Assessing TrueAllele® Genotype Identification on DNA Mixtures Containing up to Five Unknown Contributors

Mark W. Perlin, PhD, MD, PhD, Jennifer Hornyak, MS; Cybergenetics, Pittsburgh, PA USA
Ruth Dickover, PhD, Garett Sugimoto, MS, Kevin Miller, PhD; Kern Regional Crime Laboratory, Bakersfield, CA

ABSTRACT

Manual review of complex DNA evidence does not fully address the data’s identification information. Therefore, computer methods have been developed for mathematical interpretation of mixed or low-template DNA. The genotype modeling approach computationally separates out the contributor contributions, with uncertainty represented through probability. Comparison of a contributor genotype to another genotype, relative to a population, calculates a likelihood ratio (LR). Validating an interpretation method on a broad range of DNA mixtures having known composition can help predict an expected LR outcome in a particular case. This randomized experimental design examined 40 DNA mixture items. The 4 mixture sets had 2, 3, 4 or 5 contributors, with each item specified as a random mixture weighting of randomly assigned known references. Each mixture's known genotypes had the same or varying DNA amounts. The TrueAllele® genotype modeling method computationally separates out the contribution information. The study found that this genotype modeling method produces reliable match results, regardless of the DNA mixture composition. The false exclusion rate (Type II error) was estimated as 0.05 to 0.10 across 40 DNA mixture items. The LR values were highly sensitive, preserving considerable identification information. It was also highly statistically reproducible, allowing for accurate and reliable calculation of LR determinants.

CONCLUSIONS

The computer interpretation of DNA evidence is a twenty-first century necessity. With ever-increasing numbers of STR loci, DNA mixtures having three or more contributors, low-level or degraded samples, and the potential for subjective examination bias, human analysis cannot be expected to fully process all the data. Thus, rigorous and objective mathematical DNA mixture interpretation is the pathway of practices.

The match statistic distribution of inclusion and exclusion gave reproducible match values. The computer was highly sensitive, preserving considerable identification information. It was also extremely specific, providing for accurate and reliable calculation of LR values. The LR values were highly sensitive, preserving considerable identification information. It was also highly statistically reproducible, allowing for accurate and reliable calculation of LR determinants.

REFERENCE