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Applying genomic information for conservation and utilisation of the indigenous Tswana goat of Botswana

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Introduction

The indigenous Tswana constitutes 71% of the Botswana goat population (Botswana statistics, 2013). It is well adapted to the harsh conditions of the country such as poor nutrition, frequent droughts, high heat, diseases and parasites (Nsoso *et al*., 2004). These goats are mostly kept by rural farmers in the communal areas under traditional management systems and contribute significantly to food security, socio-economic and cultural needs. Due to their large numbers, they are a source of foundational stock for breed improvement programs in the country. However, there is a danger that indiscriminate crossbreeding and replacement with exotic breeds may result in the loss of the Tswana as a unique indigenous genetic resource in Botswana.

Genomic information of indigenous breeds contributes to designing effective strategies for improving productivity, breed development and conservation programs. It also provides an insight into population structure and relationships between breeds (Kim *et al*., 2016). Most studies on indigenous goats to date have been performed using microsatellite markers including, Tswana goats (Maletsanake *et al*., 2013), South African goats (Pieters *et al*., 2009) and indigenous types of sub-Saharan Africa (Chenyambuga *et al*., 2004). More recently Lashmar *et al*. (2016) and Mdladla *et al.* (2016) have used the Goat50K SNP array to characterise different indigenous South African goat breeds.

In Botswana, no molecular-based research on SNPs has been performed to genetically characterize the indigenous goats. This study aims to evaluate the genetic diversity and population structure of indigenous Tswana goat in the Central region of Botswana using the Illumina Goat50K SNP chip.

Material and methods

Samples and genotyping

Ethical approval for sampling was received from the Ethics Committee at the University of Pretoria (ECO42-15). Hair samples were collected from 48 unrelated Tswana goats from communal farmers in the Central region of Botswana. The hair samples were shipped to Labogena DNA platform in France for DNA extraction and genotyping with the Illumina Goat50K SNP Bead chip.

Data analysis

Plink version 1.07 software (Purcell *et al*., 2007) was used for analysis. Quality control was performed and SNP which did not adhere to the following thresholds were discarded: individual call rate ≤ 0.97, SNP call rate ≤ 0.97, MAF ≤ 0.05 and SNPs that deviated significantly from Hardy-Weinberg Equilibrium (HWE) ($P<0.001$). The observed and expected heterozygosity values and average inbreeding coefficient (F_{IS}) were calculated using Plink software (Purcell *et al*., 2007). Pairwise linkage disequilibrium was assessed through the correlation coefficient (r^2) and 23789 SNPs exceeded the correlation coefficient (r^2) threshold of 0.2 in a window of 50 SNP, while a set of 25239 SNPs remained for downstream analyses. Effective population (Ne) size was calculated using SNep version 1.1 (Barbato *et al*., 2015).

Results and Discussion

The average call rate across 48 samples was 99.6% and no individuals were removed for having a call rate below 97%. A total of 5203 SNP markers were removed during quality control. The average MAF across the chromosomes was 0.32±0.13.

The average observed and expected heterozygosity values of Tswana goats was 0.419±0.02 and 0.423±0.03, respectively. High levels of genetic diversity have also been observed in the indigenous Barki goats of Egypt (Kim *et al*., 2016) and South African ecotypes (Mdladla *et al*., 2016). Indigenous goats kept under communal management systems are subjected to natural selection, and are generally adapted to their natural environments, while maintaining high within and between population genetic variability (Kim *et al*., 2016).

The average inbreeding coefficient (F_{IS}) of 0.009±0.05 was lower than the 0.12±0.16 previously reported by Moletsanake *et al*. (2013) using microsatellite markers on the Tswana goat population kept at the experimental farm. In communal grazing systems with limited or no fencing, no controlled breeding seasons are enforced with limited control over the use of bucks.

Linkage disequilibrium (LD) declined with an increasing distance between SNP pairs, and the most rapid decline was seen over the first 10kb (Figure 1). The pattern of LD decay with distance is consistent with the report of Visser *et al*. (2016) on Angora breeds. The low level of LD at large distance ranges indicates that the studied population have not been under intense selection or have had large effective population size in the recent past. The persistence of LD over short distances however, indicates that SNP chips of higher density will be needed to obtain sufficient statistical power to apply genome-wide association studies or genomic selection (Lashmar *et al*., 2016).

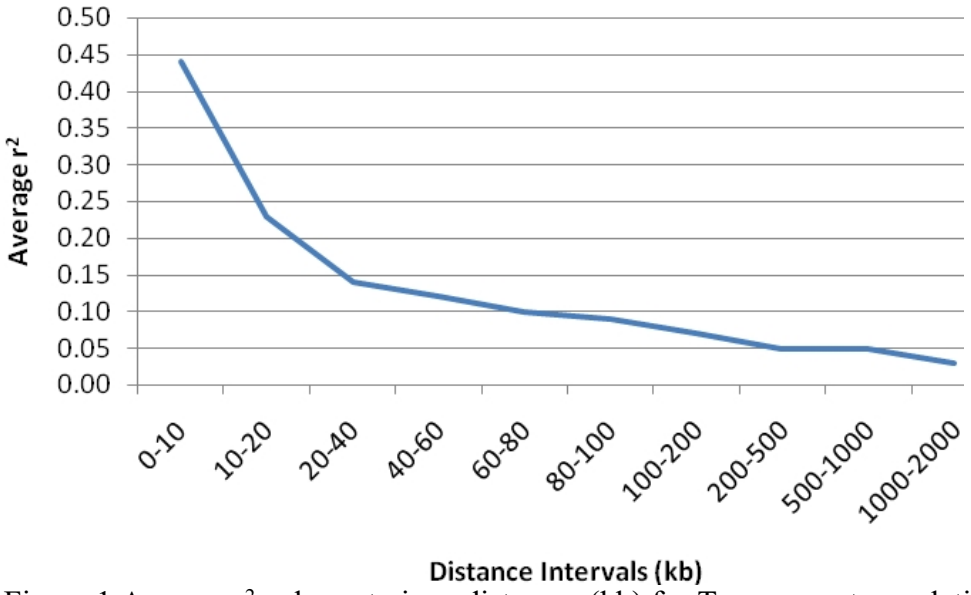

Figure 1 Average r^2 values at given distances (kb) for Tswana goat population

Ne showed a progressive decrease from 900 to 50 generations ago with an estimated size of 1700 animals in the past 50 generations (Figure 2). The large effective population size confirms that the studied population has not been exposed to directional selection or a coordinated mating system.

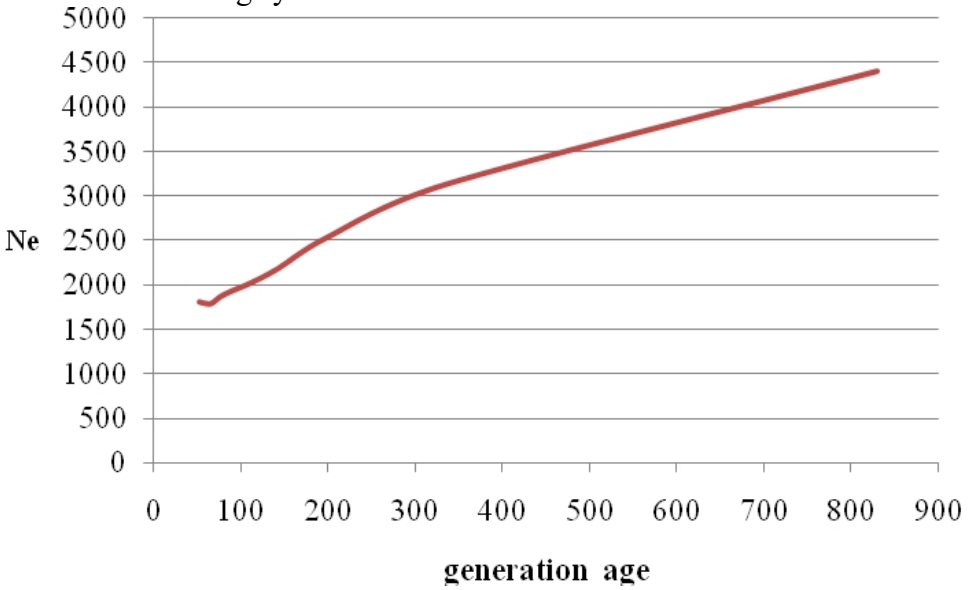

Figure 2 Effective population size (Ne) from 900 to 50 generations ago for the indigenous Tswana goats

Conclusions

The indigenous Tswana goat exhibits a relatively high level of genetic diversity, and a large effective population size. This is the first genomic data available for the Tswana goat and can be used as a bench mark for further investigation. Genetic diversity is an essential component for population survival, genetic improvement and adaptation to changing environments. It is therefore important to maintain this genetic diversity to ensure optimal utilization of Tswana goat for sustainable production and contribution to the food security in

Botswana.

List of References

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

Botswana, S., 2015. Annual agricultural survey report of 2013. Gaborone, Botswana. www.statsbots.org.bw.

Chenyambuga, S.W., O. Hanotte, J. Hirbo, P.C. Watts, S.J. Kemp, G.C Kifaro., P.S. Gwakisa, P.H. Petersen & J.E.O. Rege, 2004. Genetic characterisation of indigenous goats of Sub-saharan Africa using microsatellite DNA markers. Asian-Aust.J.Anim.Sci. 17(4): 445-452

Kim, E.S., A.R. Elbeltagy, A.M. Aboul-Naga, B. Rischkowsky, B Sayre, J.M. Mwacharo & M.F Rothschild, 2016. Multiple genomic signatures of selection in goats and sheep indigenous to a hot arid environment. Hered. 116(3):255-264.

Lashmar S.F., C. Visser & E. van Marle-Köster, 2016. SNP-based genetic diversity of South African commercial dairy and fiber goat breeds. Small Rumin. Res.136:65-71.

Maletsanake, D., S.J. Nsoso & P.M Kgwatalala, 2013. Genetic variation from 12 microsatellite makers in an indigenous Tswana goat flocks in South-eastern Botswana. *Livest. Res. Rural. Dev. 25(2): 21.* -

Mdladla, K., E.F Dzomba, H.J Huson & F.C. Muchadeyi, 2016. Population genomic structure and linkage disequilibrium analysis of South African goat breeds using genome wide SNP data. Anim. Genet. 47(4): 471-482.

Nsoso, S.J., B. Podisi, E. Otsogile, B.S Mokhutshwane & B. Ahmadu, 2004. Phenotypic characterization of indigenous Tswana goats and sheep breeds in Botswana: Continuous traits. Trop. Anim. Health. Prod. 36(8):789-800.

Pieters A., E. van Marle-Köster, C. Visser & A. Kotze, 2009. South African developed meat type goats: A forgotten animal genetic resource? Anim. Gen. Res. Info. 44:33-43.

Purcell S., B. Neale, K. Todd-Brown, L. Thomas, Ferreira MAR, D. Bender, J. Maller, P. Sklar, P.I. De Bakker, M.J. Daly & P.C. Sham, 2007. PLINK: a tool set for whole-genome association and population-based linkage analyses. Am. J. Hum. Genet. 81: 559–575.

Visser, C., S.F. Lashmar, E. Van Marle-Köster, M.A Poli, & D. Allain, 2016. Genetic diversity and population structure in South African, French and Argentinian Angora Goats from genome-wide SNP data. PloS one, 11(5).