



A78 Three Match Statistics, One Verdict

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After attending this presentation, attendees will learn how to present multiple DNA match statistics in court, how to testify on the results of computer-based DNA mixture interpretation, and why some DNA interpretation methods are more informative than others.

The presentation will impact the forensic science community by enabling practitioners to introduce in court computer-based interpretation of DNA evidence that can often provide more informative match results.

There is currently no consensus on the interpretation of DNA mixtures. Some groups advocate inclusion methods, while others prefer the likelihood ratio (LR). Key methodological distinctions include the use of qualitative or quantitative peaks, thresholds, and computer mixture interpretation. These issues all appeared in a recent criminal trial, and were integrated in a way that produced a harmonious resolution.

In 2006, Pennsylvania dentist John Yelenic was brutally murdered in his home. State Trooper Kevin Foley, boyfriend of the victim's estranged wife, was arrested for this crime. The major physical evidence was DNA extracted from the victim's fingernails. The STR data generated by the FBI laboratory showed a two person mixture largely containing the victim's own DNA, along with a seven percent unknown second contributor.

The prosecution presented three different DNA match statistics:

- A CPI (inclusion) statistic of 13 thousand was given by the FBI. The CPI method ignored both the victim profile evident in the data, as well as the quantitative peak height information.
- An obligate allele interpretation (subtraction) was done independently by Dr. Cotton. Her method did use the victim profile, though not the peak heights, and produced a match statistic of 23 million. The match improvement came from two loci that had four alleles.
- A quantitative computer interpretation (addition) was reported by Dr. Perlin. This approach used the victim information, together with quantitative peak heights, to produce a match statistic of 189 billion. The genetic calculator employed a comprehensive scientific model of the STR data generation process to infer unknown genotypes.

At the pretrial *Frye* admissibility hearing, it was explained that all three methods were LR's. Each method used progressively more of the evidence data, and all are generally accepted by the relevant scientific community. All methods were admitted into evidence.

At the 2009 trial, the three experts explained their underlying data assumptions to the jury. It was shown how each method analyzed the DNA to infer a genotype (up to probability), and how its LR match statistic followed automatically from the genotype. The jury was shown how a mixture interpretation that uses more of the available evidence becomes a more powerful DNA microscope. While the defense tried to show that multiple match statistics could be confusing, the prosecution's experts demonstrated how multiple interpretations are persuasive. The jury convicted the former trooper of first degree murder.

All three DNA LR's used in this case were correct, although some extracted more match information from the data than others. Given the weakness of the 13 thousand CPI statistic, the multiple DNA statistics proved instrumental in securing a just verdict. The jury had no difficulty understanding the different data assumptions behind each method, and was persuaded that more informative use of the data produced a greater LR. Based on this experience, we suggest that all scientific evidence and interpretations should be presented in court, and that experts withhold nothing from the jury.

DNA Match, Computer Interpretation, DNA Mixture