Genetic diversity among Swakara sub-populations and their founders

Andiswa Njilo[1, 2], Farai C. Muchadeyi,[1] and Edgar F. Dzomba[1]

[1]Biotechnology Platform, Agricultural Research Council, Onderstepoort, South Africa

[2]Discipline of Genetics, School of Life Sciences, University of KwaZulu-Natal, Pietermartizburg, South Africa

Background

Originally derived from the Karakul breed of Uzbekistan, the Swakara is a fat-tailed breed known for its high-quality pelts. Introduced into Southern Africa in the 1900s, the Karakul was subjected to intense crossbreeding with indigenous Namaqua Afrikaner and Blackhead Persian breeds to produce the Swakara, whose pelt is superior with unique features. Selection and crossing of Karakul to indigenous white-wooled breeds resulted in a sub-vital factor in the pure white sub-population that causes the lamb to die within 48 hours of birth. With a complex ancestral background, little is known about the genomic architecture of the sub-populations, making it difficult to understand the factors contributing to the occurrence of genetic disorders. Determine the genetic structure of Swakara and its relationship with presumed founding breeds.

Figure 1. Flocks of Blackhead Persian (left) and Namaqua Afrikaner sheep (right)

Methodology

A total of 244 sheep tissue samples from 8 sub-populations sampled in Namibia, South Africa and Germany were genotyped using the OvineSNP50 beadchip at the Agricultural Research Council, Biotechnology Platform

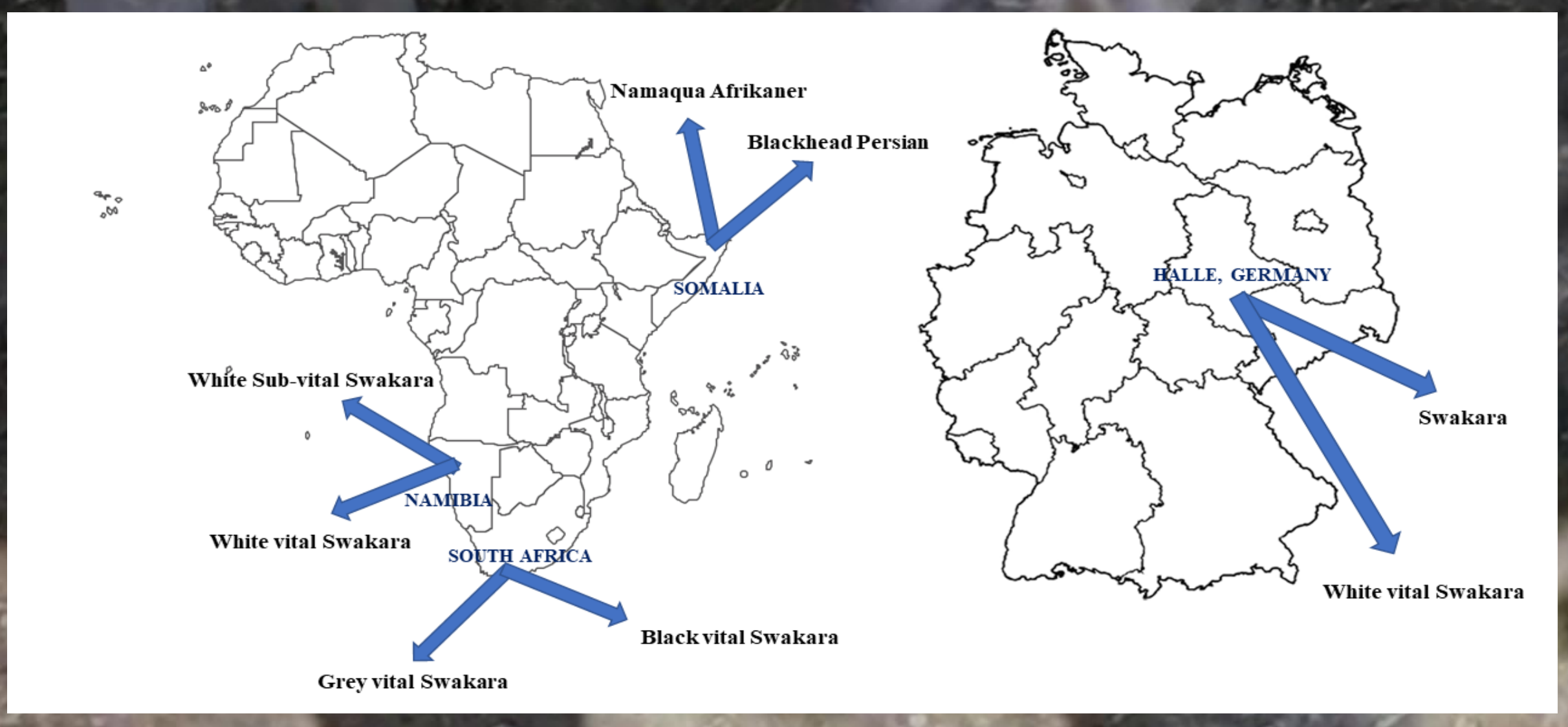

Figure 2. Geographic location and distribution of sampled sheep breeds

Results

Table 1. Genetic diversity measures for each sub-population of sheep breeds and whole population

	N	SNP %	HO	HE	F_{IS}
BHP	14	64	0.36±0.20	0.32±0.15	-0.12±0.07
BVS	50	66	0.30±0.17	0.31±0.16	0.04±0.08
BRVS	24	62	0.34±0.19	0.31±0.16	-0.11±0.09
NQA	10	70	0.30±0.18	0.35±0.14	0.13±0.10
SWA	5	64	0.41±0.22	0.36±0.12	-0.15±0.07
WSV	33	64	0.30±0.17	0.30±0.16	0.01±0.11
WVS	63	65	0.29±0.15	0.31±0.15	0.08±0.09
GVS	42	71	0.30±0.16	0.31±0.16	0.03±0.10
ALL	241	71	0.32±0.13	0.35±0.14	0.10±0.09

Genetic diversity ranged from H_O = 0.29±0.15 for the White Subvital to H_O = 0.41±0.22 for the Swakara, and the highest inbreeding was observed in the Namaqua Afrikaner (F_{IS} = 0.13±0.10) and White Vital Swakara (F_{IS} = 0.08±0.09) The principal component analysis produced five clusters with PC1 explaining 27.35% of the total variation separating cluster 2, which contained the Namaqua Afrikaner only, from clusters 1 and 3-5, to which the Black Vital, Brown Vital, Grey Vital, White Sub-vital and Swakara all belonged. PC2 accounted for 19.25% of the total variation separating cluster 1 from all the other clusters. The PCA demonstrated the effect of geographic origin with sheep breeds sampled from Germany clustering together, separating from the Southern African sheep.

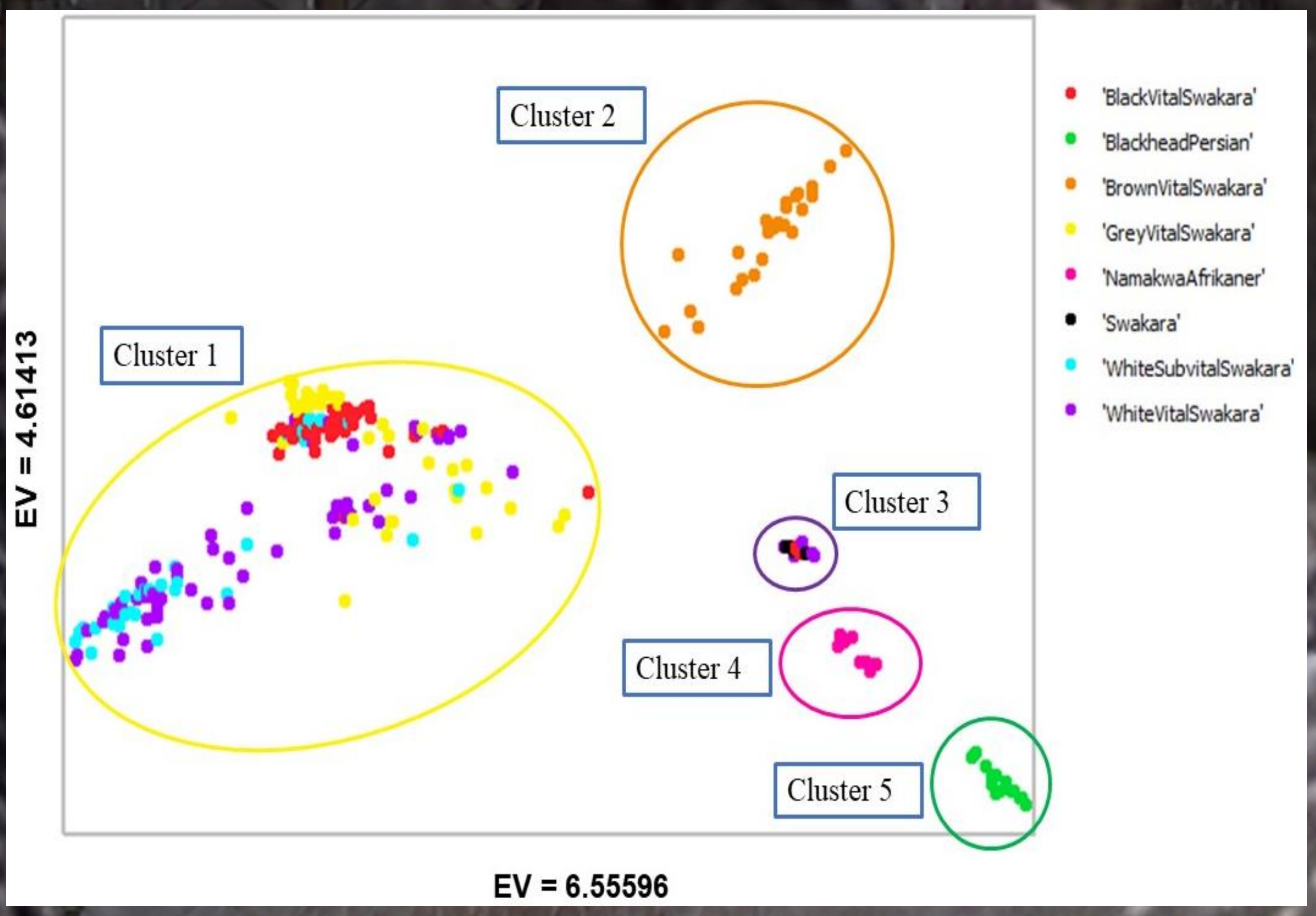

Figure 3. PCA based population clustering of sheep breeds from three different countries (SA, Germany, and Namibia)

Separation of animals in the PCA resulted in four different clusters being produced (Figure 4). The first principal component (PC1) explained 27.35% of the total variation and separated cluster 2 from cluster 1, 3, 4 and 5. The second PCA (PC2) accounted for 19.25% of the total variation and separated cluster 1 from all the other clusters. The Black-head Persian and Namaqua Afrikaner clearly separated from the rest of the Swakara sub-populations forming two separate clusters. The PCA demonstrated the effect of geographic origin with the sheep breeds sampled from Germany clustering together, those from Southern Africa clustering together and the Somalian-influenced breeds separating together from all the other clusters. The genetic division of breeds based on geographic history has similarly been reported by Kijas *et al.*, (2012) in a study of global sheep where European, Asian, American, and African sheep displayed phylogeographic patterns. Furthermore, individuals belonging to the same breed but sampled in different regions e.g., White vital clustering differently further supports the idea of geographic history having an influence on breed cluster.

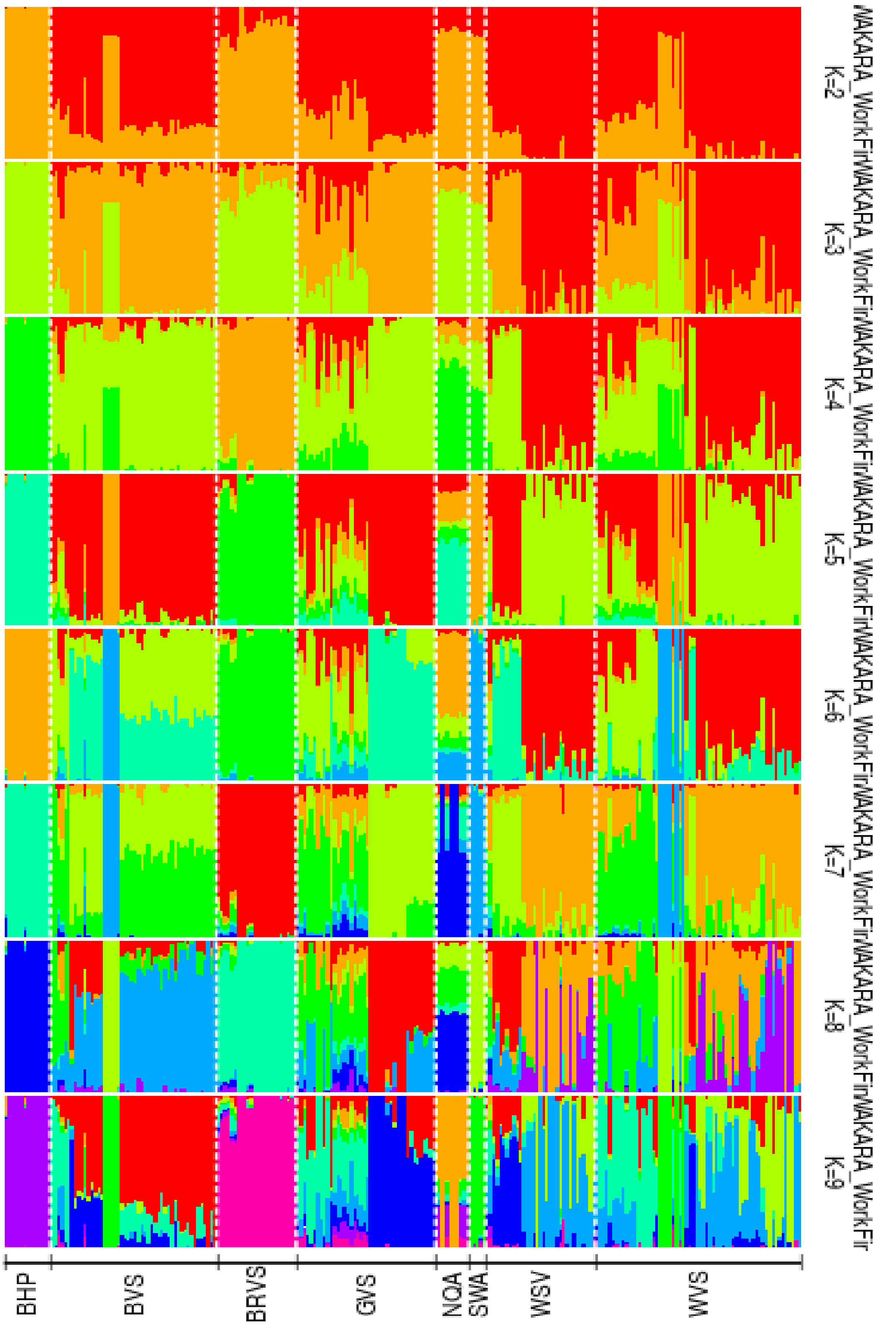

Figure 4. ADMIXTURE based clustering of sheep breeds from K = 2 to K = 9. BHP, Blackhead Persian; BVS, Black Vital Swakara; GVS, Grey Vital Swakara; NQ, Namaqua Afrikaner; SW, Swakara; WSV, White Subvital Swakara; WVS, White Vital Swakara.

The cross-validation error was calculated, and the optimal K value was found to be K=9. The compete and clear separation of the Blackhead Persian from the rest of the populations at K=2 is observed in Figure 5. The White Vital and White Subvital Swakara which clustered together from K=1 to K=2, started separating at K=3. At K=3 and K=4 saw the Black Vital, Swakara and White Vital clustering the same way witnessed in the PCA. From K=4 to K=9 the White Vital showed high levels of admixture whereas the Swakara was showing that it was less admixed. From K=2 to K=9 the Blackhead Persian maintained its homogeny showing no diversity and forming its own cluster. Similar to the PCA, the Brown Vital Swakara maintained its clustering with very little admixture.

Per marker F_{ST} analysis was used to study candidate genes from SNPs having a threshold of $F_{ST} > 0.80$ and their associated traits. It showed SNPs within QTLs associated with milk production, wool quality, and coat colour. Seven notable genes between cluster 3 and all the clusters across 5 different chromosomes were found to be related to immune response: *ATG10* (1 and 3), *UBR1* (3 and 9), *PCDH15* (3 and 9), *DOCK10* (3 and 4), *A2M* (3 and 4), *CYFIP1* (3 and 4), and *XRC44* (3 and 8), which is important for overall ovine health and survival. Three genes were found to be related to growth: *TRHDE, ACBD6 and CD86*,

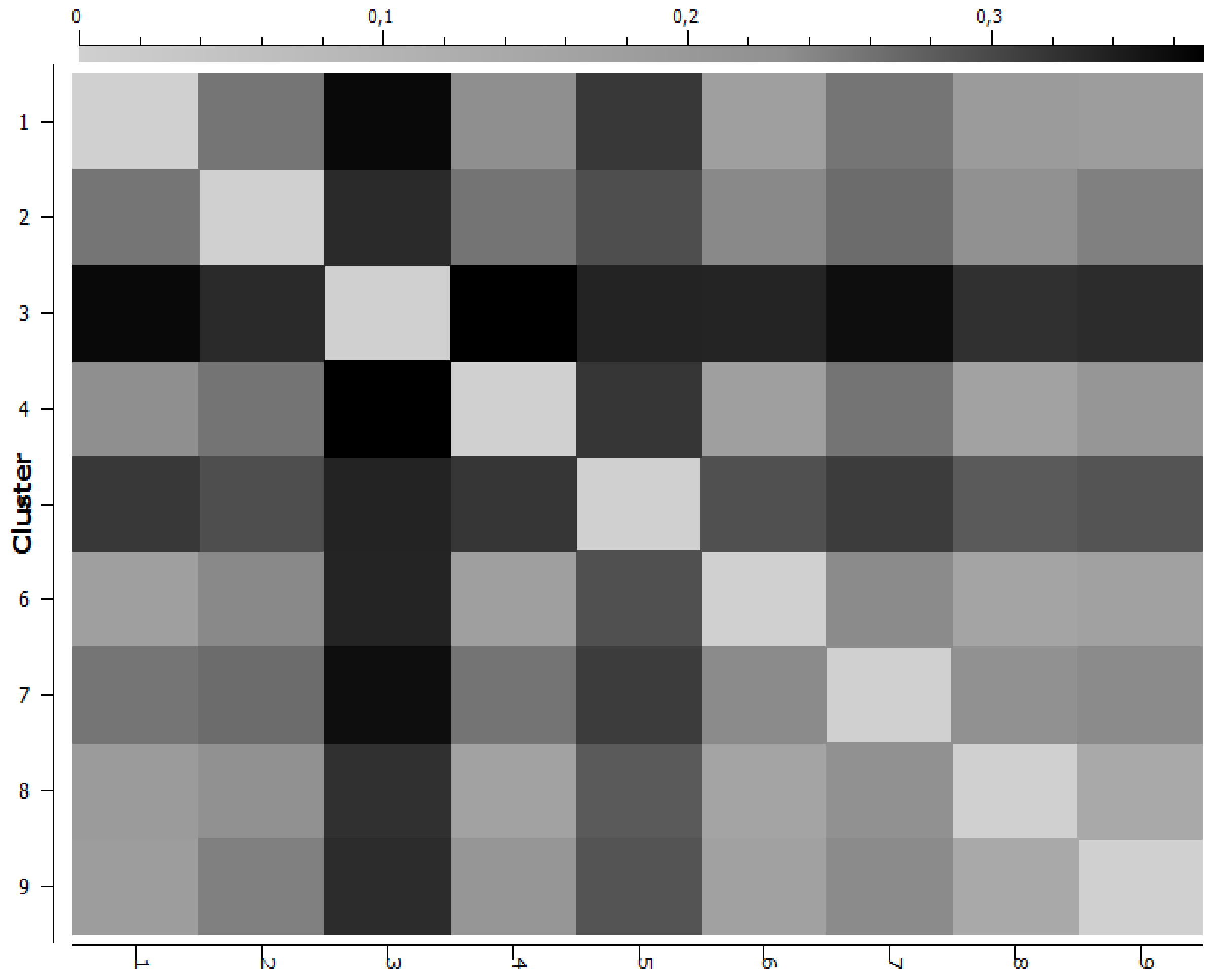

Figure 7. Genetic differentiation of sheep clusters

Conclusions

- The morphological consequence of selective breeding is clearly observed in the number of different coat-coloured sub-populations of the Swakara where the effects of selection have been detected and shown to have resulted as a response of a human-led breeding objective.
- The identification of coat colour genes (*SL41A2, PLEKHA8*) within the Swakara sub-populations is significant as it was an indication of selection targets and clearly differentiated it from Namaqua Afrikaner and Black head Persian
- Geographic isolation showed to have no influence on the variation but rather the influence of founder effects was observed in these sub-populations.
- High F_{ST} levels observed in the Namaqua Afrikaner compared to other indigenous Southern African sheep breeds may be attributed to genetic divergence as a result of natural selection pressures.

References

- BUDURAM, P. 2004. *Genetic characterization of Southern African sheep breeds using DNA markers.* University of the Free State.
- KIJAS, J. W., TOWNLEY, D., DALRYMPLE, B. P. FOR THE INTERNATIONAL SHEEP GENOMICS, C. 2009. A Genome Wide Survey of SNP Variation Reveals the Genetic Structure of Sheep Breeds. *PLOS ONE,* 4**,** e4668.
- MALESA, M. T. 2015. *Population genetics of Swakara sheep inferred using genome-wide SNP genotyping.*
- SCHOEMAN, S. J. S. A. J. O. A. S. 1998. Genetic and environmental factors influencing the quality of pelt traits in Karakul sheep. 28.