

Characterization of Genetic Diversity, Level of Admixture and Risk to Extinction of South African Indigenous and Village Pig Populations Emanating From Crossbreeding With Prevailing Exotic Breeds



Mandisa G. Mbuyazi^{1,2}, Edgar F. Dzomba¹, Farai C. Muchadeyi³ and Nompilo L. Hlongwane²
¹Discipline of Genetics, School of Life Sciences, University of KwaZulu-Natal, Pietermaritzburg, South Africa
²Biotechnology Platform, Agricultural Research Council, Onderstepoort, South Africa
³Animal Production and Health Section, Joint FAO/IAEA Division of Nuclear Techniques in Food and Agriculture, International Atomic Energy Agency, Vienna, Austria



Introduction

Genetic diversity, including the variation within and between different populations, is key to a population's ability to adapt to changing production conditions and climate change. South Africa is home to diverse pig populations, including indigenous and village pig breeds. These pig populations are valuable genetic resources that have adapted to local environments and possess unique traits. However, South African pig production is colonized by commercial breeds due to their superior production traits. Recently, approximately 35% of pig breeds were classed as at risk or already extinct, the majority of which are those from developing countries of Asia and Africa. This study aims to undertake a comprehensive assessment of the status of South African indigenous and village pig population as an important and unique animal genetic resource.



Figure 1: South African map showing the locations of the population sample sites.

Materials and Methods

A total of 144 pig ear tissue samples were collected from the villages of South Africa, extracted and genotyped using Illumina PorcineSNP80 BeadChip. SNP quality control and data combination was done using the Golden Helix Variation Suite (SVS). SNPs with call rate > 85%, Minor Allele Frequency (MAF) < 0.02 and Hardy Weinberg (HWE) < 10⁻⁴ were removed to generate a data set for analysis. To evaluate genetic variability, observed (H_o) and expected (H_e) heterozygosity, total number (N_a) and effective number (N_e) of alleles, and F (Wright's inbreeding coefficient) index were computed. Using the filtered dataset combined with data from previous studies, QC filtering was performed for SNPs high in LD (r² = 0.5) and Identity-by-descent (IBD ≥ 0.65) to detect and prune closely related and duplicate samples using SVS to produce a dataset for population structure analysis using the PCA and ADMIXTURE.

Results & Discussion

Within the populations, genetic diversity ranged from H_o=0.309 ± 0.119 to H_o = 0.339 ± 0.148 for the Mopani and Alfred Nzo populations, and from H_e=0.364 ± 0.129 to H_e =0.376 ± 0.121 for ALN and CAP respectively. The expected heterozygosity was higher than observed heterozygosity which attribute the discrepancy to forces such as inbreeding. High inbreeding coefficients were observed in the Mopani (F_{IS}=0.163 ± 0.166) and OR Tambo (F_{IS}=0.125 ± 0.214) populations. The heterozygote deficiency within breed (F_{IS}) was positive indicating that mates are closely related on average than expected. Inbreeding is quite common in village pig farming as proper breeding strategies are absent (Kidoido & Korir, 2013) . The average number of alleles per locus was 2.42, and the effective number of alleles was 1.64. The N_e resulted lower in all breeds due to the presence of low-frequency alleles that can be

Table 2: Population genetic variability parameters.

Population	N	PIC	P	Na	Rt	Ne	P	I _p
ALN	28	0.215	100	2.37±0.12	2.19	1.63±0.29	0.62	0.07
ORT	32	0.220	100	2.43±0.16	2.10	1.65±0.28	0.50	0.10
CAP	35	0.219	100	2.13±0.20	2.08	1.66±0.29	0.53	0.17
MOP	49	0.218	100	2.76±0.29	2.23	1.65±0.29	0.40	0.13

easily lost by genetic drift, thus reducing the genetic variability of the breeds, and increasing their risk of extinction. The principal component analysis produced three clusters with PC1 explaining 18.25% and 10.42% of the total genetic variability separating clusters 2 and 3 from clusters which contained Duroc pig breed only. PC2 explained 10.42% of the total variation and separated cluster 1 from all the other clusters. K=9 was the optimal ADMIXTURE clustering where admixed structuring was observed in all the village pig populations. The Duroc was not admixed and clustered in a way that aligned with the PCA results. Considerable low F_{ST} values ranging from 0.025 to 0.078 were observed between village populations. A phylogenetic analysis of the sampled pig populations The results suggested

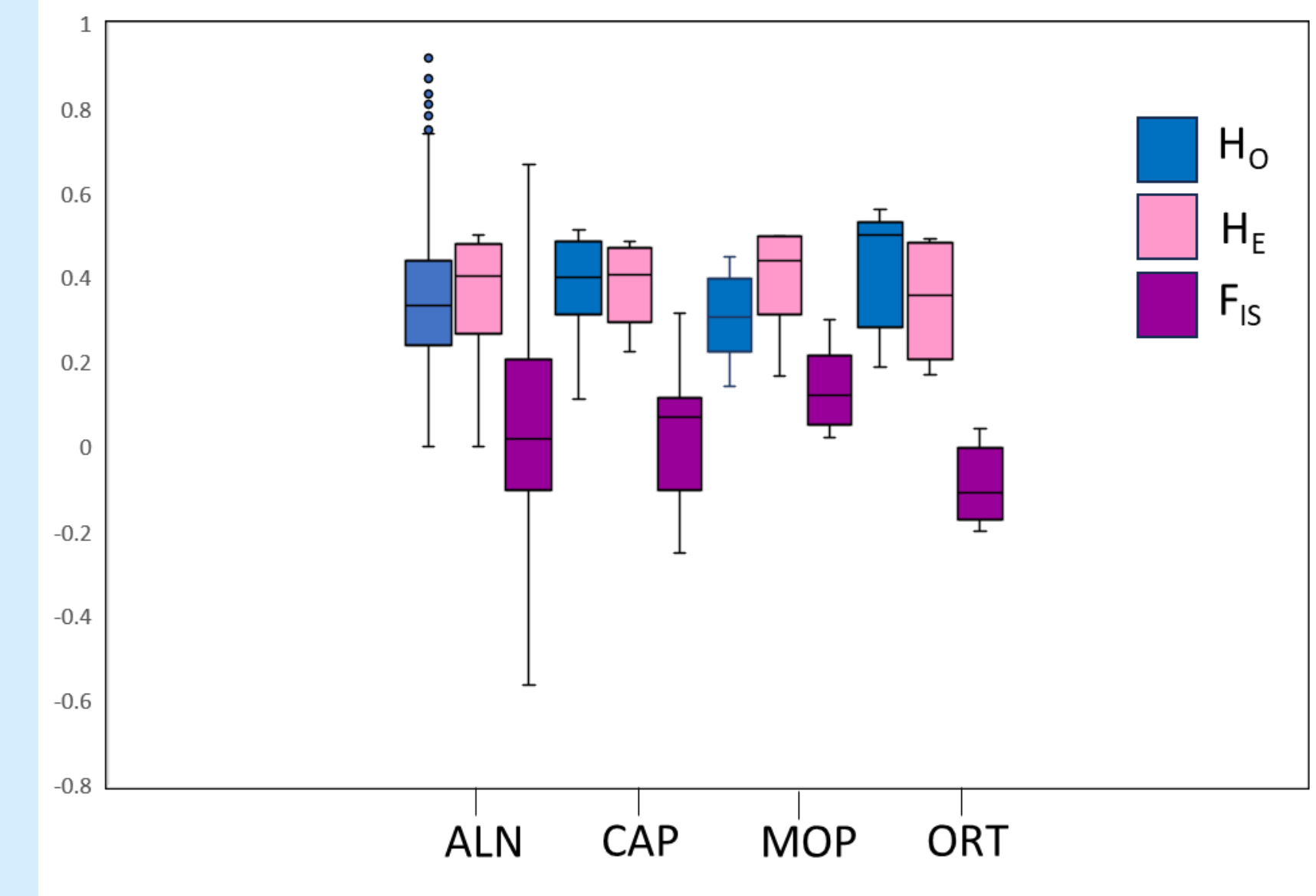


Figure 2: Heterozygosity analysis (observed heterozygosity, expected heterozygosity, and heterozygote deficiency within breed).

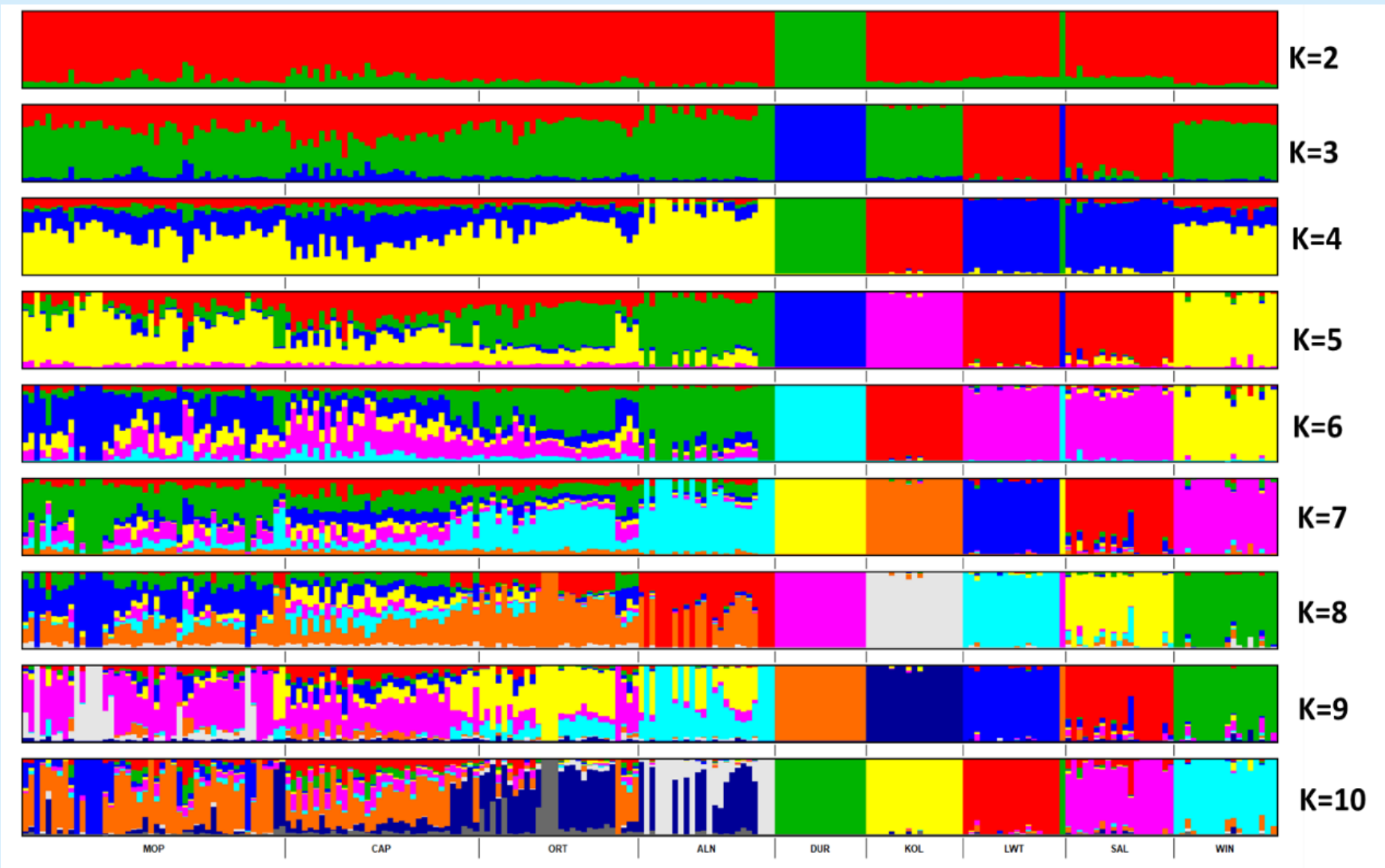


Figure 5: Ancestry proportions at K = 2 to K = 10 estimated by means of ADMIXTURE. The number of ancestral populations K is represented by one vertical line with K coloured segments.

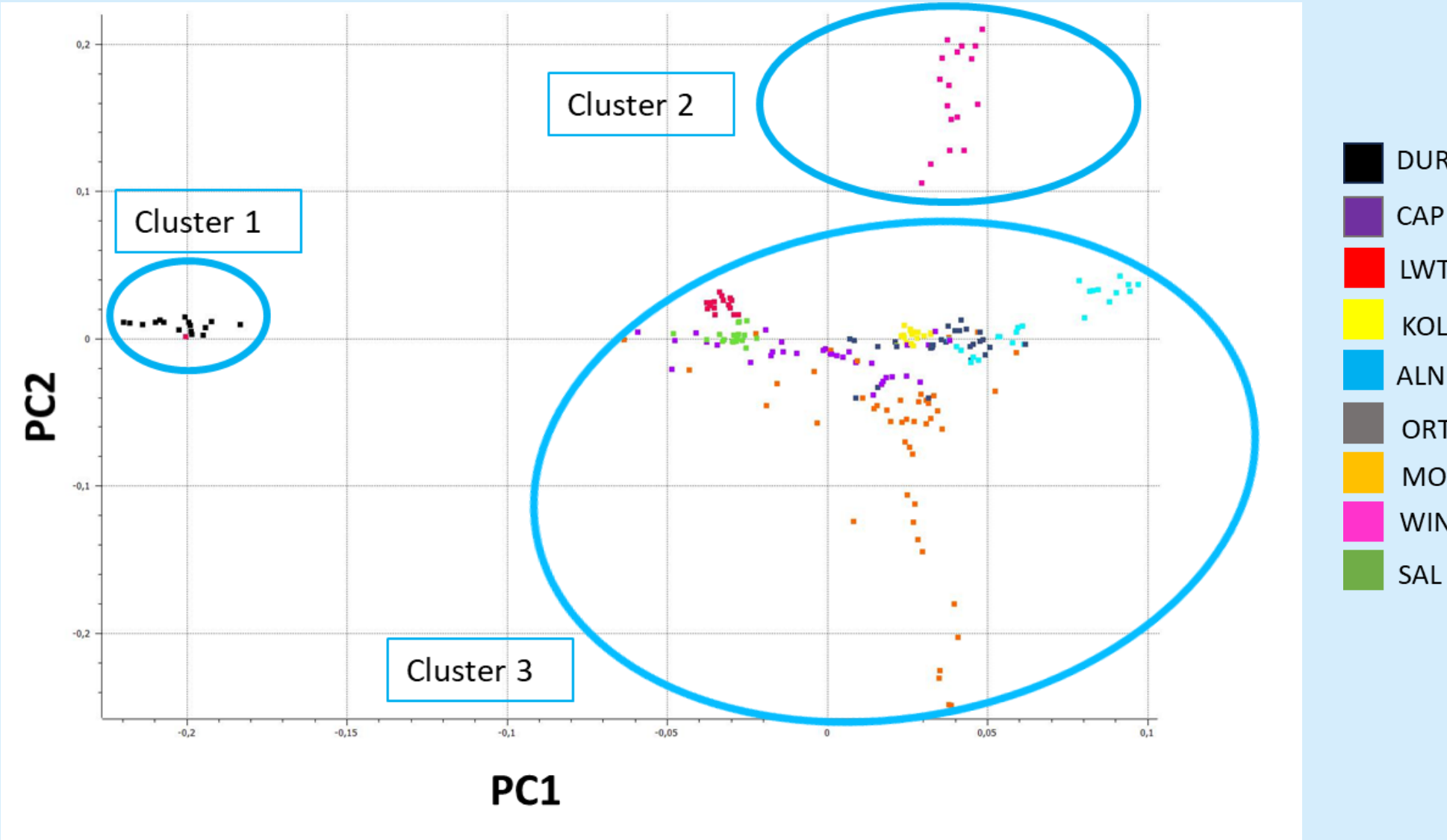
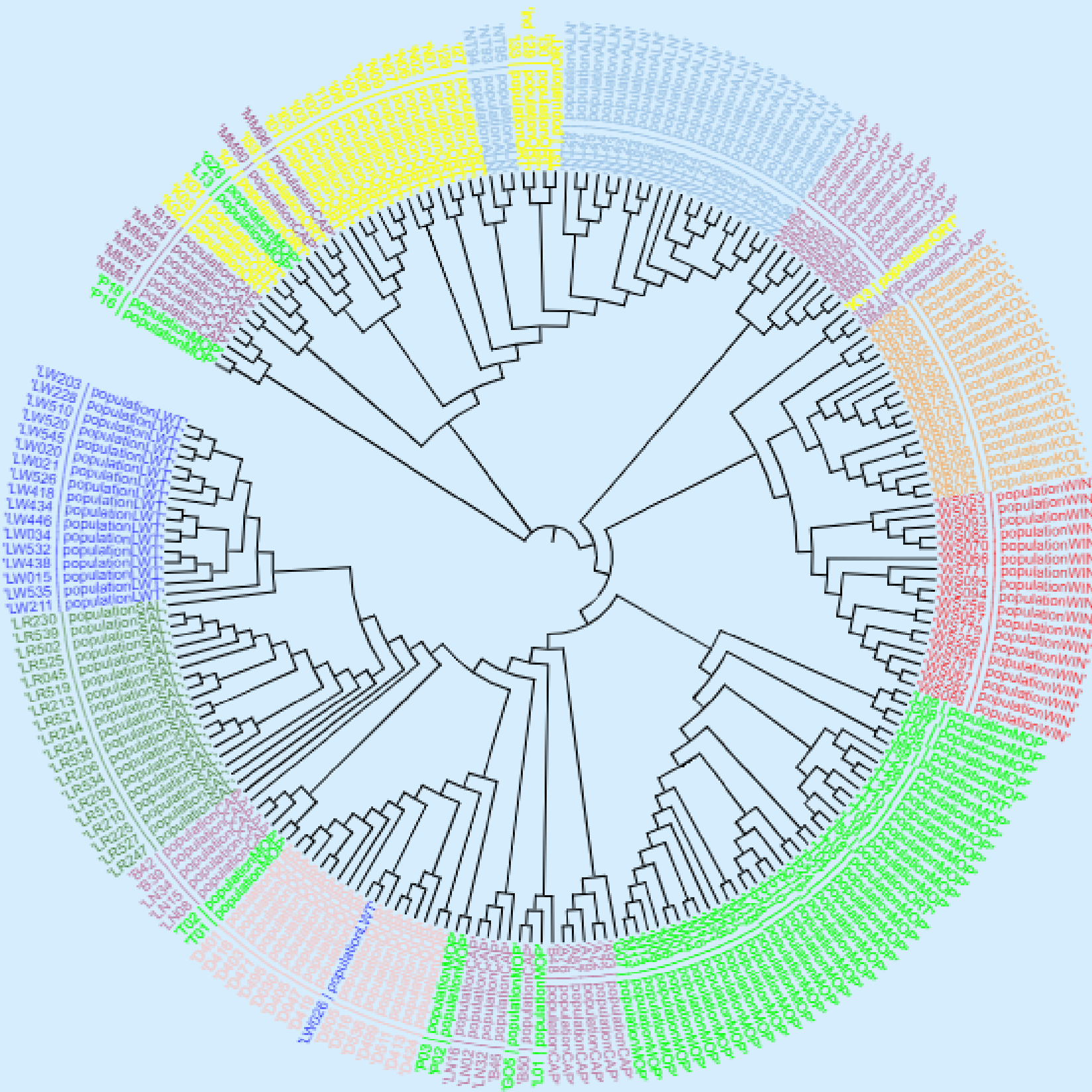


Figure 3: Principal Component Analysis Results of the pig populations (23 891 SNPs).

Conclusion

The investigated pig breeds and populations showed a decline in population size over the years and were highly admixed. Further studies investigating the mating systems and their effects on population diversity and structure are being pursued.



References

- Kidoido, M. M. and Korir, L. (2013). The Uganda pig value chain impact pathways narrative.
- Hlongwane, N. L., Hadebe, K., Soma, P., Dzomba, E. F., & Muchadeyi, F. C. (2020). Genome Wide Assessment of Genetic Variation and Population Distinctiveness of the Pig Family in South Africa. *Frontiers in Genetics*, 11(May), 1–19. <https://doi.org/10.3389/fgene.2020.00344>



Acknowledgements