B109 Hair of the Dog: DNA Analysis of Probative Canine Hairs in the Wayne Williams Investigation

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After attending this presentation, attendees will be educated in the probative value of archived crime-scene animal hair. The collection, sampling, and testing strategies used in this case are presented for implementation in other laboratories.

This presentation will impact the forensic community by addressing the needs of the forensic community by assessing the potential for DNA analysis to augment microscopic examinations of animal hairs in cold case criminal investigations. Microscopy is becoming a lost art in the field of forensic science and fewer criminalists are developing the expertise this discipline requires.

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Forty percent of homes in the United States have one or more dogs and thirty-four percent have one or more cats. Therefore, animal biological material is abundant in the domestic environment and is frequently present on evidence collected during crime-scene investigations. Historically, microscopical comparisons of animal hair have been made. This can be difficult due to the amount of variation found in the color, length, and texture of animal hairs both within and between individuals and the lack of published research on the validity of animal hair comparisons. The advent of molecular diagnostic tools for the analysis of animal DNA has enhanced the utility and significance of crime-scene animal hairs.

For a two-year period from July, 1979, to May, 1981, a series of murders targeting African-American children—which became known nationwide as the Atlanta Child Murders—were perpetrated on the citizens of Atlanta, Georgia. In June, 1981, 22-year-old Wayne Williams was charged with first degree murder in the deaths of two of adult male victims: Jimmy Ray Payne and Nathaniel Cater. In addition to the two murder charges, Atlanta prosecutors included ten pattern cases to establish a connection between the Payne and Cater murders and those of area children. Microscopic comparisons of fibers and dog hair from Williams' home and vehicle were made to those collected from the victims. Twenty-four deaths were ultimately attributed to Williams by Fulton County authorities.

At the request of the Georgia Innocence Project and pursuant to a court order, the Georgia Bureau of Investigation selected dog hairs that had been determined to be microscopically similar at the time of the 1982 trial and submitted them for DNA analysis. Due to the length of time since the hairs were collected, their storage on slides, and the poor condition of some of the victims upon autopsy, a strategy was developed and agreed upon that would optimize testing and minimize sample consumption. Three hairs each from the two indicted cases and three of the pattern cases were removed from their slides and dry mounted for submission to the laboratory. It has been reported that successful amplification of human hairs for nuclear profiling is dependent upon follicular material adhering to the root. Although all tested dog hairs had visible roots, none of the submitted hairs had attached follicular material. The dog hairs collected from the two indicted cases were all shorter secondary hairs while the selected hairs from the pattern cases were all longer guard (primary) hairs. In an effort to assess the likelihood of obtaining nuclear DNA (nDNA) for individual profiling, three hairs with visible roots from one of the pattern cases were pooled in a single extraction. Since the hairs were microscopically similar, it was decided that the opportunity to obtain a nDNA profile outweighed the risk of contamination had the hairs originated from different sources. However, when the pooled hairs failed to yield quantifiable canine nDNA, the course of action was clear. Further testing targeted individual hairs and mitochondrial DNA (mtDNA) sequencing of a 402 base-pair region of the canine hypervariable region 1 (HVI). Subsequent sequencing of two individual hairs from each indicted case and one hair from each remaining pattern case all yielded the same haplotype as the pooled hairs. The shorter hairs from the indicted cases necessitated amplification of shorter HVI regions that were assembled to obtain full sequence coverage. Reference hairs collected from the Williams' family dog for microscopical comparison were then tested and yielded the same mtDNA haplotype as the probative hairs. That sequence has been observed twelve times in our database of 1,219 dogs.

There was no difference in our ability to obtain a mtDNA profile between hairs that had been Permounted and those that had been dry mounted. Hairs with brownish decomposition material on their surface still yielded good mtDNA for profiling. The biggest factor in successful mtDNA amplification was hair type, with longer, thicker guard hairs being the most successful. Even with visible roots, archived dog hairs failed to yield sufficient nDNA for genotyping, but mitochondrial sequencing was valuable in supporting the original microscopical comparisons. **Dog, Hair, Mitochondrial DNA**

 ** Presenting Author*