SUMMARY

A comprehensive molecular study was conducted in order to reveal levels of genetic polymorphism in bontebok and blesbok antelope and to define the degree of genetic substructure between the two subspecies. Gene markers were also used to assign individuals to specific categories (subspecies, hybrid). The results of this study can be used in further management of each subspecies.

The levels of genetic diversity revealed in the control region reflected each subspecies demographic history. Only one control region lineage was revealed by SSCP and sequence analysis in bontebok while five others were found in blesbok. The subspecific control region haplotypes demonstrated the unique evolutionary lineages of the species. Sequence divergence estimates were used to approximate a time divergence (1 – 2 MYA) since the two subspecies shared a common ancestor.

Haplotypic diversity of blesbok was compared to other antelope species and found to substantially lower. This finding may be explained by evidence that blesbok failed to expand a range out of South Africa throughout their evolution during the Pleistocene. This endemic antelope may have not been as successful as its conspecifics (topi, wildebeest, hartebeest) in withstanding severe climate changes and as a result declined. However, the control region data does reflect population expansion in the present blesbok populations.

Microsatellite data confirms the genetic partitioning and differing levels of allelic diversity found at the control region. Both sets of gene markers are neutral and expected to be strongly influenced by the effects of genetic drift. Analysis of eight polymorphic

microsatellite loci also revealed many private (subspecies specific) alleles that can be used to assign individuals into subspecies classes through cluster and likelihood analyses. Hybrid detection in a test group of animals was impaired by the high frequency of shared alleles between subspecies. Distributions of allelic frequencies were used to reveal the demographic histories of each subspecies.

The class II major histocompatibility complex (MHC) DRB locus was characterized by SSCP and sequence analysis in both subspecies. Allele sequences were generated in order to assess polymorphism at a coding nuclear gene and uncover mechanisms that govern maintenance of polymorphism. The results of this study have revealed that the allelic diversity of the African antelope species far exceeds the reported polymorphisms of any other wild ungulate species. High levels of polymorphism were found within the blesbok (23 alleles) while a lack of diversity was recorded in bontebok (6 alleles). These levels of diversity reflect past demographic events of both subspecies. A majority of the polymorphism was found at the antigen binding sites where nonsynonymous changes were significantly greater than synonymous changes. This and the apparent trans-species relationship among alleles in a bovid phylogeny suggest the evolution of diversity by heterosis or frequency dependent selection.

Bontebok antelope have economic and ecological value to South Africa and should be regarded as a conservation priority. The polymorphism remaining in bontebok populations should be conserved through careful breeding and management plans. I suggest that translocation of bontebok between small populations should proceed to establish gene flow and prevent further breeding between closely related individuals.