

Historical demographic profiles and genetic variation of the East African Butana and Kenana indigenous dairy zebu cattle

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Keywords: Bayesian Skyline Plots, Effective population size, mitochondrial DNA, Population expansion

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Abstract

The history of African pastoralism remains debated. Butana and Kenana cattle from Sudan are part of the East African zebu *Bos indicus* type of cattle. Unlike other indigenous zebu cattle in Africa, they are unique due to their reputation for high milk production. They are regarded as dairy cattle, the only ones of their kind in the African continent. In this study, we sequenced the complete mtDNA *D*-loop of 70 animals to understand the maternal genetic variation, demographic profiles and history of the two breeds. We find very high mtDNA diversity but low levels of genetic structure and variation within and between breeds. Bayesian coalescent-based analyses reveal that the two breeds have different historical and demographic profiles, with earlier population expansion of the Butana breed compared to the Kenana. Unexpectedly, the maternal ancestral populations may have separated prior to their introduction into the African continent, with first the arrival of the ancestral Butana population. We also reveal distinct demographic history between the two breeds with the Butana showing a decline in its effective population size (N_e) in the recent past ~ 600 years. Our results provide new insights on the early history of cattle pastoralism, indicative of a large ancient effective population size. They are calling for the design of appropriate breeding strategies for the effective management of these two breeds, with the potential of improving milk production in the marginal semi-dry areas of the African continent.

Submitted to Journal of Animal Genetics

Mitochondrial DNA analysis sheds light onto expansion of zebu cattle (*Bos taurus indicus*) pastoralism across East and southern Africa

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Keywords: Bayesian Skyline Plots, African cattle, mitochondrial DNA, Population expansion

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Abstract

The history of introduction and subsequent dispersal of zebu cattle and associated pastoralist lifestyle across eastern and southern Africa has continued to intrigue geneticists, historians and archaeologists alike. Here, through a Bayesian coalescent analysis of 13 full mitochondrial genome and 111 complete D-loop sequences including 72 full mtDNA sequences and 150 D-loop retrieved from the Genbank, we model the expansion dynamics of zebu cattle from the North, East and South of the African continent as a proxy to revealing and understanding their genetic history and that of pastoralism. We observe a high level of genetic diversity among the zebu cattle represented by several unique haplotypes supporting frequent admixture of diverse genetic stocks within and outside the African continent. Common to all geographic regions, is a gradual decline in effective population size (N_e) reminiscent of a bottleneck following the initial arrival of zebus in the continent. This is however followed by an increase in N_e in each region that commences at different time periods but within the past 5000 years indicating the possibility of regional differences in the introduction, adoption and spread of zebu cattle pastoralism. Based on the expansion profiles, our results lend support to the fact that zebu cattle arrived on the African continent via Egypt before spreading southwards in to Sudan. Another wave most likely led to a separate introduction of the species into Ethiopia and Kenya via the Horn and East African coastline. Given the almost simultaneous expansion of cattle in Ethiopia, Kenya and South Africa, it is likely that the dispersal of zebu cattle pastoralism southwards was a very rapid process that involved both demic and cultural diffusion

*(In preparation, targeting **Proceedings of the royal society B**)*

Dynamics of domestication and trading revealed by the global genetic diversity of the dromedary

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(Under review in *Proceedings of the royal society B*)