rhino is 3.5 million years. The estimated time of divergence between the two species agrees well with fossil evidence (Hooijer, 1969), but the two million year divergence time for the two geographically separated subspecies is surprising; the mtDNA analysis suggests that little or no gene flow has occurred between the races for this period.

The intraspecific variation in mtDNA observed here in the white rhino is consistent with levels of intraspecific variation found in other species such as macaques, apes, rodents, sheep and goats. The intergeneric difference (7%) for the mtDNA of *Ceratotherium* and *Diceros* is somewhat lower than observed in mtDNA studies on other taxa.

We may tentatively conclude that, whereas morphological divergence between *simum* and *cottoni* has been slow (due perhaps to similar selection pressures or convergent evolution), the mtDNA analysis exposes significant genetic differences in these two forms. A second *C.s. simum* individual's mtDNA was subsequently studied, with essentially similar results. However, more sampling is required, in particular to verify the basic level of intraspecific variation in a particular race of white rhino, so that we can be certain that the differences between the northern and southern races are not in fact normal intraspecific polymorphic differences. in addition to increasing the sample size (ideally about 10 rhino from each race should be studied), the number of restriction enzymes could also be increased. *Comments by Oliver Ryder (Zoological Society of San Diego)* While the analysis of mitchondrial DNA of northern and southern white rhinos displays clear differences, no significant differences have been elucidated from protein electrophoretic studies carried out at the University of California, San Diego (A. Merenlender and D._Woodruff). Twenty-six presumptive loci were examined from five northern white rhinos, 14 southern white rhinos and five black rhinos (all *michaeli).* The electrophoretic difference between the northern and southern forms was approximately one-tenth that between white and black rhinos, whereas the. mitochondrial DNA studies had shown a difference between the northern and southern races which was about one-half of the mitochondrial DNA differences between the white and black rhinos.

Additional samples of northern white rhinos have been obtained from animals in captivity at Dvur Kralove, Czechoslovakia and will be subjected to mitochondrial DNA analysis. Additionally, chromosome studies of both black and white rhinos are very limited and should be undertaken. Both of these projects are underway in research supported by the Zoological Society of San Diego and the Ellen B. Scripps Foundation.

The phylogenies derived from fossil, electrophoretic, and mitochondrial DNA studies agree, but questions arise over the rates of evolution and times of divergence between the taxa. It is known that the rates of divergence in different animal lineages vary greatly and it would seem that the genetic loci studied by protein electrophoresis may have a particularly slow rate of evolution in rhinos in comparison to other vertebrates. This is consistent with the mitochondrial DNA findings. The fact that the protein electrophoretic studies indicate that genetic distances between the northern and southern white rhino are no more than those that can be expected in a single randomly mating population, while the mitochondrial DNA studies indicate longstanding genetic isolation, may be due to the difference in rates of evolution of nuclear genes (assayed by protein electrophoresis) a mitochondrial DNA or they may be due to a rehybridization event. Limited breeding occurring between rejoin populations that had been sepa-rated for some time has led merging of nuclear genes with retention of mitochondial DNAs of only a single population. Generally, the phenomena require recent genetic interaction of the previously separated populations.

While conservation decisions may need to be ma immediately, a clearer understanding of the systematics both white and black rhinos will require further studies chromosomes, protein electrophoresis, mitochondrIal a nuclear DNA genes.

Comments by Don Melnick (Columbia University)
In applying genetic methods to conservation goals we must be careful to avoid placing too much importance on subspecies designations and, instead, assess the distribution of genetic, morphological and ecologic variation throughout a species' range. It is these variants that we wish to conserve in the most efficient, cost-effective w and not the somewhat arbitrary taxonomic distinction between so-called subspecies.

With this in mind, it is necessary to investigate the distribution of genetic diversity (Nel, 1973) across the remaining black rhinoceros populations, in order to establish how much of the species variability can be attributed differences within populations as opposed to difference between populations. This will help us avoid some of the difficulties which have arisen in interpreting the results oft white rhino studies.

The relevance of genetic diversity analysis to rhino conservation in Africa can be Illustrated by an example of two Asian primate species (Melnick, 1987). Only 5% of the genetic diversity found among rhesus monkeys across Asia can be attributed to differences between animals in different regions. The remaining 95% of species diversity is intrapopulation diversity that can be found in any single region. In contrast, 41% of the genetic diversity found among long-tailed macaques can be attributed to difference between regional populations of this species. Hence, if the strategy were devised to conserve the greatest amount on genetic diversity in these primates it would entail the conservation of many more regional populations of the long-tailed macaque than the rhesus monkey. Given the scarcity of resources available for the conservation of the black rhino, we need to determine which of these two types of genetic structure exist.

With the assistance of the New York Zoological Society, the AAZPA and the AERSG, a genetic survey of the black rhino has commenced, with the aim of analyzing mtDNA and bloc proteins in reasonably-sized samples from populations different parts of Africa. Thus far, blood samples from 3 individual black rhinos have been collected in Zimbabwe by P. du Tout, sampling is underway in Kenya and some samples may also become available from South Africa. Sampling very opportunistic, since it usually depends on translocation exercises. It may be very difficult if not impossible to get samples from central Africa. In addition to the wild-caught rhinos, we have collected, with the help of participating zoo blood samples from 12 captive rhinos of Kenyan origin. protocol for tissue collection has been developed and ha been circulated to those who may be in a position to obtain samples.

ECOLOGICAL ADAPTIONS OF RHINOS

Summary of discussion
N. Owen-Smith noted that the feeding ecology of northern white rhinos may well differ to that of the southern white rhinos. The latter graze on short, nutritious grasses while the northern animals live in a wetter habitat, with long fibrous grasses. K. Hillman-Smith confirmed that this is a possibility but relevant research has not yet been undertaken in Garamba National Park. Casual observations indicate that

the northern rhinos may eat more dicotyledons than the southern, and they have to survive in tall grasses he such as *Hyparrhenia* and *Loudetia* in the wet season, and in burnt areas during the dry season. Their social behaviour appears similar to that of the southern rhinos although ranges are about 10 times larger; this may be due to the very low population density in Garamba.

It was generally agreed that estimations of divergence times, subspecies designations and other phylogenetic/taxonomic aspects do not necessarily allow us to identify "evolutionary significant units" (ESU's). Important ecological adaptations may remain hidden from biochemists investigating genetic material and blood proteins, and will almost certainly not be picked up through skull measurements, so it is necessary to investigate the range of habitats in Africa (with their varying selection pressures) in order to outline common-sense strategies for both continental and national rhino conservation initiatives. If a group of rhinos from one part of the species' range is not likely to adapt to different environmental factors when moved to another part of the range, then it is obviously important to conserve representatives of the original populations of both regions.

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APPLICATION OF DECISION ANALYSIS TO BLACK RHINOS
Discussion Leader LYNN MAGUIRE

INTRODUCTION
Purpose
The presentation had three purposes: (if) to introduce several issues crucial to the management of small wild or captive populations; (ii) to propose for discussion some strategies for the coordinated management of wild and captive populations of black and white rhinos; and (ill) to examine two elements of the proposed strategies using formal methods for decision making under uncertainty. These methods have proved useful in developing management plans for other endangered species, including black-footed ferrets (Maguire, 1987a) and tigers (Maguire, 1987b).

Small population management
Several features of the demography and genetics of small populations have important implications for their management.

(I) The concept of *minimum viable population size* (MVP) (Schaffer, 1981) suggests that populations cannot be self-sustaining below some minimum level. Small populations are particularly vulnerable to extinction due to stochastic fluctuations: demographic (e.g. sex ratios at birth), environmental (e.g. variations in food supply), catastrophic (e.g. fire), and genetic (e.g. fixation of deleterious alleles).

(ii) Due to nonrandom mating systems, unequal family sizes, fluctuating population size, and other factors, real populations have an *effective population size* (Ne) that is often far lower than census size, which means that genetic variation Is lost much faster than would appear on the basis of total numbers. Loss of genetic variation is a concern because variation is the raw material for short and long term fitness, in the wild and in captivity.

(iii) Although a relatively small number of founders can capture most of the variation from a larger population initially, this variation will be lost quickly if the population stays small. Black rhinos have declined quickly, suggesting that the remaining animals may provide a good sample of previous levels of genetic variation, but not for long.