B150 Forensic DNA Identification of Feline Hairs: Casework and a Mitochondrial Database

Joy L. Halverson, DVM, MPVM, Questgen Forensics, 1902 East 8th Street, Davis, CA 95616; Leslie Lyons, PhD, Department of Population Health and Reproduction, School of Veterinary Medicine, University of California, Davis, CA 94022*

After attending this presentation, attendees will have a greater awareness in the forensic community of the tools and utility of individual identification of pets as part of criminal investigation. DNA identification of animal hairs via mitochondrial haplotyping can provide a useful link between a victim and a suspect.

This presentation will demonstrate that animal hairs are a common finding in a carefully scrutinized environment such as a crime scene. The application of forensic DNA analysis techniques to hairs and other animal-derived samples opens previously unrecognized avenues of criminal investigation.

DNA typing of samples from pets, including cats, has contributed to homicide investigations and convictions in the United States and Canada. Indeed the first example of forensic DNA identification of animal hairs was a homicide investigation in Nova Scotia in which cat hair was found in the pocket of a jacket discarded near the murder scene. STR profiles of the hair matched that of Snowball, a cat belonging to the suspect's parents. While animal hairs are the most frequent animalderived sample recovered by crime scene investigators, such hairs are usually shed telogen hairs.Despite the availability of feline STR markers, there is often insufficient nuclear DNA to perform STR typing. As in humans, mitochondrial DNA can be extracted from the hair shaft and characterized by DNA sequencing or other sequence detection methods. Assigning the significance of a DNA match between an evidence sample and reference animal requires knowledge of the frequency of the mitochondrial type in the domestic cat population. This paper presents the database derived from DNA sequencing of the mitochondrial control region from 155 purebred cats and 105 mixed breed cats.

Domestic cats have elements of complexity in the mitochondrial control not seen in dogs or humans. Between a relatively short Hv1 region and the Hv2 region is an AT-rich region with 3-5 tandem, 80 base pair repeats. While this repeat region can be avoided by the amplification and sequencing of just the 3' half of the control region, the 5' end is rich in polymorphism. Roughly 50% of cats actually show length polymorphism when the entire control region is amplified. Two to three fragments 80 base pairs apart can be electrophoretically separated demonstrating that the variability is derived from the tandem repeat region. A systematic analysis of this variability is required to ascertain its utility in reliable individual identification.

In order to generate a feline mitochondrial database, primers were designed to amplify the entire feline mitochondrial control region (approximately 1100-1300 base pairs) analogous to 16000 bp to 400 bp of the Andersen human mitochondrial genome. A total of 260 cats, including 155 purebred cats representing 14 foundation cat breeds, as well as 105 mixed breed cats were analyzed. The samples from the purebred cats had been held in storage for some years and many were too degraded to amplify the entire region. Sets of internal primers were designed to amplify smaller, overlapping regions for sequencing. These primers are also being investigated for nested PCR amplification, a procedure often required for processing of evidence hairs. Nested amplification through the tandem repeat region presents additional challenges that are being investigated. A separate study has been undertaken to ascertain whether heteroplasmy was detectable in feline hair samples and, if so, to what degree. Results from the study are important for the continued validation of feline mitochondrial haplotyping.

Feline mitochondrial typing was useful in a recent homicide investigation. In Iowa in 2000, Tracy Ann Carson disappeared; her body was found 7 months later. The body had been wrapped in a large piece of fabric, partially burned and buried; spring flooding unearthed it. Investigators found a variety of animal hairs on the fabric. Feline hairs taken from the fabric had mitochondrial haplotypes consistent with the three cats owned by the suspect. Based on a previous database based only on the 3' end of the feline control region, the haplotype frequency of the two siblings cats was 31% (the most common type) and the haplotype frequency of the third cat was 1.25%. Just before trial the suspect, Ben O'Donnell, pleaded guilty to second degree murder.

DNA typing of animal-derived samples opens new possibilities for linking suspects to crime scenes or victims. The close relationship between people and their pets is a potentially valuable source of evidence to the observant investigator. The value of such evidence will be determined by the scientific validation of both its power and its limitations.

Animal Hairs, DNA Identification, Mitochondrial DNA

 ** Presenting Author*