A137 A Cold-Case Investigation Utilizing Canine STRs, mtDNA, and Y-STRs

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After attending this presentation, attendees will understand that forensic analysis of canine DNA is under utilized in crime scene investigations. Due to the number of homes with dogs, the close relationships between owners and their pets, and the easy transfer of pet hair to various substrates, pet hair has the potential to provide valuable probative information. Attendees will be educated on the discriminatory power of canine DNA through presentation of a multi-pronged approach to analysis of dog hairs in a cold-case homicide investigation.

This presentation will impact the forensic science community by stimulating interest in and increasing awareness of an untapped source of potential DNA evidence. The application of this technology can provide investigative leads, elucidate connections between victims and suspects, and contribute powerful empirical data at trial.

In May, 2006, the nude body of an eighteen-year-old female was discovered wrapped in a sheet and shower curtain and deposited in a wooded area. The cause of death was asphyxiation, and she had been dead less than twenty-four hours. At the medical examiner's office, vacuum sweepings were taken from the sheet, shower curtain, and transport sheet. Microscopic comparisons performed by the Federal Bureau of Investigations (FBI) Trace Evidence Unit identified some of the hairs obtained from the vacuum sweepings as dog. The victim did not own pets. Her boyfriend was eliminated as a suspect, and the case went cold. The FBI determined that the hairs were visually similar to those from dogs owned by the man who first discovered the body. To eliminate him as a possible suspect, the questioned hairs, along with exemplars from two dogs belonging to the man, were submitted to the Veterinary Genetics Forensic Laboratory at the University of California, Davis, for DNA analysis and match comparison. The hairs were further sorted at George Washington University for length and root swelling to optimize DNA yield.

Ten hairs were chosen for DNA extraction using a phenol:chloroform protocol and then quantified for canine DNA using a TaqMan-based quantitative PCR assay. One hair from the sheet and one hair form the transport sheet yielded sufficient DNA to proceed to genotyping. Amplification was performed using a panel of 15 autosomal short tandem repeat (STR) markers and the SRY gene for sex identification. Both hairs yielded a partial DNA profile from a male canine that excluded the two suspect dogs as the source. However, amplification of Y-chromosome STRs and sequencing of the canine hypervariable region I (HVSI) of the mitochondrial DNA (mtDNA) provided insights into the relationship between the questioned and known hairs. The questioned hairs yielded Y-STR profiles that matched the Y- chromosome haplotype obtained from the male suspect dog and a mitochondrial haplotype that matched both suspect dogs. Furthermore, the questioned hairs shared an allele at every locus with the female dog, qualifying her as a possible parent or offspring. The male dog was excluded as a parent or offspring at three loci. The two suspect dogs shared a mtDNA haplotype as well as alleles at all loci but one, indicating a potential sibling relationship. Due to the shared Y and mtDNA haplotypes, the amount of allele sharing between the questioned and known hairs, and the exclusion of the male dog as the sire or offspring of the hairs collected from the victim, investigators were advised to locate male siblings of the two suspect dogs as possible sources of the hairs recovered from the victim.

Dog, DNA, Cold Case

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