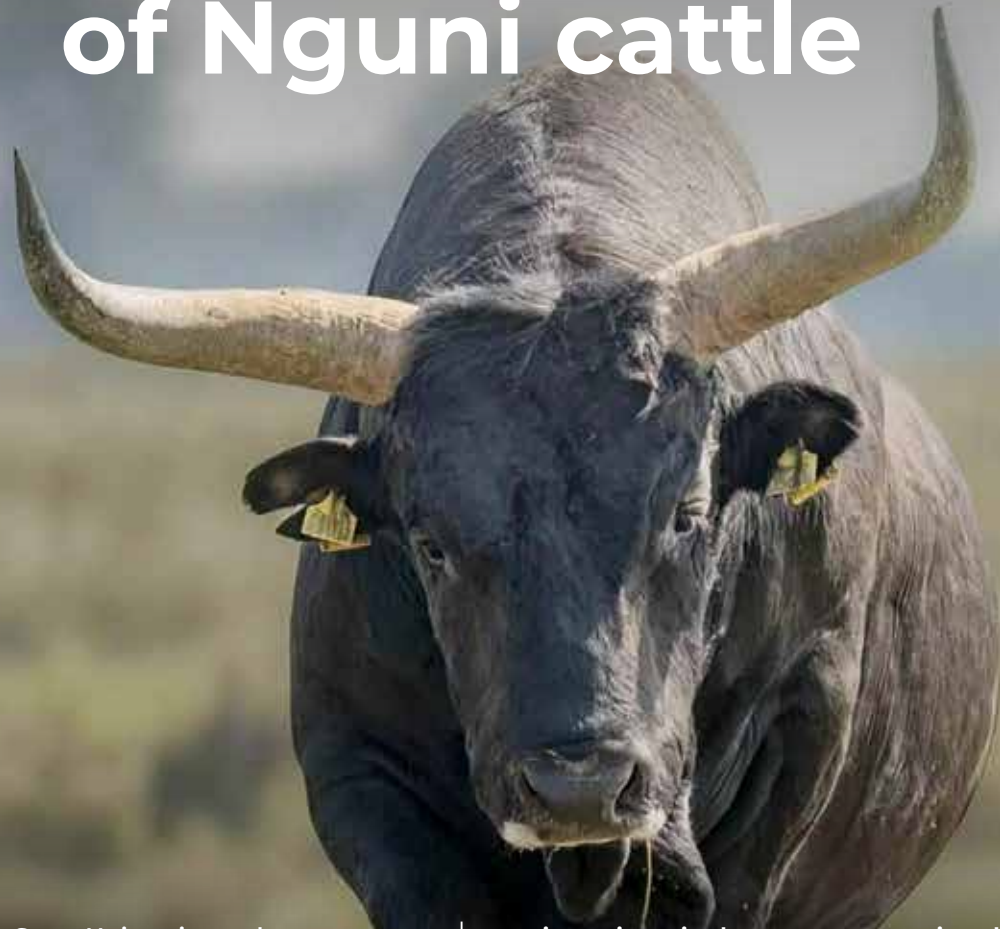


A cow's tail: the maternal heritage of Nguni cattle



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Nguni cattle are the product of thousands of years of human ingenuity combined with the selective forces applied by Africa's diverse ecosystems. Their ancestry stretches back to both the Near East and the Indian subcontinent.

About eight thousand years ago, cattle were domesticated from the wild auroch, a species now

extinct since its last representative died in 1627. The auroch was described by Julius Caesar as "a little below the elephant in size" and "[t]heir strength and speed are extraordinary." Lest his comparison with elephants seems farfetched, the important caveat is that he was no doubt comparing auroch with the now extinct northern African elephant which is considerably smaller than the African elephant familiar to South Africans. Nonetheless, archaeological evidence indicates that male auroch stood between 155 cm and 180 cm at the withers. In comparison, modern improved Nguni cattle stand approximately 135 cm at the withers.

Despite their large size, and their apparent aggression – Caesar claimed that “they spare neither man nor wild beast which they have espied” – auroch were domesticated at least twice.

In the Near East auroch domestication resulted in flat backed taurine cattle, while those domesticated in India resulted in the humped indicine or zebu cattle. It is also possible that auroch were domesticated independently in northern Africa, but the evidence is complicated, sometimes contradictory, and difficult to interpret. Regardless if northern Africa was another centre of cattle domestication, we can be sure that the descendants of cattle from the Near East and India were brought to Africa

To study the genetics of Nguni cattle in particular, research team members of the Zulu Kingdom Archaeology Project took samples of hair pulled from the tails of cattle.

The hair follicle that remains attached to the hair contains enough DNA to analyse. The hair samples were shipped to Horsburgh’s Molecular Anthropology Laboratories in the US, where we sequenced complete mitochondrial genomes from 175 cattle.

To understand the results of our work, we need to step back for a quick primer on genetics in general, and the genetics of African cattle in particular. DNA is one of the primary information storage molecules in most forms of life. It exists in a twisted ladder shape, in which the sides or the rails of the ladder provide stability to the molecule and the rungs contain the information.

The information carrying capacity of a DNA molecule can be conceptualised by using a four-letter alphabet of chemical structures, known as bases: adenine (A), cytosine (C), guanine (G) and thymine (T). It is the order of the bases that contains the information necessary to build an organism. It certainly does that, but it also carries information about the history of an organism – it can tell us which individuals are more closely related to each other.

Mutations are random changes in the DNA molecule. They are chemical mistakes, resulting in, for example, a change in a sequence from AATG to AATC. Sometimes those changes have biological consequences. They can cause a change in a protein which can be damaging, useful, or inconsequential. Unless the change is so detrimental that it results in the death of an animal, or their inability to reproduce, then that mutation can let us track relatedness. All the descendants of the individual in which the G mutated to a C, will inherit the C which allows us to infer that all the organisms with the C are more closely related to each other than they are to all the individuals with the G.

In animals, most of the cell’s DNA is contained in a nucleus, separated from the rest of the cell by a membrane. Contained within the nucleus are all the chromosomes inherited from each of the individual’s parents. In humans, we inherit twenty-three chromosomes from each parent, for a total of forty-six. Cattle have more chromosomes, inheriting thirty from each parent. Curiously, even though cattle have more chromosomes than humans, the chromosomes are smaller on average, and they have approximately the same number of DNA bases.

All of this DNA, however, is not the DNA we focused on in this study. Sitting outside the nucleus, is a small membrane wrapped structure called a mitochondrion (plural: mitochondria). It carries its own independent genome, which carries genes largely devoted to energy production in the cell and the manufacture of proteins. The mitochondrion itself produces the molecules that are the units of chemical energy for the cell.

Importantly for our purposes, mitochondria, and therefore mitochondrial genomes are inherited only from mothers. Sperm have a small number of mitochondria in the section between the head and the tail, and they provide the energy to allow sperm to swim but they are excluded from the egg upon fertilization. Mitochondrial genomes, therefore, allow us to track maternal lineages across time and space.



When examining the variability in mitochondrial genomes, we group individuals together who share a common maternal ancestor, and we give them a haplogroup name. This is exactly the same as putting together all the people descended from your mother's, mother's, mother's, mother's, mother's, mother's mother in the same haplogroup. You have other relatives, but for the purposes of mitochondrial DNA analysis, and assignment to a particular haplogroup, it is the unbroken line of mothers that counts.

Almost all the African cattle studied so far are members of a haplogroup called T1. This means they all share a common maternal ancestor, and therefore the mutation that occurred in that maternal ancestor. Because we have some information on the pace at which mitochondrial genomes accumulate mutations over time and can count the mutations that have happened in the descendants of that one maternal ancestor, we can calculate how long ago that T1 maternal ancestor lived. She was running around the Near East approximately 12,000 years ago.

One of the things that is interesting about that calculation, is that it means that she was an auroch, and not a cow. And further that her descendants remained auroch for about four thousand years before they were domesticated.

We divide the members of the haplogroup T1, again based on shared mutations, into six subhaplogroups, inventively called T1a, T1b, T1c, T1d, T1e,

and T1f. The lineage T1b is common in northern Africa and becomes more common the further south you move. In a previous study where we sequenced thirty-five Nguni cattle from a single farm in the Western Cape, we found that the overwhelming majority of individuals were members of the subhaplogroup T1b. A further thirty-one of them were members of a subgroup of T1b called T1b1. One individual belonged to each of T1, T1b, T1c and T1d.

In the current study, we sequenced complete mitochondrial genomes from 175 cattle. Consistent with the previous study of Western Cape Nguni cattle, most of the individuals are members of T1b1 with a small number of T1, T1c and T1d. In the image, you can see a network which joins together related DNA sequences, with the circles representing individuals. The larger the circle, the more individual cattle had the relevant DNA sequence. The cattle from our earlier study are represented in green, and those from the current study are represented in blue. You can see that the cattle in the current study are more genetically diverse than those in the earlier study of just Nguni cattle from one farm in the Western Cape.

Consistent with all the previous work done with African cattle, none of the individuals show signs of maternal ancestry among Indian cattle. This is despite the clear evidence of Indian ancestry in the morphology of Nguni cattle – the presence of the hump, among other characteristics – and despite studies of nuclear DNA showing Indian ancestry in other African cattle. There are two explanations for this pattern currently on the table. It is possible that when Indian cattle were brought to Africa, the individuals were almost exclusively male, so few Indian mitochondrial lineages were ever brought to Africa. It is also possible that Indian mitochondrial lineages in Africa did not survive the rinderpest panzootic in the 1890s, but that they had been present earlier. Genetic data from archaeological cattle in Africa are few, but those that are available have not yet shown any evidence of ancient Indian maternal lineages.

As fragments of ancestral herds were moved south, some portion of the genetic diversity of the parent herd was not included. This is a common pattern in migrating populations known as the founder effect. It reflects

that each founding population contains only a subset of the genetic variation present in the ancestral population. In the case of African cattle, this process has been repeated myriad times over thousands of years. The genetics of Nguni cattle then, have been shaped by both the unique selective environment and a progressive reduction in genetic diversity as their ancestors migrated southwards.

