B41 How to Deal With Low Likelihood Ratios (LRs) in Mixed DNA Samples

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Learning Overview: After attending this presentation, attendees will better understand a method of how to deal with a low LR when making inclusionary statements about a Person Of Interest (POI) in a mixed DNA sample.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by presenting a graphical tool for the comparison of low LRs produced for minor contributors in mixed DNA samples to the general population. This can be used by the expert as an additional check for an exclusion opportunity and as a communication tool for helping the fact finder understand how the POI compares to the population at large.

The reporting of an LR calculated from probabilistic genotyping software has become more popular since 2015 and has allowed for the use of more complex mixtures at court. The meaning of "inconclusive" LRs and how to communicate the significance of low LRs at court is now important. Typically, mixtures that result in LRs <1,000 for a POI are those that are made up of multiple contributors and/or where the contributor position that best fits the POI has relatively high levels of drop-out. These mixtures are a challenge to interpret, but doing so is the only way to make exclusionary interpretations of the POI. However, when the human expert cannot exclude, or said another way, makes an interpretation that the POI is included as a possible contributor, the next step is to calculate the LR. When the resulting LR is small, but greater than one, it can be a challenge for the expert to communicate the meaning of a low LR to the jury.

Some have advocated the use of a verbal scale as an attempt to help communicate the meaning of low LRs to the fact finder.[1,2] This may be quite useful at times, although the verbal scale is related to the LR in a general manner and is not specific to the sample in question. It may be more helpful to have a communication tool that is directly related to the deconvolution and specific genotypes of the sample in question.

Gill and Haned proposed using a non-donor performance test as a measure of how robust the LR is for POI compared to a distribution of LRs from a population.[3] Understanding the use of a non-donor distribution may enhance communication between scientists and the court when discussing the significance of a low, but greater than 1, LR for low-level contributors in mixed DNA samples. The use of the database comparison function in the probabilistic genotyping software STRmix™ allows for this check to be performed on a routine basis.

A tool is presented here that uses the distribution of sub-source (DNA profile) LRs obtained from non-donors as a method for assisting in communicating the value of the sub-source LR for a POI.[4] The non-donor distribution is useful for examining calibration and discrimination for profiles that have produced LRs less than approximately 1,000. The output of the tool is a graph that can show the position of the LR for the person of interest set against the non-donor LR distribution. An LR for a POI that is less than 99.9% of the non-donor LRs would be considered uninformative.

Reference(s):

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2. Scientific Working Group on DNA Analysis Methods. *Recommendations of the SWGDAM Ad Hoc Working Group on genotyping results reported as likelihood ratios*. (2018). https://docs.wixstatic.com/ugd/4344b0_dd5221694d1448588dcd0937738c9e46.pdf.
3. Gill P,. Haned H., (2013) A new methodological framework to interpret complex DNA profiles using likelihood ratios. *Forensic Sci. Int. Genet*. 7 (2):251–63.
4. Schuerman C., Kalafut T., Buchanan C., Sutton J., Bright J.-B. (2020) Using the Nondonor Distribution to Improve Communication and Inform Decision Making for Low LRs from Minor Contributors in Mixed DNA Profiles. *Journal of Forensic Sciences* 65(4): 1072-1084.

Likelihood Ratio, DNA Mixtures, DNA

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