Spotting the Issues: The Science and the Law

Eric J. Carita
Forensic DNA Consultant
Owner – Ace Forensic Consulting Services, LLC.
Forensic Science: the application of natural sciences to matters of the law.
Criminalistics:

The recognition, identification, individualization, and evaluation of physical evidence using the methods of the natural sciences in matters of legal significance.
DNA 101
Basic Genetics
What is DNA?

DNA is…

The inherited genetic material that makes us what we are
DNA in the Cell

- Cell nucleus
- Chromosome
- Double stranded DNA molecule
- Individual nucleotides
Base Pairing of DNA Strands

Butler, J.M. (2001) *Forensic DNA Typing*, Figure 2.2, ©Academic Press
One set of 22 autosomes (plus X)

Two alleles* for each autosomal genetic marker

Paternity Testing

One set of 22 autosomes (plus X or Y)
Forensic DNA Testing is Nothing like CSI!
Locard’s Principle of Exchange

Anytime there is contact between two surfaces, there will be a mutual exchange of matter across the contact boundary.
Transfer of DNA Evidence

• Locard’s Theory
• Biological fluids
  – Saliva
  – Semen
  – Blood
• Epithelial (Skin) Cells
  – Touch DNA
  – Fingerprints
How much do you need?

The size of the blood sample necessary for RFLP

What we need today

“Touch DNA”
Common Sources of Touch DNA

From Hands:
- Gloves
- Knife handles
- Weapon handles
- Firearm grips
- Plastic bag handles
- Steering Wheels
- Rope
- Shoe laces
- Electrical cords
Common Sources of Touch DNA continued...

Wearer:

- Baseball caps
- Sweatbands
- Shirt/jacket collars
- Socks
- Waistbands of pants
- Eyeglasses

* Mixtures v. Single Source
TOUCH DNA CASES

Commonly swabbed areas
DNA Testing
DNA analysis using STRs and the DNA Database

Individuals tested → Blood sample → DNA is extracted → DNA quantitation → PCR amplify → DNA profiles
Qiagen EZ1 DNA Extraction Robot
Quantitation: How much DNA?
## Quantitation Results

<table>
<thead>
<tr>
<th>Sample Name</th>
<th>Location</th>
<th>Sample Type</th>
<th>Human [Auto] ng/µL</th>
<th>Human [Y] ng/µL</th>
<th>Human:Male Ratio</th>
<th>Mixture Detection</th>
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DNA Amplification with the Polymerase Chain Reaction (PCR)

Separate strands (denature)

Make copies (extend primers) (anneal)
In 32 cycles at 100% efficiency, 1.07 billion copies of targeted DNA region are created.
Short Tandem Repeats (STRs)

Repeat number varies between alleles. PCR primers bind to flanking regions that are constant.

Homozygote = Two copies of same allele.
Heterozygote = Two different alleles.
Flanking region with unique sequence in “constant” region = locus specific amplification.
Capillary Electrophoresis
Homozygote – 13 Mom / 13 Dad

Heterozygote – 10 Mom / 11 Dad

Amelogenin

X,X = Female
X,Y = Male
Conclusions

• Included / Match
• Cannot Be Eliminated
• Excluded
• Inconclusive
• Insufficient for comparison

Inclusionary = stat
(Yee, Mattei, Coy)

Rarely complained about (but beware)

(Cameron)
Highly Debated
(STRmix / TrueAllele)
Spotting the Issues
But what do I look for?

Step 1: Discovery Material

- Can’t identify potential issues without the underlined information
- More is better: Ask for it, see what you get, argue it if necessary
DNA Discovery Request

Necessary material to be provided by the laboratory:

1. A copy of all DNA laboratory reports.
2. A copy of all DNA laboratory case jacket / casefile / file folder notes, from evidence intake through evidence disposition, including LIMS chain-of-custody receipts and all CODIS related information / paperwork.
3. A copy of all Serology / Forensic Biology laboratory reports.
4. A copy of all Serology / Forensic Biology laboratory case jacket / casefile / file folder notes, from evidence intake through evidence disposition, including LIMS chain-of-custody receipts.
5. A copy of all Serology / Forensic Biology / DNA reports from private or outsourcing laboratories.
6. A copy of all Serology / Forensic Biology / DNA laboratory case jacket / casefile / file folder notes from private or outsourcing laboratories, from evidence intake through evidence disposition, including LIMS chain-of-custody receipts.
7. A copy of all pertinent non-laboratory generated paperwork or reports associated with the case (e.g. hospital reports, police reports, reports from testing performed by a private laboratory, grand jury minutes, trial testimony, etc.).
8. A copy of all MtDNA and/or STR data (Genotyper®, GeneMarker®, Genescan®, GeneMarker®, Sequencher®, etc.) generated (including all evidentiary and exemplar profiles, with their associated controls).
9. A list of acronyms / abbreviations used throughout all laboratory notes.
10. A copy of all communications logs (written and electronic) between all relevant parties pertaining to this case. This would include, but not limited to, attorneys, investigators, inspectors, state or local law enforcement, and other analysts or supervisors / administrators associated with this case.
11. Electronic copies (in CD form) of all DNA data generated for this case. This would include electronic copies of...
   a) all reported data
   b) all DNR (Data Not Reported) runs
   c) all raw data, Genescan®, Genotyper®, GeneMapper®, SeaScan®, GeneMarker®,
      or pertinent mtDNA and/or STR generated runs.
   d) all matrices (if applicable) for all runs

12. A copy of the DNA and Serology / Forensic Biology protocols (SOP), Laboratory Quality Manual, and work instructions (including all appendices) pertaining to the dates in which the testing was performed and the results reported. These should include interpretational guidelines, stutter thresholds, calling and asterisk thresholds, statistical calculations, database references, and CODIS related guidelines. Any changes made to the SOPs, Quality Manual, and/or Work Instructions, between the dates in which the testing was started and the report finalized, are to be documented and/or noted.

13. A copy of the contamination log for the primary analyst, secondary analyst, and technical reviewer (if applicable). These would include individual instances of contamination throughout the analysts working history and are sometimes referred to as instances of “contamination”, “unexpected results”, “corrective action”, “sample switching”, “mislabeling”, or other similar terms.

14. Copies of the primary analyst’s, secondary analyst’s, technical reviewer’s, and administrative reviewer’s (if applicable) CVs.

15. A copy of proficiency test results for all analysts (Primary, Technical Reviewer, and Administrative Review) spanning 2 years prior to (4 proficiency tests) and two years following (4 proficiency tests) the testing and reporting of all evidentiary and known exemplar DNA samples associated with this case. The test results should identify the (1) proficiency testing company, (2) proficiency test number, (3) the analyst, and (4) the results of the proficiency test. Any discrepancies with testing results should include (1) the discrepancy, (2) what corrective action(s) were taken, and (3) any internal and external communication logs between the laboratory, analyst, and testing company.

16. Specification of which databases were used in any and all calculations presented in this case.

17. A copy of the database or databases used in the calculation of the allele frequencies or statistical correlations performed within this case.
18. Copies of journal articles, if any, in which the databases used in this case were published.

19. A copy of the last two laboratory external audits (ASCLD-LAB, ISO-17025, Legacy, NFSTC, etc.) including all (1) findings, (2) laboratory responses to findings, and (3) remediation performed by the laboratory for the listed findings.

All paperwork should be sequentially numbered (page # / total number) to ensure that all pages are present.

Thank you,

Eric J. Carita
Forensic DNA Consultant / Owner
Ace Forensic Consulting Services, LLC.
Evidence Handling / Collection

- By law enforcement?
- By Laboratory?
- Packaging – cross contamination?
- Fruit of the poisonous tree or cross examination challenges for both PD & Lab?
- Statements, Reports, GJM = defendant or belongings searched prior to recovered item?
- Were was evidence found?
BIG NO-NO!!!
Location?
Together then separated

Transfer prior to collection – exterior of shorts to interior of underwear?
SOP / Protocols

- Are the protocols accurate & abide by audit standards?
- Were all the procedures performed per the laboratory protocols
- Were all of the analyses, interpretations, and comparisons performed per lab protocols
- Were all statistical correlation performed per laboratory protocol?
Controls

- Positive and Negative Controls

- Expected Results

- Demonstrate the reliability and validity of the reagents, platforms, & results

- Failure = DNA results not being used
Positive

Negative
Mixtures
What is a Mixture?
Mixture

- A profile consisting of DNA from two or more individuals
- Can be determined based upon results at one or more loci.
- Mixture Interpretation - Simple or complex based upon the number of contributors, peak height ratios, and number of loci detected.
# of Contributors?
Mixture Detection?

Factors:
1. Quantity
2. Quality
3. Ratio
Mixture Analysis & Interpretation

- The more contributors, the more complex
- The more low-level quantities of DNA, the more complex
- Easily distinguishable Major contributor?
- Following lab protocols and Mixture Interpretational Guidelines?
Different Thresholds

Example values (empirically determined based on own internal validation)

- **150 RFUs**: Peak real, but not used for CPE
- **50 RFUs**: Peak not considered reliable

**Asterisk Peaks**:

- **Called Peak - Allele #**: Peak real, can be used for CPE

**Stochastic Threshold**
(Dropout/Interpretation/LOQ/Reporting/MIT)

**Analytical Threshold**
(Reporting/Noise/Limit-of-Detection/PAT)

Noise

DNA Mixture Interpretation
Current SWGDAM Guidelines
Possible Alleles at locus = 11-21
Mixture of at least 2 people

Suspect Profile = 14,16

SWGDAM – Drop-out Possible = Uninterpretable / Inconclusive
4 Loci example
Mixture of multiple individuals – Lab reports inconclusive

Suspect Profile

Locus 1
11
12* 13*

Locus 2
8
9
10*

Locus 3
11
14
15,15

Locus 4
12,14
10,10
15,15

Stochastic
Analytical

Brady Issue - Potential Exculpatory Data?
Two Main Schools of Thought

- Comparisons based upon data generated.
- Goal of DNA testing is to exclude known.
- Absence of DNA profile is an exclusion.
- Does not ignore potential exculpatory data.
- Conservative Approach.

- SWGDAM “Guidelines”
- Recommendations, not Audit Standards
- If in Stochastic Zone then inconclusive.
- Ignore Potential Exculpatory Data?
- Conservative Approach.
Mixture Conclusions

- The Great Debate: Inconclusive vs. Exclusion

- Inconclusive – Based upon:
  - Number of Contributors (2 vs. 3 vs. 4 person mixture)
  - Potential for drop-out (missing genetic info)
  - Major Contributor?
  - Low-level quantities of DNA (Conclusion: NSC)
  - Possible degradation (sheared or cut DNA)
  - Capability to perform a stat (Yee, Coy, Mattei)

- Question: What is detected and what is assumed to be missing?
NSC v. Excluded?

Evidence

No 15
No 28

No 17, <19
No 14
No 13
No 19

No 17
No 9
No 15

No 13
No 21

Known
NSC v. Excluded?

Excluded at 11 of 15 loci

Lab Reports: NSC

I Conclude: Excluded (Based upon data detected and making no assumptions)

What to do?

LR Stats
Cybergenetics

TO: ERIC J. CARITA
ACE FORENSIC CONSULTING SERVICES, LLC.
NORTH GROSVENORDALE, CT 06253

September 22, 2016

REPORT
Cybergenetics

Victim:

Defendant:

Evidence Items:
1. Item 1.2.1.1
   Item 2.1.1
   Snake of weeder (50 Brown Street)

METHODS:

- The DNA Identifiler® data profiles referenced in this report were previously developed and addressed in a DNA Testing Report issued by the Massachusetts State Police Crime Laboratory.
- The TrueAllele® Casework system processed each evidence item in independent replicate computer runs to infer possible DNA contributor genotypes from the samples.
- The United States Federal Bureau of Investigation generated the population allele frequencies.
- The DNA match statistics were calculated using Vihan™ version 3.3 SPM (31 Jan 2016) at a theta value (co-
  ncertainty coefficient) of 1%.
- All evidence genotypes were compared with all reference genotypes to compute likelihood ratio (LR) DNA match statistics.

RESULTS:

TrueAllele assumed that the evidence sample data (Item 1.2.1.1) contained two or three unknown contributors, and objectively inferred evidence genotypes solely from these data. Degraded DNA was considered. Following genotype inference, the computer then compared repeated genotypes from this evidence item to a provided reference genotype (Item 2.1.1), relative to ethnic populations, to compute LR DNA match statistics. Based on these results:

A match between the weeder (Item 1.2.1.1) and [redacted] was:

- 25.8 million times less probable than a coincidental match to an unrelated African-American person.
- 2.44 billion times less probable than a coincidental match to an unrelated Caucasian person, and
- 839 million times less probable than a coincidental match to an unrelated Hispanic person.

DNA Match Tables

All evidence genotypes were compared with all reference genotypes to compute LR DNA match statistics.

1. Likelihood ratio:

<table>
<thead>
<tr>
<th>Item</th>
<th>Description</th>
<th>LR</th>
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<tbody>
<tr>
<td>1.2.1.1</td>
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</table>

2. log_{e}(LR), or the powers of ten in the LR number

<table>
<thead>
<tr>
<th>Item</th>
<th>Description</th>
<th>LR</th>
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</thead>
<tbody>
<tr>
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*The LR shown is the conservative value calculated across three ethnic populations.
Commonwealth vs. Ronjon Cameron

- Beware the combination of a reported “inconclusive” conclusion, an implied inclusion (nonexclusion), and the lack of statistics.
- Implied “inclusion” by the prosecution based upon the DNA results.
- No report but implied through expert testimony
- No statistic to support the implied conclusion.
What to look for when interpreting a mixture profile...Expert

• Always analyze Q before K...Prevents Cognitive Bias.
• Each Individual locus.
• Examine Mixture as a whole.
• Smaller loci (> efficient) vs. Larger Loci (< efficient)
• Complexity of mixture.
• Possibly degradation.
• Intimate sample, Property, Ownership, etc.
\[ p + 1.96 \sqrt{\frac{(p)(1-p)}{N}} \]

\[ p^2 + 2pq + q^2 = 1 \]

\[ 1 - \alpha^{1/N} \]

**Forensic DNA Statistics**

\[ AA + 2AB + 2AC + BB + 2BC + CC = 1 \]

\[ P = .5 \times .5 \times .5 \times .5 \times .5 = 1/32 \]
Statistics

• Key is to spot stats issues prior to and during trial
  – Prosecution and Defense Fallacies?
• What statistic is being implemented?
  – Report and Discovery Materials
• Is it being calculated correctly per the laboratory SOP?
  – SOP and Discovery Materials
• What does the statistic actually mean or represent?
  – Study, study, study, or expert explains and educates.
• Does conclusion and stat jive?
• Defendant has NOTHING to do with the statistic!!!
Common Statistics Used In Forensics

- Random Match Probability (RMP)
- Restricted / Unrestricted CPE / CPI
- Counting Method (YSTR & MtDNA)
- Likelihood Ratios
  - Unlike years ago, LHR stats can calculate a LH or probability of exclusion, not just inclusion.
  - Feb 1\textsuperscript{st} – LHR stats online for ID at MSP Lab.
  - Only for older cases with previous inculpatory results.
Statistics

Is not:

Prosecutor’s Fallacy.

A) There is only a 1 in 100 million chance that the DNA profile came from someone else.

B) There is only a 1 in 100 million chance that the defendant is not guilty.
Is not:

Defense Fallacy.

A) Therefore, everyone else with the same genotype has an equal chance of being guilty.

B) Therefore, every possible genotype in a mixture has an equal chance of having committed the crime.
Statistics are not:

1. The probability that someone else is guilty.
2. The probability that someone else left the DNA.
3. The probability that the defendant is not guilty.
United States Court of Appeals, 9th Circuit
(Troy Don Brown v. Farwell and State of Nevada)

Statements of the DNA Analyst:

1. 1 in 3 million randomly selected people would match the DNA found in victim’s underwear.

2. 99.999967 percent chance that the DNA found in the underwear was from Brown.

Source probability ≠ Random match probability.
Math in the Courtroom

• “Mathematics, a veritable Sorcerer in our computerized society, while assisting the trier of fact in the search for the truth, must not cast a spell over him.”
  - People v. Collins, 438 P. 2d 33, Cal. 1968

• Trial by Mathematics, L. Tribe, 84 Harv. L. Rev.1329:
  • “directness and precision may overshadow basic concepts and fundamental bases of the trial system.”

• “significance, appropriateness, and dangers of mathematical proofs may depend dramatically on whether such proof is meant to bear on occurrence, identity, or frame of mind.”

• “Without the probability assessment, the jury does not know what to make of the fact that the patterns match: the jury does not know whether the patterns are as common as pictures with two eyes, or as unique as the Mona Lisa.”
“We … hold that DNA evidence is only admissible when both the evidence of a match and the statistical significance of the match are admissible. Thus we reject the State’s overly simplistic argument that statistics go simply to the weight, not the admissibility of the DNA matching evidence.”

We have also held that in a criminal trial we will "not permit the admission of test results showing a DNA match (a positive result) without telling the jury anything about the likelihood of that match occurring." Commonwealth v. Curnin, 409 Mass. 218, 222 n.7 (1991)

See Commonwealth v. Daggett, 416 Mass. 347, 357 (1993) (Abrams, J., concurring) ("expert testimony concerning a DNA match must be accompanied by some background information indicating the probability that the match in question might have occurred by chance")
Commonwealth v. Thad T., 59 Mass. App. Ct. 497, 505-506 (2003) (same). We have explained our approach by stating that "[e]vidence of a match based on correctly used testing systems is of little or no value without reliable evidence indicating the significance of the match, that is, 'evidence of the probability of a random match of [the victim's or] the defendant's DNA in the general population.'"

See Commonwealth v. Curnin, supra at 230 (Appendix) ("The fact that two DNA samples produce the same DNA prints, and therefore contain the same alleles, is of little probative value in a criminal prosecution until it is determined how often that combination of alleles occurs in a given population").
Defense Arguments to Uninterpretable / Inconclusive Conclusions

• Results not probative because expert cannot make a “conclusion”.
  – How is jury suppose to interpret “inconclusive” and use that conclusion if Lab / Expert can’t make a conclusion.
  – Should the jury even hear “inconclusive” results / conclusions?
Defense Arguments to Uninterpretable / Inconclusive Conclusions

• Uninterpretable / Inconclusive conclusions makes a “inclusionary” inference (Cameron).
  – If you could have excluded the defendant than you would have…
  – But since you didn’t exclude, there has to be something “inclusionary” about the comparison.
  – Jury could make “Inclusionary” inference because defendant wasn’t excluded.
  – Does jury have “expertise” to make their own “inferred” conclusion.
How Prosecution may deal with Uninterpretable / Inconclusive Results

• If it doesn’t help the State’s case…

• Not call Lab’s expert because fear that results may confuse jury or call into question “forensics”…CSI Effect.
  – Will defense call Lab expert?

• “evidence / results are not probative to the case, so jury just ignore it.”
How Prosecution may deal with Uninterpretable / Inconclusive Results

- Attempt to turn “uninterpretable” / inconclusive results to their advantage… (Cameron).

- Although profile is low-level and the lab reports “inconclusive”, the defendant matches minor peak.

- Show expert evidentiary vs. known profile and show jury all those areas where the defendant matches.

- Ask expert “yes” and “no” questions.
But the DNA results are good…

- What issues are there when the results are accurate, reliable, and valid?
- How to approach the evidence and cross?
- Yourself or expert: Spotting the limitation to the testing for your specific case and the scenario.
- How can the data help your case?
Limitations: Anitus Argument

1. Can’t determine how DNA was deposited.
2. Can’t tell when DNA was deposited.
3. Mixtures: Can’t tell order (even with major)
4. Primary vs. Secondary Transfer
5. Quant Results: # of skin or sperm cells
6. Case specific

Associated with many crimes including:

Property Crimes
Robbery
Homicide
Assault/Sexual Assault
etc., etc., etc.
Limitations: Anitus Argument

1. Can’t determine how DNA was deposited.

No tests to determine how.

No tests to determine primary vs. secondary transfer.

Does the argument of primary vs. secondary transfer make sense.

If the State can’t determine how, then it rounds up your closing argument.
Limitations: Anitus Argument

2. Can’t tell when DNA was deposited.

DNA has been detected on items, clothing, swabbings collected from individuals but not originally tested days, weeks, months, years after being deposited.

Burdon of the State to demonstrate the DNA was deposited at the time of the crime by the alleged.

Depends upon scenario / circumstances of the case…does it make sense?

Expert will or should know how the State’s expert will testify.
Limitations: Anitus Argument

3. Mixtures: Can’t tell order (even with major)

Being included can’t tell the order, even if your client is the major contributor.

3 person mixture:
- #1, #2, #3
- #1, #3, #2
- #2, #1, #3
- #2, #3, #1
- #3, #1, #2
- #3, #2, #1

4 person mixture:
- 10 different combinations
- N (n+1) / 2
Limitations: Anitus Argument

4. Primary vs. Secondary Transfer

Part of can’t tell “how”.

Could object come in contact with owned property (defendant’s: couch, car seat, clothing, etc.) – expect to have an abundance of their DNA on it.

How was area searched?

Necessary anti-contamination protocols adhered to?

Packaging and handling of the evidence?
Limitations: Anitus Argument

5. Quant Results: # of skin or sperm cells

How much DNA is there in the sample?

0.0020 ng/ul = 20 pg/ul
Amplify 10ul = 200 pg total: can give a beautify DNA profile
7 pg / skin cell
Equivalent of 28 skin cells tested

Humans naturally shed thousands of skin cells a day

Primary vs. Secondary?
Firearm under passenger seat...lot of DNA from def in his own car. Can’t tell how this very small amount got there.
If you hire an expert…

Evaluate all of the relevant discovery material.

They spot potential issues along with you…TEAM!!!

Communicate: educate, train, inform, guide you

Defense hypotheses (that make scientific sense) and play Devil’s Advocate with you (prosecution).

Aid you in cross exam & direct…be there if necessary.

Scientists: unbiased conduit between the evidence and the jury.

Don’t blow smoke up your butt…hurts you and your client.
Confused?: It’s OK!!!

Talk to other attorneys who have had DNA cases.

Attend trainings just like this one.

Read / study up…great bedtime reading.

Call an expert to just ask a question…we don’t bite.
HARD!!!
Any Questions…

Eric J. Carita
Forensic DNA Consultant / Owner
Ace Forensic Consulting Services, LLC.
P.O. Box 521
North Grosvenordale, CT 06255
1-860-377-4067
AFCS.ejcarita@yahoo.com
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