cluster closer to Boer, fibre or dairy groups respectively. Australian Boer goats belong to the well defined Boer group which includes worldwide Boer population but also populations with Boer ancestry such as Australian Contender and Australian Savanna goats. The Kalahari Red individuals clustered within the Boer branch but not in separate and defined groups indicating little to no differentiation between Australian Boer and Kalahari populations. More analysis is under way to describe the genetic structure of the Australian goat population better using admixture approaches. This analysis will also produce allele frequencies to define the breed composition for genotyped individuals of unknown breed.

Currently, only a small number of goats are performance recorded annually (predominantly Boer, Granleese *et al.* 2023), with KIDPLAN breeding values calculated by Sheep Genetics (Meat & Livestock Australia). Expanding the scope of genetic recording to include a broader range of goats and more detailed performance data is critical to advancing the Australian goat industry. Estimating the genetic diversity and breed structure of Australian goats is the first step towards a genomic reference population that will facilitate the development of a multibreed genetic evaluation, fostering genetic improvement across various breeds.

CONCLUSION

First results towards establishing an Australian goat reference population have highlighted the genetic differentiation existing between Australian Boer, Rangeland, dairy and fibre goats. Despite their potential multiple ancestries, Rangeland goats appear to be a separate breed clearly distinct from other populations. Australian based Kalahari Red goats are genetically similar to Boer goats, indicating they can be treated as the same breed. Ongoing studies aim to refine genetic structure and breed composition, aiming to enhance genetic evaluations and breeding strategies.

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