DNA Mixture Interpretation Principles: Observations from a NIST Scientific Foundation Review

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Common Aspects of SOPs Across Forensic Labs

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SWGDAM Interpretation Guidelines for Autosomal STR Typing by Forensic DNA Testing Laboratories – APPROVED 01/12/2017:

- “I. The laboratory’s interpretation guidelines and thresholds shall be based on and supported by applicable internal validation studies, publications, and scientific literature.
- VIII. (1.7) The laboratory shall establish a stochastic threshold for use with binary methods.
- IX. (1.8) The laboratory shall establish peak height ratio expectations for heterozygous genotypes.
- X. (1.9) For DNA mixtures, the laboratory shall establish guidelines for determination of the minimum number of contributors to a sample.

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- “XI. (1.10) The laboratory shall establish guidelines to determine whether DNA typing results are suitable for comparisons.
- XII. (2 Introduction) The primary goal of mixture interpretation shall be to determine the possible genotype combinations of the contributors.
- XIV. (2.3) Interpretation guidelines for mixtures must be based on mixture studies conducted using known contributors that represent the number of contributors and the range of general mixture types for which the procedure will be used in casework (e.g., mixture proportions and template quantities). The laboratory guidelines shall be sufficiently detailed to ensure confidence in the separation of the “major” versus “minor” components.

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- “XVII. (3.1.3) The laboratory shall establish guidelines for inclusionary, exclusionary, and inconclusive determinations based on comparisons of DNA typing results from known samples to both single-source and mixed evidentiary samples.”

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- FBI Director's Forensic Quality Assurance Standards for DNA Testing Laboratories *Proposed:*
- "8.3.2.1 Mixture interpretation validation studies shall include samples with a range of the number of contributors, template amounts, and mixture ratios expected to be interpreted in casework."

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- “STANDARD 9.6 The laboratory shall have and follow written guidelines for the interpretation of data that are based on and supported by internal validation studies. The laboratory shall:
- 9.6.1 Have criteria to evaluate quantitation standards, internal size standards, allelic ladders and analytical controls.
- 9.6.2 Have criteria for the interpretation of non-allelic peaks.
- 9.6.3 Have criteria for the interpretation of allelic peaks.
- 9.6.4 Define the thresholds used for interpretation. As appropriate to the interpretation model utilized, the laboratory shall establish the following thresholds:
  - 9.6.4.1 Analytical Threshold
  - 9.6.4.2 Stochastic Threshold

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- Continued: “STANDARD 9.6 The laboratory shall have and follow written guidelines for the interpretation of data that are based on and supported by internal validation studies. The laboratory shall:
- 9.6.5 Define criteria for uninterpretable data.
- 9.6.6 Have and follow procedures for mixture interpretation that address the following:
  - 9.6.6.1 The assessment of the number of contributors.
  - 9.6.6.2 The separation of contributors (e.g., major versus minor).
  - 9.6.6.3 The criteria for deducing potential contributors.

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- “STANDARD 9.9 The laboratory shall define criteria for the formulation of inclusionary, exclusionary, and inconclusive conclusions.
- STANDARD 9.10 The laboratory shall have and follow procedures for statistical calculations and the reporting of results and conclusions that address the following:
  - 9.10.1 The assumptions that can be made when formulating conclusions.
  - 9.10.2 Performing statistical analysis in support of any inclusion that is determined to be relevant in the context of the case.
  - 9.10.3 Documenting of the genetic loci and assumptions used for statistical calculations, at a minimum, in the case notes.
  - 9.10.4 Not using uninterpretable data in statistical calculations

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- Continued: “STANDARD 9.10 The laboratory shall have and follow procedures for statistical calculations and the reporting of results and conclusions that address the following:
  - 9.10.5 The approaches to performing statistical calculations.
    - 9.10.5.1 For autosomal STR typing, the procedure shall address homozygous and heterozygous typing results, multiple locus profiles, mixtures, minimum allele frequencies, and where appropriate, biological relationships.
    - 9.10.5.2 For lineage marker testing, the procedure shall address parameters specific for the applicable lineage marker statistical calculations.
    - 9.10.5.3 The laboratory shall use loci that are shown to be in Hardy-Weinberg equilibrium and statistically unlinked, when using the product rule for statistical calculations.

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- Continued: “STANDARD 9.10 The laboratory shall have and follow procedures for statistical calculations and the reporting of results and conclusions that address the following:

  - 9.10.6 The source of the population database(s) used in any statistical calculations.
  - 9.10.7 The criteria for source attribution declarations, when applicable.

- STANDARD 9.11 The laboratory shall have and follow a procedure to address the reinterpretation of legacy data.

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Take-home messages:

- Make sure your SOP is based on your validation studies.
- Make sure your validation studies cover the scope of complexity of what is commonly seen in casework
  - Best to even go a little beyond the normal scope – show how the tools and policies fail when pushed beyond their limits.
- Make sure your SOP defines scope of complexity that can be interpreted with the given tools and supporting validation studies.
- Maximize consistency across analysts within the lab.
- Minimize SOP statements of “based on analyst experience…”