UPPING THE MIXTURE GAME: NEWLY-ADOPTED STR MARKERS FOR ENHANCED DNA MIXTURE DE-CONVOLUTION

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De-convolution of complex mixtures has limitations in resolving component contributors. Various improvements in polymerase chain reaction coupled with capillary electrophoresis (PCR-CE) chemistry and downstream statistical analyses have been developed and implemented to attempt to better resolve two or more person DNA mixtures. However, CE outputs describe STR variation solely based on allele size and do not exploit the full genetic information contained within target markers to distinguish between or among component contributors.

Massively parallel sequencing (MPS) for typing forensically-relevant STR loci has dramatically impacted our understanding of allele diversity by identifying sequence variation within STR repeat and flanking regions. Recent literature has described STR sequence variation in large population groups and has demonstrated that there are enormous amounts of diversity and complexity within the currently utilized STR markers for forensic genetic analysis. However, some of the current core CODIS loci lack any observed repeat or flanking region sequence diversity. Thus, there is a need to explore novel STRs to complement existing markers as increased variation can facilitate mixture de-convolution.

This presentation will highlight the *in silico* and empirical testing of over 100 newly-adopted STRs from individuals comprising Caucasian, African American and Hispanic US populations. STR sequence variation within these marker amplicons was detected using massively parallel sequencing, STRait Razor v3.0, and in-house analysis workbooks to identify candidate loci better suited for distinguishing component contributors and stutter in simulated simple and complex DNA mixtures generated from empirical population sequence data. Additional population genetic analyses were performed to characterize the newly-adopted STR markers, which were carefully selected based on their high heterozygosity, reduced allele length spread, and increased sequence variation. The incorporation of newly-adopted forensically-useful markers into a novel STR panel in conjunction with current core CODIS markers will allow the forensic scientist to more effectively address the challenges of interpretation of some complex mixture samples, increase the number of resolved profiles being compared to reference and suspect profiles, and expand the DNA database by increasing the number of forensic samples uploaded.