

CANINE-SPECIFIC MULTI-PLEX STR KIT FOR USE IN FORENSIC CASEWORK

Mikko Koskinen

Finnzymes Oy, Espoo, Finland

A 19-locus multiplex genotyping system, comprised of 18 short tandem repeat (STR) loci and a sex-linked zinc finger locus for gender determination, was used to generate canine population genetic data for assessing the weight of DNA profiles derived from dog biological material. All forward primers were 5' fluorescence dye labeled to facilitate automated genotyping. Allele frequencies and distributions were estimated for 236 unrelated, pedigreed and 431 mixed breed dogs residing in the United States. Interestingly, gametic phase disequilibrium was greater among mixed breed than that observed among pedigreed dogs. Average random match probability for a complete 18 STR profile is approximately 1 in 2×10^{33} using the regional database and 1 in 4×10^{39} using the breed dataset (without correction for population substructure). Genetic diversity distributions among and within both datasets were compared. Each pedigreed dog sample population was genetically distinct and could be differentiated from the mixed breed dog population. However, genetic diversity is slightly clinally distributed among the different US regions. The results herein provide further support for using the allele frequency data with the canine STR multiplex to convey the significance of identity testing for forensic casework, parentage testing and breed assignments.

This research was partially funded by the National Institute of Justice (NIJ Grant No. 2004-DN-BX-K007). This research has been presented at the 2008 NIJ Grantees Conference and at the 2008 International Society for Animal Genetics Conference in Amsterdam, The Netherlands).