

haplotypes detected in African elephants across 81 locations in 22 countries, 62% were present in only a single country. Applying our mtDNA results to a previous microsatellite-based assignment study would improve estimates of the provenance of elephants in 115 of 122 mis-assigned cases. Nuclear partitioning followed species boundaries and not mtDNA subclade boundaries, consistent with the species barrier between them. For taxa such as elephants in which nuclear and mtDNA markers differ in phylogeography, combining the two markers can triangulate the origins of confiscated wildlife products. This may be especially relevant given that record numbers of ivory seizures have been reported in recent years. We will also discuss other recent findings based on genetic analyses of elephant populations and how they may impact the conservation of Africa's elephants. Funded by a US Fish and Wildlife Service African Elephant Conservation Grant.

Conservation genetics of Greater One-horned Rhinos in India – from identifying individuals to determining conservation priorities

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Being a major flagship species in its range distribution and emerging from a catastrophic population decline in the past, the greater one-horned Rhino (*Rhinoceros unicornis*) population management and conservation requires a multi-disciplinary effort, including the use of molecular tools for genetic monitoring of natural populations. In India, seven protected areas harbour more than 70% of the extant global population of this species. The contemporary populations of rhino are distributed across a landscape of fragmented habitat patches of protected areas, with restrictions to the natural movement and gene flow among them due to various land use patterns. This demanded an investigation on whether this distribution pattern facilitates any demographic and genetic exchange of rhinos among the protected areas in India and whether any genetic management of these populations are required in order to ensure their future survival. Genetic population monitoring of rhinos was initiated in 5 different protected areas of India, viz. Kaziranga National Park, Orang National Park, Pobitora Wildlife Sanctuary of Assam and Gorumara National Park and Jaldapara National Park of West Bengal, with 98% of the total rhinos present in the country. Microsatellite markers were optimized to identify individual rhinos and Y-chromosome linked markers to identify gender from noninvasively collected dung samples, along with optimization of sampling techniques to meet the requirements of genetic studies. Using these techniques, genetic census of rhinos was carried out successfully in Gorumara National Park. The optimized technology finds wider applications in forensic DNA investigation of rhino poaching cases. The same genetic markers were used to carry out a wider investigation of genetic population structuring and gene flow among the protected areas. Significant level of genetic differentiation was observed between Assam and West Bengal, especially, Gorumara National Park showing a unique genetic signature. Given the degree of population genetic structure observed, prolonged separation of these protected areas is unwanted as this could lead to further loss of genetic diversity, consequently, affecting long term viability of the species.