Forensic Report Wording and Statistics
- Interpreting DNA Results -

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Overview

- Introduction – the quest to standardize DNA interpretation
- Report Wording – general definitions
- Statistics – options
- Conclusions – advice for litigants
Standardization between and among Forensic Laboratories

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

Biology/DNA Scientific Area Committee (SAC)
- Subcommittees
  - Biological Methods
  - Biological Data Interpretation and Reporting
  - Wildlife Forensics
Standardization between and among Forensic DNA Laboratories

- **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).
Standardization between and among Forensic DNA Laboratories

SWGDAM Interpretation Guidelines for Autosomal STR Typing by Forensic DNA Testing Laboratories

SWGDAM Contamination Prevention and Detection Guidelines for Forensic DNA Laboratories

SWGDAM Recommendations for the Efficient DNA Processing of Sexual Assault Evidence Kits.

SWGDAM Guidelines for the Validation of Probabilistic Genotyping Systems

SWGDAM Guidelines for the Collection and Serological Examination of Biological Evidence

SWGDAM Guidelines for STR Enhanced Detection Methods

SWGDAM Interpretation Guidelines for Y-Chromosome STR Testing

SWGDAM Guidelines for Missing Persons Casework

SWGDAM Training Guidelines
SWGDAM Validation Guidelines for Forensic DNA Analysis Methods

SWGDAM QAS Clarification Document

SWGDAM Mitochondrial DNA Analysis Interpretation Guidelines

SWGDAM Mitochondrial DNA Nomenclature Examples

The FBI Director's Databasing Quality Assurance Standards for DNA Databasing Laboratories - Effective 09/01/2011

The FBI Quality Assurance Standards Audit for DNA Databasing Laboratories - Final, Effective 09/01/2011

The FBI Director's Forensic Quality Assurance Standards for DNA Testing Laboratories - Revisions Approved, Effective 09/01/2011

Forensic Quality Assurance Standards Audit for Forensic DNA Testing Laboratories - Effective 09/01/2011
Then there’s the data...

Challenges in DNA Interpretation
Understanding Results Obtained & Sharing Them

Data → Stats → Report

Interpretation

Slide adapted from J. Butler, AAFS2014
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.”


Slide adapted from J. Butler, AAFS2014
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**: RMNE (CPI) used in paternity testing
- **1991**: Evett et al. describe LRs for mixtures
- **1992**: NRC I report (p.59) supports CPI
- **1996**: 2-person mixtures predominate
- **1997**: Weir et al. describe LRs for mixtures
- **1999**: RMNE (CPI) becomes routine in U.S.
- **2000**: CPI becomes routine in U.S.
- **2006**: NRC II report (p.130) supports LR over CPI
- **2008**: NIJ burglary report increases touch evidence
- **2010**: SWGDAM guidelines (RMP, CPI, LR)
- **2012**: ISFG DNA Commission LR with drop-out

**2008**
- ISFG DNA Commission
- LR over CPI

Slide adapted from J. Butler, AAFS2014

**LR** = likelihood ratio
**CPI** = combined probability of inclusion
**RMNE** = random man not excluded
Data cannot be standardized

Challenges in DNA Interpretation

• **Increasing sensitivity** of DNA kits over time
  • Now detection of as little as 15pg of DNA vs. 1 ng of DNA, i.e. 1 ng versus .015ng
Data cannot be standardized

Challenges in DNA Interpretation

- Increasing sensitivity of DNA kits over time

- Drop-out occurring, i.e. loss of data
- # of contributors?
- Do you have confidence in the data?
Data cannot be standardized

Challenges in DNA Interpretation

- Increasing sensitivity of DNA kits over time

Analytical Threshold (AT): the minimum height at and above which detected peaks can be reliably distinguished from background noise.
Data cannot be standardized
Challenges in DNA Interpretation

- Increasing sensitivity of DNA kits over time

**Stochastic Threshold (ST)**

ST: the minimum height above which it is reasonable to assume that allelic 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 E-Symposium, April 14, 2005

- Why?
  - Different levels of experience
  - Different mixture interpretation “guidelines”
  - 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**."
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.
How low can you go? How low should you go?

- 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
    • 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 five individuals. Due to the complex nature 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
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
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 assumptions required 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

\[
p\left( \frac{E | H_{\text{prosecution}}} {E | H_{\text{defence}}} \right)\]
LR – the road to probabilistic genotyping

Note: the formula $2p$ may be incorporated into RMP as well as LR to account for drop out

- Probabilistic genotyping –
  *Software* determines the most probable explanation for the DNA profile (e.g. Lab Retriever, STRmix™, TrueAllele®)
Probabilistic Genotyping

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

  ![Semi-Continuous Diagram]

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

  ![Fully Continuous Diagram]

Slide adapted from M. Coble, GRC2016
3:1 Mixture Ratio
The ideal (statistical) tool

- Not all laboratories have the ideal tool in their toolbox

- Why?
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 2017

This document contains guidelines and not minimum standards. In the event of a conflict between the FBI Quality Assurance Standards for Forensic DNA Testing Laboratories (QAS) and these guidelines, the QAS and the QAS Audit Documents have precedence over these guidelines. The use of the term ‘shall’ or ‘must’ is not intended to transform these guidelines into standards.

These revised guidelines supersede the SWGDAM Short Tandem Repeat (STR) Interpretation Guidelines (2010). They are intended to be applied prospectively and not retroactively. With the underlying assumption that work performed prior to the issuance of these revisions was appropriate and supported by validation, revision of the applicable guidelines is not intended to invalidate or call into question the previous work. Laboratories are encouraged to review their standard operating procedures and validation data in light of these guidelines and to update their procedures as needed.
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
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.
Began in May 2015

TEXAS FORENSIC SCIENCE COMMISSION
CLARIFICATION REGARDING THE TERM
“CURRENT AND PROPER MIXTURE INTERPRETATION PROTOCOLS”

in cases set for trial. When these prosecutors received their new reports, they noticed significant changes in the statistics results in some (but not all) of the cases. The cases involved complex DNA mixtures, usually with difficult evidentiary samples such as gun swabs, steering wheel swabs, items of clothing, or other examples of “touch DNA” where multiple people may have contributed DNA to the sample.
DNA samples in Travis County cases will undergo extra scrutiny

By Calily Bien
Published: June 13, 2016, 5:23 pm  |  Updated: June 13, 2016, 5:32 pm

AUSTIN (KXAN) — The abrupt closure of the Austin Police Department’s DNA lab will impact cases that are moving through the Travis County court system.

On Monday, the Travis County District Attorney’s Office said they have hired a leading expert in forensic DNA to review all casework by the APD DNA lab before the plea or trial of pending cases.

Last week, APD suspended operations at its DNA lab after an audit conducted by the Texas Forensic Science Commission determined the lab did not have enough properly trained staff. The report also indicated the lab was not up to date on standard protocols.

The audit, which was conducted over a 3-day period in May and June, focused on the lab’s DNA analysis assessment and a review of the lab’s forensic biology operations.

Since 2010, the lab had been using a testing standard that “is neither scientifically valid nor supported by the forensic DNA community,” according to the report. The Scientific Working Group on DNA Analysis Methods (SWGDAM) recommended in 2010 that DNA labs implement a dual threshold when testing evidence, APD’s lab only used one.
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
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Strengthening Forensic Science in the United States: A Path Forward

Committee on Identifying the Needs of the Forensic Sciences Community, National Research Council
This PDF is available from the National Academies Press at: http://www.nap.edu/catalog/12589.htm