

Department of Biological Sciences Faculty of Science

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The history and adaptation of African cattle: A genomic perspective



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Following a complex history of introduction, crossbreeding, migrations and adaptation African indigenous cattle are amongst the most diverse livestock populations. Here, I will review, following the analysis of full genome sequencing data, our current knowledge of the history of African cattle and its adaption to environmental challenges. If taurine (humpless) cattle were first introduced on the African continent, most of the populations are today taurine x indicine (zebu – humped) crosses. The sole presence of taurine mitochondrial DNA suggests a pattern of malemediated zebu introgression with recent evidence of selection for mitochondrial – autosomes genomes compatibility. Uniquely, today we do find African cattle in nearly all the agroecologies of the continent, from the driest to the humid-infested tsetse-fly ones. Positive signatures of selection analyses provide new insights into the genome adaptation to these environmental selection pressures. It is expected that this knowledge will guide cattle breeding programs in addressing the challenges of climate change and the need for improved productivity.