LOOKING TOWARDS UTILITY OF ROUTINE CANINE STR TYPING IN FORENSIC INVESTIGATIONS

Brittania J. Bintz, M.S.
Western Carolina University, Forensic Science Program

There is increasing interest in the use of domestic canine DNA for forensic investigations. Recently, several laboratories have independently developed highly multiplexed short tandem repeat (STR) assays for canine genotyping. The Canine Genotypes Panel 2.1 is a commercially available, forensically validated kit for multiplex amplification of 19 markers targeting 18 autosomal loci and one sex determining locus. Here, we report internal validation of the kit as well as the development of a regional canine database using the SmallPond DNA Profile Matching System. To build the database, DNA was extracted from buccal swabs obtained from domestic dogs with varying degrees of admixture in the southeastern United States (N>250). DNA was amplified using the Canine Genotypes Panel 2.1 and fragment analysis was performed using an Applied Biosystems 3130xL Genetic Analyzer. Resulting profiles were uploaded into the SmallPond software and allele frequencies were calculated and compared to estimates previously published by Kanthaswamy et. al. The utility of the database for canine identification was assessed by comparing genotypes obtained from 35 unknown fecal samples to reference data stored in the database and random match probabilities were calculated. Approximately 77% of all fecal samples tested were positively identified. Our findings demonstrate that the highly-optimized Canine Genotypes Panel v2.1 is capable of discriminant identification of domestic dogs with a high degree of precision even with compromised samples. We further show that our regional database is a sufficiently robust investigative resource for canine identifications.