



B102 Deliberations on Y-Chromosomal Short Tandem Repeat (Y-STR) Interpretation, Present and Future

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After attending this presentation, attendees will better understand the proper analysis of Y-STR profiles, with particular consideration paid to rapidly mutating loci and mixed haplotypes, and the current and future approaches for statistical analysis of Y-STR matches.

This presentation will impact the forensic science community by informing attendees of issues related to the application and interpretation of male-specific STR testing.

Y-STR typing methods were developed shortly after autosomal STR typing became adopted in forensic laboratories. It was quickly recognized that a male-specific typing test could be valuable in cases in which male DNA would otherwise be swamped by the amount of female DNA in certain samples. This opened up investigative opportunities for sexual assault cases that may have previously been passed over, particularly cases in which no spermatozoa were detected, either because the incident was not immediately reported or no ejaculation occurred.

Despite its advantage over autosomal STR typing in these cases, Y-STR typing was not implemented by forensic laboratories as readily. While the methodology required to obtain Y-STR profiles is nearly identical to that used in obtaining traditional STR profiles, a completely new approach to interpretation and statistical analysis had to be developed. What does the Y-STR profile mean? First, it is a true haplotype rather than a DNA profile of independent loci. All of the loci are linked and theoretically inherited as a group. Second, a match to an individual male is also likely to be a match to any patrilineal relative and to an unknown number of unrelated males. Third, the strength of the match is limited by the size of the database used for comparison and by the number of loci tested. Fourth, samples containing haplotypes from more than one male proved very difficult to reliably interpret.

New kits that include more Y-STR loci are now commercially available; however, only a small percentage of the samples in the commonly used Y-STR population databases contain haplotypes with these additional loci. Some of the new kits also have rapidly mutating loci that can assist in differentiating close male relatives. What impacts do the additional loci and the rapidly mutating loci have on conclusions and statistics, particularly for mixed haplotypes?

A two-hour block of time has been scheduled for deliberations on the present and future approaches to Y-STR interpretation. The panel convened for this session consists of analysts, researchers, and statisticians with extensive experience in the development of Y-STR interpretation approaches and in the application of Y-STR analysis to forensic casework. The discussion will include topics such as the cost-benefit of searching more haplotypes or more loci, comparing the counting method with the likelihood ratio methods, familial/pedigree studies, and the impact of future typing technologies.

Y-STR, Interpretation, Statistics