# The **Genetic Distance** between **Nguni** and **Mashona** Animals

JASON REDING

## INTRODUCTION

Sanga cattle are indigenous to Southern Africa. Classified as *Bos taurus africanus*, these cattle are visually distinguishable by their *cervico-thoracic* humps. The formation of this subspecies is a result of historical crossbreeding between taurine and indicine cattle subspecies in Eastern Africa. The four main Sanga breeds recognised in South Africa include the Afrikaner, Drakensberger, Nguni and Tuli.

As pastoralist Nguni people migrated further south into Africa, they brought their cattle along with them. Through selection and environmental interactions, Nguni cattle developed into the well-adapted breed we know today. As Zulu, Xhosa and Ndebele people settled in different areas, they developed distinctive cattle ecotypes although all are essentially still Nguni. Mashona cattle originated from the Shona people of eastern Zimbabwe and are classified as Sanga type. They are bred in a wide spreading territory covering most of the eastern half of Zimbabwe and an adjoining region of Mozambique that is free of the tsetse fly. This breed is reared for meat production, and it is said they make docile working animals. A herd book was established in 1954, after a decade of selection for beef production and polledness. The Mashona breed is usually black or red and the majority of Mashona are polled.

An investigation into Mashona breed types at a genomic level was conducted to identify whether these animals are genetically distinct from other Sanga-type breeds, and more specifically how they cluster in relation to the Nguni breed.

## Breed clustering through a "Gene Box"

Recently ten animals representing Mashona cattle were genomically tested. These samples were collected and presented for analysis, to assess the level of genetic relatedness as well as shared ancestry between these 10 Mashona genotypes and other Sanga breed genotypes.

To assess any genetic differences between the animals, principal component analysis is used to visualise and explore the vast number of genetic variables in a much simpler format. A "Gene Box" is a three-dimensional tool that allows one to elucidate genetic variances at a simpler level. To verify the use of this tool, the investigation was split into three categories. As we progress through each category, more breeds of different genetic backgrounds are included with Category 3 being the most scientifically accurate.

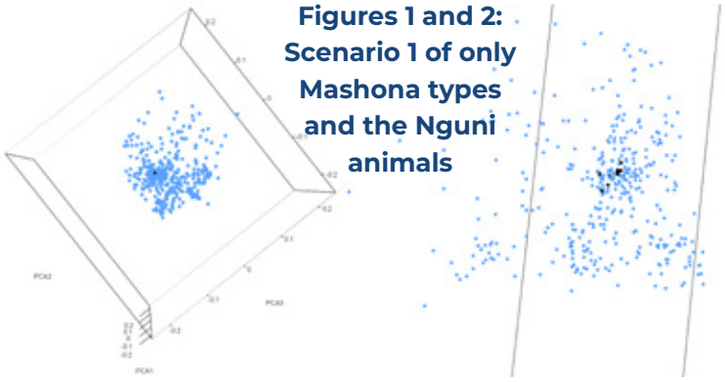
Table 1 refers to the number of genotypes in each respective breed used in this investigation. Each breed is distinctly colour-coded in the "Gene box" to easily differentiate between them. The Mashona animal types were colour-coded as black and the Nguni's as blue. The three different Sanga breeds were coded as orange (Breed 1), red (Breed 2) and green (Breed 3) with the Zebu indicus type being yellow, respectively.

**Table 1: Number of genotypes for each breed and breed type used in the analysis**

| BREED | COLOUR | NUMBER OF ANIMALS GENOTYPED |
|---|---|---|
| Mashona types | Black | 10 |
| Nguni | Blue | 380 |
| Sanga breed 1 | Orange | 308 |
| Sanga breed 2 | Red | 226 |
| Sanga breed 3 | Green | 1679 |
| Zebu | Yellow | 458 |

## CATEGORY 1

In this scenario, the Mashona genotypes were only assessed alongside the Nguni genotypes. As seen in Figures 1 and 2, the Mashona types and Nguni animals cluster distinctively together in one large cluster. As these animals do not cluster separately, this is an indication that they share a similar ancestry and genetic composition.



**Figures 1 and 2: Scenario 1 of only Mashona types and the Nguni animals**

## CATEGORY 2

Here the Nguni and Mashona genotypes merged with the three other recognised Sanga breeds in South Africa. Looking at Figure 3, we observe distinct clusters. The three Sanga breeds form the orange, green and red clusters with the Nguni breed, in blue, clustering in the middle. Here we see the largest genetic diversity within the green cluster. Once again, the Mashona animals cluster with the Nguni breed. As there are obvious clusters of the distinct Sanga types, yet there is no distinct clustering between the Nguni and Mashona breeds, this once again indicates a similarity in genetic composition.

**Figure 3: Here you see the Nguni and Mashona distinctively clustering in the middle.**

## CATEGORY 3

All the Sanga cattle genotypes from Category 2 were collated with a *Zebu indicus* breed of African origin. The addition of the *Zebu indicus* breed increased the variation in genetic composition and allowed for a greater analysis of genetic differences between all the animals in the dataset. As seen in Figure 4, the distance between the Sanga breeds increased due to a data structure that allowed for the identification of genetic differences.

## In summary

**Figure 4: A "Gene box" with the 3 Sanga breeds, the *Zebu indicus* breed with the Mashona and Nguni animals**

An interesting observation was noticed between all the Categories above. In Category 1, the Mashona genotypes were seen to cluster directly in the centre of the "Gene box" with all the Nguni animals surrounding them. In Categories 2 and 3, we start to observe a few of the Mashona animals starting to appear on the outskirts of the Nguni cluster. This can be attributed to the increased number of animals in the analysis, where Categories 2 and 3 have over 2 000 more animals.

This change in the data structure allows the analysis to be more accurate at identifying the true genetic differences between the animals. A few of the Mashona-type animals cluster on the periphery of the Nguni cluster. These animals mainly differ from the Nguni animals in the third principal component. Therefore, they cluster in the same cluster as the Nguni animals but are spread out on the Z-axis. Like what is in the orange colour-coded Sanga breed, differential clustering is an indication that animals may belong to different herds or lines within a herd due to the use of different sires.

The level of distinct clustering between the specific Sanga and Zebu breeds indicates differences at a genetic level and infers unique breed ancestry. The lack of separate clustering between the Nguni and the tested Mashona-type animals is indicative of a shared breed ancestry and genetic similarity. ■