



W10 DNA Mixture Interpretation Principles: Observations From a National Institute of Standards and Technology (NIST) Scientific Foundation Review

*John M. Butler, PhD**, NIST, Gaithersburg, MD 20899; *Sheila Willis, PhD**, NIST, Gaithersburg, MD 20899; *Melissa K. Taylor, MA**, Gaithersburg, MD 20899; *Rich Press, MSc**, NIST, Gaithersburg, MD 20899; *Hariharan Iyer, PhD**, Gaithersburg, MD; *Peter M. Vallone, PhD**, NIST, Gaithersburg, MD 20899-8314; *Bruce J. Heidebrecht**, Maryland State Police, Forensic Sciences Division, Pikesville, MD 21208; *Jennifer Gombos Breaux, MFS**, Clarksburg, MD 20871; *Eugene Y. Lien, MS**, New York City Office of Chief Medical Examiner, New York, NY 10016; *Keith Inman, MCrim**, Department of Criminal Justice Administration, Hayward, CA 94542; *Roger Frappier, MSc**, The Centre of Forensic Sciences, Toronto, ON M3M 0B1, CANADA; *Charlotte J. Word, PhD**, North Chesterfield, VA 23235-0153; *Lisa C. Schiermeier-Wood, MS**, VA Dept of Forensic Science, Richmond, VA 23219; *Joel D. Sutton, MSFS**, United States Army Criminal Investigation Laboratory, Forest Park, GA 30294; *Robin W. Cotton, PhD**, Boston University School of Medicine, Boston, MA 02118; *Jack Ballantyne, PhD**, University of Central Florida Department of Chemistry, Orlando, FL 32816-2366; *Ray Wickenheiser, MBA**, New York State Police Crime Laboratory System, Albany, NY 12226-3000

Learning Overview: After attending this presentation, participants will better understand the principles involved with DNA mixture interpretation, knowledge of core foundational literature supporting these principles, and approaches to establishing interpretation guidelines for DNA mixtures, including approaches that involve probabilistic genotyping software.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by discussing the importance of having documented research and validation studies to support measurement and interpretation claims in forensic science.

DNA mixture interpretation has become more challenging in recent years due to several factors, including submission of more touch evidence samples to aid investigations and the generation of more sensitive DNA test results with new Short Tandem Repeat (STR) typing kits. This sensitivity enables recovery of DNA results from low quantities of biological material. However, the Polymerase Chain Reaction (PCR) signal amplification process, which provides the DNA test sensitivity, also introduces artifacts into the resulting data, such as stutter products, as well as ambiguity in the form of allele drop-out, allele drop-in, and heterozygote imbalance that occur due to stochastic effects. These artifacts, combined with allele sharing among contributors to the mixture, make pairing contributor alleles into their donor genotypes more difficult and increase uncertainty associated with the mixture interpretation process. Probabilistic genotyping software programs are being implemented in many laboratories to aid evaluation of low-template DNA results, either from single-source samples or trace components of mixtures.

The NIST has been congressionally-funded to perform scientific foundation reviews of select forensic disciplines. These reviews are intended to establish what is well-known and well-supported empirically in a forensic field and identify gaps that need further study. DNA mixture interpretation was selected as the initial NIST scientific foundation review, given the existence of abundant literature and a need expressed by members of the community. Multiple interlaboratory studies conducted by the NIST and others have noted variability among accredited laboratories using validated approaches on the same DNA mixture data.

Since September 2017, a NIST review team has been studying issues surrounding DNA mixture interpretation. An important goal of this project is to identify, consolidate, and share core principles and supporting publications with the community to encourage deeper learning and understanding of DNA mixture interpretation. More than 500 articles related to DNA mixture interpretation have been gathered and examined to better understand capabilities and limitations as reflected in the scientific literature. An external DNA Mixture Resource Group, composed of 13 experienced practitioners and technical leaders, has provided valuable input and feedback to the NIST team on a regular basis. Findings from this study will be shared, along with primary considerations identified.

The report from this study, entitled *DNA Mixture Interpretation: A NIST Scientific Foundation Review*, is in the process of being written to cover a variety of topics in seven chapters. Chapter 1 introduces the need and approach to the study. Chapter 2 provides historical perspective and reviews current methods for DNA mixture interpretation. Chapter 3 discusses the NIST review team efforts and input received from outside experts along with data sources and literature evaluated. Chapter 4 covers case context and relevance issues important to high sensitivity methods where DNA transfer and persistence are possible. Chapter 5 examines measurement uncertainty issues and notes some approaches to helping validation studies become more performance-based rather than task-driven. Chapter 6 explores capabilities and limitations of new technologies, along with forces at play that influence acceptance and adoption of new approaches, and touches on training challenges and needs going forward. Chapter 7 summarizes key takeaways and considerations to help the field move forward. The report Appendix contains an in-depth reference list with annotated foundational articles.

DNA, DNA Mixtures, DNA Evidence Interpretation