Forensic DNA 201:

Mixture Interpretation and Other Advanced DNA Topics

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NIST and NIJ Disclaimer

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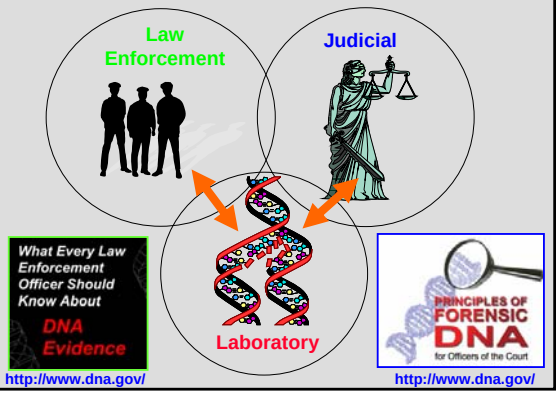
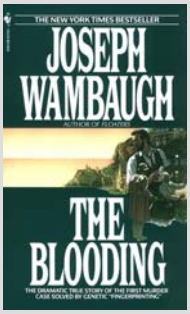
Interfaces Between Disciplines Are Crucial



http://www.dna.gov/ http://www.dna.gov/

Lessons from the First Case Involving DNA Testing



Describes the first use of DNA (in 1986) to solve a double rape-homicide case in England; about 5,000 men asked to give blood or saliva to compare to crime stains

- Connection of two crimes (1983 and 1986)
- Use of DNA database to screen for perpetrator (DNA only done on 10% with same blood type as perpetrator)
- **Exoneration of an innocent suspect**
- DNA was an investigative tool – did not solve the case by itself (confession of accomplice)

A local baker, Colin Pitchfork, was arrested and his DNA profile matched with the semen from both murders. In 1988 he was sentenced to life for the two murders.

Impact of Forensic DNA Testing

Guilt Innocence

Colin Pitchfork

Kirk Bloodsworth

Josiah Sutton

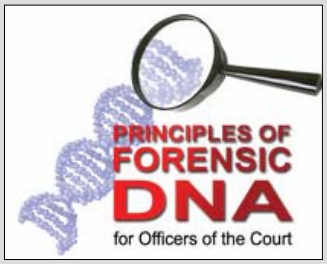
Roger Coleman

Innocence Project

http://www.innocenceproject.org/

DNA Training for Officers of the Court

PRESIDENT'S DNA INITIATIVE *Advancing Justice Through DNA Technology*



- CD-ROM available from the U.S. National Institute of Justice (http://www.ncjrs.gov)
- On-line training available at http://www.DNA.gov

http://www.dna.gov/training/otc/

Principles of Forensic DNA for Officers of the Court

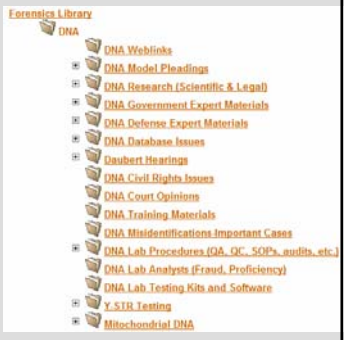
1. Introduction
2. Biology of DNA
3. Practical Issues Specific to DNA Evidence
4. Forensic DNA Laboratory
5. Assuring Quality in DNA Testing
6. Understanding a Forensic DNA Lab Report
7. Statistics and Population Genetics
8. Mitochondrial DNA & Y-STR Analysis
9. Forensic DNA Databases
10. Collection of DNA Evidence
11. Pretrial DNA Evidence Issues
12. Victim Issues
13. Trial Presentation
14. Postconviction DNA Cases
15. Emerging Trends

http://www.dna.gov/training/otc/

Information Resources for Defense Attorneys

http://www.nlada.org/Defender/forensics/for_lib/Index/DNA/exhibits/index_html

Defense Lawyers and Experts are becoming more united and informed



Common Defense Attacks

Compiled from Forensic Bioinformatics website

http://www.bioforensics.com

- Contamination
- Statistical Weight of a Match
- Degradation/PCR Inhibition of "True" Perp
- Artifacts (N+4 stutter, etc.)
- Thresholds Set Too High (missing peaks)
- Examiner Bias
- **Improper Mixture Interpretation**
- Meaning of a Database Hit

Forensic Bioinformatics 6th Annual Conference **The Science of DNA Profiling: A National Expert Forum** August 17 - 19, 2007 Dayton, OH

See http://www.bioforensics.com/conference07/index.html

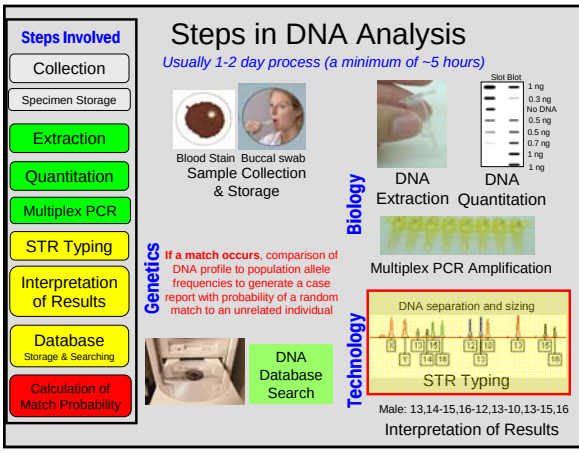
Presentation Outline

- How DNA Results are Obtained
  - Where do these "1 in a zillion" numbers come from?
- Mixture Interpretation
  - How to detect if a mixture is present in a DNA result?
  - Why are mixtures challenging to interpret?
- Other Topics
  - Why are partial profiles not as informative?
  - What measures exist for quality control in labs?
  - Why are protocols used in forensic labs?

How Are DNA Results Obtained?

Steps in DNA Analysis

Usually 1-2 day process (a minimum of ~5 hours)

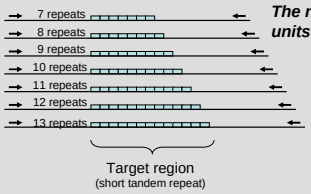


Short Tandem Repeat (STR) Markers

An accordion-like DNA sequence that occurs between genes

TCCCAAGCTCTTCCTCTTCCCTAGATCAATACAGACAGAAGACA
GGTG**GATAGATAGATAGATAGATAGATAGATAGATAGATAGA**
TAGATAGATATCATTGAAAGACAAAACAGAGATGGATGATAGAT
ACATGCTTACAGATGCACAC

= 12 GATA repeats ("12" is all that is reported)

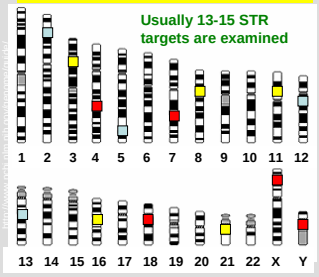


The number of consecutive repeat units can vary between people

The FBI has selected **13 core STR loci** that must be run in all DNA tests in order to provide a common currency with DNA profiles

What is a DNA Profile?

Human Genome
23 Pairs of Chromosomes (~3 billion bp)

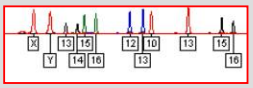


Unique regions of the human genome are targeted

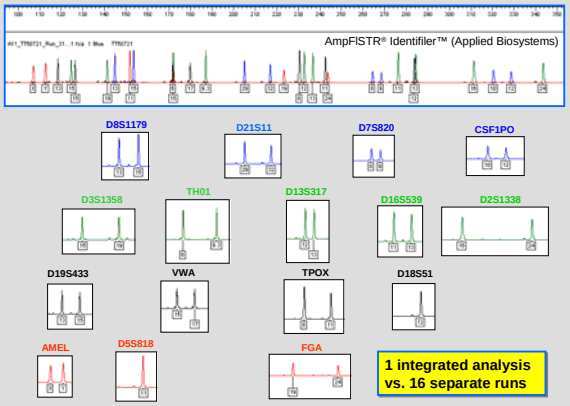
These regions consist of a few hundred base pairs

The regions are copied by the **polymerase chain reaction (PCR)** – billions of exact copies are made

The copied fragments are labeled with fluorescent dyes for detection purposes



Information is tied together with multiplex PCR and data analysis



1 integrated analysis vs. 16 separate runs

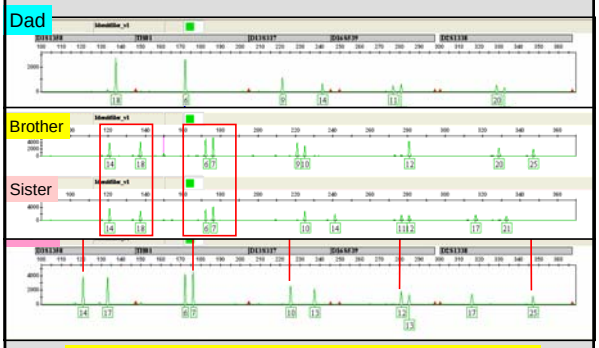
DNA Testing Requires a Reference Sample

A DNA profile by itself is fairly useless because it has no context…

DNA analysis for identity only works by comparison – **you need a reference sample**

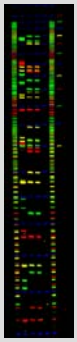
Crime Scene Evidence compared to **Suspect(s)** (Forensic Case)
Child compared to **Alleged Father** (Paternity Case)
Victim's Remains compared to **Biological Relative** (Mass Disaster ID)
Soldier's Remains compared to **Direct Reference Sample** (Armed Forces ID)

Autosomal Paternity Example

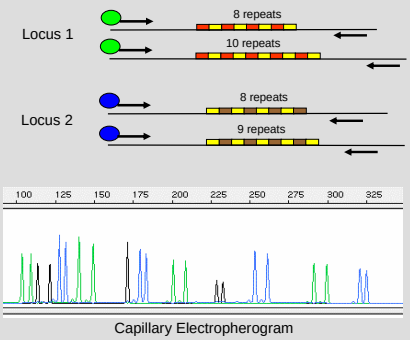


What would be entered into a DNA database for searching:
14,17-6,7-10,13-12,13-17,25 …

STR Allele Separation Can Be Performed by Gel or Capillary Electrophoresis with Detection of Fluorescent Dyes Labeling Each PCR Product

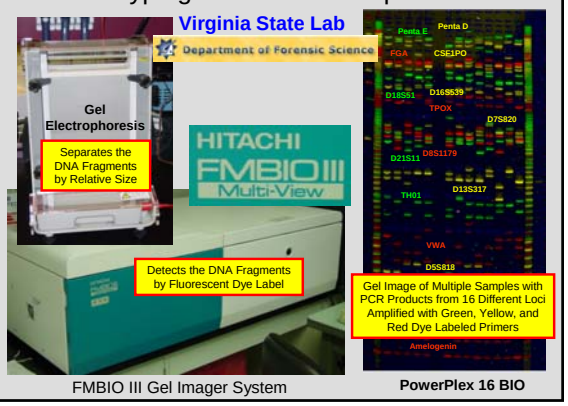


Scanned **Gel Image**

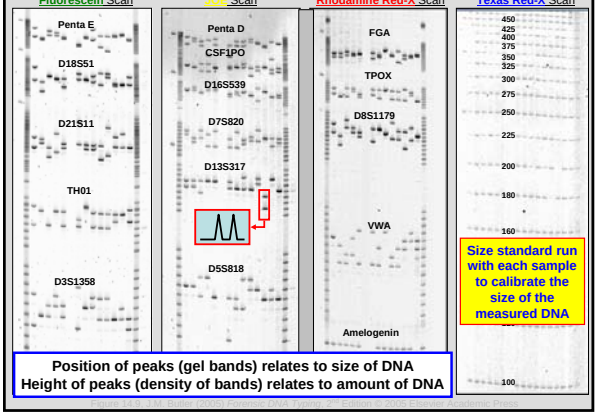


Capillary Electropherogram

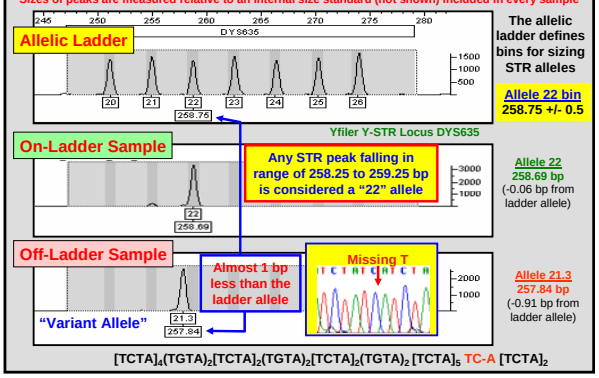
STR Typing with Gel Electrophoresis



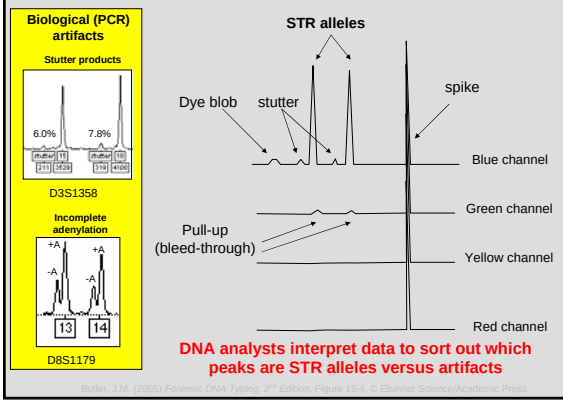
Color-Separated PowerPlex® 16 BIO Samples



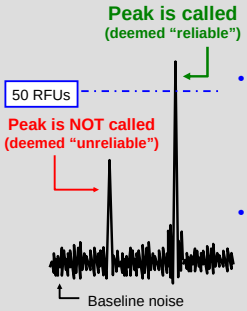
A Locus-Specific Allelic Ladder Composed of Common Alleles is Used to Calibrate Size Measurements



Deciphering Artifacts from the True Alleles



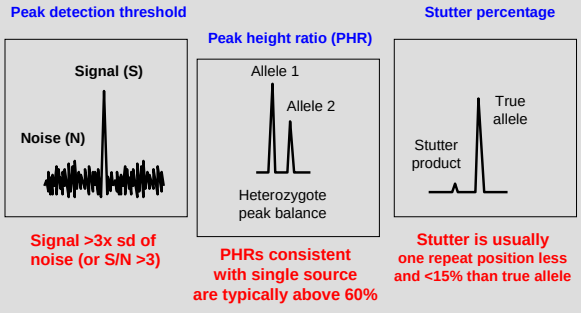
Thresholds for Measuring DNA Data



- **Detection (analytical) threshold**
  - Dependent on instrument sensitivity ~50 RFU (relative fluorescence units)
  - Impacted by instrument baseline noise
- **Dropout (stochastic) threshold**
  - Dependent on biological sensitivity ~150-200 RFU
  - **Important in mixture interpretation**

STR Data Interpretation Involves Determining What is a True Allele (Peak)

All of these issues impact mixture interpretation



STR Data is Tabulated by Genotype Calls for Each Locus

	AMEL	CSF1PO	FGA	TH01	TPOX	VWA	D3S1358	D5S818
Ind(1)	X,Y	11,12	19,21	6,7	8,8	15,18	14,18	10,13

The number of repeats observed for each locus is tabulated

This data format is stored in databases and used for comparisons/matches

Finally a case report is written based on tabulated STR genotype calls

A Report is Generated Based on the STR Allele Calls

http://www.dfs.virginia.gov/services/forensicBiology/manuals/procedures/03-III-PP16 BIO 2003/17-Chapter 11 –Report Writing.pdf (See pp. 2, 3, and 30)

Elements of a Virginia State Lab Report Department of Forensic Science

METHODS SECTION:

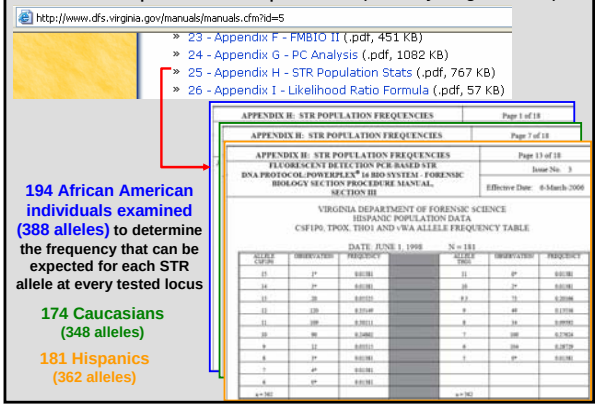
- The method of deoxyribonucleic acid (DNA) analysis used was the Polymerase Chain Reaction (PCR).
- The PCR amplification kit used was the **PowerPlex® 16 BIO system**.
- The PowerPlex® 16 BIO system contains 16 genetic loci (FGA, TPOX, D8S1179, vWA, Penta E, D18S51, D21S11, TH01, D3S1358, Penta D, CSF1PO, D16S539, D7S820, D13S317, D5S818 and Amelogenin, a gender determining locus which is not used for statistical purposes).

RESULTS SECTION:

A DNA profile was developed from the buccal swabs from SUSPECT (Item __). **SUSPECT cannot be eliminated as a contributor of the foreign DNA profile** previously developed from the vaginal sample (Item __) and reported in the Certificate of Analysis dated ____.

"**The probability of randomly selecting an unrelated individual with a DNA profile matching** that developed from the EVIDENCE, SPERM OR NON-SPERM FRACTION OF EVIDENCE, MAJOR PROFILE OF THE EVIDENCE, ETC. at the LOCI USED FOR CALCULATION loci **is approximately 1 in _____ in the Caucasian population, 1 in _____ in the Black population, and 1 in _____ in the Hispanic population.**"

STR Population Frequencies (used by Virginia DFS)



194 African American individuals examined (388 alleles) to determine the frequency that can be expected for each STR allele at every tested locus

174 Caucasians (348 alleles)

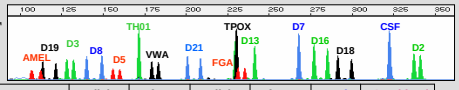
181 Hispanics (362 alleles)

How Are Such Large Numbers Generated with Random Match Probabilities?

RMP = the probability of randomly selecting an unrelated individual with a DNA profile matching that found in the evidence

- Each allele is sampled multiple times to produce a statistically stable allele frequency in the populations of interest (e.g., African American, Caucasian, and Hispanic); each population is calculated
- Using a theoretical model from genetics called Hardy-Weinberg equilibrium, **the predicted frequency of a genotype at a particular locus is calculated** (p^2 for homozygotes and 2pq for heterozygotes)
- Since the forensic STR loci are on separate chromosomes and thus inherited independently, **the result from each locus can be multiplied together with the other tested loci** to produce an estimate of the rarity of a particular multi-locus DNA profile; often referred to as **the product rule**

DNA Profile Frequency with all 13 CODIS STR loci



D3S1358
2pq
= 2(0.2533)(0.2152)
= 0.10902
= 1 in 9.17

D7S820
p^2
= (0.1772)(0.1772)
= 0.0314
= 1 in 31.85

Locus	allele	freq.	allele	freq.	1 in	Combined
D3S1358	16	0.2533	17	0.2152	9.17	9.17
VWA	17	0.2815	18	0.2003	8.87	81
FGA	21	0.1854	22	0.2185	12.35	1005
D8S1179	12	0.1854	14	0.1656	16.29	16,364
D21S11	28	0.1589	30	0.2782	11.31	185,073
D18S51	14	0.1374	16	0.1391	26.18	4,845,217
D5S818	12	0.3841	13	0.1407	9.25	44,818,259
D13S317	11	0.3394	14	0.0480	30.69	1.38 x 10^9
D7S820	9	0.1772			31.85	4.38 x 10^{10}
D16S539	9	0.1126	11	0.3212	13.8	6.05 x 10^{11}
THO1	6	0.2318			18.62	1.13 x 10^{13}
TPOX	8	0.5348			3.50	3.94 x 10^{13}
CSF1PO	10	0.2169			21.28	8.37 x 10^{14}

PRODUCT RULE

The Random Match Probability for this profile **in the U.S. Caucasian population** is **1 in 837 trillion (10^{12})**

The Same 13 Locus STR Profile in Different Populations

1 in 837 trillion

1 in 0.84 quadrillion (10^{15}) in U.S. Caucasian population (NIST)
1 in 2.46 quadrillion (10^{15}) in U.S. Caucasian population (FBI)*
1 in 1.86 quadrillion (10^{15}) in Canadian Caucasian population*

1 in 16.6 quadrillion (10^{15}) in African American population (NIST)
1 in 17.6 quadrillion (10^{15}) in African American population (FBI)*

1 in 18.0 quadrillion (10^{15}) in U.S. Hispanic population (NIST)

These values are **for unrelated individuals** assuming no population substructure (using only p^2 and 2 pq)

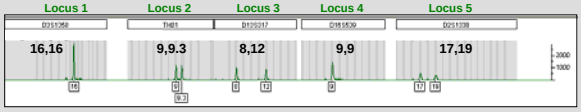
NIST study: Butler, J.M., *et al*. (2003) Allele frequencies for 15 autosomal STR loci on U.S. Caucasian, African American, and Hispanic populations. *J. Forensic Sci.* 48(4):908-911. (http://www.cstl.nist.gov/biotech/strbase/NISTpop.htm)

*http://www.csfs.ca/pplus/profiler.htm

DNA Mixtures: Detection and Interpretation

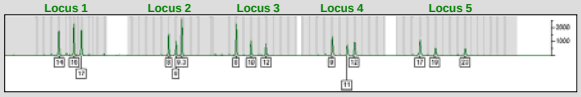
Single Source vs. Mixture Samples

Single Source Sample



One or two peaks observed at each locus (tested DNA region)

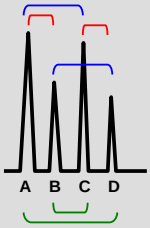
Mixture Sample



More than two peaks observed at more than two loci (tested DNA regions)

Different possible combinations could have given rise to the particular mixture observed

With Some Mixtures, Multiple Genotype Combinations Are Possible



AC
BD
AB
CD
BC
AD

Depends on PHR and proportion of mixture components from the various contributors

Peak Height Ratios (PHR)
Minimum Peak Height (mPH)
Proportion (p) or mixture proportion (M_x)

From Report to the **Virginia Scientific Advisory Committee** by the DNA Subcommittee – Addendum January 8, 2008

(authored by Dr. Norah Rudin and Dr. Artie Eisenberg)

- "Among the many reasons that Forensic DNA analysis has become the gold standard for forensic science is the relatively discrete nature of the data. For strong, single source samples, a profile can readily be determined, and is subject to little or no analyst judgment. **However, ambiguity may arise when interpreting more complex samples, such as those containing multiple contributors, of poor quality (e.g. degraded or inhibited DNA), of low quantity (e.g. contact samples), or various combinations of these challenging situations**…"

http://www.dfs.virginia.gov/about/minutes/saCommittee/20080108.pdf

From Report to the **Virginia Scientific Advisory Committee** by the DNA Subcommittee – Addendum January 8, 2008

(authored by Dr. Norah Rudin and Dr. Artie Eisenberg)

- "…**These kinds of samples are encountered with increasing frequency, as the sensitivity of the technology has increased, and as law enforcement has become more sophisticated about the kinds of samples they submit for analysis**. Difficult samples are also frequently encountered when reanalyzing historical cases, in which samples were not collected and preserved using the precautions necessary for DNA analysis…"

"Cold cases" or Innocence Project samples…

http://www.dfs.virginia.gov/about/minutes/saCommittee/20080108.pdf

From Report to the **Virginia Scientific Advisory Committee** by the DNA Subcommittee – Addendum January 8, 2008

(authored by Dr. Norah Rudin and Dr. Artie Eisenberg)

- "It is for these types of challenging samples, where the evidence profile may not exactly "match" a reference profile, that confirmation bias becomes a concern. **The interpretation of an evidentiary DNA profile should not be influenced by information about a subject's DNA profile.** Each item of evidence must be interpreted independently of other items of evidence or reference samples. Yet forensic analysts are commonly aware of submitted reference profiles when interpreting DNA test results, creating the opportunity for confirmatory bias, despite the best intentions of the analyst…"

http://www.dfs.virginia.gov/about/minutes/saCommittee/20080108.pdf

Mixture Basics

From J.M. Butler (2005) *Forensic DNA Typing, 2nd Edition*, p. 154

- Mixtures arise when two or more individuals contribute to the sample being tested.
- Mixtures can be challenging to detect and interpret without extensive experience and careful training.

Even more challenging with poor quality data when degraded DNA is present…

- Differential extraction can help distinguish male and female components of many sexual assault mixtures.

Y-chromosome markers can help here in some cases to isolate male DNA…

Sources of DNA Mixtures

- **Two (or more) individuals** contribute to the biological evidence examined in a forensic case (e.g., sexual assault with victim and perpetrator or victim, consensual sexual partner, and perp)

Victim Reference and Spouse or Boyfriend Reference

- **Contamination** of a single source sample from
  - evidence collection staff
  - laboratory staff handling the sample
  - Low-level DNA in reagents or PCR tubes or pipet tips

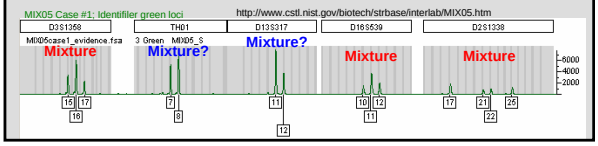
Examine Staff Profiles (Elimination Database), etc.

Reference elimination samples are useful in deciphering both situations due to possibility of intimate sample profile subtraction

Detecting the Presence of a Mixture

From J.M. Butler (2005) *Forensic DNA Typing, 2nd Edition*, p. 155

- The probability that a mixture will be detected improves with the use of more loci and genetic markers that have a high incidence of heterozygotes.
- The detectability of multiple DNA sources in a single sample relates to the ratio of DNA present from each source, the specific combinations of genotypes, and the total amount of DNA amplified.
- Some mixtures will not be as easily detectable as other mixtures.



Steps in the Interpretation of Mixtures

(Clayton *et al.* 1998)

Step #1 Identify the Presence of a Mixture

Step #2 Designate Allele Peaks

Step #3 Identify the Number of Potential Contributors

Step #4 Estimate the Relative Ratio of the Individuals Contributing to the Mixture

Step #5 Consider All Possible Genotype Combinations

Step #6 Compare Reference Samples

Clayton *et al.* (1998) *Forensic Sci. Int.* 91:55-70

Two Parts to Mixture Interpretation

- Determination of alleles present in the evidence and **deconvolution of mixture components** where possible
  - Many times through comparison to victim and suspect profiles
- **Providing some kind of statistical answer** regarding the weight of the evidence
  - There are multiple approaches and philosophies

Statistical Approaches with Mixtures

See Ladd *et al.* (2001) *Croat Med J.* 42:244-246

- **Inferring Genotypes of Contributors** - Separate major and minor components into individual profiles and compute the random match probability estimate as if a component was from a single source
- **Calculation of Exclusion Probabilities** - CPE/CPI (RMNE) – The probability that a random person (unrelated individual) would be excluded as a contributor to the observed DNA mixture
- **Calculation of Likelihood Ratio Estimates** – Comparing the probability of observing the mixture data under two (or more) alternative hypotheses; in its simplest form LR = 1/RMP

DNA Advisory Board (DAB) Recommendations on Statistics

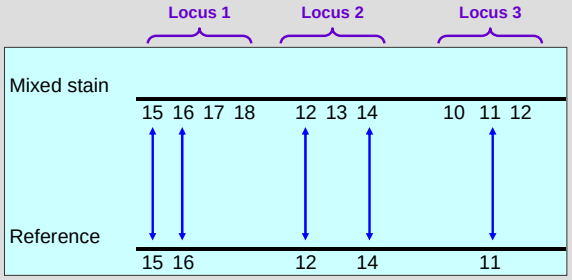
February 23, 2000
Forensic Sci. Comm. 2(3); available on-line at
http://www.fbi.gov/hq/lab/fsc/backissu/july2000/dnastat.htm

"The DAB finds either one or both PE or LR calculations acceptable and strongly recommends that one or both calculations be carried out whenever feasible and a mixture is indicated"

- Probability of exclusion (PE)
  - Devlin, B. (1992) Forensic inference from genetic markers. *Statistical Methods in Medical Research*, 2, 241–262.
- Likelihood ratios (LR)
  - Evett, I. W. and Weir, B. S. (1998) *Interpreting DNA Evidence*. Sinauer, Sunderland, Massachusetts.

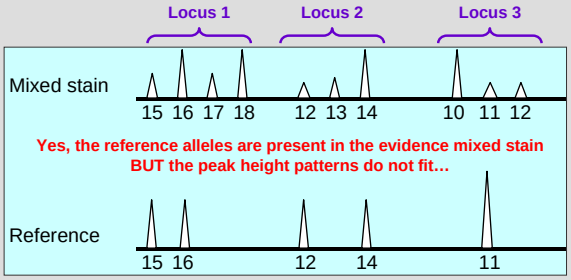
Mixture Example

Comparing Alleles Only



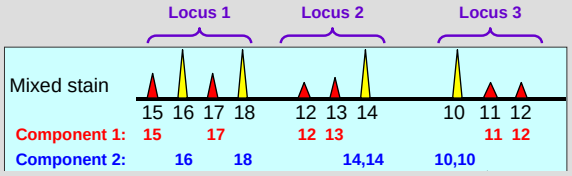
Mixture Example

Showing Importance of Using Peak Height Information



Mixture Example

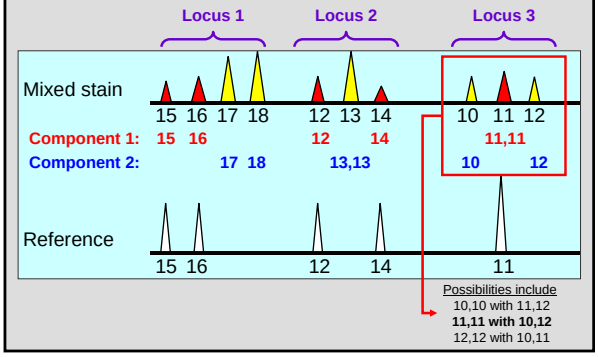
Solving Components Prior to Comparison to Suspect Reference



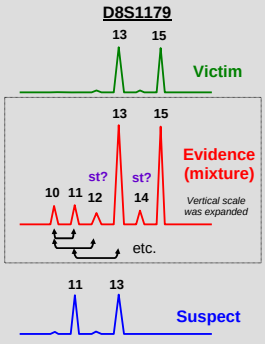
Reference (suspect) does not match either component of the mixed stain and therefore could not have contributed to the evidence sample

Mixture Example

Different Evidence Sample…



Another Mixture Example



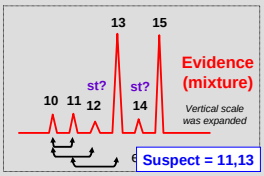
Conclusions from the evidence:

1. **Major contributor = 13,15 (victim) –** *to be expected with an intimate sample like a fingernail or vaginal swab*
2. Alleles 12 and 14 are **likely stutter products** of the major contributor's 13 and 15 alleles but could also be masking minor contributor alleles
3. A number of minor contributor combinations are possible (e.g., 10,11 or 10,12 or 10,13 or 11,13, etc.)
4. Could have more than two contributors present in this mixture

"Suspect cannot be excluded" BUT statement needs to be qualified by statistics because a large percentage of the population might also not be able to be excluded…

Probability of Exclusion Calculation
for a Single STR Locus

The case may grow stronger against a suspect with information from additional STR loci…



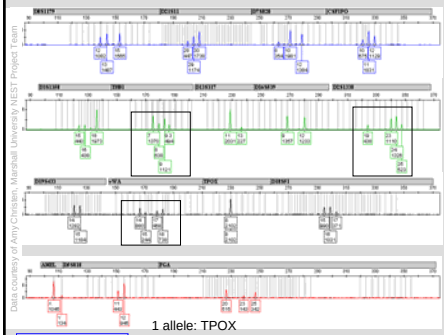
The fact that in this case a suspect is included is not very informative because ~9 out of 10 people examined from any population could potentially be included in the evidence mixture…

From VA DFS STR Allele Frequencies
http://www.dfs.virginia.gov/manuals/manuals.cfm?id=5

D8S1179 alleles	AA (n=384)	C (n=346)	H (n=366)
10	0.0287	0.1069	0.0820
11	0.0495	0.0925	0.0465
12	0.1094	0.1416	0.1093
13	0.2422	0.3093	0.3224
14	0.2969	0.1965	0.2623
15	0.1849	0.0896	0.1202
SUM	0.9115	0.9364	0.9426
Sq SUM = PI	0.8308	0.8769	0.8886
PE = 1-PI	0.1692	0.1231	0.1114
PE (%)	**16.9%**	**12.3%**	**11.1%**
	African Am.	Caucasians	Hispanics

"Suspect cannot be excluded" BUT we would expect to see, for example, only 11.1% of Hispanics excluded (or 88.9% cannot be excluded) based on results at this one locus

Mixture Profile Overview



Data courtesy of Amy Christen, Marshall University NIST Project Team

Evaluation Notes:

1. Loci seen with 1,2,3,&4 alleles (**a mixture** with at least 2 contributors)
2. Imbalance at amelogenin (female & male mixture with female as major)
3. Decent overall signal with D8 in ~1500 RFU (out of stochastic range)
4. Large MW loci have decent signal with D18 in ~1000 RFU range (degradation unlikely)
5. Ratio of **major to minor around 3:1** (from amelogenin X/Y ratios)

1045/134 = 7.8
~3 female (X,X): 1 male (X,Y)

1 allele: TPOX
2 alleles: D19, D5, D13, D16
3 alleles: D8, D21, D7, CSF, D3, D18, FGA
4 alleles: TH01, D2, VWA

DNA Degradation

Intact sample

Target region for PCR

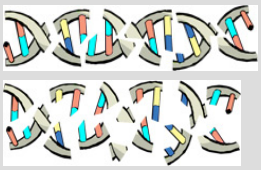
300 base pair PCR product can be produced

Degraded sample

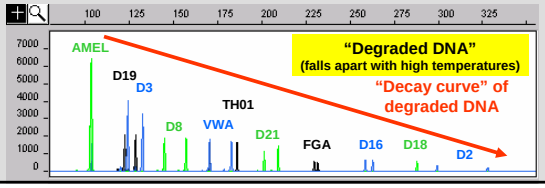
Target region for PCR is fragmented

300 base pair PCR product can not be produced or only in limited quantities

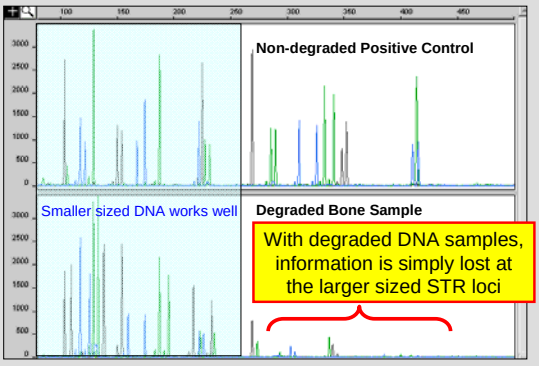
Degraded DNA



Larger segments of DNA cannot be recovered when DNA molecules have fragmented into small pieces (caused by heat, water, or bacteria)



DNA Degradation Means **Less Loci Work**



Impact of Degraded DNA Samples

- Comparison to a phone number (string of 13 numbers)

  001-301-975-4049

- If you only had "4049"…this information would be of limited value since it is not as specific (and could match other phone numbers from different area codes)
- DNA profiles are essentially a string of numbers – **if the DNA is damaged, then the string of numbers is shorter and less informative…**

  ----------4049 or ----301-9-------

The Statistic (Determining the Weight of the Evidence) Should Be **Calculated from the Evidence**

Evidence (partial profile):

	Type	Statistic
Locus 1	16,17	1 in 9
Locus 2	17,18	1 in 9
Locus 3	21,22	1 in 12
Locus 4	12,14	1 in 16
Locus 5	28,30	1 in 11

		Product = 1 in 171,000

Match Observed at All Loci that May Be Compared

Reference (full profile):

	Type	Statistic
Locus 1	16,17	1 in 9
Locus 2	17,18	1 in 9
Locus 3	21,22	1 in 12
Locus 4	12,14	1 in 16
Locus 5	28,30	1 in 11
Locus 6	14,16	1 in 26
Locus 7	12,13	1 in 9
Locus 8	11,14	1 in 31
Locus 9	9,9	1 in 32
Locus 10	9,11	1 in 14
Locus 11	6,6	1 in 19
Locus 12	8,8	1 in 3
Locus 13	10,10	1 in 21

		Product = 1 in 665 trillion

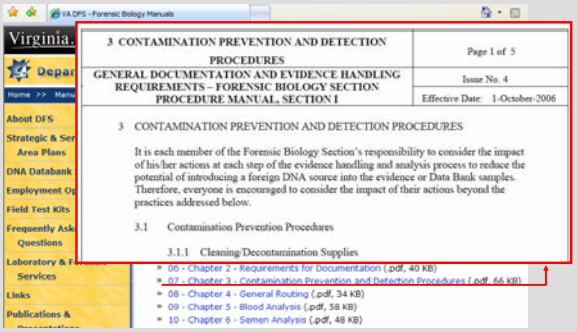
The reference sample is still a "match" – just not as much information is available from the evidence for comparison

Quality Control Measures Used in Forensic Laboratories

Checks and Controls on DNA Results

Community	FBI DNA Advisory Board's Quality Assurance Standards *(also interlaboratory studies)*
Laboratory	ASCLD/LAB Audits and Accreditation
Analyst	Proficiency Tests & Continuing Education
Method/Instrument	Validation of Performance *(along with traceable standard samples)*
Protocol	**Standard Operating Procedure is followed**
Data Sets	Allelic ladders, positive and negative amplification controls, and reagent blanks are used
Individual Sample	Internal size standard present in every sample
Interpretation of Result	Second review by qualified analyst/supervisor
Court Presentation of Evidence	Defense attorneys and experts with power of discovery requests

Virginia's State Forensic Laboratory Makes Their Standard Operating Procedures Available



http://www.dfs.virginia.gov/manuals/manuals.cfm?id=5

Standard Operating Procedures (SOPs)

- Based on **validation studies** performed in a laboratory
- Validation studies help define a range over which reliable results can be expected (e.g., a detection threshold of 150 RFU with DNA profile peaks)
- An SOP **helps to ensure consistency** from case-to-case and analyst-to-analyst within a laboratory and should keep analysts within the scope of reliable results defined by the validation studies
- **SOPs may differ between labs** (e.g., Virginia vs. FBI)

Summary

- "DNA" + "Match" ➔ "Guilty" in the minds of many jurors
- Consider the assumptions with the weight of the evidence particularly for mixtures
- The technology is advancing rapidly with new capabilities becoming available…
- Training for both the scientific and legal communities is vital to make the most effective use of the wonderful power of DNA technology

If You Want to Know More Regarding Recent Advances…
See Review Article on "Forensic Science" in *Analytical Chemistry*

Describes 181 forensic DNA articles published in 2005 and 2006 (**560 references** covering DNA, trace evidence, drugs and poisons)

Forensic Science

Brettell, T.A., Butler, J.M., Almirall, J.R. (2007) Forensic science. *Anal. Chem.* 79: 4365-4384

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Available at http://www.cstl.nist.gov/biotech/strbase/NISTpub.htm

Status of Genetic Marker Systems Used in Forensic DNA Testing

- **STRs** – widely used in casework and national databases world-wide
- **miniSTRs** – smaller versions of STR loci that can work well on degraded DNA
- **Y-STRs** – permits examination of male-only DNA
- **mtDNA** – used in specialty labs for highly degraded specimens or hair that contains limited amounts of DNA
- **SNPs** – potential for identifying ethnicity of evidence sample; still in research and likely to be limited in use

Thank you for your attention…

Our team publications and presentations are available at:
http://www.cstl.nist.gov/biotech/strbase/NISTpub.htm

Questions?

See also http://www.dna.gov/research/nist
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