E29 Conservation Genetics of Bioko Monkeys

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After attending this presentation, attendees will understand how genotypic information from three endangered primate species can be used to further develop forensic wildlife molecular methods.

This presentation will impact the forensic science community by demonstrating how the use of genetic information can be used to assess the genetic health of three endangered primate species. More importantly, it will illustrate how this information can be used by forensic biologists to develop testing methods that can be used to deter crimes against wildlife.

Wildlife forensics deals with the legal and environmental aspects of crimes against animals. Newer research in this field is exploring the use of molecular approaches to forensic testing which can be used to deter crimes against wildlife. The focus of this research is three endangered primate species, *Procolobus pennantii pennantii* (red colobus), *Colobus satanas satanas* (black colobus), and *Mandrillus leucophaeous poensis* (African drill), from Biko Island. Biko Island is home to a multitude of unique species and is one of the world's top biodiversity hot spots. Many of the primate species on the island are endangered due to a thriving bushmeat market and habitat degradation. Despite legislative efforts and hunting bans making it illegal to kill these endangered species, the people on the island continue to do so with little to no consequence. While it is difficult to fine or prosecute individuals who hunt these creatures, the availability of genetic testing which can be implemented for forensic testing purposes, may deter hunters from preying on these protected species.

The goal of this research is to genotype the three endangered primate species mentioned above in an effort to determine genetic health of the populations for conservation efforts while evaluating loci for phylogeographic utility. No previous studies regarding the loss of heterozygosity of these primates have been published. Therefore, this research is desperately needed. Three classes of loci — traditional, bioinformatic and International Haplotype Map Project (HapMap) pairs — totaling 67 loci across the whole genome, have been identified as potentially valuable for genetic testing within these populations. This research focused on those loci located between chromosomes 1 and 2, of which there are 19 in total. Of the three species of interest, 49 individuals were genotyped using the three primer methods indicated above. Loci were scored as homozygous or heterozygous. Currently, four loci with heterozygosity ranging from 9% to 33% have been identified for use in determining the genetic health of these populations. Additionally, two of these loci are promising candidate markers for implementation in forensic conservation efforts.

Wildlife Forensics, Bioko Primates, Genome Sequencing

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