

**THE POPULATION GENETIC STRUCTURE OF AFRICAN BUFFALO (SYNCERUS
CAFFER, SPARRMANN 1786) IN UGANDA BASED ON MITOCHONDRIAL DNA**

CONTROL REGION SEQUENCE VARIATIONS

BY

MASEMBE CHARLES

(BVM), MAK.

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Abstract

Until the 1950's and 60's the African buffaloes (*Syncerus caffer*) in Uganda were abundant and widely distributed. However recently, the buffaloes have been decimated and their range restricted to protected areas as a result of bottlenecks, habitat fragmentation and other human activities. In this study I investigated the effects of the recent reduction in population size and fragmentation on the distribution and patterns of genetic diversity in the buffaloes using mitochondrial DNA control region sequence variations. Eighty four samples from four national parks were used in this study. Despite the documented reduction in population sizes, fairly high levels of nucleotide diversity ($\pi = 3.1\%$ to 5.4%) were observed. In the total sample, 78 haplotypes were identified and an overall π of 4.4% was observed. Despite the high mobility of buffaloes, significant genetic differentiation among all populations was also observed even between populations separated by short geographical distances (K_{ST} [0.03 – 0.09]; F_{ST} [0.06-0.14]).

The observed mtDNA haplotypes did not coincide with the geographical origin of the individuals. These results are interpreted in light of the recent catastrophes faced by the buffaloes and should

raise conservation and management concerns as far as *Syncerus caffer* populations in Uganda are concerned.