



DNA Mixture Interpretation Workshop | Karin Crenshaw

Reporting DNA Mixture Results and Statistics



Overview

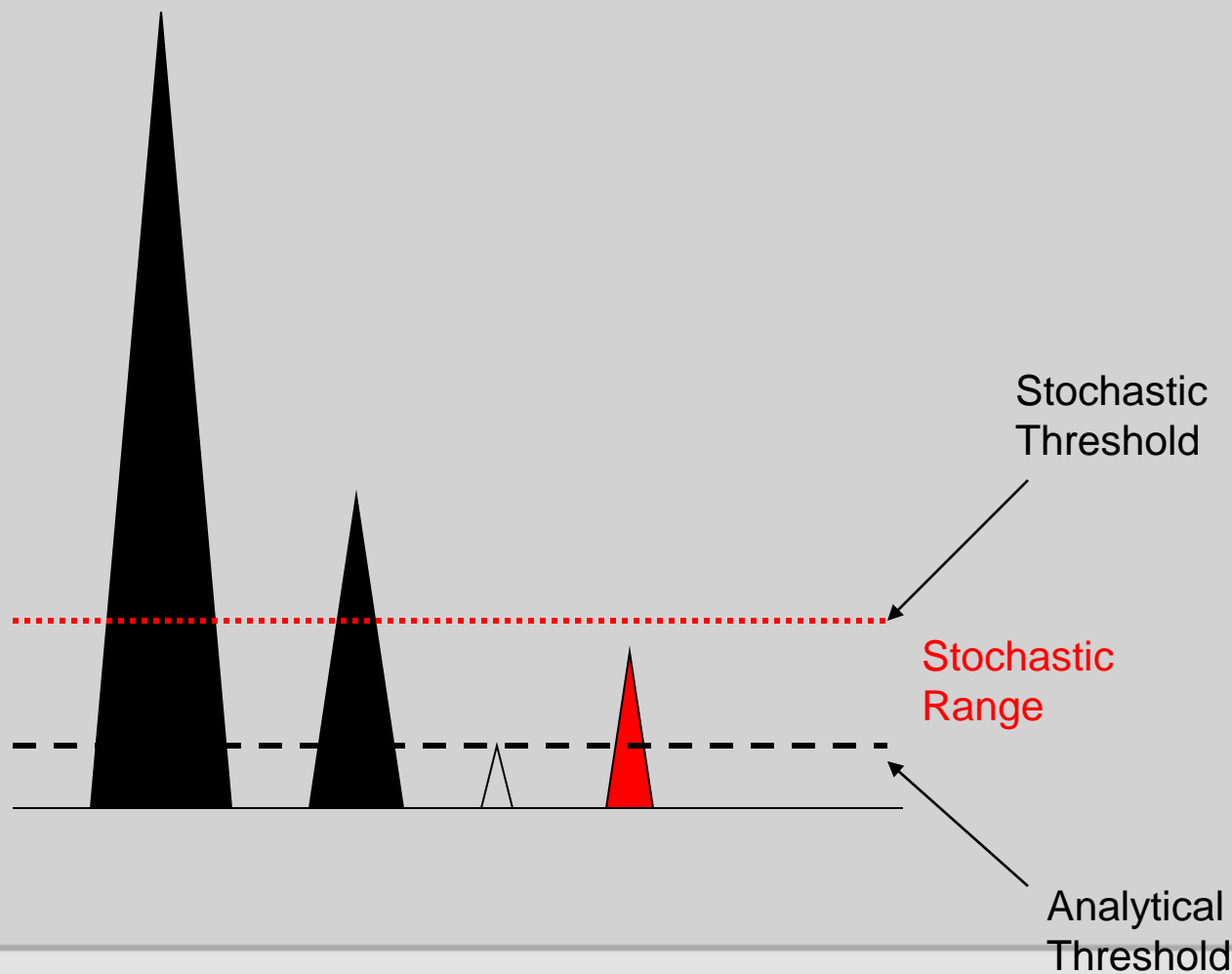
- Types of Mixtures
- Options for Reporting Mixtures
- RMP, PE, or Likelihood Ratio
- Stochastic Alleles
- Report Wording
- Practical Examples from P.B.S.O.
- Questions

What is a Mixture?

According to the SWGDAM Interpretation Guidelines:

- **When three or more alleles are present at one or more loci (excepting tri-allelic loci) and/or the peak height ratios between a single pair of allelic peaks for one or more loci are below the empirically determined heterozygous peak height ratio expectation.**
- **Generally, the minimum number of contributors to a mixed sample can be determined based on the locus that exhibits the greatest number of allelic peaks.**

Factors Involved in Mixture Analysis



Types of Mixtures:

No two Mixtures are exactly alike....requires Validation Studies and proper training to interpret properly

- Major/Minor with the alleles all above the stochastic threshold.
- No Major/Minor with alleles all above the stochastic threshold.
- Mixtures with alleles that fall below the stochastic threshold. Also includes mixture with more than three individuals that are indistinguishable.

Options for Reporting Mixtures:

- Give qualitative statement (exclusions) with no statistic
- The known individual cannot be excluded (is included) as a possible contributor, can choose from:
 - Calculate RMP on Major profile or Restricted RMP
 - Calculate probability of exclusion (CPE), or Restricted CPE for multiple major contributors
 - Calculate likelihood ratio (LR)
- Report result as inconclusive or uninterpretable
- The DNA profile is consistent or inconsistent with originating from a common source.

For court purposes it is necessary to provide a statistic if an inclusion is being made

2-Step Process for Reporting Results:

- **Step 1 = Determine type of mixture, decide on the appropriate statistical approach, the loci that will be used in the calculation, and calculate the statistic.**
- **Step 2 = Compare to the known DNA profiles, determine inclusions/exclusions, write wording for report.**

What Type of Statistical Calculation Should Be Performed?

- Answer depends on the type of mixture
 - RMP (Random Match Probability)
 - Major profile or Deduced Profile from Intimate Sample, Mixtures with assumption of number of contributors
 - CPE (Combined Probability of Exclusion)
 - Non-distinguishable mixture profile or Minor profile
 - LR (Likelihood Ratio)
 - Mixtures with assumed number of contributors and only alleles above stochastic are utilized

RMP (Random Match Probability)

- Used consistently for Single Source profiles
- Can also be used for Major DNA profile from a mixture.
- Intimate Samples – given the reference standard of the owner, the other contributor can be deduced out and treated as single source profile.
- Indistinguishable Mixtures – must assume the number of contributors, then can use data that falls below stochastic threshold.

RMP Calculations

- **For a single major contributor to a mixture**

Heterozygote Genotype = $2pq$

Homozygote Genotype = $p^2 + p(1-p)\theta$

- ❖ **For single alleles where the allele falls below the stochastic threshold, have several formula options available or can just not use the locus in statistical calculations**

Application of RMP to Indistinguishable Mixtures (Modified RMP):

- **Acceptable as long as the assumption as to the number of contributors is clearly noted.**
- **Can apply a “restricted” approach, utilizing the peak height ratio information to eliminate certain allelic combinations from the calculations.**
- **This approach will allow the use of stochastic alleles under certain conditions**

General Report Wording for Modified RMP:

Assuming N number of contributors, the probability of randomly selecting an unrelated individual who could be included as a contributor to the mixture obtained from a swabbing/cutting/etc. of the item (Exhibit X.QX) is listed below for the following populations:

1 in X (billion, trillion, etc.) US Caucasians

1 in X (billion, trillion, etc.) US African Americans

1 in X (billion, trillion, etc.) US Southwest Hispanics

*Note: Wording provided by Todd Bille



CPE (Combined Probability of Exclusion) or CPI (Combined Probability of Inclusion)

- Also known as RMNE (Random Man Not Excluded)
- Probability that a random person (unrelated individual) would be excluded as a contributor to the observed DNA mixture
- Does not require an assumption as to the number of contributors to the mixture
- Assumes that there is no allele dropout (All alleles are above the stochastic threshold)
- All contributors are unrelated
- All contributors come from the same population group
- Does not utilize all of the data's probative value

Uses of CPE/CPI

- **If major/minor contributors can not be determined based on unambiguous profiles**
- **For the minor contributor to a mixture, using all of the alleles present for each locus that does not have stochastic alleles, unless a “restricted” approach is used for multiple major contributors**
- **If the number of contributors cannot be determined**

Calculating CPE/CPI

PI = (sum of allele frequencies)² for each locus

$$\text{CPI} = \text{PI}_1 * \text{PI}_2 * \dots * \text{PI}_N$$

$$\text{CPE} = 1 - \text{CPI}$$

Unrestricted = Utilizes all of the alleles at each locus, and cannot be performed at a locus that contains a stochastic allele.

Restricted = Can separate out the alleles above the stochastic threshold as separate from the ones below and perform CPE/CPI on that locus.

LR (Likelihood Ratio)

- Ratio of probabilities
- Both probabilities are conditional, meaning that they are based on a hypothesis
- Expressed as: $LR = \frac{\text{Pr}(E/S) \text{ or the } H_p}{\text{Pr}(E/U) \text{ or the } H_d}$

Numerator = Probability of the evidence if the sample originated from the suspect (or suspect and unknown contributor)

Denominator = Probability of the evidence if the sample originated from one or more unknown individuals

Calculating Likelihood Ratio:

- **Uses the general formulae for each possible genotype**

Heterozygote Genotype = $2pq$

Homozygote Genotype = $p^2 + p(1-p)\theta$

- **Must assume the number of contributors to the mixture**
- **Loci used in calculations should display no indication of allelic dropout**
- **Assumes that any unknown contributors are not related.**

General Report Wording for Likelihood Ratios:

- **The probability of the evidence is “x” times more likely if the stain came from “suspect” than if it came from an unknown, unrelated individual.**
 - **Keep in mind that it is NOT appropriate to state that “The probability that the stain came from “suspect” is “x” times greater than it coming from an unknown individual”**

Report Wording Considerations:

- **Using “source” or source attribution statements**
- **Cannot be excluded v. Included**
- **Make sure to include any assumptions being made in the wording**
- **Exclusion conclusions do not require statistical analysis**

Practical Examples from Palm Beach County Sheriff's Office

***The following are examples only of possible wording for
reporting statistics***

Example #1: Major/Minor (no stochastic alleles)

	Mixed Blood B
D3S1358	(16), 17
TH01	6, 7, 9.3
D21S11	28, 30, 31.2, 32.2
D18S51	13, 14, 15, 17
Penta_E	(5), 12
D5S818	9, 12
D13S317	11, 13
D7S820	8, (9), 10
D16S539	11, 12, 13
CSF1PO	(10), (11), 12
Penta_D	9, 11, 12, 15
AMEL	X, (Y)
vWA	14, 16, 18
D8S1179	11, (13), 16
TPOX	8, (9)
FGA	19, 20, 22
Generate CMF	

* CPE, RMP, or LR for all loci

Example #1 (Report Wording)

1) A DNA profile was obtained from the blood stain and indicates the presence of two individuals.

A. Victim is the source of the major DNA profile.

B. Suspect cannot be excluded as a contributor to this DNA mixture.

The estimates of the combined probability of inclusion (i.e. the chance of selecting an unrelated individual at random that would be expected to be included) for the observed DNA mixture profile is approximately:

Caucasian: 1 in XXXX African American: 1 in XXXX Hispanic: 1 in XXXX

NOTE: Source attribution statements at P.B.S.O indicates a RMP of less than 1 in 300 Billion for all three population groups.



Example #2: Major/Minor (stochastic effects)

D3S1358	14, (16), (17)
TH01	6, (8), (9)
D21S11	28, (29), 30
D18S51	(12), 14, 15
Penta_E	7, (10), (12), 19
D5S818	11, 12, (13)
D13S317	8, (10), 12
D7S820	9, (11)
D16S539	(8), (9), 11
CSF1PO	(9), 10, 12
Penta_D	(10), 12, (13), 14
AMEL	X, Y
vWA	(14), 16, 17, (19)
D8S1179	13, (14), 15, (16)
TPOX	8, (9), 10
FGA	(21), 22, 23
	outside suspect's shorts

Suspect = Major DNA profile = RMP

Victim = Minor DNA profile, CPE or LR at 4 loci (no stochastic alleles)
or could calculate a restricted RMP assuming a 2 person mixture

Example #2 (Report Wording):

1) A DNA profile was obtained from the outside of the suspect's shorts and indicates the presence of two individuals.

A. Suspect is the source of the major DNA profile.

B. Victim cannot be excluded as a contributor to this DNA mixture.

The estimates of the combined probability of inclusion (i.e. the chance of selecting an unrelated individual at random that would be expected to be included) for the observed DNA mixture profile is approximately:

Caucasian: 1 in XXXX

African American: 1 in XXXX

Hispanic: 1 in XXXX

NOTE: Source attribution statements at P.B.S.O indicates a RMP of less than 1 in 300 Billion for all three population groups.



Example #3: Mixture with NO Major/Minor

D3S1358	14, 16, 17	
TH01	6, 8, 9	
D21S11	(28), 29, 30	
D18S51	12, (14), (15), (20)	
Penta_E	7, 10, 12, (19)	
D5S818	(11), (12), 13	
D13S317	8, 10, (12)	
D7S820	9, 11	
D16S539	8, 9, 11	
CSF1PO	9, 10, (11), (12)	
Penta_D	10, (12), (13), 14	
AMEL	X, (Y)	
vWA	14, (16), (17), 19	
D8S1179	13, 14, 15, 16	
TPOX	8, 9, (10)	
FGA	19, 21, (22), 23	
	inside susp underwear	

- CPE or LR calculation for all loci w/no stochastic alleles (12 loci)
OR – Could calculate RMP for all the loci

Example #3 (Report Wording):

- 1) A DNA profile was obtained from the inside of the suspect's underwear and indicates the presence of two individuals. Suspect and Victim cannot be excluded as contributors to this DNA mixture.

The estimates of the combined probability of inclusion (i.e. the chance of selecting an unrelated individual at random that would be expected to be included) for the observed DNA mixture profile is approximately:

Caucasian: 1 in XXXX African American: 1 in XXXX Hispanic: 1 in XXXX

Example #4: Complex Mixtures

	Swabs of trigger of gun
D3S1358	(14), 15, 16, 17
TH01	6, 7, (8), (9)
D21S11	28, 30, (36)
D18S51	(14), (15), 15.2, (16), 17, (18), (19)
Penta_E	5, (12)
D5S818	(9), 11, (12), 13
D13S317	9, (11), 12
D7S820	7, (8), (9), 10, (11), (12)
D16S539	9, (10), 11, (12)
CSF1PO	(7), (8), 10, 11, (12)
Penta_D	2.2, 10, 11, 13
AMEL	X, (Y)
vWA	15, 16
D8S1179	(9), (12), (13), 14, 15
TPOX	(6), 8, 9
FGA	17, (19), 23

Example #4: (Report Wording)

- 1) A DNA profile was obtained from the swabs from the trigger of the gun at 16 genetic markers. This DNA profile is a complex mixture of at least 4 individuals. None of the standards submitted in this case are included as a possible contributor to this DNA mixture at all 16 genetic markers. As a result, interpretation of this complex DNA mixture with regard to inclusion and exclusion statements will not be reported.

Questions?

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