

INTERNAL VALIDATION OF THE “DOGFILER” STR AMPLIFICATION ASSAY FOR THE ANALYSIS OF CANINE DNA EVIDENCE

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Analysis of Short Tandem Repeat Polymorphisms (STR's) from canine DNA evidence is an effective tool for law enforcement during criminal investigations. As companion animals, dogs traveling with their owners may act as victims, perpetrators, or witnesses to crime. Dogs leave traces of DNA evidence in various types, such as blood and hair, which may be analyzed using canine-specific STR kits. Results from the analysis may be used to link individual dogs to a crime scene or person of interest. STR analysis of canine DNA has been ruled as admissible evidence in court in numerous criminal cases.

Although the admissibility of STR analysis of canine DNA evidence has increased, public crime laboratories have been slow to incorporate the technology as a regular internal function. This is due in part to the lack of nationally recognized standards and accreditations among the forensic science community for guiding the analysis of non-human DNA. Our goal is to demonstrate a model for analyzing canine DNA evidence as a regular internal function of public crime laboratories.

We describe our results toward translating current STR technology into a viable protocol for public crime laboratories. Internal validation studies are performed for assays previously described in literature: a human/canine DNA quantification assay, and the “Dogfiler” STR amplification kit. The impact of sample type on analysis outcome is elucidated.

DNA was extracted from samples, quantified using a human/canine-biplex quantitative PCR assay, and analyzed using the Dogfiler STR amplification kit. Sizing was accomplished by comparing resultant peaks to an allelic ladder. Internal validation studies included sensitivity, precision, species specificity, and evaluation of casework-type samples. Casework-type samples included buccal swabs, blood, shed hair and hair collected directly from groomed locations. Shed hairs were examined for the presence or absence of bulb tissue, and then tested as individual or bundled samples.

The canine DNA analysis process was effective for generating STR profiles from blood, buccal swabs, and hair samples. Sensitivity and precision studies yielded results similar to those exhibited by human DNA quantification and STR amplification kits. Biplex components of the human/canine DNA quantification assay exhibited specificity for human and canine DNA, respectively. The Dogfiler STR amplification kit exhibited specificity for canine DNA. Hairs collected from grooming locations exhibited increased DNA content relative to shed hair collected from the same dog. Partial profiles were generated from individual shed hairs with bulb tissue.

Our validation studies demonstrate an effective protocol for analyzing canine DNA evidence. Blood and saliva samples may be collected as reference or evidence samples. Hair collected from grooming locations may be collected as additional reference samples. Shed hair may be analyzed as evidence samples, although shed hair lacking bulb tissue should be bundled. Quantification using a human/canine-biplex assay permits simultaneous determination of species-specific DNA concentrations. The use of an allelic ladder during profile interpretation promotes standardization in allele sizing. Future studies will focus on translating this protocol into a regular internal function of forensic laboratories.

