B152 The Use of Relationship Likelihood Ratios (LRs) as a Diagnostic for Probabilistic Genotyping: Validation and Casework Experience Through the Years

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Learning Overview: The goal of this presentation is to illustrate how familial relationship LRs can be used as an additional diagnostic for probabilistic genotyping through validation and to highlight casework examples.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by helping to implement familial relationship diagnostics in individual labs.

Since 2016, DNA Labs International (DLI) has been online with STRmix™ expert forensic software. Validated for use with the Applied Biosystems® AmpFℓSTR® Identifiler® Plus on the Applied Biosystems® 3130xl Genetic Analyzer, and now with the Applied Biosystems® GlobalFiler® and Promega® PowerPlex® Fusion 6C on the Applied Biosystems® 3130xl and 3500xL Genetic Analyzers, thousands of casework samples have been evaluated.

At DLI, STRmix™ is used to aid the analyst in deconvoluting a DNA evidence sample and develop an LR. An LR is a ratio of two probabilities giving a numerical value that shows strength of support for one scenario over another. In the case of DNA, in the simplest of terms, it is saying whether it is more likely to observe the DNA profile if it originated from the individual of interest than from an unknown individual. The software also develops several types of relationship LRs, including sibling, parent/child, half siblings, uncle/aunt/niece/nephew, and first cousins where it addresses if it is more likely to observe the DNA profile obtained if a person of interest is part of an evidence sample versus a relative of the person of interest. This is of interest to both the prosecution and defense as members of a family share more alleles in common than unrelated individuals and can, therefore, lead to potential false inclusions or exclusions of individuals. It became clear from a few specific casework samples that the relatives LR table provided in the STRmix™ report can be indicative of the inclusion of relatives into the mixture in question and can falsely inflate the LR for a person of interest.

As a result, additional validation studies were performed involving mixtures made from multiple family trees using different amplification kits and instruments. Diagnostic ranges were developed for comparison of the unified LR to the sibling LR as well as the unified LR to the parent/child LR, as these were shown to be the most affected. This diagnostic range, in conjunction with other diagnostics and the LR itself, may indicate when a relative LR should be of noted concern and would necessitate requesting standards of primary relatives of the person of interest for comparison. However, the LR value can be dependent on the quality of the profile and the overall presence of the applicable contributor in that profile as well.

Casework examples highlighting possible familial relationships and what was done to address them will be presented. Additionally, the diagnostic ranges that DNA Labs International employs for relative LRs that were developed during validation and how they were determined will be examined. This will benefit attendees by providing information on ways the familial LRs developed by STRmix™ can be explored during validation and how it relates to casework.

Probabilistic Genotyping, Familial Relationships, Validation