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Genetic structure of tiger populations in India and its significance in forensics

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The goal of tiger conservation is to maintain sufficiently large populations of each subspecies in its natural habitat that ensured high probabilities of long term survival. Poaching for illegal trade is a serious threat across its range. Success in tiger conservation is to curtail global trafficking in tiger parts and products. Development of genetic tools has enabled tracking poaching of endangered species to their source population. Project is aimed at establishing genotyping data profile of tiger population in India and use for tracking poaching cases to its geographic origin. We examined genetic structure of tigers based on mitochondrial and nuclear DNA using scat samples collected from tiger reserves and tissue samples. Mitochondrial DNA data indicates unique haplotype in *cytochrome b* gene, which was used to differentiate population from northern (Rajaji to Pakke Tiger Reserves) to rest of the tiger populations. A major challenge in developing genotyping profile from nuclear DNA is to identify suitable microsatellite loci which are suitable for poor to good quality scat samples therefore, we screened 60 loci. Of these, 26 loci ranged from moderate to good for using them on such samples that were <200 bp. We examined genetic structure of samples collected from Rajaji-Corbett Population (RC), Ranthambhore Tiger Reserve (RTR), Buxa Tiger Reserve (BTR), Central India (CI) and zoo (Z) tiger populations. The mean observed heterozygosity ranged 0.28 to 0.69 and was in the order of CI>RC>BTR>Z>RTR. The observed mean effective allele per locus ranged 1.53 to 3.76 with the highest in RC population. F_{st} values for population structuring indicates a population differentiation from moderate to high among examined populations and observed values ($F_{st}>0.033$) are suitable for Bayesian based population assignment. Genetic variation within population was c.82%, where as, among population was 18%. We discuss population assignment based on Bayesian approach for tracking tiger poaching.

Biography

S P Goyal, MSc and PhD (Zoology) is working with the Wildlife Institute of India, Dehra Dun, India for last 27 years. He worked on a number of species ranging from Fruit bats to elephant. He is Nodal Officer, Wildlife Forensic Cell of the Institute. One of the important tasks is to develop protocols for species identification which is needed in implementation of national laws and International treaties. He has initiated a research work on "*Panthera tigris* genome: Implications in forensics" mainly to establish reference genetic database to determine geographic origin of poaching cases and has immense global significance. He has widely traveled across world to acquire new technologies for use in developing wildlife forensics and in other issues of wildlife conservation.

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