Overview

- Introduction - background
- Report Wording – general definitions
- Statistics – options
- Conclusions – advice for litigants

Standardization between and among Forensic Laboratories

- Not just a DNA laboratory challenge
- 2009 NAS Report
  - Recognized significant improvements are needed in forensic science
  - Ensure the reliability of the disciplines
  - Establish enforceable standards
  - Promote best practices and their application
Standardization between and among Forensic Laboratories

**National Commission on Forensic Science**
- In 2013, the Department of Justice established the National Commission on Forensic Science in partnership with the National Institute of Standards and Technology to enhance the practice and improve the reliability of forensic science.
- This unique partnership draws upon each agency’s core strengths to promote scientific validity, reduce fragmentation, and improve federal coordination of forensic science.

https://www.justice.gov/ncfs

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Work Products Adopted by the Commission

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Standardization between and among Forensic Laboratories

**Organization of Scientific Area Committees (OSAC)**
- Created in 2014, part of an initiative by NIST and the Department of Justice to strengthen forensic science in the United States.
- The organization is a collaborative body of more than 600 forensic science practitioners and other experts who represent local, state, and federal agencies, academia, and industry.
- NIST has established OSAC to create a sustainable organizational infrastructure that produces consensus documentary standards and guidelines to improve quality and consistency of work in the forensic science community.

http://www.nist.gov/forensics/osac/index.cfm
Standardization between and among Forensic Laboratories: OSAC

Biology/DNA Scientific Area Committee (SAC)
- Subcommittees
  - Biological Methods
  - Biological Data Interpretation and Reporting
  - Wildlife Forensics

Scientific Working Group on DNA Analysis Methods (SWGDAM)
- Serves as a forum to discuss, share, and evaluate forensic biology methods, protocols, training, and research to enhance forensic biology services as well as provide recommendations to the FBI Director on Quality Assurance Standards (QAS) for forensic DNA analysis.
- Established in 1988 first as TWGDAM (Technical Working Group)

http://www.swgdam.org/
Standardization between and among Forensic DNA Laboratories

SWGDAM

- Adherence to the FBI’s Quality Assurance Standards (QAS) is required by Federal law as a condition of a laboratory’s participation in the national DNA Index System.
- The Federal DNA Identification Act provides, in pertinent part, “the index described in subsection (a) shall include only information on DNA identification records and DNA analyses that are— (1) based on analyses performed by or on behalf of a criminal justice agency in accordance with publicly available standards that satisfy or exceed the guidelines for a quality assurance program for DNA analysis, issued by the Director of the Federal Bureau of Investigation under section 210303.” see 42 U.S.C. 14132(b)(1).

Then there’s the data...

Challenges in DNA Interpretation
Ian Evett on Interpretation

“The crucial element that the scientist brings to any case is the interpretation of those observations. This is the heart of forensic science: it is where the scientist adds value to the process.”

Data cannot be standardized

Challenges in DNA Interpretation

- DNA mixtures have always existed
- More than one contributor to a DNA profile

> 2 peaks at more than one marker.

Historical Perspective on DNA Mixture Approaches

1985
- Evett et al. describe LRs for mixtures
- RMNE (CPI) used in paternity testing
- CPI becomes routine in U.S.

1991
- Evett et al. describe LRs for mixtures

1992
- CPI becomes routine in U.S.

1996
- Weir et al. describe LRs for mixtures

1997
- NRC I report supports CPI

1998
- DAB Stats (Feb 2000) CPI and LR okay

2000
- NRC II report supports LR
- ISFG DNA Commission LR over CPI

2006
- ISFG DNA Commission LR with drop-out

2008
- ISFG DNA Commission LR with drop-out
- CPI becomes routine in U.S.

2010
- ISFG DNA Commission LR with drop-out

2012
- SWGDAM guidelines (RMP, CPI, LR)

1997
- ISFG DNA Commission LR with drop-out

LR = likelihood ratio
CPI = combined probability of inclusion
RMNE = random man not excluded

Slide adapted from J. Butler, AAFS2014

Data cannot be standardized

Challenges in DNA Interpretation

- Increasing sensitivity of DNA kits over time
  - Now detection of as little as 15 pg of DNA vs. 1 ng of DNA,
    i.e. 1 ng versus 0.015 ng
Data cannot be standardized

Challenges in DNA Interpretation

• Increasing sensitivity of DNA kits over time
  
  Analytical Threshold (AT)
  AT: the minimum height at and above which detected peaks can be reliably distinguished from background noise.

• Drop-out occurring, i.e., loss of data
• # of contributors?
• Do you have confidence in the data?

Stochastic Threshold (ST)
ST: the minimum height above which it is reasonable to assume that allele dropout has not occurred within a single-source sample.
Data cannot be standardized

Challenges in DNA Interpretation

- Increasing sensitivity of DNA kits over time

Analyst Training

- Challenges in analyst training
  - Every analyst interprets the same way, every time
    - in every laboratory

“If you show 10 colleagues a mixture, you will probably end up with 10 different answers”

- Peter Gill, Human Identification II Symposium, April 14, 2006

  - Why?
    - Different mixture interpretation “guidelines”
    - Different levels of experience
    - Different DNA kits
    - Different instruments
    - Different statistical tools

Therefore there is no concordance in current forensic practice on what constitutes a “correct” mixture solution.
A Complexity/Uncertainty Threshold

New Scientist article (August 2010)

- How DNA evidence creates victims of chance
  - 18 August 2010 by Linda Geddes

- From the last paragraph:
  - In really complex cases, analysts need to be able to draw a line and say "This is just too complex, I can't make the call on it," says Butler. "Part of the challenge now, is that every lab has that line set at a different place. But the honest thing to do as a scientist is to say: I'm not going to try to get something that won't be reliable."


Slide adapted from J. Butler, AAFS2014

How low can you go?

How low should you go?

- Hidden Perpetrator
  - Absence of evidence is not evidence of absence
  - A perpetrator does not always leave a DNA profile at a crime scene

Confirmation Bias – red herring

- Discovery of DNA must be significant in relation to a crime
- Is the DNA profile relevant to the crime event?
How low can you go?
How low should you go?

- Innocent transfer
  - The transfer of DNA to an item may have occurred prior to or have no relation to the crime event
  - Is there an innocent explanation?

Report Wording

In general, report wording will resemble the following...

- "Cannot be excluded" = "Included": the evidentiary profile is consistent with/ matches the profile from a known individual
- What you should expect:
  - A statistic
    - … unless it’s an intimate item (e.g. vaginal swabs) or there is a reasonable expectation a person’s profile is on an item.
- What you don’t expect:
  - The inclusion to change
  - The statistic to change…
Report Wording

- “Cannot be included” = “Excluded”: the evidence profile is not consistent with/does not match the profile from a known individual
- What you should expect:
  - No statistic, ever
  - Exclusions do not require weight
  - This result should not change

Report Wording

- “Inconclusive”
  - Typically results from one of two reasons
    - Poor DNA profile
    - Inability to perform a statistic

Inconclusive

- Poor DNA profile: no comparisons
  - Extremely partial profile
  - Complex mixture

A DNA profile was obtained and indicates the presence of at least two individuals. Due to the complexity of this DNA mixture, the results are not suitable for comparative analysis. Comparisons for inclusions and exclusions will not be performed.
Inconclusive

- Cannot perform a statistic
- Cannot exclude an individual, but statistical "rules" do not allow for a calculation to be generated
- To report an inclusion a statistic must be generated

Statistics

“All models are wrong, but some are useful”
- George Box (statistician)

Statistics

- The purpose of statistics is to give significance/weight to an inclusion
- The weight can be calculated by a variety of approved statistical tools – see NRC II
- Statistical tools utilize population databases to determine the frequency (how often) of a piece of DNA appears in the population
The ideal (statistical) tool for the job?

- **RMP**
  - Random match probability
  - Product rule
- **CPE/CPI**
  - Combined probability of exclusion/inclusion
  - Random man not excluded
- **LR**
  - Likelihood ratio

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**RMP**

- The probability of randomly selecting an individual that would be included in the profile
- Single-source profiles
- Mixtures
  - Number of contributors necessary
  - Utilizes intensity differences to deduce major/minor profiles

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**CPE/CPI**

- Mixtures
  - The probability that an individual randomly picked out of the general population would be excluded/included from matching a given DNA profile
  - Generally thought to be conservative
  - No assumption as to the number or identity of contributors
  - Does not take into account intensity differences within a profile
  - Requires that all data be present for a given profile
Likelihood Ratios

- Single source or mixed DNA profiles
- Whereas RMP and CPE/CPI generate individual probabilities, LR generates a probability for an entire profile
- Number of contributors necessary
- Compares two competing scenarios that may explain a DNA profile
- Returns how likely the data are under one (or more) scenario than the other

\[
\frac{p(E \mid H_{\text{prosecution}})}{p(E \mid H_{\text{defence}})}
\]

LR – the road to probabilistic genotyping

- Probabilistic genotyping – Software determines the most probable explanation for the DNA profile

Probabilistic Genotyping

- Semi-Continuous – information is determined from the alleles present – peak heights are not considered.

- Fully Continuous – incorporation of biological parameters (peak heights, mixture ratio, stutter percentage, etc...).
The ideal (statistical) tool

- Not all laboratories have the ideal tool in their toolbox

Why?

3:1 Mixture Ratio
The evolution of statistics in forensics

• The way statistical tools are applied to forensic DNA profiles has changed over time...and continues to evolve.

SWGDAM Interpretation Guidelines

• Approved in January 2010

The document provides guidelines for the interpretation of DNA typing results from short tandem repeats (STR) and supersedes the Dynamic Working Group Analysis Guidelines (SWGDAM Short Tandem Repeat (STR) Interpretation Guidelines) (2004). The revised guidelines are provided to be employed in the interpretation of STR data to ensure the quality and consistency of results by providing a framework for allele detection and interpretation, and appropriate statistical approaches to the interpretation. The document is required to be used in conjunction with the SWGDAM Diagnostic Protocol and the SWGDAM Interpretation Guidelines to ensure the correct resolution and validation data is applied when these guidelines are used to support these procedures as needed.
SWGDAM Interpretation Guidelines

- Approved in January 2010

4.7 For calculating the OPE or RIF, any DNA typing results used in the analysis should be treated
the same manner as if the results were from a single source DNA sample. This includes applying the
same assumptions and methods to each DNA result in the same manner as if the results were from
the same mixture component. However, different calculations may be necessary for the
same mixture component depending on different assumptions as to the number of contributors are made and clearly
related to the case details and report.

4.8 When using OPE and RIF results in calculations to calculate the exclusivity that
a single-source sample will not be excluded and that can be considered as a factor in the
interpretation. Therefore, the laboratory should be aware of the possibility of
misinterpretation due to the use of these methods and the limitations of the interpretations.

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2010 SWGDAM Interpretation Guidelines

Table 1 – Isolate Statistical Analysis for DNA Typing Results

<table>
<thead>
<tr>
<th>Company of DNA Typing Result</th>
<th>RIF</th>
<th>CPI/CPI</th>
<th>LR (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Single Source</td>
<td>+1</td>
<td>+1</td>
<td>1</td>
</tr>
<tr>
<td>Single Major Contributor to a Mixture</td>
<td>+2</td>
<td>+2</td>
<td>2</td>
</tr>
<tr>
<td>Multiple Major Contributors to a Mixture</td>
<td>+3</td>
<td>+3</td>
<td>3</td>
</tr>
<tr>
<td>Single Minor Contributor to a Mixture</td>
<td>+1</td>
<td>+1</td>
<td>1</td>
</tr>
<tr>
<td>Multiple Minor Contributors to a Mixture</td>
<td>+2</td>
<td>+2</td>
<td>2</td>
</tr>
<tr>
<td>Individual or Mixture</td>
<td>+1</td>
<td>+1</td>
<td>1</td>
</tr>
</tbody>
</table>

(1) Restricted to unprocessed
(2) Restricted
(3) All potential alleles identified during interpretation are included in the statistical calculation.

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In the news...
In the news

• What do these labs have in common?

Issues with:
• Low level and/or mixed samples
• Poor training/understanding of mixture interpretation and statistics

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The Washington Post

National accreditation board suspends all DNA testing at D.C. crime lab

By Keith L. Alexander  April 27, 2015

The problems with the District lab have centered on the analysis of evidence that includes DNA from more than one person — and their conclusions regarding the likelihood that a certain person’s genetic material is included in the sample.

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THE TEXAS TRIBUNE

New Protocol Leads to Reviews of "Mixed DNA" Evidence

by Tenti Laughlin | Sept. 12, 2015 | 2 Comments

TEXAS FORENSIC SCIENCE COMMISSION

"CURRENT AND PROPER MIXTURE INTERPRETATION PROTOCOLS"

In cases of the trial, when these prosecutors received their new reports, they noticed significant changes in the evidence provided to them by the lab. In all of the cases, the lab had told the DNA evidence, usually with difficult evidence samples such as pubic hair, showing mixed results, areas of clothing, or other examples of "mixed DNA," where multiple people may have contributed DNA in the sample.
Conclusions

1. Know how to read and interpret a laboratory report

   - Each laboratory is going to be different
   - Until there is standardization across forensics there will be variation in how inclusions and exclusions are reported.
   - Know which statistical tools your DNA laboratory uses and their limitations
2. Communication with the laboratory
- If they are using a LR, what hypotheses were used
  - Do they account for your explanation of the evidence?
  - Are they fair?
- Find out why a sample was inconclusive
  - If it is because a statistic cannot be conducted by the lab can the profile be outsourced for additional analysis?

3. Understand your samples
- DNA is circumstantial; it is rarely a silver bullet
- Be careful not to give DNA profiles more weight than they deserve
  - Hidden perpetrator
  - Uncertainty of association with a crime event
    - Confirmation bias
    - Innocent transfer
  - Low level mixed samples vs. high level single source samples
Bibliography

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- Scientific Working Group on DNA Analysis Methods (SWGDAM): http://www.swgdam.org/
- Misleading DNA Evidence: Reasons for Miscarriages of Justice (Elsevier 2014) by Peter Gill
- NRC II: The Evaluation of Forensic DNA Evidence, National Research council (NRC) Committee on DNA Forensic Science: An Update, 1996

Strengthening Forensic Science in the United States: A Path Forward
Committee on Identifying the Needs of the Forensic Science Community, National Research Council
The PDF is produced from the National Academies Press at http://www.nap.edu/catalog/12846.html