## E36 Low Copy Number Y-STR Evidence: Will "Junk" DNA Dilute the Power of the Phrase "DNA Match" and Debase the "Gold Standard?"

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After attending this presentation, attendees will become aware of the emerging issues surrounding low copy number Y-STR evidence in criminal trials and the concerns of prosecuting and defending these types of cases.

This presentation will impact the forensic science community by challenging participants to debate about the wisdom of prosecuting cases using low copy number Y-STR DNA evidence, and whether new guidelines are needed to maintain the integrity of forensic DNA technology.

The phrase "DNA match" carries terrific power. It derives from the notion that the DNA associated with a crime is essentially unique; it can virtually and statistically single out the accused as the source of the DNA evidence. What happens when laboratories and prosecutors begin calling "DNA matches" with one-in-four probabilities, when the DNA evidence might actually match three members of the jury? Will that "DNA match" claim sometimes be wrong, associating some accused individuals as included when they might be excluded? Will subjectivity and bias increase? Will powerful science be mixed with junk science? Will the meaning of the phrase "DNA match" become diluted?

These concerns are increasing in the forensic courtroom setting, especially in Y-marker cases. The Y-chromosome short tandem repeat (Y-STR) markers have been used in criminal investigations to help detect low levels of DNA where other kits have failed, targeting only the male contribution in the evidentiary sample. As DNA science and technology advances, forensic labs are now able to get test results from smaller quantities of DNA, even when these test results yield incomplete and partial DNA. In some instances, these Y-results are reported as "DNA matches" even when the profile is derived from only one loci detected. In fact, lab analysts have reported such test results, defended them in court, and have been supported by their management teams.

The use of low copy, Y-STR DNA results leads to differing mixture interpretations. Typically, Y-STR loci produce single alleles at each of the ten (out of the eleven loci available in the kit) loci in single source samples of male DNA. As a result, lab analysts interpret these Y-STR results as single source samples. When forensic analysts observe multiple peaks at any one of these ten loci, they commonly report that more than one male contributor is present in the tested sample. Absent from this forensic analysis is when a particularly challenging problem arises: while many individuals have only one allele at each of these ten loci on the Y-chromosome, some individuals have two or even three alleles at some loci. Accordingly, a laboratory report interpreting the Y-result as a mixture of at least two contributors and "matching" the defendant's DNA haplotype could likewise be interpreted as a DNA exclusion. The use of this low copy, Y-STR DNA evidence at a criminal trial could ultimately result in the most egregious failure in the criminal justice system: the conviction of the innocent, while allowing perpetrators to walk free.

This presentation will show examples of this emerging issue from actual casework and trials. Attendees will learn about the challenges presented by this new issue, and be challenged to engage in a debate within the forensic science community about the wisdom of such practices, and whether new guidelines are needed to maintain the integrity of forensic DNA technology.

**Y-STR, DNA, Mixtures**

 ** Presenting Author*