B11 A “Whodunit” Solved Utilizing Mixture Interpretation Software With Quantitative Genotyping

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After attending this presentation, attendees will appreciate how useful touch DNA samples can be and gain an understanding of how mixture interpretation tools can be pivotal in deconvoluting difficult mixtures. The algorithms used in the ArmedXpert™ software will also be introduced.

This presentation will impact the forensic science community by demonstrating how a complex DNA mixture from a perplexing case was able to be interpreted, using quantitative genotyping, and led to a useful investigative lead.

Touch DNA is DNA which is deposited when someone touches or comes in contact with an item and leaves sloughed off skin cells behind. It is usually present in very low quantities and full DNA profiles are often difficult to obtain due to the low number of cells which are usually deposited. Because of the nature of touch DNA samples, it’s very rare that a Combined DNA Index System (CODIS) -worthy profile is developed; however, with the help of mixture interpretation software, difficult mixtures, such as those obtained when swabbing for touch DNA, can more readily be interpreted and can result in useful investigative information.

In 2012, the United States Army Criminal Investigation Laboratory (USACIL) received a case involving the abduction of a young child. A little girl was playing on a playground when she was approached by an unknown male who proceeded to kidnap her. Shortly after being captured, the child was able to flee to safety; however, even after she gave a description of the man, investigators had no idea who the abductor was. The child’s pants were subsequently submitted to the laboratory and, during analysis, the pockets were swabbed for touch DNA since it was alleged that the assailant touched that area.

The resulting DNA profile was analyzed using ArmedXpert™, a mixture interpretation software tool that was developed in-house and for which USACIL currently holds a patent. It uses a simple deconvolution strategy based on three rules: (1) shared alleles are shared in proportion to the unshared alleles; (2) where possible, peak height ratios are defined as 100%; and, (3) minimum allele heights are maintained. This software has been invaluable in streamlining the analysis and interpretation process. It has also provided a relatively high level of consistency in final results as determined by the statistical analysis of mixed DNA profiles used during internal competency testing.

With the help of the mixture interpretation software, the DNA profile obtained from the pants’ pockets was able to be interpreted as a mixture of three individuals where the owner could be assumed, a family member could be identified, and a full unknown male DNA profile could be teased out for CODIS submission. In the months following case completion, approximately 150 standards were submitted for comparison; however, no matches were made. Finally, months after the unknown profile was uploaded to CODIS, it hit on an arrestee who has since accepted a plea deal and is currently serving 25 years.

Touch DNA, Complex Mixture, Mixture Software