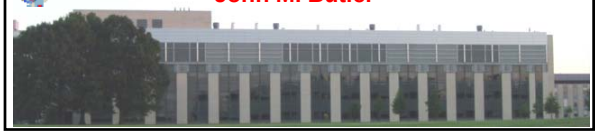
Forensics @ NIST
December 6, 2010 – Gaithersburg, MD

Mixture Interpretation

Michael D. Coble
John M. Butler



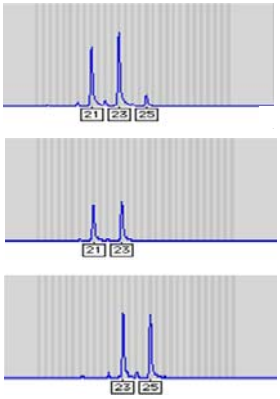
The Forensic Institute

Forensic e-Symposium™
The Forensic Institute

April 14, 2005

"If you show 10 colleagues a mixture, you will probably end up with 10 different answers."
- Dr. Peter Gill

"Don't do mixture interpretation unless you have to"
- Dr. Peter Gill (1998)



Evidence

Victim

Suspect?

Mixture Case Summaries

Elements of DNA Mixture Interpretation

Principles (theory)

Protocols (validation)

Practice (training & experience)

Consistency across analysts

ISFG Recommendations
SWGDAM Guidelines

Laboratory SOPs

Training within the Laboratory

Periodic training will aid accuracy and efficiency within the laboratory.

NIST's Role in Mixture Interpretation

NIST Mixture Interpretation Interlaboratory Study 2005 (MIX05)

John M. Butler and Margaret C. Kline

Biotechnology Division, National Institute of Standards and Technology, 100 Bureau Drive MS 8311, Gaithersburg, MD 20899-8311

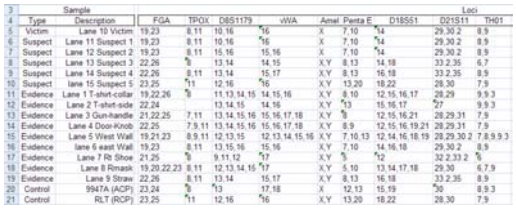
94 labs enrolled, 69 labs participated

"Some of the primary benefits we hope to gain from this study include **recommendations for a more uniform approach to mixture interpretation** and training tools to help educate the community."

http://www.cstl.nist.gov/biotech/strbase/interlab/MIX05/MIX05poster.pdf

NIST Software Tools

mixSTR (Dave Duewer)



	Sample		Loci									
	Type	Description	FGA	TPOX	D8S1179	vWA	Amel	Penta E	D18S51	D21S11	TH01
Victim	Victim	Lane 10 Victim	19,23	8,11	10,16	16	X	7,10	14	29,30.2	8,9
Suspect	Suspect	Lane 11 Suspect 1	19,23	8,11	10,16	16	X	7,10	14	29,30.2	8,9
Suspect	Suspect	Lane 12 Suspect 2	19,23	8,11	15,16	15,16	X	7,10	14	29,30.2	8,9
Suspect	Suspect	Lane 13 Suspect 3	22,26	8	13,14	14,15	X,Y	8,13	14,18	33.2,35	6,7
Suspect	Suspect	Lane 14 Suspect 4	22,26	8,11	13,14	15,17	X,Y	8,13	16,18	33.2,35	8,9
Suspect	Suspect	lane 15 Suspect 5	23,25	11	12,16	16	X,Y	13,20	18,22	28,30	7,9
Evidence	Evidence	Lane 1 T-shirt-collar	19,22,26	8	11,13,14,15	14,15,16	X,Y	8,10	12,15,16,17	28,29	9,9.3
Evidence	Evidence	Lane 2 T-shirt-side	22,24		13,14,15	14,16	X,Y	13	15,16,17	27	9,9.3
Evidence	Evidence	Lane 3 Gun-handle	21,22,25	7,11	13,14,15,16	15,16,17,18	X,Y	8	12,15,16,21	28,29,31	7,9
Evidence	Evidence	Lane 4 Door-Knob	22,25	7,9,11	13,14,15,16	15,16,17,18	X,Y	8,9	12,15,16,19,21	28,29,31	7,9
Evidence	Evidence	Lane 5 West Wall	19,21,23	8,9,11	12,13,15	12,13,14,15,16	X,Y	7,10,13	12,14,16,18,19	28,29,30.2	7,8,9,9.3
Evidence	Evidence	lane 6 east Wall	19,23	8,11	13,15,16	15,16	X,Y	7,10	14,16,18	29,30.2	8,9
Evidence	Evidence	Lane 7 Rt Shoe	21,25	8	9,11,12	17	X,Y	8	12	32.2,33.2	6
Evidence	Evidence	Lane 8 Rmask	19,20,22,23	8,11	12,13,14,16	17	X,Y	5,10	13,14,17,18	29,30	6,7,9
Evidence	Evidence	Lane 9 Straw	22,26	8,11	13,14	15,17	X,Y	8,13	16,18	33.2,35	8,9
Control	Control	9947A (ACP)	23,24	8	13	17,18	X	12,13	15,19	30	8,9.3
Control	Control	RLT (RCP)	23,25	11	12,16	16	X,Y	13,20	18,22	28,30	7,9

NIST Software Tools

Virtual MixtureMaker (Dave Duewer)

Mixture females and Hispanics.xls [Compatibility Mode]

	Profiles		Alleles			# Alleles / Locus																
	#1	#2	#Sep	#Mix	Ratio	Avg	SD	#1	#2	#3	#4	#5	#6+	D8S1179	D21S11	D7S820	CSF1PO
ZT80870	MT94890	63	55	0.87	3.44	0.63	0	1	7	8	0	0	11,13,14,16	28,29,30,34	8,9,10	10,11,12
MT94890	ZT80870	63	55	0.87	3.44	0.63	0	1	7	8	0	0	11,13,14,16	28,29,30,34	8,9,10	10,11,12
GT37869	TT51435	64	55	0.86	3.44	0.73	0	2	5	9	0	0	10,12,13	28,30,30.2,31.2	10,11	9,10,11,12
TT51435	GT37869	64	55	0.86	3.44	0.73	0	2	5	9	0	0	10,12,13	28,30,30.2,31.2	10,11	9,10,11,12
TT51483	TT50722	63	55	0.87	3.44	0.81	0	3	3	10	0	0	11,13,14,15	30,31	8,9,10,11	10.3,11,12,13
TT50722	TT51483	63	55	0.87	3.44	0.81	0	3	3	10	0	0	11,13,14,15	30,31	8,9,10,11	10.3,11,12,13
ZT80815	ZT80870	64	54	0.84	3.38	0.62	0	1	8	7	0	0	11,13,14	28,29,34	8,11,12	10,11,12,13
TT51399	UT57305	63	54	0.86	3.38	0.72	0	2	6	8	0	0	11,13,14	28,29,30.2,32.2	8,11,12	10,12
UT57305	TT51399	63	54	0.86	3.38	0.72	0	2	6	8	0	0	11,13,14	28,29,30.2,32.2	8,11,12	10,12
ZT80869	UT57308	63	54	0.86	3.38	0.81	0	3	4	9	0	0	14,15	29,30,32.2	9,10,12	10,11,12,13
UT57308	ZT80869	63	54	0.86	3.38	0.81	0	3	4	9	0	0	14,15	29,30,32.2	9,10,12	10,11,12,13

Training and Education

David L. Duewer,[1] Ph.D.; Margaret C. Kline,[2] M.S.; Janette W. Redman[2]; Pamela J. Newall,[3] M.A.; and Dennis J. Reeder,[2,4] Ph.D.

AAFS 2008 DNA Mixture Workshop

DNA Mixture Interpretation: Principles and Practice in Component Deconvolution and Statistical Analysis

Full-day workshop at AAFS meeting in Washington, D.C.
***Tuesday, February 19, 2008** - Marriott Wardman Park Hotel*

Chair: John Butler (NIST)
Co-Chairs: Ann Marie Gross (MN BCA) and Gary Shutler (WSP Crime Lab)

Repeat Multiplex Signal Intensity

Margaret C. Kline, David L. Duewer,* Janette W. Redman, and John M. Butler

Chemical Science and Technology Laboratory, National Institute of Standards and Technology, Gaithersburg, Maryland 20899

Mixture Workshop (Promega/ISHI 2009)

http://www.cstl.nist.gov/biotech/strbase/mixture.htm

Handout >200 pages
Literature list of >100 articles

13 Modules Presented

Introductions (Robin)
SWGDAM Guidelines (John)
Analytical thresholds (Catherine)
Stutter (Mike)
Stochastic effects (Robin)
Peak height ratios (Charlotte)
Number of contributors (John)
Mixture ratios (John)
Mixture principles (Charlotte)
Statistics (Mike)

Case Example 1 (Robin)
Case Example 2 (Charlotte)
Case Example 3 (John)

Catherine Grgicak	Mike Coble	Robin Cotton	John Butler	Charlotte Word
Boston U.	NIST	Boston U.	NIST	Consultant

NIJ Grant to Boston University
funded ~150 state & local lab analysts to attend

AAFS 2011 Mixture Workshop

February 22, 2011 (Chicago, IL)

DNA Mixture Analysis: Principles and Practice of Mixture Interpretation and Statistical Analysis Using the SWGDAM STR Interpretation Guidelines

Topics (Speakers)

SWGDAM Guidelines (John Butler)
Mixture Fundamentals (Mike Adamowicz)
Validation & Thresholds (Joanne Sgueglia)
Mixture Statistics (Todd Bille)
Case Summary Analysis (John Butler)
Worked Case Example (Mike Coble)
Complex Mixtures (Gary Shutler)
Software Survey (Mike Coble)
Updating Protocols (Jennifer Gombos)
Training Staff (Ray Wickenheiser)

Planning for ~200 people

FREE
DNA MIXTURE INTERPRETATION
WORKSHOP nfstc NU
NFSTC | LARGO, FL | MARCH 15 -17 | 2011

Topics (Speakers)

Evolution of DNA Mixture Interpretation (Jack Ballantyne)
Current SWGDAM Guidelines (Mike Coble)
Validation (Mike Coble)
Modified Procedures (Mike Coble)
Deconvolution of Mixtures (Chris Maguire)
Mixture Statistics (Todd Bille)
Practical Experience from VDFS (Brad Jenkins)
Y-STR Mixtures (Jack Ballantyne)
Thresholds (John Buckleton)
Reporting Mixtures (Karin Crenshaw)
Pros and Cons of Statistical Approaches(John Buckleton)
Legal Considerations (Jules Epstein)

SWGDAM Mixture Interpretation Subcommittee

- **John Butler** (NIST) – chair
- **Mike Adamowicz** (CT)
- **Terry Coons** (OR)
- Jeff Modler (RCMP)
- **Phil Kinsey** (MT)
- Todd Bille (ATF)
- Allison Eastman (NYSP)
- **Bruce Heidebrecht** (MD)
- **Tamyra Moretti** (FBI DNA Unit I)
- **George Carmody** (Carleton U)
- **Roger Frappier** (CFS-Toronto)
- **Jack Ballantyne** (UCF/NCFS)
- **Gary Sims** (CA DOJ) - co-chair
- **Joanne Sgueglia** (MA)
- **Gary Shutler** (WA)
- Cecelia Crouse (PBSO)
- **Hiron Poon** (RCMP)
- Steve Lambert (SC)
- **Steven Myers** (CA DOJ)
- **Ann Gross** (MN BCA)

The 15 members in bold font were involved with most of the writing (July-Oct 2009)

Started in January 2007

SWGDAM STR Interpretation Guidelines

- The January 14, 2010 approved SWGDAM STR Guidelines were **publicly released April 8, 2010** on the FBI website for the CODIS group: http://www.fbi.gov/hq/lab/html/codis1.htm
  (underneath the Audit document information).
  - The direct links are:
  - http://www.fbi.gov/hq/lab/html/codis_swgdam.htm (html text version)
  - http://www.fbi.gov/hq/lab/html/codis_swgdam.pdf (pdf version)

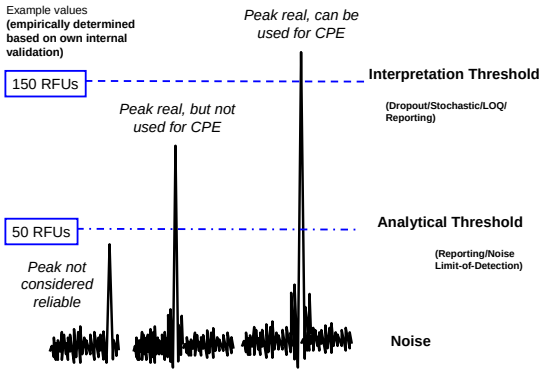
SWGDAM Interpretation Guidelines for Autosomal STR Typing by Forensic DNA Testing Laboratories

- Guidelines
  - Not Standards
  - No lab should be audited against this document
- Autosomal STR Typing
  - This document does not address Y-STRs, mtDNA testing, or CODIS entries
- Forensic DNA Testing Laboratories
  - Databasing labs may have different issues since they are working with known single source samples

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

Different Thresholds



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

Software tools can help with one or both of these…

4. Statistical Analysis of DNA Typing Results

- 4.1. The laboratory ***must perform statistical analysis*** in support of any inclusion that is determined to be relevant in the context of a case, irrespective of the number of alleles detected and the quantitative value of the statistical analysis.

Buckleton & Curran (2008): "There is a considerable aura to DNA evidence. Because of this aura **it is vital that weak evidence is correctly represented as weak or not presented at all.**"

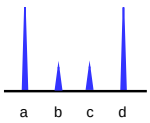
Buckleton, J. and Curran, J. (2008) A discussion of the merits of random man not excluded and likelihood ratios. *Forensic Sci. Int. Genet.* 2: 343-348.

4. Statistical Analysis of DNA Typing Results

- 4.1. The laboratory must perform statistical analysis in support of any inclusion.
- 4.2. For calculating the CPE or RMP, any DNA typing results used for statistical analysis ***must be*** derived from **evidentiary items** and not known samples.
- 4.3. The laboratory must not use inconclusive/uninterpretable data (e.g., at individual loci or an entire multi-locus profile) in statistical analysis.

Statistical Approaches with Mixtures

- **Random Man Not Excluded (CPE/CPI)** - The probability that a random person (unrelated individual) would be excluded as a contributor to the observed DNA mixture.



$p = f(a) + f(b) + f(c) + f(d)$

$q = 1 - p$

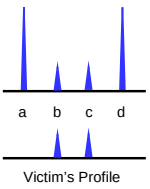
$PI = [f(a) + f(b) + f(c) + f(d)]^2$

$CPI = PI_{M1} \times PI_{M2} \cdots$

$CPE = 1 - CPI$

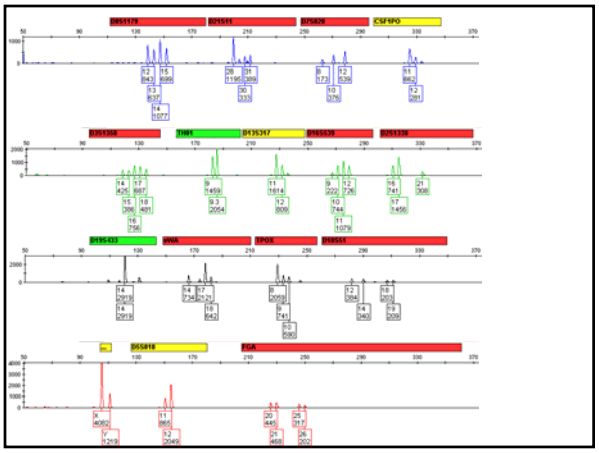
Statistical Approaches with Mixtures

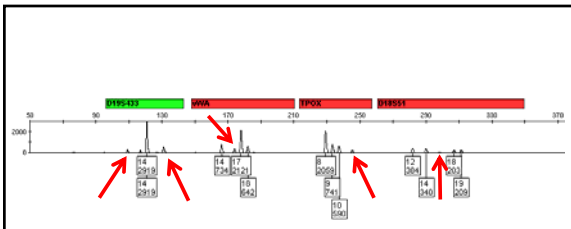
- **Likelihood Ratio** - Comparing the probability of observing the mixture data under two (or more) alternative hypotheses.

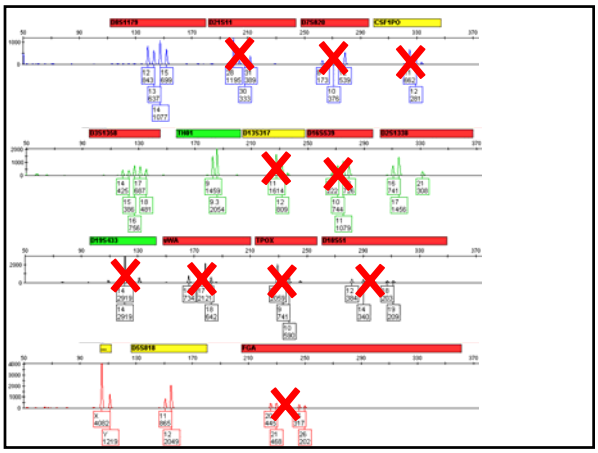


$$\frac{P(E|H_1)}{P(E|H_2)} = \frac{1}{P(E|H_2)} = \frac{1}{2 * f(a) * f(d)}$$

E = Evidence
H_1 = Prosecutor's Hypothesis (the suspect did it) = 1
H_2 = Defense Hypothesis (the suspect is an unknown, random person)







Available Loci (CPI Stats)

- D8S1179 PI = 0.5927
- D3S1358 PI = 0.9704
- D2S1338 PI = 0.0658
- D5S818 PI = 0.5550

- CPI = 0.021

~2.1% of the Hispanic population can be included in this mixture

How not to handle this result

- "To heck with stochastic thresholds", I am just going to see if the suspect profile(s) can fit into the mixture allele pattern observed – and then if an allele is not present in the evidentiary sample I will try to explain it away as possible allele dropout due to stochastic effects.

- This is what Bill Thompson calls "painting the target around the arrow (matching profile)…"

Thompson, W.C. (2009) Painting the target around the matching profile: the Texas sharpshooter fallacy in forensic DNA interpretation. *Law, Probability and Risk* 8: 257-276

Expert Software for Mixture Analysis

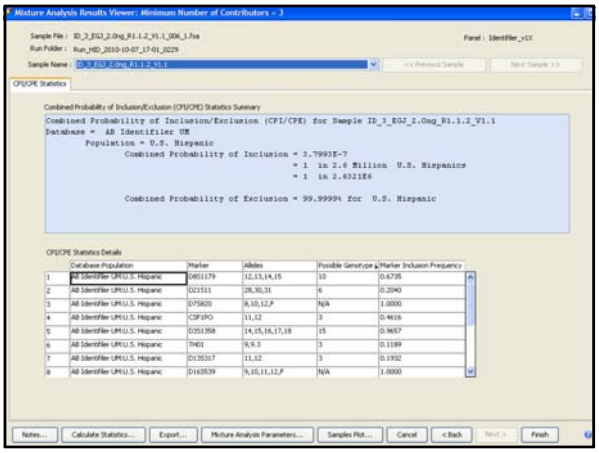
GeneMapper ID-X Software — Now Featuring an Integrated Mixture Analysis Tool

Cybergenetics TrueAllele®

FSS-i3

GeneMarker® HID

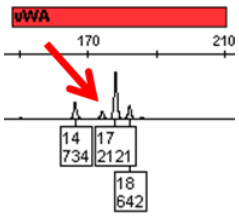
NicheVision Inc.



Software Limitations…

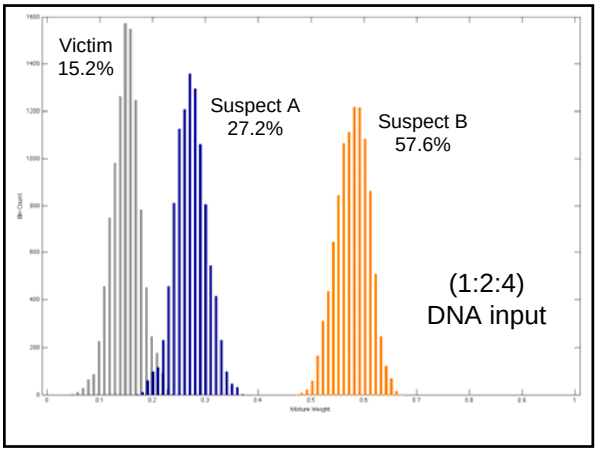
The "16" allele is considered an artifact (stutter) peak from allele 17 and is ignored.

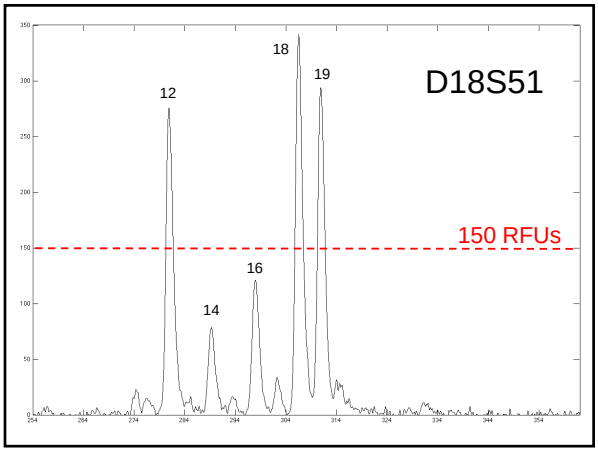
This marker is included in the CPI calculation.

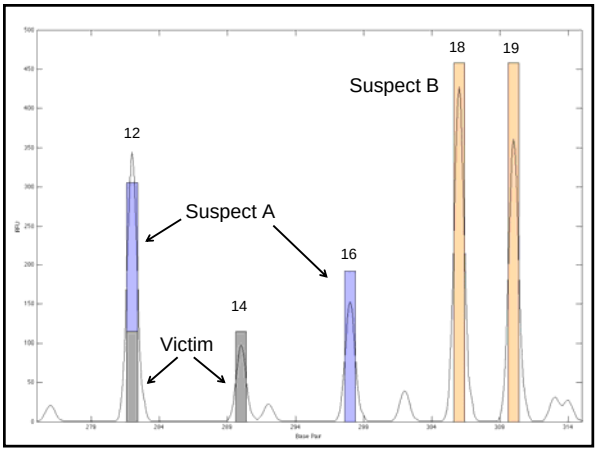


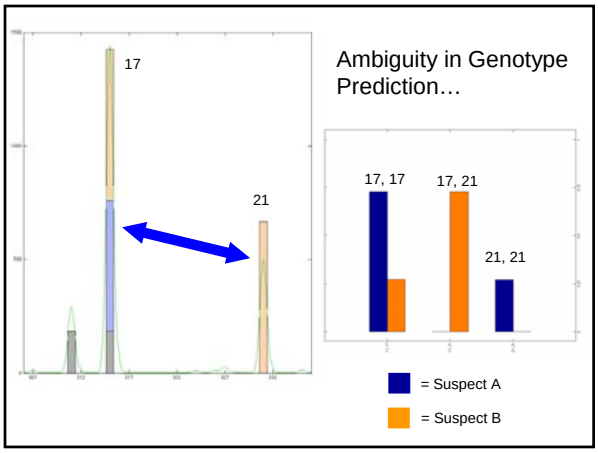
True Allele Software

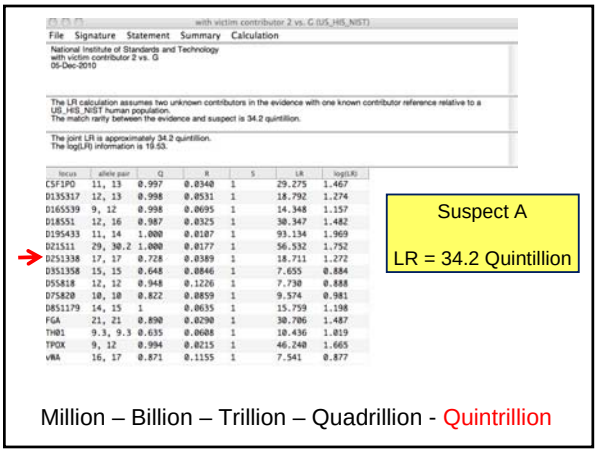
"Markov Chain Monte Carlo Testing"

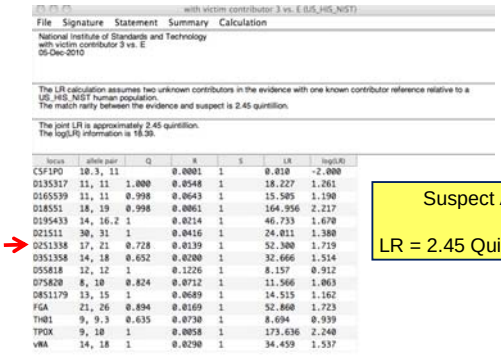












Suspect A

LR = 2.45 Quintillion

Million – Billion – Trillion – Quadrillion - Quintrillion

Benefits of Increased Information

Manual Calculation (CPI)	Mixture Software (CPI)
1 in 2.1% included	1 in 2.6 million included

True Allele Software
(LR)

2.45 Quintillion and 34.2 Quintillion

The NIST Human Identity Project Team
(Forensic DNA & DNA Biometrics)

Funding from the **National Institute of Justice (NIJ)** through the NIST Office of Law Enforcement Standards and the **FBI S&T Branch** through the NIST Information Access Division

…Bringing traceability and technology to the scales of justice…

John Butler — *Project Leader, Forensic DNA*
Erica Butts
Mike Coble
Dave Duewer
Becky Hill
Margaret Kline
Kristen Lewis
Jan Redman
Pete Vallone — *Project Leader, DNA Biometrics*

Workshops & Textbooks
Mixtures, mtDNA & Y
Concordance & LT-DNA
Kinship Analysis
Rapid PCR & Biometrics
Direct PCR & DNA Extraction
Software Tools & Data Analysis
Variant alleles & Cell Line ID
STRBase Support

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