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Assessing inbreeding levels in two pilot community-based breeding program sites with common breeding objectives in South Africa

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Introduction

Inbreeding in communally kept herds of indigenous goats compromises the genetic variation, fitness, and adaptability of these populations (Nandolo *et al.*, 2019). Community-based breeding programs (CBBP) are a low-cost approach to improve the output potential of indigenous livestock populations under communal production systems, whilst prioritizing farmer participation in the definition of breeding objectives (Haile *et al.*, 2020). CBBP were implemented in two sites to address the production and breeding challenges for an improved system. These communities keep indigenous goats with the goal of breeding fast-growing, white coat colour goats with a large body frame. When initiating a CBBP, it is recommended to assess the level of inbreeding, genomic haplotype sharing and the degree of relatedness among the breeding stock, to avoid the mating of closely related individuals and the loss of genetic diversity which may impede genetic progress (Ofori and Hagan, 2020). Therefore, the aim of this study was to assess the inbreeding levels as a potential constraint on genetic progress and herd productivity in the two pilot sites of uMkhanyakude District in KwaZulu-Natal and Buffalo City in Eastern Cape, South Africa.

Materials & Methods

Research permit, Section 20 of the Animal Diseases Act No. 35 of 1984 (Reference: 12/11/1/1(a) (6336BM) was granted by the Department of Agriculture, South Africa. Ethics clearance was obtained from the Onderstepoort Veterinary Institute Animal Ethics, Agricultural Research Council (Reference: AE22.15) and the Animal Research Ethics Committee, Tshwane University of Technology (Reference: AREC2024/08/002). A total of 3545 animals were tagged and recorded in the CBBP. The average herd size was 15.8 ±17.5 in Buffalo City and 19.7 ±18.6 in uMkhanyakude.

A subset of 212 goat hair samples were randomly collected from 195 participating herds and genotyped using the Illumina 65K Goat SNP BeadChip (IGGC) at the Agricultural Research Council, Biotechnology Platform. Quality control (--geno 0.1, --mind 0.1, --maf 0.05 and linkage disequilibrium pruning using –indep-pairwise with a window size of 50 SNPs, a step size of 5 SNPs and an r^2 threshold of 0.2) was done using PLINK v1.9 resulting in 54,820 independent variants and 206 samples for downstream analyses.

Inbreeding coefficient (F_{IS}) and their standard deviations were determined using Plink v1.9. Runs of homozygosity (ROH) and genomic inbreeding F_{ROH} were calculated using the detectRUNS package in R v4.4.0. ROH hotspots were determined using the *snpInRUNS* function of the detectRUNS package and the genes overlapping with the top 1% most frequently occurring SNPs were annotated using Biomart Ensembl. An analysis of haplotype sharing was performed with Refined IBD using Beagle v4.0 with default conditions (window=40.0, lod=3.0, length=1.5, trim=0.15, scale=0). Genomic clustering was performed using the R package LEA. The optimal number of ancestral clusters was determined by selecting the K-value that minimized the cross-entropy loss. Results were visualised using

ggplot2. Reference genotypes from Savanna (n=20) selected for white colour, Kalahari Red (n=20) selected for uniform red colour, Boer (n=20) selected for white body and brown head, and Indigenous Veld Goat ecotypes, including Nguni (n=20), Cape Speckled (n=20), and Cape Lobear (n=20) from the Agricultural Research Council, Biotechnology Platform database, were added to the dataset for cluster analysis.

Results

Inbreeding coefficients (F_{IS}) in Buffalo City and uMkhanyakude were 0.21 ±0.03 and 0.29 ±0.02 respectively, and the genomic inbreeding coefficients based on ROH (F_{ROH}) were 0.08 ±0.04 and 0.14 ±0.02 (Table 1).

Table 1. Mean ± SD observed and expected heterozygosity, F_{ROH} and F_{IS} in Buffalo City and uMkhanyakude districts.

District	HO	HE	F_{IS}	F_{ROH}
Buffalo City	0.39 ± 0.02	0.50 ± 0.00	0.21 ±0 .03	0.08 ± 0.04
uMkhanyakude	0.36 ± 0.01	0.50 ± 0.00	0.29 ± 0.02	0.14 ± 0.02

Table 2 shows the average lengths of the ROH within the standard ROH bin sizes. The 1-2Mb range had the highest % of ROH, Buffalo City (55.5%) and uMkhanyakude (61.0%) the average ROH sizes were 1.35 in both populations. The genomic inbreeding coefficient was highest in the 4-8Mb length class across both regions (F_{ROH} = 0.002).

Table 2. Average lengths of the ROH within the standard ROH length class as well as the F_{ROH} per ROH length class.

	Buffalo City		uMkhanyakude	
Class	Average Length	% ROH	Average Length	% ROH
0-1Mb	0.87	23.45	0.88	24.0
1-2Mb	1.35	55.5	1.35	61.0
2-4Mb	2.64	14.87	2.56	13.0
4-8Mb	5.43	3.9	5.08	1.0
>8Mb	17.28	2.28	15.59	1.0

ROH hotspots that were in the top 1% most frequently occurring ROH segments (Fig. 2) overlapped with 998 genes, of which 654 had known functions. Some of the overlapping genes found in the uMkhanyakude population included *melanocortin 2 receptor (MC2R)* and *melanocortin 5 receptor (MC5R)* located on chromosome 24, which are involved in melanogenesis.

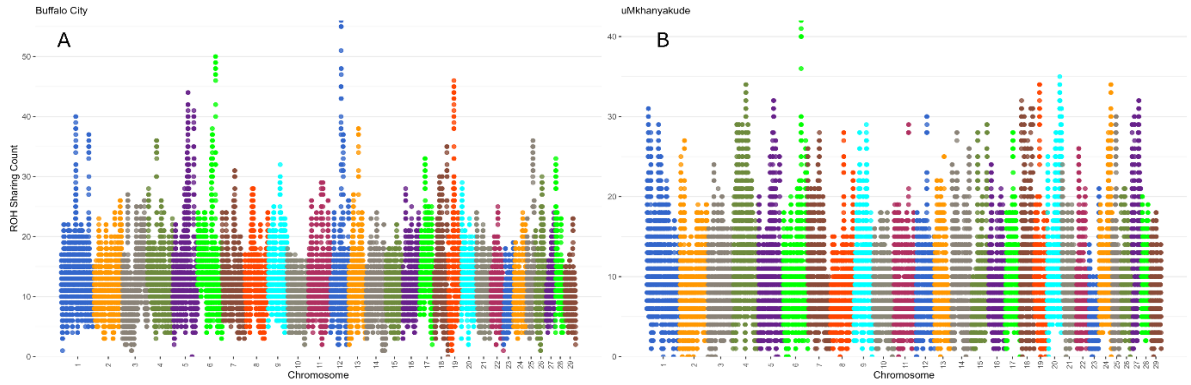

Figure 2. Manhattan plots of the ROH hotspots in Buffalo City (A) and uMkhanyakude (B). Each point represents an SNP, and colours are alternated between chromosomes. Peaks indicate genomic regions with a high frequency of ROH among individuals.

The average length of IBD segments was 11.33 ± 11.16cM in Buffalo City and 8.05 ± 6.46cM in uMkhanyakude, indicating a higher degree of haplotype sharing in Buffalo City herds (Table 3). The observed IBD segments ranged from 3cM to 99.03cM in Buffalo City and 3cM to 77.69cM in uMkhanyakude, suggesting the presence of both distant and recent shared ancestry among goats within each region. The number of IBD segments was higher in Buffalo City (31.1 ±31.5) than in uMkhanyakude (22.8 ±12.7).

Table 3. Mean ± SD IBD sharing within each district.

District	Segment Length	Number of Segments
Buffalo	11.33 ± 11.16	31.1 ± 31.5
uMkhanyakude	8.05 ± 6.46	22.8 ± 12.7

The optimum number of ancestral clusters was K = 4 (cross entropy = 0.82) and the seven populations fell into four unique clusters (Fig. 3). The Buffalo City goats clustered together with the Xhosa Lobear goats in Cluster 2. The uMkhanyakude goats fell into cluster 4 with the Nguni reference goats.

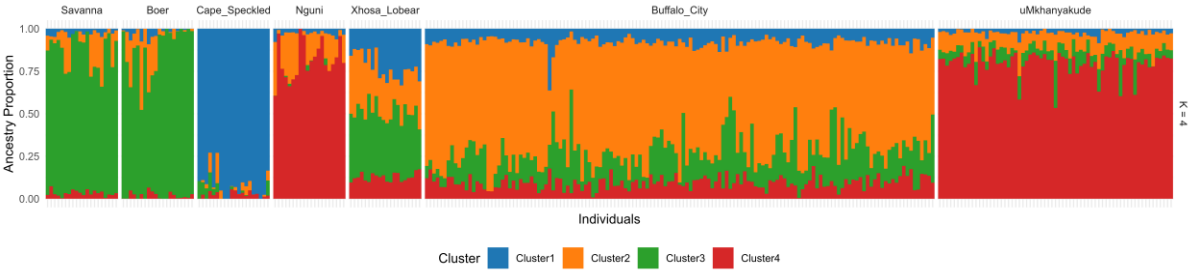

Figure 3. Genomic clustering of study populations and reference breeds, including the Boer, Savanna and Xhosa Lobear, Nguni and Cape Speckled Indigenous Veld Goat ecotypes.

Discussion

The breeding objectives and traits of interests of the participating farmers were fast-growth, large-frame and white coat colour. Localised cultural purposes drive the market demand and highlight the potential for improvement in these sites. This study establishes the impact of preferential selection and if the trait of interests is selected with the current breeding structure. Southern African farmers contribute to high proportions of recent inbreeding with the preference of the white coat colour within their herds (Nandolo *et al.*, 2019, Nguluma *et al.*, 2020). In addition, the ratio of males to females in the participating herds was 1 to 11

(Segakoeng *et al.*, 2026), and bucks are often kept in mating herds for over 3 years. Participants also castrate young males without performance records using coat colour as a selection preference. These circumstances may contribute to high levels of recent inbreeding which have been reported to negatively impact birth weight (Kasap *et al.*, 2020), pre-weaning survival and early growth (Rashidi *et al.*, 2015), and reproductive performance (Sajjad Khan *et al.*, 2007). This may impede the breeding goals of fast growth if the inbreeding levels are not reduced to more acceptable levels.

The majority of ROH were in the 1-2Mb bin size in both regions indicating historic genetic bottleneck events in both regions, however the highest inbreeding levels were in the 4-8Mb although differences were minimal amongst the length classes, suggesting more recent inbreeding. These results are similar to those reported by Chalebgwa *et al.* (2025) in Tswana goats from Botswana. Among the genes found in the ROH hotspots were the *MC2R* and *MC5R* located on chromosome 24. These genes are involved in melanin production and may be under selective pressure due to preferential selection for white coat colour goats. Intense artificial selection of white goats may result in the repeated use of a few breeding bucks and inadvertently lead to hypopigmentation on vulnerable areas such as the muzzle, ears and back. This makes goats prone to sunburn and is also regarded as a defect by the Indigenous Veld Goat Breeders Society (IVG, 2025). High IBD values were observed within herds and among neighbouring herds in Buffalo City increasing the likelihood that offspring from different herds inherit identical chromosomal segments from a common ancestor (Blondeau Da Silva *et al.*, 2024). The Buffalo City goats are genetically Cape Lobear, and the uMkhanyakude herds are Nguni ecotype. This genetic characterization of animals within the CBBP adds value in niche markets and directs the design of the selection, improvement strategies of each site.

Conclusions

The farmers have a selection criterion not matched with breeding structure, castrate with no proper selection or growth performance and the uncontrolled mating in communal setting and continuous use of few breeding males across multiple herds in neighbouring villages has impact on the current structure.

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