

**Detection of Genetic Substructure and Diversity in the Endemic South African  
Antelope Species, *Damaliscus pygargus***

by

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DEDICATION

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## ACKNOWLEDGEMENTS

to Nico

I wish to express my gratitude to my promoter, Prof. L. H. Nel for his encouragement and guidance that has sustained me throughout this study. His willingness to tackle a new avenue in molecular evolution and his strong interest in the conservation of species has made this research possible. I would also like to thank Prof. Nel for sharing his love of rock photography and science with his students. I am also grateful to the long distance support of my co-promoter, Dr. R. S. Barrett. You have seen me through the intricacies of population genetics for over eight years. I also appreciate her quick replies and useful comments to my framing questions through e-mail. I have also inspired to pursue scientific research by Dr. William Turner over a decade ago. He is also indebted to you for his continual support over the years.

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## LIST OF ABBREVIATIONS

BOLA	Bovine Leucocyte Antigen
dS	synonymous
dN	nonsynonymous
ESU	Evolutionary significant unit
Kf	Kinship coefficient
LIS	Low ionic saccharose
MU	Management unit
MYA	Million years ago
NJ	Neighbor joining
PBR	Peptide binding region
Ps	Proportion of allele shared
SSCP	Single strand conformational polymorphism
TBE	Tris Borate EDTA
UPGMA	Unweighted pair group mean algorithm
UV	Ultraviolet

## ABSTRACT

The antelope (*Damaliscus pygargus*) is an endemic species in South Africa belonging to the contemporary antelope tribe Alcelaphini. The species is subdivided into two subspecies based on phenotypic differences and historic geographic isolation. This study has revealed strong molecular evidence of genetic structuring between (*D. p. pygargus*, bontebok) and (*D. p. phillipsi*, blesbok) based on neutral and coding gene markers. Examination of the control region demonstrated extreme lack of diversity within bontebok revealing only one unique matriline, which was not found within blesbok. Microsatellite analyses confirmed the mitochondrial data and showed strong genetic partitioning and differences in genetic diversity for each subspecies. Allelic diversity of the major histocompatibility class II gene DRB was investigated and found to be extremely polymorphic in numbers of alleles, number of amino acid site changes, and genetic distance. I suggest that the evolution of DRB diversity is governed by over-dominant selection and/or heterosis as evidenced by the high number of non-synonymous changes found within the peptide binding region as well as the high number of heterozygous animals. The results of this study reflect past demographic events experienced by each subspecies. Erosion of molecular genetic variation in bontebok is most likely due severe reduction in population size caused by over-hunting and stochastic events. Blesbok antelope display moderate levels of genetic diversity, which was expected given their relatively stable demographic history. Based on the genetic findings from this study, I recommend the retention of the subspecies designation and that each group be managed separately. Furthermore, I suggest careful management of the remaining bontebok herds in order to conserve the unique genetic diversity of these rare antelope for future evolutionary change.