

THE EVALUATION AND IMPLEMENTATION OF GeneMarker®HID (Softgenetics), PowerPlex® Fusion 6C (Promega), and STRmix™ (ESR) FOR FORENSIC CASEWORK

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Adding seven loci to the CODIS core effective January 1, 2017 requires forensic science laboratories to validate and implement one of the newer megaplex STR kits. However, the additional loci may increase the time required by the analyst to analyze results and document edits. Most of the new megaplex STR kits utilize 6-dyes to accommodate the extra loci, which then necessitates forensic labs to validate new DNA analysis software to accommodate the additional dye. Finally, the forensic community is transitioning to probabilistic genotyping software to make full use of the peak heights, especially regarding DNA mixtures. Our laboratory has chosen Promega's Fusion 6C STR amplification system, Softgenetics' GeneMarker HID analysis software, and ESR's STRmix probabilistic genotyping software to address the new requirements and operational considerations.

Given that $n-1$ repeat stutter percentage increases with allele size, the use of a single stutter threshold for a locus is not optimal. Since previous analysis software options can only have a single locus stutter threshold, the filter would either under or overcompensate at any given allele depending on the value used (locus minimum, average, or maximum) thus requiring manual edits. Another common practice is to manually add a label (e.g., an asterisk *) to the electropherogram for subthreshold peaks in a lab defined range such as above the analytical threshold, but below the stochastic threshold. Our laboratory contracted Softgenetics to modify the GeneMarker HID software to incorporate allele-specific stutter and subthreshold peak labeling options. These modifications minimize the number of manual edits required, saving analysis time. In allele-specific stutter mode, GeneMarker HID software can successfully analyze $n-1$, $n+1$, $n-0.5$, and $n+0.5$ repeat stutter positions including when stacked. Mock samples analyzed with allele-specific stutter thresholds in comparison to locus-specific had less manual edits. Peaks in overlapped stutter positions were correctly evaluated. GeneMarker HID is a cost-effective option relative to some others, significantly reducing costs for forensic laboratories with a large number of analysts. To illustrate the full DNA analysis workflow, mock two and three person female-male mixtures were prepared at various ratios with and without degradation, were amplified with Fusion 6C and analyzed by GeneMarker HID. The DNA profile results were then exported to STRmix. Likelihood ratio results are presented for true contributors and non-contributors.