



A75 Frequency of Apparent False Inclusions in Complex Y-STR Mixtures

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After attending this presentation, attendees will gain an understanding of the limitations of Y-STR mixture statistical analysis; use of a Y-STR mixture analysis tool (Y-MAT) that utilizes random mixtures from a database of over 2500 profiles; and, use of the Y-MAT to ascribe meaningful weight to Y-STR mixtures.

This presentation will impact the forensic science community by explaining how Y-STR analysis is a powerful tool for the forensic community. However, Y-STR mixture interpretation has a serious limitation in the inability to ascribe a meaningful statistical analysis. As such, partial matches to Y-STR mixtures can result in misleading conclusions. Y-MAT provides a method to obtain.

Y-STR analysis is a powerful tool in the DNA arsenal for human identification, particularly in the forensic arena. A serious limitation, particularly in forensic samples, is in interpreting mixtures that have more than one male contributor. The fallacy is that the Y-STR profile is donated as a block of loci, rather than as independent loci such as the autosomal loci used in conventional STR analysis. As such, partial profiles that are observed in a complex mixture may represent dropout, or alternatively may be an exclusionary event and therefore it is presently impossible to conduct a valid statistical analysis. But without statistics, the jury cannot properly weigh the significance of the evidence. If a suspect's Y-STR profile is observed in over ninety percent of the loci in a mixture, intuitively it seems reasonable that that he is likely one of the DNA donors. However, this could be misleading as a mixture of profiles from random individuals will often yield a profile combination that the suspect will match at 12, 13, 14, or even more of the 16 loci tested.

The development of a method will be described that, rather than comparing the mixture to individual profiles where dropout would confound the evaluation of the data, creates mixtures of two, three, or four random individuals from a database of over 2,500 individuals. This allows the determination of the expected frequency of partial or entire matches of an individual's Y-STR profile to the random mixtures. A software program was then developed that facilitates conducting literally thousands of comparisons in less than an hour. It also allows the incorporation of random individuals either from the entire database or it can be limited to a specific race. This tool enables the analyst and the jury to weigh the relative significance of the evidence.

The software program was applied to a real case involving a three person mixture. The suspect, in this case, was indicted by a match at 15 out of 16 loci from another agency's data that did not include statistics. Of 1,000 three-person random mixtures, the suspect was included in 254 at 15 loci and 105 at 16 loci. This data dramatically shows that the intuitive conclusion that the data implicates the suspect could be misleading as over one-third of random three-person mixtures would include the suspect. Thus the genetic data only weakly supports the conclusion that DNA source is that of the suspect. Combine this with the fact that autosomal data did not support the conclusion, and the finding reached by the jury could be significantly different.

Y-MAT continues to be developed to further investigate the discriminating power of Y-STR's in forensic science. As seen, the tool is proving useful in determining the probability of a selected suspect matching frequencies in criminal cases, thereby providing the ability of ascribing meaningful weight to Y-STR matching statistics. The preliminary indications are a lack of confidence in 4 person Y-STR mixtures, and a significant note of caution in ascribing probative significance in matches against mixtures of three.

Y-STR Mixtures, Random Matches, Y-STR Analysis Tool