Smithsonian Scientists Provide Hi-Tech Method to Study Endangered Species

The conservation and management of endangered species is a primary focus for the National Zoo’s research staff who have pioneered in research and veterinary science methods for decades. Now Zoo and National Museum of Natural History (NMNH) scientists and a former Smithsonian pre-doctoral fellowship student are credited with refining a noninvasive technique, faecal sampling followed by molecular analysis of faecal DNA, to obtain information on wild mammals without the need to capture, handle or observe them. This method has previously been criticized because, if conducted inappropriately, it yields too many scoring problems and genotyping errors making the results unreliable.

The endangered San Joaquin kit fox (Vulpes macrotis mutica) population in California, which has been studied by the Zoo for 17 years, was chosen as the research target. Researchers from the Conservation and Research Center and the Genetics Program joined forces with colleagues from the University of Washington and University of Montana along with trained locator dogs to collect hundreds of faecal samples (scats) in the Carrizo Plain National Monument. The location of each scat collected was georeferenced using a Global Positioning System (GPS) unit. The team’s previous research had shown that the trained dogs were 100% accurate at distinguishing kit fox scats from those of other species. DNA was extracted from every scat sample and sex markers and six microsatellite loci were examined; then five previously recommended tests for reducing and tracking error as well as several new spatial tests developed by the investigators were applied. Results showed very low rates of genotyping error, and analyses of the individual scat genotypes provided information on kit foxes that was in good agreement with data gathered using more traditional, invasive techniques (trapping and radio collaring). Results on fox movement patterns, for instance, agreed with prior field observations.

An important conclusion of this study is that a systematic collection of “fresh” scats followed by molecular typing can provide reliable data on species, differentiate individuals and provide data on sex. Genetic data can further reveal relatedness, movements, and latrine use. The technique, with some further testing, may prove useful in deducing the probable diameter of a fox home range since it was found that 96% of foxes deposited scats within a distance no greater than 2,107 m. Finally, researchers foresee faecal sampling, when paired with appropriate steps to ensure genotype reliability, as being quite applicable to studies of other elusive or rare animal populations.

Rare Vulture Cited in India

By Raju Lal Gurjar, Wildlife Institute of India

Breeding and roosting sites of the critically endangered Indian Long-billed Vulture (Gyps indicus) have been discovered in the Satpura Tiger Reserve, Madhya Pradesh, India. A total of 48 vultures are living in a hill complex cliff. The site is quite inaccessible to humans and wild animals from both the ground level and from the top of the cliff.

Satpura Tiger Reserve, Hosangabad, Madhya Pradesh (22° 15’ - 22° 45’ N; 77° 50’ - 78° 30’ E) is in the Satpura range (Mahadeo Hills). Bori Wildlife Sanctuary and Pachmarhi Wildlife Sanctuary are a part of Satpura Tiger Reserve. The forests are tropical dry deciduous, tropical moist deciduous and sub-tropical. The biodiversity is rich with over 1,300 species of plants, including numerous rare bryophytes and pteridophytes, 50 mammal species, 30 reptile species and 254 species of birds, including the vultures.

Current Literature


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