A125   Virginia TrueAllele® Validation Study: Casework Comparison

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After attending this presentation, attendees will better understand why computer interpretation of complex DNA evidence is scientifically reliable.

This presentation will impact the forensic science community by enabling practitioners to make better use of DNA evidence already generated in their laboratory. Human review may greatly understate the evidential value of complex STR data; however, when such data are truly informative, computer reinterpretation can preserve more of the evidence, and bring that strength of match into the courtroom.

Modern criminal justice requires rapid and reliable processing of DNA evidence. Such reliability is a hallmark of admissible evidence, and encompasses sensitivity, specificity, and reproducibility. However, when confronted with complex mixtures or touch DNA, human interpretation can become a challenging task.

The result is that much evidence may be reported with an artificially low DNA match statistic, or is not reported on at all (i.e., "inconclusive"). Mathematical computing can overcome these limitations by statistically separating out contributor genotypes from the DNA mixture. These genotypes are objectively inferred by thorough consideration of the evidence data, and can be compared with reference genotypes to determine match strength.

This case study examined 111 comparisons from 92 items of evidence in 72 criminal cases involving DNA mixtures. For each item, a TrueAllele® computer provided a DNA match statistic that was reported in a supplemental case report issued by the Virginia DFS laboratory.[1] The sensitivity, specificity, and reproducibility of the computer results were examined. Comparison was made to the match information obtained by human review of the same data using Combined Probability of Inclusion (CPI) or modified CPI (mCPI). The study found TrueAllele® computer interpretation to be a reliable method for interpreting DNA mixture evidence.

Out of 111 DNA match comparisons, current mCPI human review could report on 55 of them (49.5%), finding an average match statistic of 156. TrueAllele® computer interpretation had greater sensitivity, providing 102 match statistics (91.9%) with an average value of 86.9 billion. Thus, the computer preserved more of the evidence (91.9% matches by computer, versus 49.5% manually), as well as the DNA identification information it contained (86.9 billion average match statistic, versus 156 manually).

The computer did not simply "add zeros" to the DNA match statistic. In fact, TrueAllele® statistics were lower than the corresponding human CPI values in 15 reported items. Moreover, the computer found no statistical support for a match in some cases. While, on average, TrueAllele® does find more matches and computes stronger statistics, the system objectively examines DNA evidence without any bias towards the defense or prosecution.

In addition to increased average sensitivity, TrueAllele® also maintained excellent specificity. The computer can quantify nonmatch information for exclusionary purposes through a negative log likelihood ratio (or "log(LR)"). In contrast, CPI or mCPI human interpretation methods give only positive log(LR) values, since their match statistics are never less than one. The study examined ten thousand TrueAllele® cross-case comparisons where it was expected to find no match, and found no false positives—the log(LR) was always a negative number. The average exclusionary nonmatch information in this assessment was a log(LR) of -19.693 (1 in 49.3 quintillion).

The computer objectively gave reproducible DNA match statistics. Replicate computer runs on the same evidence data showed a within-item log(LR) standard deviation of 0.305. Thus, on average, independent computer runs on the same evidence item gave statistically similar (within an order of magnitude) DNA match statistics.

DNA, whether single source or complex mixture, can provide compelling evidence that implicates criminals and exonerates the innocent. Current human review of DNA mixture data applies stochastic thresholds that can discard half the evidence and greatly understate the evidential import of what's left. As demonstrated in this casework comparison study, TrueAllele® computer interpretation more effectively preserves DNA evidence and match information. Societal safety and criminal justice may be better served by using this validated computer technology to reliably review complex DNA mixture evidence.

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.

Computer Interpretation, DNA Mixture, Likelihood Ratio