Unravelling of Genes Associated with Coat Colour and Coat Colour Patterns in South African Meat-type Goats.

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CHAPTER ONE: SIGNATURES OF SELECTION

INTRODUCTION

- Meat-type goats contribute to their farmers food and income security, as they are breed for selling and home meat consumption (Visser and van Marle-Koster, 2018).
- Coat colour is an important production trait as it can determine the selling price of a goat, and in the commercial sector, coat colour forms part of maintained breed standards which are used to characterise the breeds and maintain their genetic resources (Mdladla et al., 2017).
- Coat colour has also been linked to goat adaptation to harsh environments, for instance, the Red coat of the Kalahari Red has been reported to contribute to the breeds higher tolerance to heat, while the white coat of the Savanna is said to protect the goats from cold weather (Ncube et al., 2020).
- The lack of knowledge about the genetic mechanisms underlying production traits such as coat colour is a contributing factor towards the lag seen in South African goat genetic improvement (Visser and van Marle-Koster, 2018).
- Therefore, there is a need for a detailed study of South African meat-type goat coat colour genes.

METHODS AND MATERIALS

Sampling

Figure 1: Goat coat colour and coat colour patterns sampled. Coat colours and patterns sampled included white (n = 67), red (n = 68), white and red head (n = 97), black (21), brown (n = 9), grey (n = 14), patched (n = 17), and belted (n = 17).

Sample Genotyping

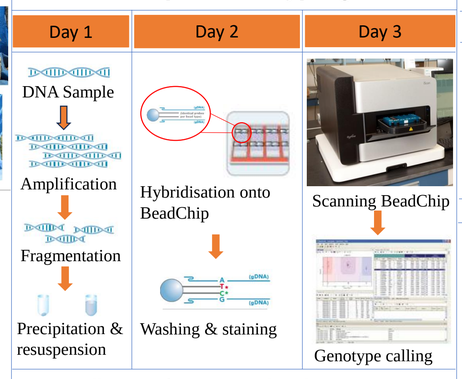

Figure 2: Illumina Infinium protocol used to genotype goat blood samples.

Data Analysis

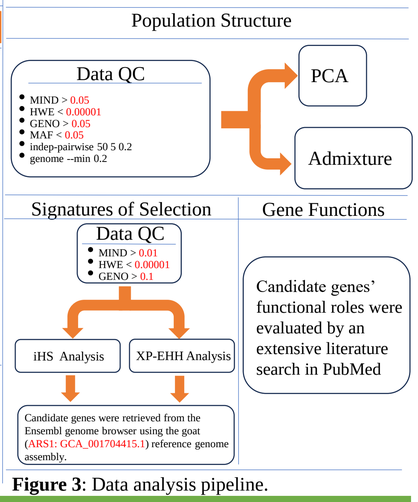

Figure 3: Data analysis pipeline.

RESULTS (PCA & ADMIXTURE)

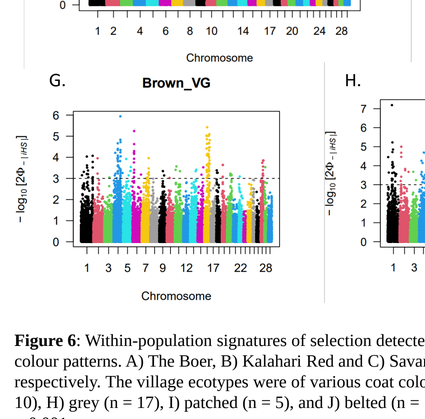

Figure 4: Principal component analysis (PCA) of the three commercial meat-type breeds and ecotype populations. Commercial meat-type goats included the Boer, Savanna, and Kalahari Red breeds. Ecotype populations included goats from Venda, Zulu, Xhosa, and Tswana villages. This analysis was carried out in the R software using the R package adegenet.

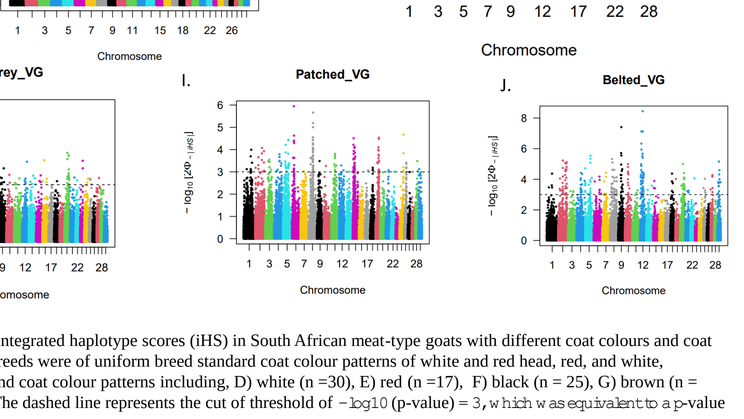

Figure 5: Admixture analysis of the three commercial meat-type breeds and ecotype populations. Admixture was plotted for A) K = 1 – 5, and B) K = 6 – 10. Commercial meat-type populations included the Boer, Kalahari Red (KR), Savanna breeds. Ecotype populations included goats from Tswana, Venda, Xhosa, and Zulu villages. The optimal K = 8 represents the most appropriate number of ancestral populations. This analysis was carried out in R using the R package LEA.

RESULTS (WITHIN–POPULATION SIGNATURES OF SELECTION)

Figure 6: Within-population signatures of selection detected by integrated haplotype scores (iHS) in South African meat-type goats with different coat colours and coat colour patterns. A) The Boer, B) Kalahari Red and C) Savanna breeds were of uniform breed standard coat colour patterns of white and red head, red, and white, respectively. The village ecotypes were of various coat colours and coat colour patterns including, D) white (n =30), E) red (n =17), F) black (n = 25), G) brown (n = 10), H) grey (n = 17), I) patched (n = 5), and J) belted (n = 17). The dashed line represents the cut of threshold of $-\log10$ (p-value) = 3, which was equivalent to a p-value = 0.001.

RESULTS (BETWEEN–POPULATION SIGNATURES OF SELECTION)

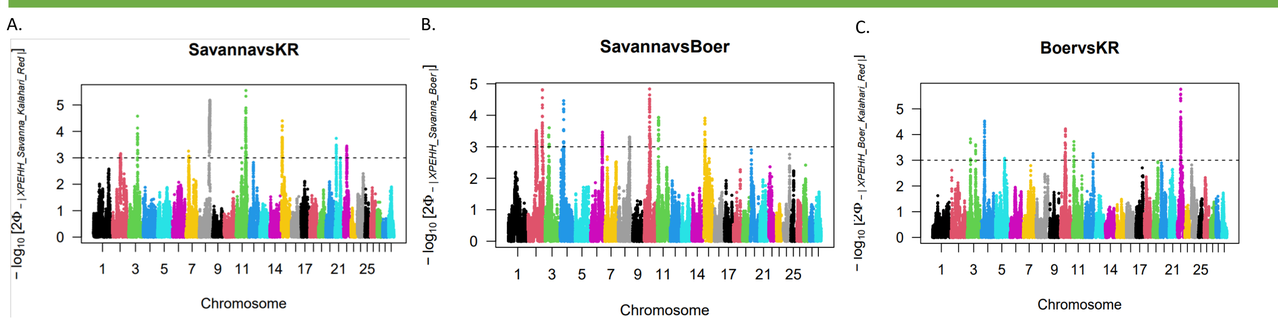

Figure 7: Signatures of selection detected using cross-population extended haplotype homozygosity (XP-EHH) tests between South African commercial meat-type goats. A) XP-EHH between the Kalahari Red and Savanna breeds. B) XP-EHH between the Savanna and Boer breeds. C) XP-EHH between the Boer and Kalahari Red breeds. The dashed line represents the cut of threshold of $-\log10$ (p-value) = 3, which was equivalent to a p-value = 0.001.

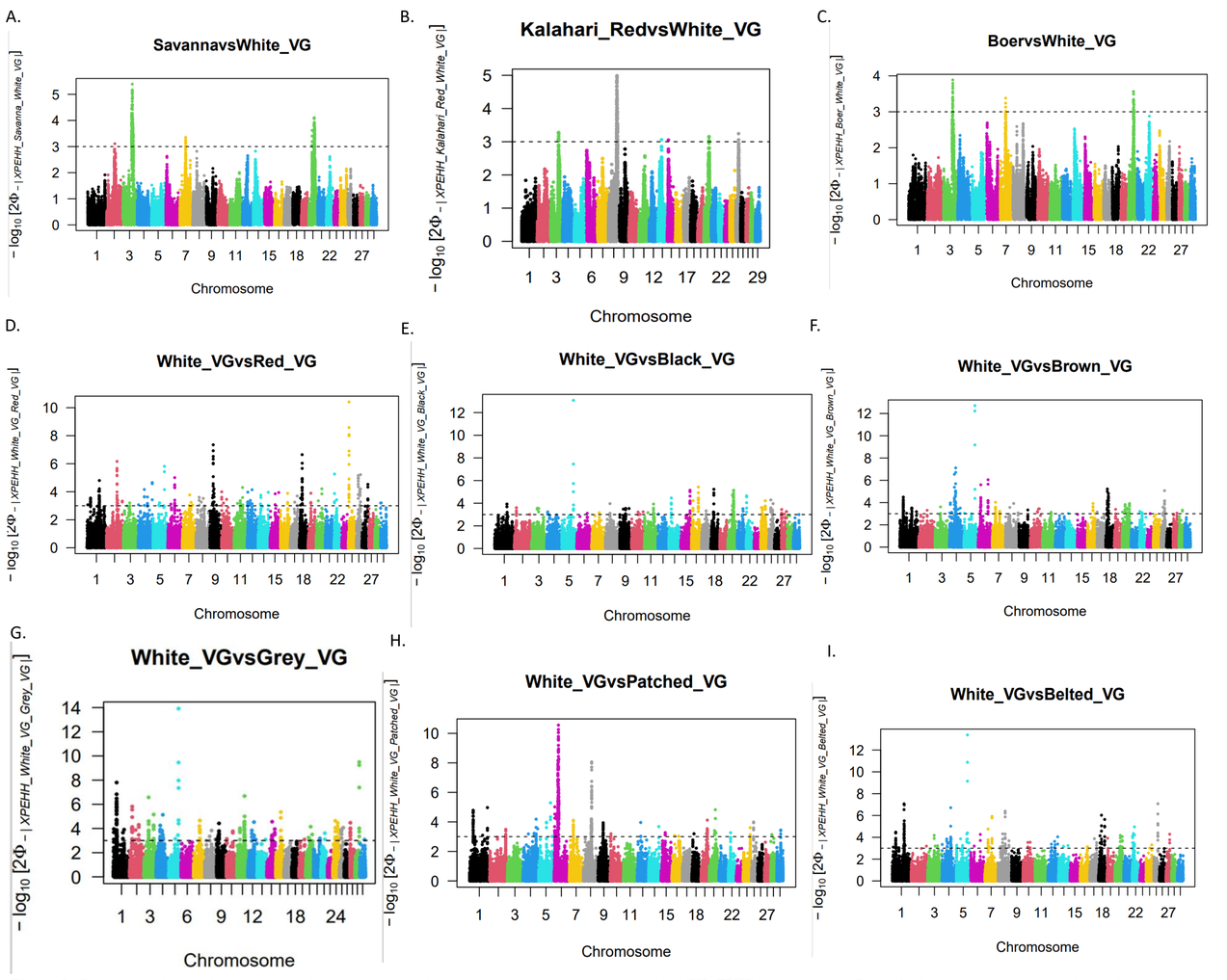

Figure 9: Signatures of selection detected using cross-population extended haplotype homozygosity (XP-EHH) tests between South African meat-type goats with white coat colour and various coat colours and coat colour patterns, including A) white of the Savanna, B) red of the Kalahari Red, C) white and red head of the Boer, D) Red, E) Black, F) Brown, G) Grey, H) Patched, and I) Belted. The dashed line represents the cut of threshold of $-\log10$ (p-value) = 3, which was equivalent to a p-value = 0.001.

DISCUSSION

Population Structure (PCA & ADMIXTURE)

- The PCA revealed separate clusters for the three commercial meat-types and the ecotypes, indicating that the commercial breeds and the village goats are genetically distinct (Mdladla et al., 2017).
- At the optimal K = 8, Admixture revealed that the three commercial meat-type breeds and the ecotypes shared similar genetic backgrounds suggesting shared ancestry, likely due to the commercial breeds' history of crossbreeding with the indigenous goats for improvement of production traits (Visser and van Marle-Koster, 2018).

Signatures of selection

- Within-population signatures of selection analysis (iHS) detected a total of 2 534 potential genes under positive selection.
- Cross-population signatures of selection analysis (XP-EHH) detected a total of 1 745 potential genes under positive selection.
- The analyses detected signatures associated with genes involved in growth, metabolism, reproduction, adaptation, and immune response.
- Several genes located on chromosomal positions previously shown to hold goat coat colour genes were also detected, for instance, the *TYRP1* gene (on chromosome 8), which has been linked to brown goat coat colour was detected in black village goats.

REFERENCES

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