Phylogeography and Genetic Diversity of the Kenyan Black Rhinoceros

(*Diceros bicornis michaeli* Zukowsky 1965)

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ABSTRACT

The Kenyan black rhinoceros population declined by over 98% in less than thirty years due to habitat destruction and extreme poaching in the 1970s; to a mere 381 animals in 1987 that were distributed in few isolated areas. Various government bodies that have managed wildlife in Kenya adopted the sanctuary approach to manage the remaining black rhinoceros subpopulations. Initially, this approach focused on creating four high security black rhinoceros nucleus breeding sanctuaries that begun taking threatened black rhinoceros in the early1980s. The approached proved very successful in rehabilitating black rhinoceros populations and new sanctuaries were seeded in Kenya. By 2008 the sanctuaries had increased to 14 and where holding over 650 animals.

However the translocations were not based on any empirical genetic information and thus, posed the risk of introducing outbreeding depression and breakdown of locally adapted genotypes in the black rhinoceros subpopulations. Kenya Wildlife Service (KWS) has also partitioned the metapopulation into lowland and highland subpopulations that are managed separately with strong emphasis in avoiding translocation of black rhinoceros between them. The genetic effect of this management strategy is not known. This study focused on generated information on the genetic status in the extant Kenyan black rhinoceros subpopulations. The information will be used by KWS in the formulation of a genetically viable management strategy for the Kenyan black rhinoceros subpopulations.

Twelve subpopulations were sampled for this study. General standard molecular methods were employed. Genetic information was obtained from 408bp mitochondrial D-loop sequence from 170 individuals and 145 individuals were genotyped at nine autosomal loci. Both model based and standard methods were used to examine the data.

Both mtDNA and microsatellite (nDNA) markers detected moderate genetic diversity in the Kenyan black rhinoceros metapopulation (h =0.78±0.027, n = 170; Ho =0.70±0.087, n=145) that is consistent with previous studies on *Diceros bicornis michaeli*. However, mtDNA and nDNA diversity varied between subpopulations; while Masai Mara had the highest mtDNA diversity, the least nDNA diversity, Lewa WC had exactly the opposite. The lack of genetic diversity detected by microsatellite data in Masai Mara unlike that detected by mtDNA illustrates the stochastic nature of the correlation between nDNA and mtDNA diversity in subdivided small populations

Findings from this study suggest that Masai Mara is fairly distinct subpopulation, with the highest inbreeding and isolation level. They also suggest that there is no distinct lowland - highland subpopulation grouping and that there is no historical gene flow barrier. The highest component of genetic diversity is still partitioned among individuals, hence to preserve genetic variability in the various subpopulations it will be important to conserve as many individuals as possible and in the event of translocation; evaluate keenly the genetic orientation of both the donor and recipient subpopulations.