F6 Results of a Survey on Probabilistic Genotyping From the Legal Community

Michael D. Coble, PhD*, University of North Texas Health Science Center, Fort Worth, TX 76107

Learning Overview: After attending this presentation, attendees will better understand the current state of training and the issues surrounding the use of probabilistic genotyping from the perspective of the legal community.

Impact on the Forensic Science Community: This presentation will impact the forensic science and legal communities by helping to: (1) determine how well the legal community is coping with the current change in DNA mixture interpretation using probabilistic genotyping software, and (2) show where and how training can help to improve the litigation of mixture interpretation and reporting using probabilistic genotyping software and likelihood ratios.

DNA mixtures of two or more individuals can be challenging to interpret for the forensic DNA scientist. Although guidance for autosomal Short Tandem Repeat (STR) interpretation of DNA mixtures from organizations such as the Scientific Working Group on DNA Methods (SWGDAM) and the International Society for Forensic Genetics (ISFG) have been provided, the challenge of interpreting complex mixtures remains an issue for the forensic DNA community.[1-3]

Probabilistic genotyping, according to SWGDAM, "refers to the use of biological modeling, statistical theory, computer algorithms, and probability distributions to calculate likelihood ratios and/or infer genotypes for the DNA typing results of forensic samples ("forensic DNA typing results")."[4] Over the past decade, there has been an "explosion" of software that uses a probabilistic approach to mixture interpretation. *All* of these programs use the likelihood ratio to convey the value of the evidence.

There are at least 45 laboratory systems in the United States that are currently using a probabilistic genotyping software system, with another 56 laboratory systems in some state of purchasing, validating, or implementing a program.[5,6] We are now at a tipping point for the use of probabilistic methods of mixture interpretation as the new "standard" for the forensic DNA community.

This presentation will provide the perspective of the legal community, through a survey conducted in late 2018, on the movement away from "binary" methods of interpretation for DNA mixtures to probabilistic methods of interpretation. Survey participants were asked about their access to training in probabilistic genotyping and likelihood ratios, how well they understand this change in interpretation and presentation of the results in court, and how well juries and judges have accepted these changes. The results will also provide advice from both prosecution and defense attorneys on issues involved with understanding and presenting this approach in court. Finally, a summary of training materials, literature, and other resources for the legal community will be presented.

Reference(s):
1. SWGDAM (2017) Autosomal STR Interpretation Guidelines. Available at: https://docs.wixstatic.com/ugd/4344b0_50e2749756a242528e6285a5bb478f4c.pdf.
2. Gill P., Brenner C.H., Buckleton J.S., Carracedo A., Krawczak M., Mayr W.R., Morling N., Prinz M., Schneider P.M., Weir B.S. (2006) DNA Commission of the International Society of Forensic Genetics: Recommendations on the Interpretation of Mixtures. *Forensic Sci Int.* 160(2-3): 90-101.
3. Gill P., Gusmão L., Haned H., Mayr W.R., Morling N., Parson W., Prieto L., Prinz M., Schneider H., Schneider P.M., Weir B.S. (2012) DNA commission of the International Society of Forensic Genetics: Recommendations on the Evaluation of STR Typing Results That May Include Drop-Out and/or Drop-In Using Probabilistic Methods. *Forensic Sci Int Genet.* 6(6): 679-688.
4. SWGDAM (2015) Guidelines for Validation of Probabilistic Genotyping Systems – available at https://docs.wixstatic.com/ugd/4344b0_22776006b67c4a32a5ffc04fe3b56515.pdf.
5. https://americansecuritytoday.com/fbi-validates-strmix-use-five-person-mixtures-video/.
6. Numbers have been updated through personal communications by the author with laboratories and software developers.

Probabilistic Genotyping, DNA Mixture Interpretation, Likelihood Ratio