W02 Interpreting and Communicating DNA Evidence in a Probabilistic Genotyping Universe

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Learning Overview: After attending this presentation, attendees will better understand the Likelihood Ratio (LR) and the limits of probabilistic genotyping and will gain tools to help explain the results of such analyses to stakeholders. The concepts to be discussed are applicable to probabilistic genotyping software in general and fundamentals of genetics and statistics. In addition, concepts of adventitious hits, false positives, and false negatives will be addressed. The relationship between a numerical result and the reliability of DNA evidence will be discussed. The appropriateness and limitations of a Bayesian framework for DNA evidence will be considered.

Impact on the Forensic Science Community: This presentation will impact the forensic science community through: (1) attendees gaining a better appreciation for the benefits and limitations of probabilistic genotyping; (2) attendees gaining an understanding of the role of proposition setting; and (3) attendees gaining experience on ways to communicate findings to other scientists, investigators, and the judicial system.

Forensic DNA typing has been called "the gold standard" of the forensic science disciplines.[1] However, there is a resurgence of focus on the limits of the interpretation and testimony related to the quality of the profile and the numerical weight that accompanies an inclusionary interpretation.[2,3] Indeed, there is some debate as to whether an interpretation of inclusion/exclusion is even appropriate.[4] Due to the implementation of probabilistic genotyping approaches, mutually exclusive hypotheses and expressing the significance of analysis in the form of the LR are being adopted in the United States.

Because of the need to better interpret mixture evidence and the availability of software tools, probabilistic genotyping has been embraced to assess a DNA mixture profile from the perspective of the genotypes from individual donors. When there are multiple donors, there can, and likely will, be many more potential genotypes to explain the mixed DNA profile than there are donors that contributed to the profile. While previously laboratories tended to attempt to deconvolve mixtures of two persons into single-contributor-possible genotypes, modern probabilistic genotyping software has the ability to deconvolute mixtures of three-, four-, or five-person mixtures. In theory, there may be no limits to the number of contributors.

There are numerous benefits to generating a probabilistic LR, such as the ability to: (1) interpret previously deemed inconclusive profiles that may support exculpatory results; (2) interpret mixtures that were considered too complex; (3) provide more consistency and less variance in mixture interpretation among analysts; (4) obtain more data to effect an interpretation; and (5) use the LR from a single locus even if <1.0 while other loci support a contributor hypothesis.

The use of probabilistic genotyping software requires understanding of such data and how to express the data in a cogent fashion. For example, some samples that used to be considered as "inconclusive" may be evaluated, which may result in a relatively low LR and a discussion as to whether low LRs are reliable. Low "numbers" have always been a part of the process, including with the Random Match Probability (RMP) and Combined Probability of Inclusion (CPI). Expression of the results can be challenging, especially when the experience of analysts and the judicial system is based on traditional methods of interpretation. There are commonalities and differences in the various methods of interpreting DNA profiles, and they need to be appreciated to support the use of advance tools, such as those for probabilistic genotyping, so that evidence can be conveyed in a meaningful and effective manner.

The overall and components of the LR and how the LR is used in a Bayesian framework shall be explained fundamentally and with examples.

Reference(s):

1. National Research Council Committee on Identifying the Needs of the Forensic Sciences Community. (2009) *Strengthening Forensic Science in the United States: A Path Forward*. ISBN: 0-309-13131-6, 352 pages http://www.nap.edu/catalog/12589.html.
2. President's Council of Advisors on Science and Technology. (2016) *Forensic Science in Criminal Courts: Ensuring Scientific Validity of Feature-comparison Methods*. Executive Office of the President's Council of Advisors on Science and Technology, Washington, DC, 2016. https://www.whitehouse.gov/administration/eop/ostp/pcast/docsreports.
3. Stiffelman B. (2019) No longer the gold standard: probabilistic genotyping is changing the nature of DNA evidence in criminal trials, *Berkeley J. Criminal Law* 24: 110–146.
4. Morrison G.S., Kaye D.H., Balding D.J., Taylor D., Dawid P., Aitken C.G.G., Gittelson S., Zadora G., Robertson B., Willis S., Pope S., Neil M., Martire K.A., Hepler A., Gill R.D., Jamieson A., de Zoete J., Ostrum R.B., Caliebe A. (2017) A comment on the PCAST report: Skip the "match"/"non-match" stage. *Forensic Sci Int.* 272: e7-e9.

Forensic DNA, Probabilistic Genotyping, Bayesian Framework