

## Abstracts

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### Casework Studies with Profiler Plus™

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DNA analysis of short tandem repeats by capillary electrophoresis is quickly catching on as one of the most popular methods of DNA analysis. Its most advantageous feature is that it allows ten loci to be analyzed simultaneously in a process known as multiplexing. Such multiplexing allows for this to be a highly discriminating tool. This presentation will cover the advantages which capillary electrophoresis allows in the interpretation of mixed stains in casework.

In 1997, the Illinois State Police conducted validation studies on Perkin Elmer's Profiler Plus™ STR kit using the ABI Prism® 310 Genetic Analyzer (capillary electrophoresis). Initial validations included studies on reproducibility, sensitivity, and precision. From these studies a mathematical model was developed which established the maximum percent difference between sister alleles of a heterozygote pair (heterozygote model). The application of this model was then examined in a mixture validation study designed to test its effectiveness in discriminating individual contributors to a mixed stain. Subsequently, the limitations of the heterozygote model were evaluated in non-probative casework prior to implementation in regular casework. This presentation will review the application of the heterozygote model to a variety of mixtures typically encountered in forensic casework.

The first example reviewed will consist of a mixture from a single probative and a single non-probative source, such as victim elimination standard and one assailant. This example makes the assumption that one of the profiles present in the mixture is that of a known individual. Such an assumption effects the way the heterozygote model is applied in order to determine the possible genotypes of the unknown contributor to the mixture. The application of this model also differs depending upon which individual is the major or minor contributor.

The second example reviewed will consist of a mixture from two probative sources, such as two assailants in a sexual assault. This example makes no assumption about a given profile necessarily being present but rather relies entirely on the heterozygote model itself to establish the majority profile and subsequent possible genotypes of the minority profile.

Upon reviewing these examples, several points were noted where caution must be exercised in the strict application of the heterozygote model and subsequent interpretation of mixtures. These points will be individually addressed and their impact discussed.