A123 How Inclusion Interpretation of DNA Mixture Evidence Reduces Identification Information

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After attending this presentation, attendees will better understand how human review of DNA mixture evidence using the inclusion method reduces identification information.

This presentation will impact the forensic science community by enabling practitioners to preserve more identification information in their DNA evidence, reaching the conclusion that human interpretation may discard considerable DNA mixture identification information that computers can preserve, which can improve criminal justice processes and outcomes.

The combined probability of inclusion (CPI) mixture interpretation method applies thresholds to quantitative STR peak data in order to simplify human review. However, this flattening of peaks into putative all-or-none allele events usually reduces evidential force. The true DNA match statistic is better estimated by a computer model that accounts for peak heights and their variation.[1]

The "weight of evidence" is an additive measure of DNA identification information, calculated as the logarithm of the likelihood ratio (LR) and measured in "ban" information units. Since CPI can be viewed as an LR, this study looked at log(LR) at individual STR loci to determine how CPI reduces match information.

The study examined 615 locus experiments obtained from 41 inclusions in 31 mixture evidence items that had a reported CPI statistic. The items were from 16 cases, and included clothing, weapons, vehicles, vaginal swabs, and skin swabs. Promega PowerPlex® 16 STR electropherograms were developed on an ABI 3130® genetic analyzer, and reinterpreted on Cybergenetics TrueAllele® genetic calculator.

There were 517 loci (84.1% of 615 experiments) for which both CPI and computer match statistics were calculated. At these loci, the computer found an average log(LR) of 0.746 ban per locus, forming a bell-shaped normal distribution having standard deviation 0.590. DNA evidence need not support an identification hypothesis at every locus, as was seen in the 52 (10.1%) experiments having negative log(LR) values.

On these 517 loci, CPI yielded an average log(LR) of 0.489 ban per locus. CPI only reports on loci that support an identification, and is silent about evidence whose weight does not support an inclusion. The CPI weight of evidence values formed a truncated normal distribution. These positive log(LR) numbers had a maximum at 0 ban per locus, monotonically decreased to the right, with a fitted standard deviation of 0.615. Comparison with the better-modeled computer log(LR) distribution showed that: (1) on average, CPI reduces identification information relative to a computer gold standard; (2) CPI discards locus evidence that does not support an inclusion; and, (3) CPI can report an inclusion at a locus where the computer finds no support for a match.

When using CPI, a locus is not reported unless evidence alleles over threshold are seen in the reference genotype. There were 97 loci (15.8% of 615 experiments) at which the computer found a statistic but CPI did not. At the 68 (70.1%) of these unreported CPI loci that had interpretable data, the computer produced log(LR) values in a normal distribution having a mean of 0.659 ban per locus and standard deviation 0.664. At the remaining 29 (29.9%), experiments exhibiting allele dropout or extreme peak imbalance, the computers log(LR) values were all negative, having mean –0.755 ban per locus and standard deviation 0.346. Overall, computer interpretation of loci that CPI did not use contributed additional weight of evidence that favored an identification.

In this study, reported CPI locus statistics with more sophisticated computer reinterpretation of the same mixture data were compared. Whenever CPI produced a result, so did the computer. However, CPI yielded (on average) a lower weight of evidence than the computer; CPI discarded evidence whenever it classified a locus as unfavorable; and CPI reported as favorable some loci that the computer found to be unfavorable. For more accurate and balanced reporting of DNA mixture evidence, laboratories using CPI should progress to more informative interpretation methods.

Reference:

1. Perlin MW, Legler MM, Spencer CE, Smith JL, Allan WP, Belrose JL, Duceman BW. Validating TrueAllele® DNA mixture interpretation. J Forensic Sci 2011;56(6):1430-47.

Interpret Mixture, Inclusion Method, Weight of Evidence

 ** Presenting Author*