

## New insights on African buffalo genetics

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**Abstract:** Along with the elephant and the wildbeest, the African buffalo (*Syncerus caffer*) is the most dominant species in terms of biomass but also the most widespread herbivore. It exhibits extreme morphological variability at large geographical scale, which has led to controversies about its taxonomic status. Nowadays, the African buffalo experience a severe reduction in population size and geographical distribution, as a result of human demographic expansion, overexploitation, habitat degradation and diseases. Using different kinds of markers on a large sampling set, we aimed to infer the genetic diversity and phylogeographic history of the African buffalo at the pan-African spatial distribution (N=766), as well as to assess the genetic health and the population structure of southern African Cape buffalo populations that face gene flow restriction (N=264). Analyses highlighted the existence of two distinct lineages at the continental scale: West and Central African populations (*S.c. nanus*, *S.c. brachyceros*, *S.c. aequinoctialis*) and East and Southern African populations (*S.c. caffer*). The two lineages likely expanded and diverged in the late to middle Pleistocene from an ancestral population located around the current-day Central African Republic. They probably adapted their morphology to colonize new habitats, hence developing the variety of ecophenotypes observed today. The finer scale axis- concentrated on southern Africa allowed identifying three genetic clusters. The splitting period suggests that the current pattern results from human-induced factors and/or from the aridification process that occurred during the Holocene. Lower differentiation estimates were observed between localities that experienced translocation over the last century. The two main clusters displayed high intra-cluster genetic diversity, low inter-cluster differentiation, and an absence of inbreeding depression signal, while the third one- a tiny population enclosed within an isolated protected area, experienced genetic drift. All those information are particularly essential within the context of conservation programs currently undertaken to restore genetic diversity of African buffalo populations.

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