

**Genetic variation, structure and dispersal among Cape buffalo  
populations from the Hluhluwe-Imfolozi and Kruger National  
Parks of South Africa**

by

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## Declaration

I declare that the thesis/dissertation, which I hereby submit for the degree  
.....at the University of Pretoria, is my own work and  
has not previously been submitted by me for a degree at this or any other tertiary institution.

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**Aan Bob, Bennie en Marelize**

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## Preamble

Developments in the field of molecular genetics, especially during the last two decades have revolutionised the field of conservation biology in several ways. Being able to characterise a species on the DNA level has taxonomic, phylogenetic, phylogeographic, conservation and forensic applications, to name but a few. Signatures of ancestry, environmental change and intervention that shape the dynamics of a species, whether of natural or anthropological origin, are contained in the DNA, and these signatures can be analysed in order to elucidate the processes affecting the existence of a species. They may be prominent or subtle, depending on the degree to which processes exerted an influence on a population or species. Sadly, these signatures often portray the remnants of human interventions that had detrimental effects on the species.

In order to devise interventions aimed at conserving biodiversity, it is vital to understand and uncover the driving forces behind population dynamics. This thesis describes the extent to which some factors influence the population dynamics and structure of one of Africa's largest and most remarkable mammals, the Cape buffalo (*Syncerus caffer caffer*). By studying the two largest buffalo populations in South Africa, the intention was to gain an in depth understanding of how present and historical events, together with geographical, ecological and behavioral factors, have impacted upon the two populations. We are convinced that through this, we can make a positive contribution towards designing more efficient management and protection strategies for the species as a whole. This is of special importance in view of an ever-increasing pressure on the resources utilized by this species.

## Summary

The Cape buffalo (*S. c. caffer*), one of Africa's largest and most magnificent mammals, initially numbered more than 3 million animals at the end of the 19<sup>th</sup> century, but presently comprises around 400 000 animals. This staggering decrease is mainly due habitat fragmentation, overhunting, drought and disease. In order to contribute to conservation management of the species, it is vital to understand the underlying factors that affect their population dynamics, and the research reported on in this thesis is aimed at quantifying and qualifying some of these factors, using a molecular genetics approach.

In South Africa, the two largest buffalo populations are found in the Kruger National Park (KNP) and Hluhluwe-Imfolozi Park (HiP), numbering ~28500 and ~3000 animals, respectively. Prior to large-scale genotyping of animals from these parks (485 and 401 from KNP and HiP respectively), a high-throughput, cost- and time-effective genetic profiling system was developed. The system comprising a panel of 17 Microsatellites, amplified in three core multiplexes and co-electrophoresed as a single injection, uncovered substantial genetic variation in the sample population. Exclusion probabilities were in excess of 0.999 and a random match probability of  $6.5 \times 10^{-17}$  was obtained, for the initial 60 KNP buffalo screened by this approach.

Population genetic parameters revealed that KNP and HiP are significantly differentiated (Msat data:  $F_{ST} = 0.159$ ; mtDNA data:  $F_{ST} = 0.275$ ), and it seems that drift has played a major role in this observed level of divergence. Little or no differentiation could however be demonstrated among most herds and subpopulations, suggesting high levels of gene flow. HiP exhibited consistently lower levels of mtDNA variation than KNP, with only 4 haplotypes (haplotype diversity:  $0.48 \pm 0.05$ ; nucleotide diversity: 0.025) recovered from the 97 animals sequenced, compared to 34 haplotypes from 162 KNP individuals (haplotype diversity:  $0.92 \pm 0.009$ ; nucleotide diversity: 0.049). The haplotypes from the two parks were also separated by a relatively small genetic distance, and the fact that they were not geographically partitioned, suggests genetic contact between the populations in the past. HiP also exhibited a reduced level microsatellite diversity (0.54 vs. 0.64 in KNP). From these

results it appears that HiP exhibits signals of a genetic bottleneck or founder event, while KNP has retained substantial genetic variation. HiP also exhibits strong signals of a population contraction, while the population from KNP is in equilibrium. Pre-bottleneck levels of variation may also have played a role in the reduction of genetic variation in HiP. A steady decline in genetic variation in HiP was observed between 1986 and 2004, suggesting episodes of low  $N_e$ . Strong sex-biased dispersal could be demonstrated for KNP but not for HiP, which may be attributed to the lack of mtDNA diversity and the small size of the park. The strong signals for male-biased dispersal in KNP are confounded by the fact that the whole population shows a positive inbreeding coefficient. However, this may indicate significant differentiation between herds despite the presence of high gene flow. The results presented provide valuable baseline information for making sound genetic management decisions.



## **Disclaimer**

This thesis consists of a series of research chapters that have been prepared as stand-alone manuscripts for publication purposes. Some unavoidable repetition may therefore occur between chapters.