

have an exceptional distribution: mitochondrial DNA derived from forest elephants is present in savanna elephant populations, suggesting that hybrid females have successfully back-crossed to unhybridized savanna males. Within species, the two markers reflect sex differences in dispersal and reproductive variance. Genetic patterns are in agreement with the observation by Petit and Excoffier (Trends Ecol Evol. 2009 24:386-93) that across almost all pairs of species that hybridize, the delimitation of species will be more effective with markers experiencing high levels of gene flow. These findings are placed in the context of similar patterns reported between other species in which the dispersal of one sex is severely circumscribed, to recent reports regarding the ancient “conversion” of populations of bears (genus *Ursus*) from one species to another through sex-specific dispersal, and to evidence for widespread genetic introgression across felids universally recognized as distinct species. These patterns are also discussed in light of recent reports of inter-species introgression across living and extinct elephantids, and a recent review of molecular studies of elephantids (Annual Review of Animal Biosciences 3:139-167; 2015). (With thanks to the US Fish and Wildlife Service African Elephant Conservation Fund)

### **Genetic status of the black rhinoceros - from DNA profiling to whole genome analysis**

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I describe the results of a range wide conservation genetic assessment of the black rhinoceros and the first assembly of a black rhino genome. We analyzed a large mitochondrial and nuclear dataset containing both extant samples and colonial-era material from museums throughout the world. We found range-wide genetic erosion and pronounced structure in this species for the first time, documenting a remarkable loss of genetic diversity. We were able to identify conservation units to maintain evolutionary potential and for population management. The genome of the southern black rhino has recently been completed and I will describe some preliminary results from the first assembly.

### **Genetic advances and the conservation of African forest and savanna elephants**

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Little or no nuclear gene flow occurs between African savanna elephants (*Loxodonta africana*) and African forest elephants (*L. cyclotis*), establishing that they comprise separate species. In elephant species, males disperse, whereas females remain with their natal social group, leading to discordance in the phylogeography of nuclear and mitochondrial (mt) DNA patterns. Nuclear gene flow is mediated by the dispersing males, while maternally inherited mtDNA exhibits low geographic dispersal. We examined the effectiveness of mtDNA for assigning the provenance of African elephants or their ivory, so that law enforcement efforts could be targeted toward poaching hot spots. For 653 savanna and forest elephants from 22 localities in 13 countries, 4258 bp of mtDNA was sequenced. We detected eight mtDNA subclades, seven of which had regionally restricted distributions. Among 108 unique haplotypes identified, 72% were found at only one locality and 84% were country specific, while 44% of individuals carried a haplotype detected only at their sampling locality. We combined 316 bp of our control region sequences with those generated by previous trans-national surveys of African elephants. Among 101 unique control region