B153 Internal Validation of the "DogFiler" Short Tandem Repeat (STR) Amplification Assay for the Analysis of Canine DNA Evidence

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Learning Overview: The goal of this presentation is to demonstrate preliminary validations for the "DogFiler" canine STR amplification assay. The long-term goals are to address the challenges of present canine STR technology and to model a strategy for canine STR analysis for the forensic science community. DogFiler was selected among other canine STR assays due to the accessibility to an allelic ladder and an allele frequency database.

Impact on the Forensic Science Community: This presentation will impact the forensic scientific community by demonstrating competence and enabling performance of canine STR analysis by public crime laboratories.

Dogs may be victims, perpetrators, or witnesses to crime, leaving traces of DNA evidence in various types, such as blood and hair, which may be analyzed using canine-specific STR assays. Results may link individual dogs to a crime scene or person of interest. Canine DNA analysis has been ruled as admissible evidence in court for numerous cases involving abuse, burglary, assault, and homicide.

Public crime laboratories have been slow to incorporate canine DNA analysis as a regular internal function. This is due in part to the lack of required tools, for example, allelic ladders and allele frequency databases, lack of participation by public crime laboratories in validations and casework application, and limitations on the robustness of current canine STR assays. Improvements are needed to promote the advantages of canine STR analysis as tool for human criminal investigations, and to facilitate wider application in public crime laboratories.

DNA was extracted from canine sources, quantified, amplified with DogFiler, and analyzed by capillary electrophoresis. Sizing was accomplished by comparing resultant peaks to an allelic ladder. Internal validation studies included determining sensitivity, evaluating stutter, resolving two-contributor mixtures, and analyzing mock casework samples. Mock casework samples included individual shed hairs comprising bulb tissue. Bundles of shed hair were analyzed as potential evidentiary samples. Bundles of hair collected directly from self-grooming locations were analyzed as potential alternate reference samples.

The sensitivity study showed that canine profiles could be generated from as little as 0.2ng template. DogFiler was used to resolve two-contributor mixtures across varying mixture ratios and input amounts. Full profiles were generated from shed hair bundles and hair bundles collected from self-grooming locations. Self-groomed hair bundles sometimes exhibited significantly greater DNA concentration likely due to the presence of saliva due to grooming. The use of an allelic ladder during profile interpretation promoted standardization in allele sizing. Future goals include applying DogFiler to casework investigations at Harris County Institute of Forensic Sciences (HCIFS) and promoting the application of canine STR analysis in public crime laboratories across the United States.

Canine, Short Tandem Repeat, DogFiler

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