B95 Multi-Software Interpretation of Complex Mixture DNA Profiles: A Comprehensive Approach to Explaining DNA Interpretation Results in Courtrooms

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After attending this presentation, attendees will understand how to use a multi-software probabilistic approach for Low Template DNA (LT DNA) mixtures in highly challenging samples to better explain evidence in court, avoiding expert discussion when using different interpretation strategies.

This presentation will impact the forensic science community by illustrating how diverse the results of different software can be and how to manage these results by providing the most conservative and reproducible data in order to deliver complete statistical information.

The goal of this study was to define a rigorous approach to LT DNA mixture interpretation using multiple probabilistic software programs. Despite several recommendations having been proposed over the past years concerning the importance of evaluating several factors which may affect inclusion or exclusion hypotheses from prosecutor or defense, a rigorous approach has still not been properly defined in order to establish a "universally accepted" methodology. Moreover, this lack of regulation and guidelines leads experts to differently interpret evidence in courtrooms by applying several statistic approaches, which are often incomprehensible to the jury and legal experts. This practice causes the ability to make a judgement "beyond any reasonable doubt" even more difficult. In order to improve judgement capability and impartiality, this study adopted two models: the semi-continuous approach (using LRmix Studio and Lab Retriever software) and the fully continuous approach (using Charles Brenner DNA•VIEW™ mixture solution software).

Both models helped to highlight the difficulties encountered when evaluating challenging Short Tandem Repeat (STR) profiles and clarified the need for extreme caution in order to achieve a correct interpretation of the DNA evidence as this can heavily affect the outcome of a trial. After thorough validation studies, this research developed the "statistic consensus approach." In practice, this approach compares all Likelihood Ratio (LR) values obtained from all software used. If all LR results are similar and convergent, then the most conservative LR value obtained is reported. On the contrary, if LR results are not similar, the interpretation process provides an inconclusive decision. This approach resembles, in a complex way, the consensus method itself, which makes use of alleles observed in different replicates.[1-3] Due to this approach, it seems possible to conclude that certain suspects under investigation are unquestionable contributors to LT DNA mixtures under investigation. Even though the application of several software programs and different models is questioned by some scientists, this approach has already been successfully tried in court. The presentation of results were made easier during the trial since this approach considers different advocated issues such as the level of conservatism, the semi-continuous model's comprehensibility, and the fully continuous model's complexity.[4] Actual cases using this approach will be presented.

Reference(s):

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LT DNA Mixture Interpretation, Statistical Consensus Profile, Probabilistic Software