

Empirical investigations of intra-specific outbreeding and subsequent introgressive hybridization in natural populations are rare, particularly among conspecific populations of large mammals. Using mitochondrial DNA data (partial control region [496 bp] and cytochrome *b* gene [343 bp] sequences analysed from 95 individuals representing 17 sampling locations scattered through the African miombo [*Brachystegia*] woodland ecosystem) (figure 1) and phylogeographic statistical procedures (gene genealogy, nested cladistic and admixture proportion analyses), we (i) give a detailed dissection of the geographical genetic structure of *Hippotragus niger*, (ii) infer the processes and events potentially involved in the population history, and (iii) trace extensive introgressive hybridization in the species. The present-day sable antelope population shows a tripartite pattern of genetic subdivision representing West Tanzanian, Kenya/East Tanzanian, and Southern Africa locations (figure 2). Nested clade analysis revealed that past allopatric fragmentation, probably caused by habitat discontinuities associated with the East African Rift Valley system, together with intermediary episodic long-distance colonization and restricted, recurrent gene flow have played an predominant role in shaping the extent of maternal genetic diversity (10.4%) and population structure. An extensive (average rate of admixture = 20.0%), but geographically circumscribed and unidirectional hybridization event in the past was inferred, resulting in an extreme (the highest discovered so far in mammals) intra-specific difference of 18.2% among morphologically monotypic sable antelopes from West Tanzania.

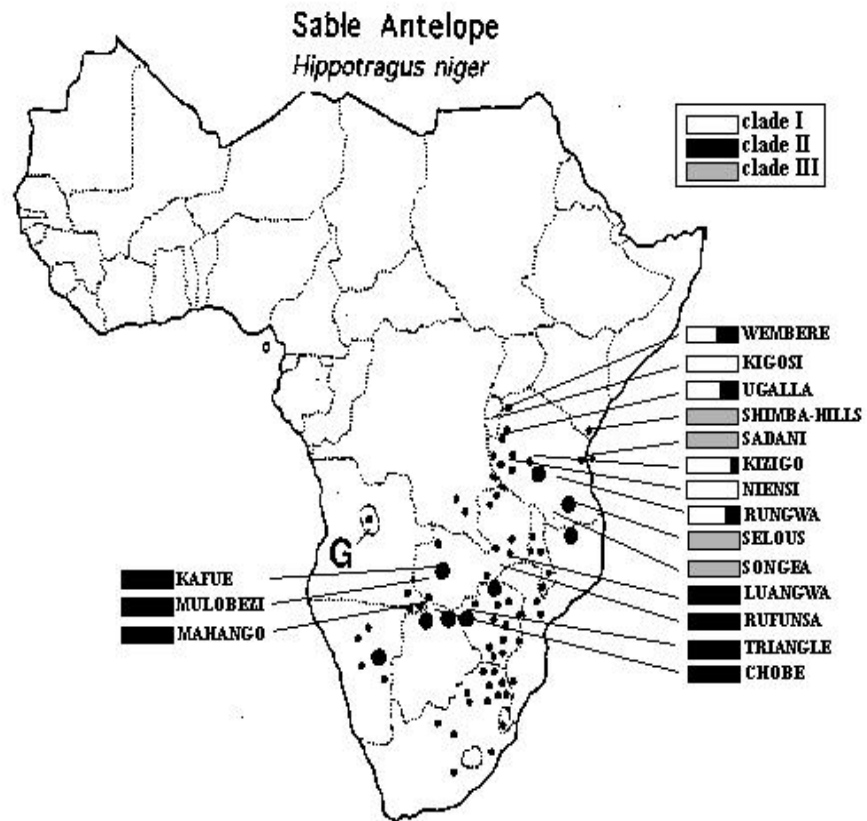


Figure 1 Schematic map showing the sampling localities of sable in Africa and geographical distribution of the three major mtDNA clades. The known extent of occurrence of the species was obtained from East (1999). Large circles designate 1.000 to 10.000 individuals; small circles designate less than 1.000 animals or present but abundance unknown. The subspecies *H. n. variani* is found only in Angola (G).

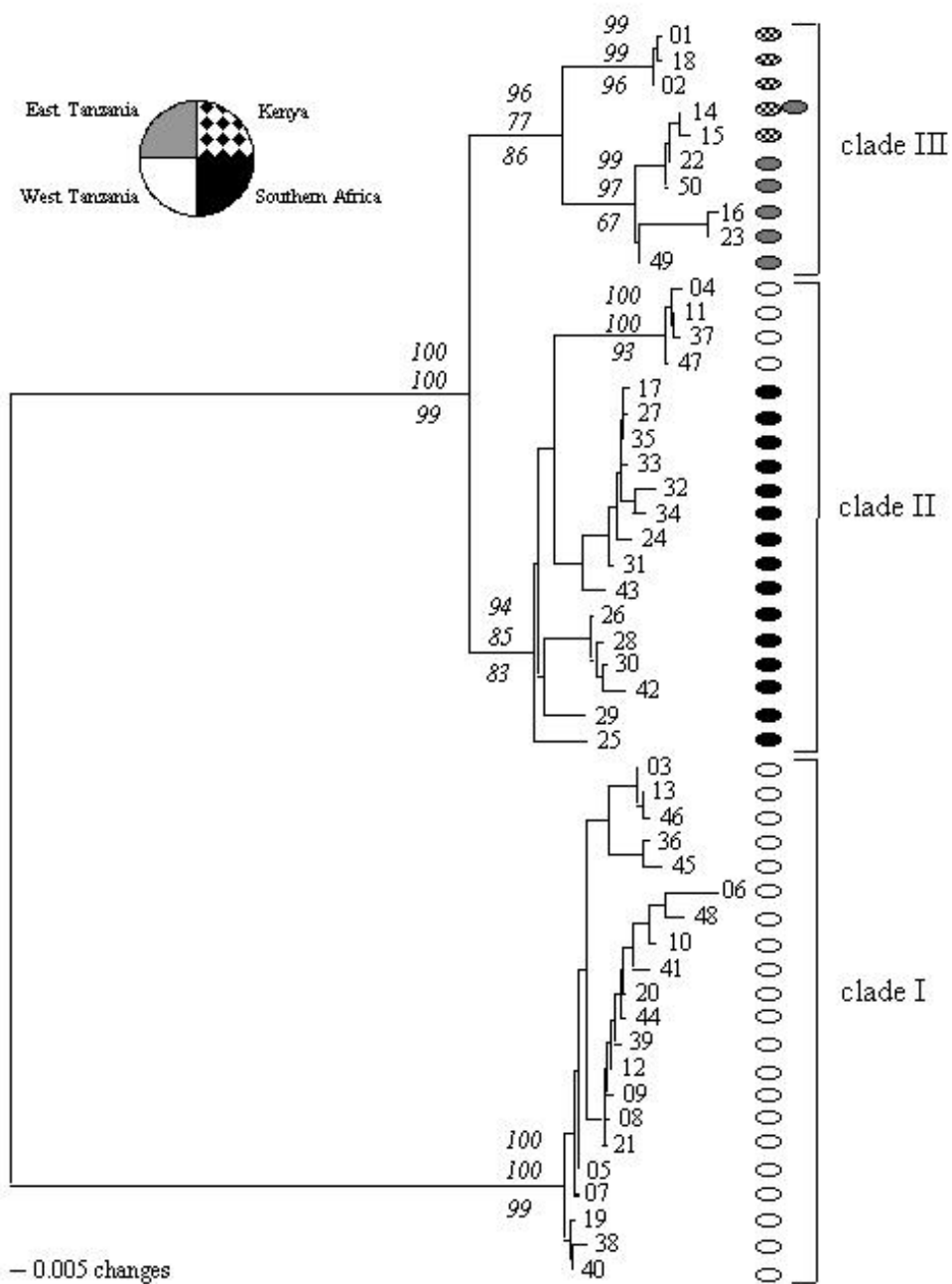


Fig. 2 *Plata et al. 2007*

Figure 2 Phylogenetic relationships among 50 unique mtDNA control-region sequences from 95 sable antelopes. Lables 01-50 represent haplotype designation numbers according to Table 1. The three major clades are indicated by brackets and the geographic origin of the haplotypes is depicted with colours as indicated. The tree shown is a neighbour-joining tree ( $L_n = -1911.6$ ) of the maximum-likelihood distances using a transition/transversion ratio estimated from the data and allowing for among-site heterogeneity ( $\Gamma$  distribution). Bootstrap

values (%) based on 1,000 replicates are given for neighbour-joining (first) and maximum parsimony (second) above branches; the maximum-likelihood support values based on 1,000 puzzling steps are given below branches (only shown for nodes of particular interest).