B51 Evaluation of the Least Square Deconvolution Approach in Interpreting DNA Mixtures

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The goal of this presentation is to present the use of mathematical models to resolve DNA Short Tandem Repeat profiles.

This presentation will provide a mechanism for interpreting DNA mixtures in forensic casework including but not limited to sexual assault evidence, trace or low copy number samples, product of conception cases, and commingled remains from mass disasters.

Introduction: DNA samples containing mixed profiles are often encountered in forensic DNA casework, stemming most often from sexual assault cases. Characteristic peak height imbalances and disproportionate intensity seen in short tandem repeat (STR) analysis indicate that DNA contributions may originate from different individuals. The U.S. Supreme Court established under *Daubert v. Merrell Dow Pharmaceuticals, Inc*. that scientists are required to show the reliability, reproducibility and validity of their scientific results. Current mixture resolution methods do not rely on all available empirical data. Mixture statistics such as the probability of exclusion fail to differentiate between the victim and suspect profiles and do not take into account the ratio of mixtures. Other statistical measures such as likelihood ratios take into account major and minor peak levels but fail to provide a measure of differing mass ratios. Least Square Deconvolution (LSD) algorithms strengthen the reliability, reproducibility and validity of mixture interpretations required by *Daubert* standards by providing a systematic mathematical approach to resolving mixtures. All available data generated in electropherograms are evaluated. LSD software computes a mass proportion for each two contributing genotypes by comparing their relative peak height and/or area measurements assuming 1) relative mass ratio is approximately preserved during PCR amplification across all loci and all alleles within a locus, and 2) allele peak heights and areas are proportional to its relative DNA mass. The software takes into consideration all possible combinations of the two contributing genotypes and computes the corresponding fitting errors. The higher mass profile is normalized against the lower mass proportion to calculate the mass ratio. The profile with the smallest fitting error is determined to be the most likely genotype scenario. Hypothesis/Methods: Evaluate the effectiveness and precision of the LSD software. Different male to female DNA ratios were PCR amplified and separated by capillary electrophoresis. Corresponding peak height and area data were entered into the LSD Software. In addition, different PCR and electrophoresis parameters were examined. Results: Preliminary results indicate LSD software can separate profiles between 10:90 and 30:70 mixture ratios. Adjusting PCR and electrophoresis parameters enhances ability to separate profiles at a mixture ratio of 5:95. Conclusion: LSD could prove beneficial to the forensic community in the future by evaluating mass ratios in mixture samples. In time this analysis system may be used to strengthen statistical measurements for mixture evidence to satisfy *Daubert* standards.

Least Square Deconvolution, DNA Mixtures, Short Tandem Repeats

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