TEXAS FORENSIC
SCIENCE COMMISSION
Justice Through Science

1700 North Congress Ave., Suite 445
Austin, Texas 78701

August 21, 2015

Members of the Texas Criminal Justice Community:

This letter provides notification to the community regarding an issue of potential concern to judges, criminal prosecutors, criminal defense lawyers, victims and defendants in the Texas criminal justice system. The concerns involve the interpretation of DNA results where multiple contributors may be present, commonly referred to as DNA mixture interpretation. The attached document details the origin and scope of the concerns.

While the Commission assesses the issues described in the attached document, we recommend any prosecutor, defendant or defense attorney with a currently pending case involving a DNA mixture in which the results could impact the conviction consider requesting confirmation that Combined Probability of Inclusion/Exclusion (referred to as "CPI" or "CPE") was calculated by the laboratory using current and proper mixture interpretation protocols. If the laboratory is unable to confirm the use of currently accepted protocols for the results provided, counsel should consider requesting a re-calculation of CPI/CPE.

The extent to which any closed criminal cases may require re-analysis will be a subject of Commission review and subsequent notification to the stakeholder community.

If you have any questions regarding these issues, please contact the Commission's general counsel, Lynn Garcia, at 512-936-0649 or lynn.garcia@fsc.texas.gov.

Sincerely,

Vincent J.M. Di Maio, MD
Presiding Officer

Unintended Catalyst: the Effects of 1999 and 2001 FBI STR Population Data Corrections on an Evaluation of DNA Mixture Interpretation in Texas

1. FBI Data Corrections: What Do They Mean?

In May 2015, the Federal Bureau of Investigation ("FBI") notified all CODIS laboratories it had identified minor discrepancies in its 1999 and 2001 STR Population Database. Laboratories across the country have used this database since 1999 to calculate DNA match statistics in criminal cases and other types of human identification. The FBI attributed the discrepancies to two main causes: (a) human error, typically due to manual data editing and recording; and (b) technological limitations (*e.g.,* insufficient resolution for distinguishing microvariants using polyacrylamide gel electrophoresis), both of which were known limitations of the technology. The FBI has provided corrected allele frequency data to all CODIS laboratories.

In May and June 2015, Texas laboratories notified stakeholders (including prosecutors, the criminal defense bar and the Texas Forensic Science Commission) that the FBI allele frequency data discrepancies were corrected. The immediate and obvious question for the criminal justice community was whether these discrepancies could have impacted the outcome of any criminal cases. The widely accepted consensus among forensic DNA experts is the database corrections have *no impact* on the threshold question of whether a victim or defendant was *included or excluded* in any result. The next questions were whether and to what extent the probabilities associated with any particular inclusion changed because of the database errors.

The FBI conducted empirical testing to assess the statistical impact of the corrected data. This testing concluded the difference between profile probabilities using the original data and the corrected data is less than a two-fold difference in a full and partial profile. Testing performed by Texas laboratories also supports the conclusion the difference is less than two-fold. For example, in an assessment performed by one Texas laboratory, the maximum factor was determined to be 1.2 fold. In other words, after recalculating cases using the amended data, the case with the *most substantially affected* Combined Probability of Inclusion/Exclusion ("CPI")[1] statistical calculation (evaluated for a mixed sample) changed from a 1 in 260,900,000 expression of probability to a 1 in 225,300,000 expression of probability.

Amended allele frequency tables are publicly available for anyone to compare the calculations made using the previously published data and the amended allele frequencies, though expert assistance may be required to ensure effective use of the tables.[2]

2. The Impact of FBI Database Errors on DNA Mixture Interpretation Using CPI

As part of their ongoing commitment to accuracy, integrity and transparency, many Texas laboratories offered to issue amended reports to any stakeholder requesting a report using the corrected FBI allele frequency data. Some prosecutors have submitted such requests to laboratories, particularly for pending criminal cases. As expected, the FBI corrected data have not had an impact exceeding the

[1] The Combined Probability of Inclusion/Exclusion is commonly referred to as either "CPI" or "CPE." They are referred to jointly in this document as "CPI" for ease of reference.

[2] https://www.fbi.gov/about-us/lab/biometric-analysis/codis/amended-fbi-str-final-6-16-15.pdf

two-fold difference discussed above. However, because analysts must issue *signed amended reports* with the new corrected data, they may only issue such reports if they believe *the analyses and conclusions in the report comply with laboratory standard operating procedures*. For cases involving DNA mixtures, many laboratories have changed their interpretation protocols and related procedures using CPI. To reiterate, changes in mixture interpretation protocols are unrelated to the FBI allele frequency data corrections discussed above. However, when issuing new reports requested because of the FBI data corrections, the laboratory's use of current mixture protocols may lead to different results if the laboratory had a different protocol in place when the report was originally issued. Changes in mixture interpretation have occurred primarily over the last 5-10 years and were prompted by several factors, including but not limited to mixture interpretation guidance issued in 2010 by the Scientific Working Group on DNA Analysis ("SWGDAM").

The forensic DNA community has been aware of substantial variance in mixture interpretation among laboratories since at least 2005 when the National Institute of Standards and Technology ("NIST") first described the issue in an international study called MIX05. Though NIST did not expressly flag which interpretation approaches were considered scientifically acceptable and which were not as a result of the study, it has made significant efforts to improve the integrity and reliability of DNA mixture interpretation through various national training initiatives. These efforts have ultimately worked their way into revised standard operating procedures at laboratories, including laboratories in Texas. Based on the MIX05 study, we know there is variation among laboratories in Texas and nationwide, including differences in standards for calculation of CPI that could be considered scientifically acceptable. However, we also know based on a recent audit of the Department of Forensic Sciences ("DFS") in Washington, DC that some of the "variation" simply does not fall within the range of scientifically acceptable interpretation. This finding does not mean laboratories or individual analysts did anything wrong intentionally or even knew the approaches fell outside the bounds of scientific acceptability, but rather the community has progressed over time in its ability to understand and implement this complex area of DNA interpretation appropriately.

While in many cases the changed protocols may have no effect, it is also possible changes to results may be considered material by the criminal justice system, either in terms of revisions to the population statistics associated with the case or to the determination of inclusion, exclusion or an inconclusive result. The potential range of interpretive issues has yet to be assessed, but the potential impact on criminal cases raises concerns for both scientists and lawyers. We therefore recommend any prosecutor, defendant or defense attorney with a currently pending case involving a DNA mixture in which the results could impact the conviction consider requesting confirmation that CPI was calculated by the laboratory using current and proper mixture interpretation protocols. If the laboratory is unable to confirm the use of currently accepted protocols for the results provided, counsel should consider requesting a re-analysis of CPI.

The Texas Forensic Science Commission is currently in the process of assembling a panel of experts and criminal justice stakeholders to determine what *guidance and support* may be provided to assist Texas laboratories in addressing the challenging area of DNA mixture interpretation. In particular, a distinction must be made between acceptable variance in laboratory interpretation policies and protocols and those approaches that do not meet scientifically acceptable standards. An emphasis on statewide collaboration and stakeholder involvement will be critical if Texas is to continue to lead the nation in tackling challenging forensic problems such as those inherent in DNA mixture interpretation.

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JOURNAL OF FORENSIC SCIENCES

J Forensic Sci, 2015
doi: 10.1111/1556-4029.12806
Available online at: onlinelibrary.wiley.com

ERRATUM

Reference: Budowle B, Moretti TR, Baumstark AL, Defenbaugh DA, Keys KM. Population data on the thirteen CODIS core short tandem repeat loci in African Americans, US Caucasians, Hispanics, Bahamians, Jamaicans, and Trinidadians. J Forensic Sci 1999;44(6):1277–86.

Since the development in the late 1990s of the original short tandem repeat (STR) typing systems that included the 13 CODIS

using the original and corrected data is expected to be less than a factor of two in a full profile. The actual minimum ratio that we could obtain for a constructed profile in the direction of the profile probability being more rare in the original as compared to the amended data was for a highly homozygous partial profile in the Jamaica dataset. It was 0.76, which is well within the factor of 10 suggested by previous studies and the National

FBI Population Data Amendment/Erratum Moving Forward

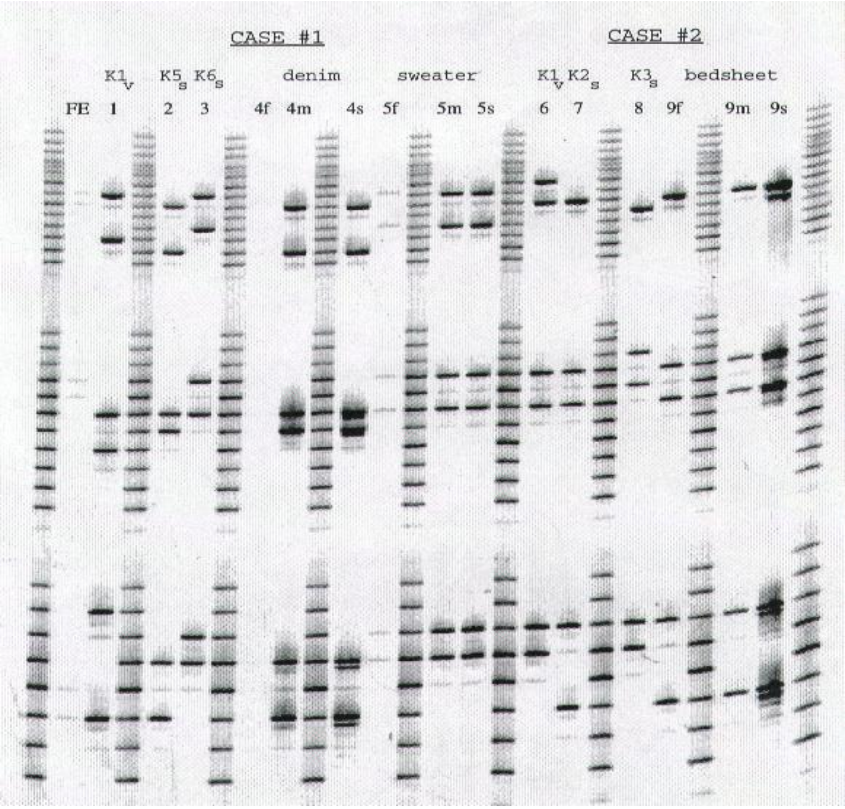
Professor Bruce Budowle
Executive Director of the Institute of Applied Genetics
Department of Molecular and Medical Genetics
University of North Texas Health Science Center
Fort Worth, Texas

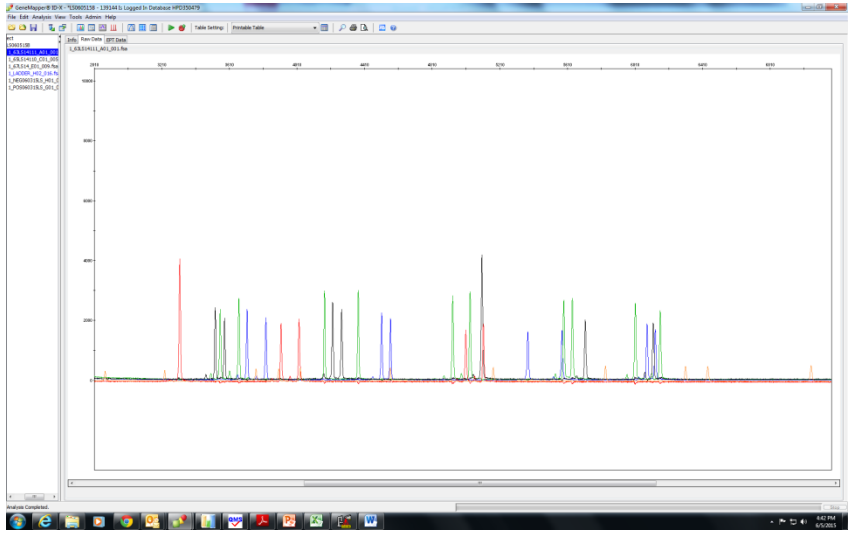
Human Identification · Computational Genomics · Biosafety and Biosecurity · INSTITUTE OF APPLIED GENETICS · Qualitas Vitae

Issue

- Population data generated in the 1990s
  - AmpFlSTR Profiler, COfiler, Identifiler, GenePrint PowerPlex,…
- Used as the basis for statistical calculations
- Quality data of the time
- Good data for statistical analyses
- Some errors occurred during typing
  - The exact number now identified
- Errors were raised in court (and other settings) from the onset
  - Issue is well-known and not new
- Addressed it with population studies

Older Technology vs. New Technology





Issue

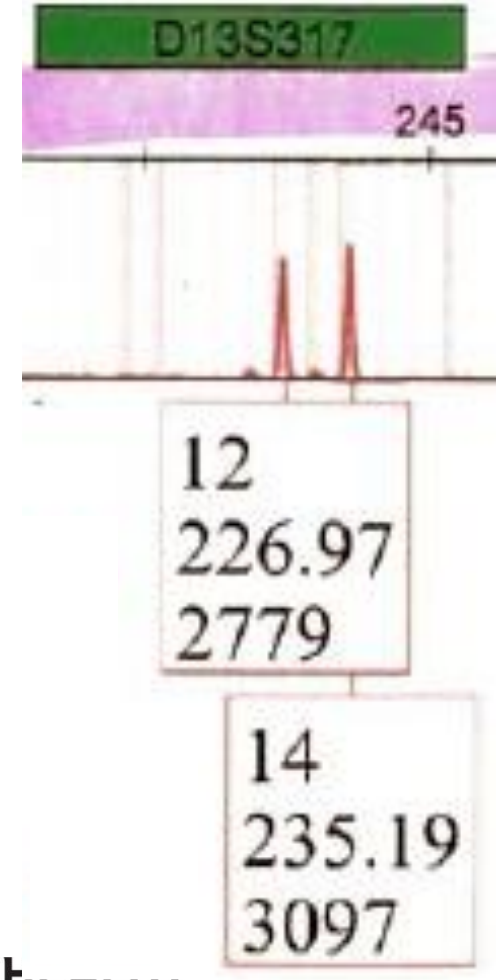
- FBI expands core CODIS STRs
- Retypes available samples primarily to generate allele frequency data on additional markers
  - GlobalFiler and PowerPlex Fusion
- Able to identify typing errors
- 27 samples
  - mostly at a single locus
  - 51 incorrect alleles out of 30,000 (0.17%)
- Magnitude of change in frequencies is 0.000012 to 0.018

Two General Categories of Errors

- Clerical errors
  - Due to manual data recording and data manipulation

- Errors due to technological limitations
  - Inherent to the STR typing system and/or analysis software of the 1990s
    - No artifact filters (stutter, elevated baseline)
    - Peak morphology and resolution differences

Sample Recorded as 8,12
Instead of 12,14



Af Amer D13 (N=179)	Allele 8	Allele 14
Original Frequency	0.0361	0.03361
Count	13	13
Amended Count	12	14
Amended Frequency	0.0335	0.0391

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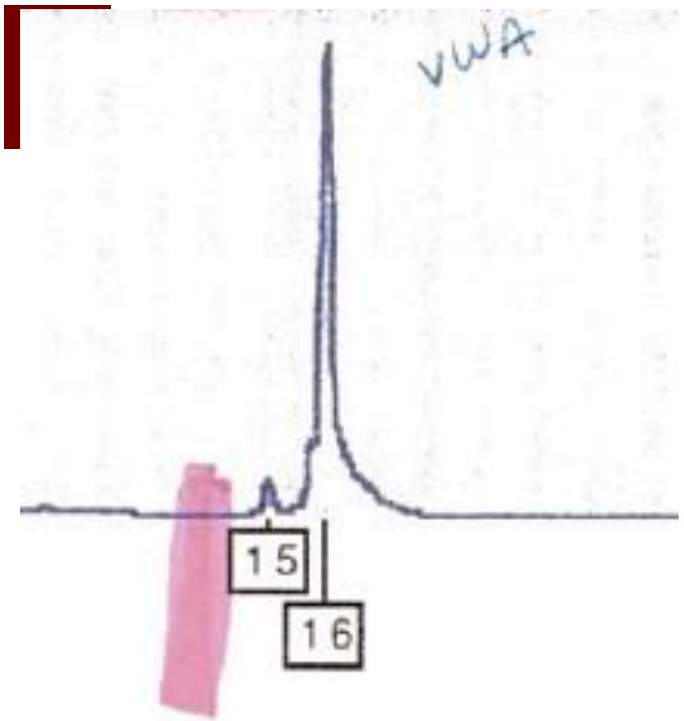
Manual Data Analysis with Transcription Error

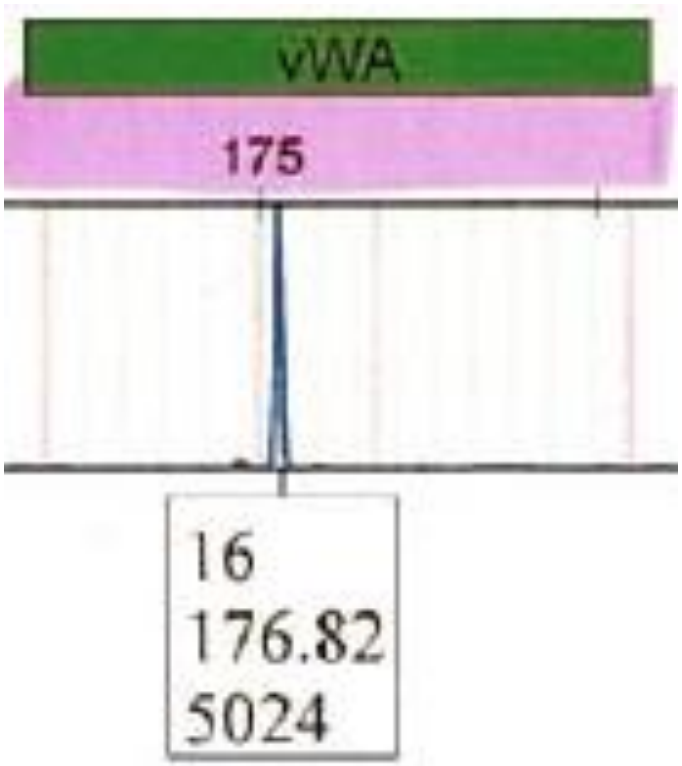
Data were recorded manually and hand-transcribed into spreadsheets for population statistics analysis.

1CH 505 FL	Penta E	D18S51	D21S11	TH01	D3S1358
C180	19-20	12-12	31.2-32.2	9-9.3	15-16
C181	7 12	15-17	27-32.2	7-9	16-16
C182	7-12	14-18	30-32.2	6-8	15-17
C183	11-14	13-16	30-31.2	7-9.3	15-18
C184	5-16	13-15	28-30	9.3-9.3	14-15
C185	10-13	14-15	28-30	7-7	14-18
C186	17	14-15	28-30	6-9.3	14-15
C187	13-14	15-17	27-32	7-9	15-18
C188	10-17	14-15	29-31	6-9.3	14-17
C189	16-17	14-15	29-31	6-9.3	14-17

8,9
Miscalled as 8,10

Stutter Labeled as Allele 15
Sample miscalled as 15,16





Allele Frequency Change Due to Error

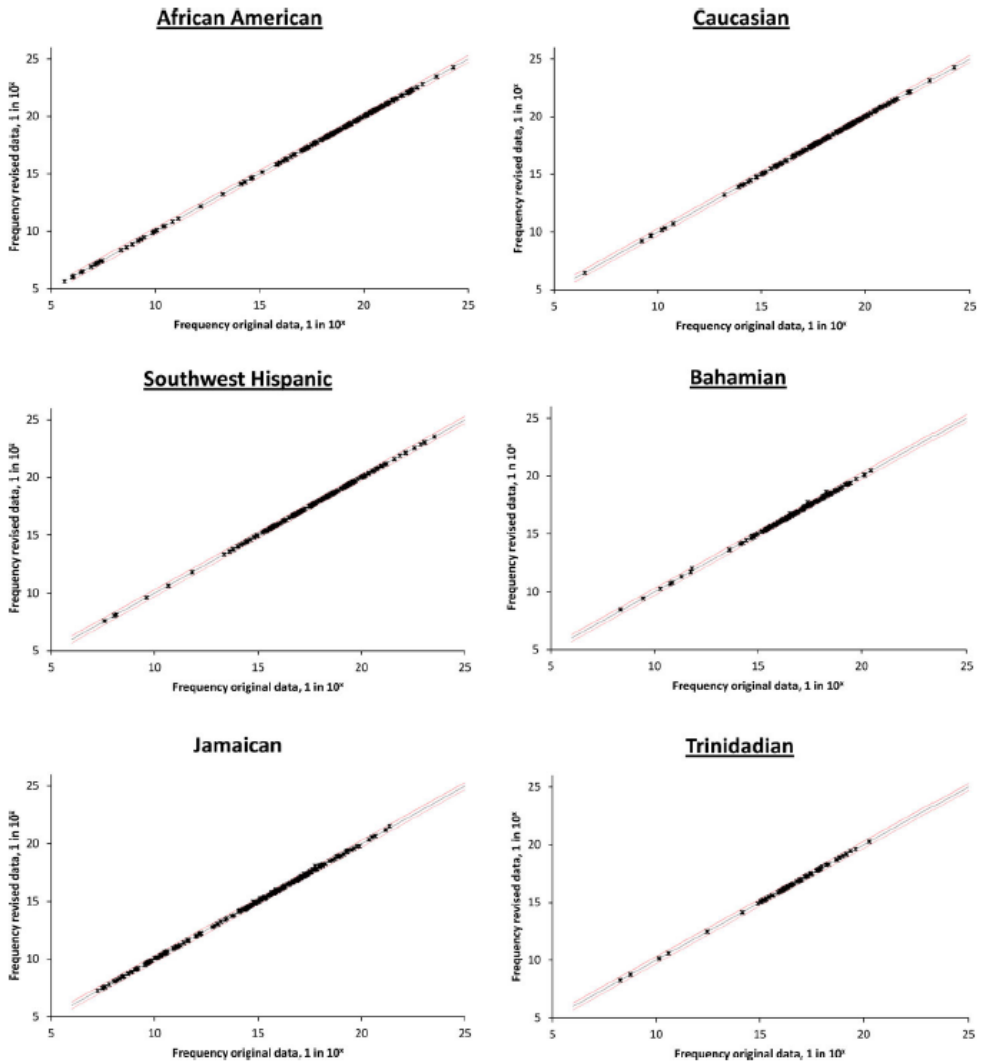
- In total across *1175 samples*, there are *51 erroneous allele calls* out of *~30,000 alleles* in the original data
  - Incorrect genotyping caused the frequency of *0.17% of alleles* to be incorrectly typed
- Average frequency change 0.002
  - range 0.000012 to 0.018181

- Of the published frequencies across 15 loci in 8 populations, ~250 out of ~1100 total allele frequencies were amended.
  - 27 genotyping errors accounted for 18% of the amended frequencies
  - 6 sample count errors (e.g., duplicates, tri-allele) accounted for 82% of the amended frequencies

Moving Forward

- These discrepancies will not materially affect any assessment of evidential value
- One could have buried the findings because the statistical impact is trivial
- However, one should not excuse error by taking the position that the statistical impact is nominal
- The actions taken by the FBI should be lauded
- Disclosed the findings so all are aware
  - Published paper
  - Media reported
  - Amended Popstats
  - CODIS Bulletins issued to NDIS-participating labs
  - Info on FBI.gov (in process)
  - Amended data publically available

Change in Frequencies Affect on RMP



Worst Case Scenarios

	African American	Caucasian	SW Hispanic	Bahamas	Jamaica	Trinidad
15 loci comb.	1.32	1.13	1.14	1.40	1.30	1.30
CSF1PO		1.01		1.03		
D13S317	1.14	1.02		1.03		
D16S539		1.01	1.03	1.03		1.07
D18S51	1.01			1.03	1.18	1.14
D19S433	1.14					
D21S11		1.05		1.03		
D2S1338						
D3S1358		1.01		1.01		
D5S818			1.02	1.04		
D7S820		1.01		1.03		
D8S1179				1.03	1.07	1.07
FGA			1.06	1.02	1.03	
TH01		1.01		1.03		
TPOX		1.01		1.03		
vWA			1.03	1.04		

Recap

- Very good quality data of the time
- Testimony in court at the time disclosed and addressed issue
- Population studies
- Even better quality today
- No issue will arise where a statistical calculation will change substantially
  - or even noticeably

Recommendations

- No need to recalculate statistics in every case ever reported
  - The difference is nominal
- Calculate with new frequencies going forward
- Recalculate upon request
  - From either prosecution or defense
- Consider recalculation if going to court with data generated previously
  - Inform DA
- Develop amended report language
- No calculations on the fly
- Because of openness no need to reach out to other parties
  - Of course there will be exceptions
  - Let DA take responsibility
  - All data are available and anyone can recalculate if desired
  - Provide allele frequency tables if requested
  - Website notification
- No real impact but facilitate

However

- Another **more significant** issue has arisen that is brought on by the requested re-calculations

- Mixture evidence interpretation!

The Outcome

Final Report on

Review of Mixture Interpretation in Selected Casework of the

DNA Section

of the

Forensic Science Laboratory Division (FSL),

Department of Forensic Sciences (DFS),

District of Columbia

Prepared by: Bruce Budowle, Frederick R. Bieber

Prepared for: Vincent H. Cohen, Jr., Acting U.S. Attorney,

District of Columbia

SCIENCE CENTER

ANSI-ASQ National Accreditation Board

ANAB

DC Department of Forensic Sciences
401 E Street SW
Washington DC, 20024
April 24, 2015

Surveillance and Remote Surveillance Audit
Conducted by Deedra Hughes and Carl Sobieralski
Lead Assessors for ANAB

600 N. Plankinton Ave., Suite 300
Milwaukee, WI 53203 USA
414-347-9858

500 Montgomery St., Suite 625
Alexandria, VA 22314 USA
703-836-0025

5300 W Cypress Street, Suite 180
Tampa, FL 33607 USA
813-443-0517

www.anab.org

Brief Partial History

- May 2014, the USAO requests assistance for LR calculations, not performed by DFS
- Identified several concerns regarding mixture interpretation by DFS
- Conference calls with DFS
- October 7, 2014, USAO representative attends a DFS Scientific Advisory Board (SAB) meeting to present the concerns raised about mixture interpretation at the DFS
- DFS performed a “non-exhaustive” review of 27 cases involving DNA evidence
  - Seven involved DNA mixtures, 3 of which included DNA mixture statistics
  - Of these 3 cases, 2 had CPI calculations one of which was modified by DFS after its review
- DFS did not review any more cases

Issues of Mixture Interpretation

- The interpretation of DNA forensic evidence is an important part of the analytical process, which often is not sufficiently defined
- Mixtures, at times, can be complex and thus present some challenges for interpreting the profile(s)
- There is variation regarding interpretation across the community
- Variation in interpretation is somewhat acceptable
- But the mere fact that variation exist does not obviate responsibility of applying an approach correctly within in the bounds of the approach established by the lab
- Misunderstandings persist and in some cases good information is being ignored

Issues of Mixture Interpretation

- Accreditation and Audits do not convey that valid mixture interpretations protocols are in place
- Mixture interpretation protocols often are scant
- Thus even with review details of process are not obvious without thorough review of actual practices
- Variation may and will occur within a laboratory system
- A review process is necessary and invaluable

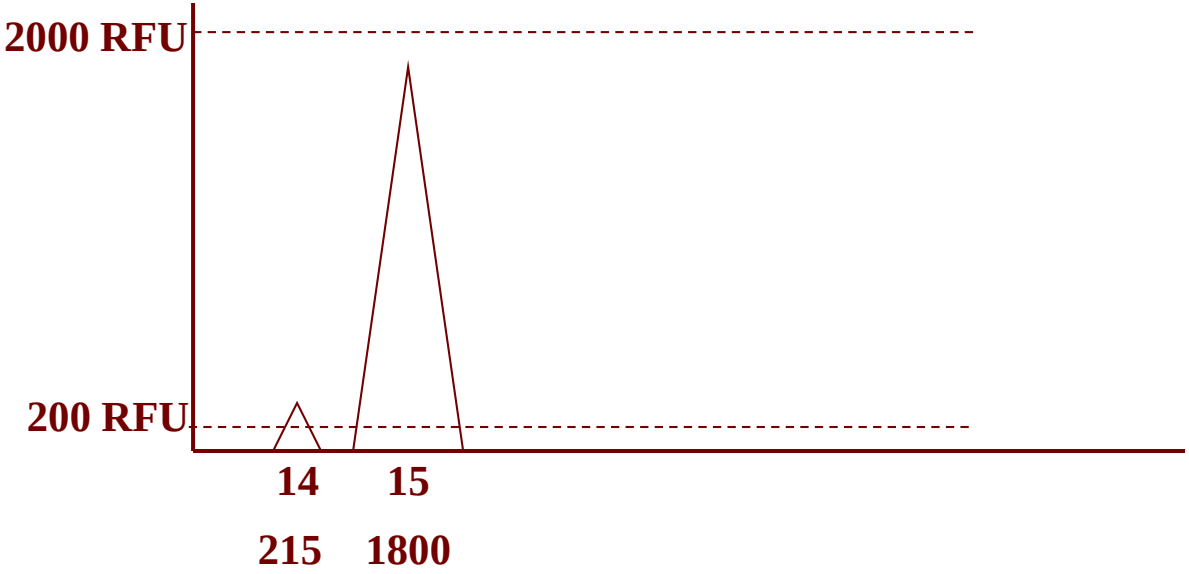
Threshold Values

- Two thresholds
  - Analytical (Detection) – 70 RFU
  - Stochastic (Interpretation) – 200 RFU
- Critical for proper mixture interpretation with STR data
- Only interpret loci where all peaks >200 RFU
- Concept is that a peak(s) below 200 RFU could have had a partner allele drop out
- **Can see this concept in guidelines going back more than a decade**

General Method Philosophy

- Using CPI
  - Assumes that the loci used exhibit no allele drop out
  - Or at least highly unlikely

Example 1

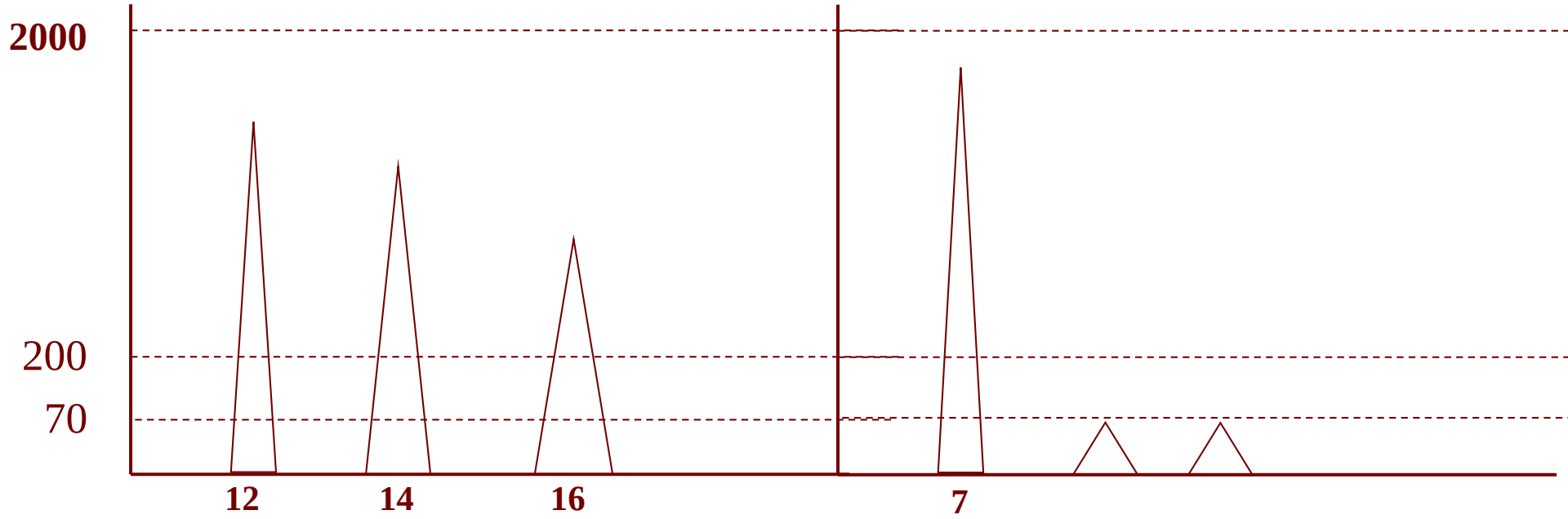


- Both peaks are >200
- If use these two alleles for CPI
- Other loci show a mixture of a minor contributor
- Minor could be probative

Example 1

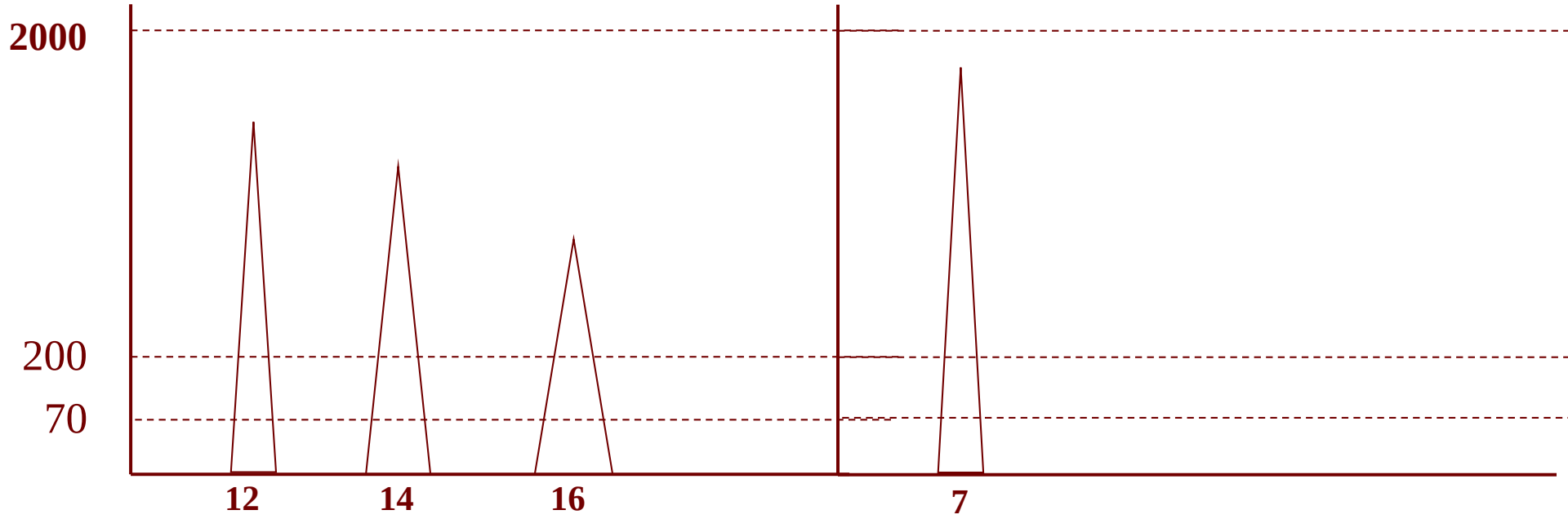
- 14 peak is above stutter threshold
- Assumes that the potential partner allele of the 14 did not drop out
- However, additive affects of stutter plus minor allele should be considered
- It is possible (and likely) that there is a 14 allele but its height is far less than 200 RFU

Example 2



- For Locus 1 three alleles for CPI
- At least two contributors
  - need to assume #contributors to consider if drop out may occur
- In this scenario, data do not support allele drop out at Locus 1
- Locus 2 only allele 7 is called - other peaks below analytical threshold

Example 2



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  - need to assume #contributors to consider if drop out may occur
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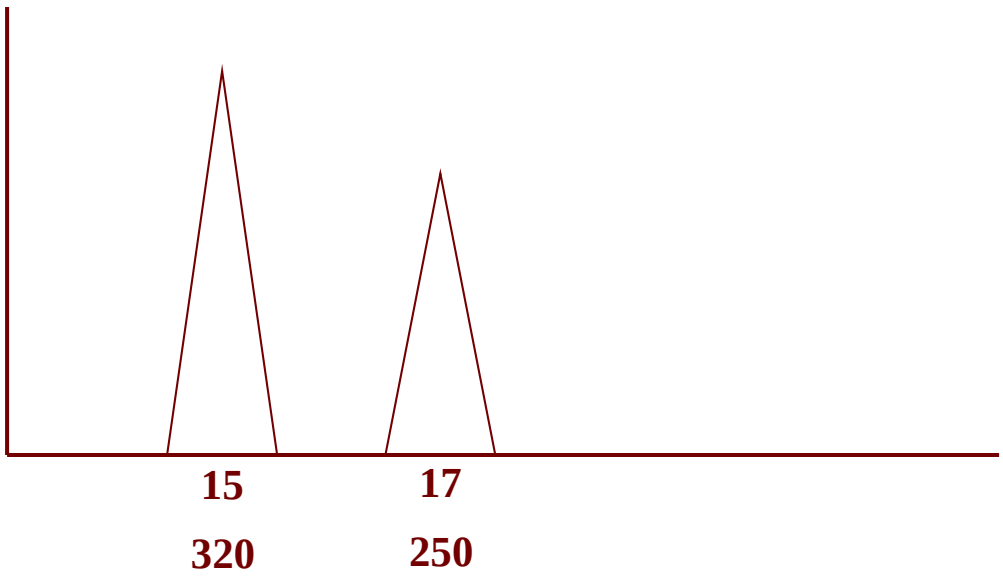
Example 3

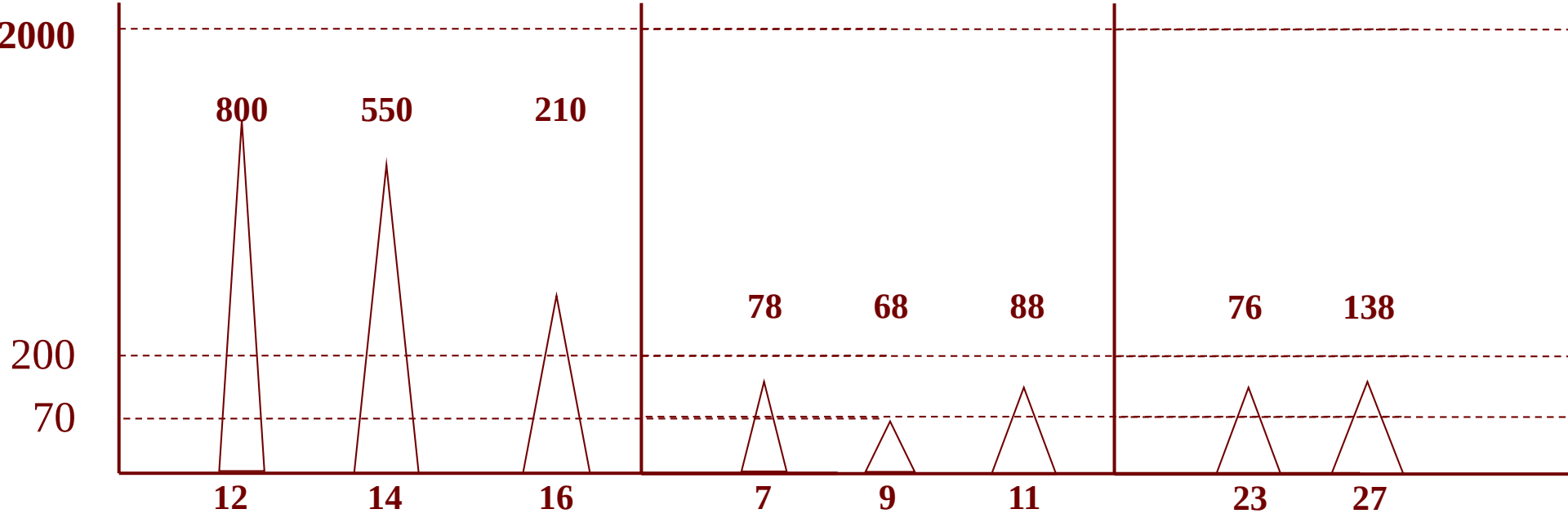


- Both peaks are >200
- These two alleles are used for calculating CPI
- Other loci show a mixture of at least two contributors

Example 3

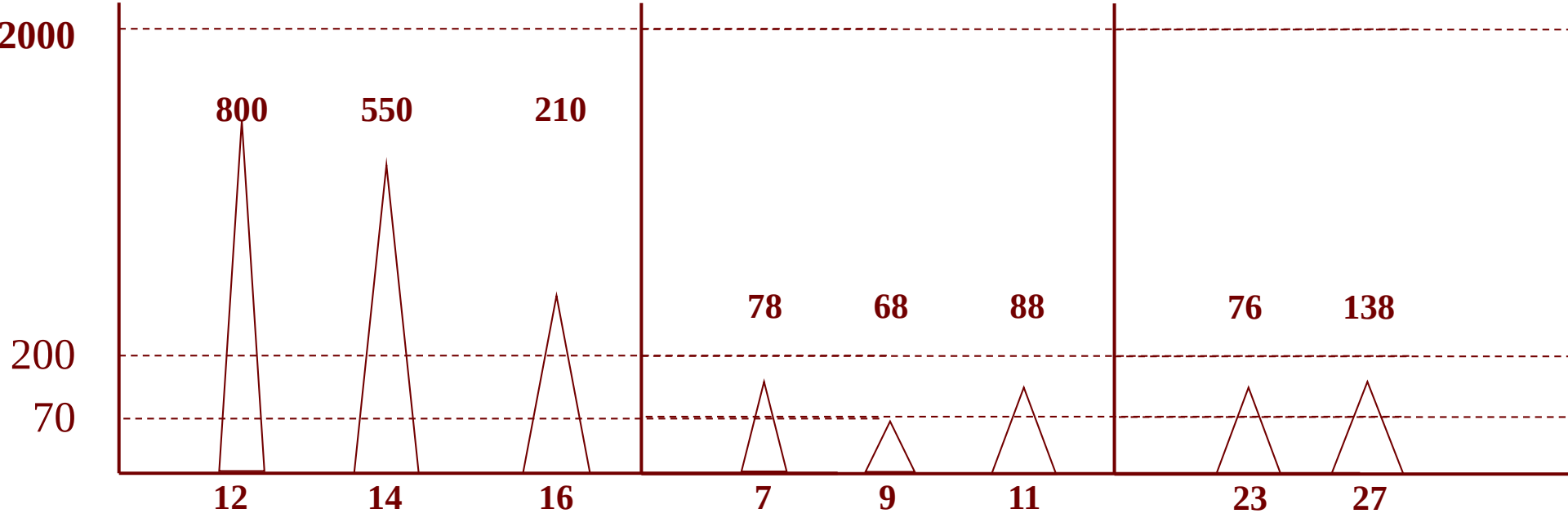
- Interpretations/Explanations
  - Homozygote 15 and homozygote 17
  - Two 15,17 heterozygotes
  - One 15,17 heterozygote and a 15,X
  - …
- All three are plausible
- The X could be any allele and thus should consider possibility of drop out
- Note in this scenario the evidence supports that one of the contributors is less than the other

Example 4



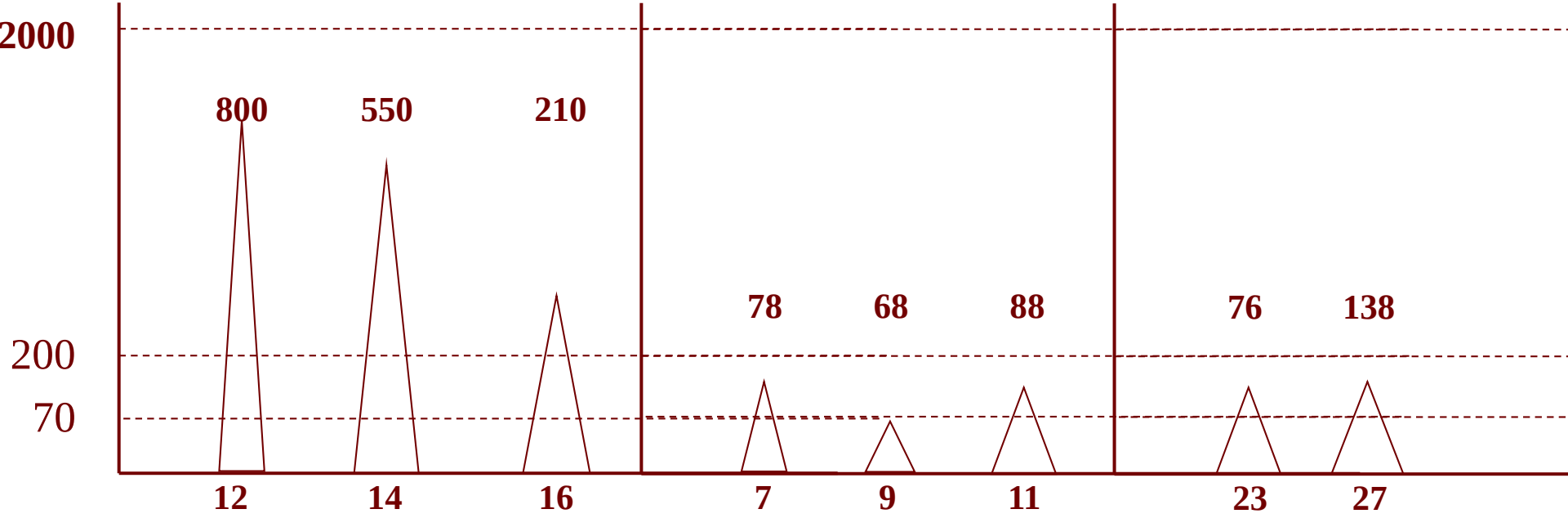
- For Locus 1 two alleles (12,14) considered a major contributor
- For Locus 2 declared 7,11 major contributor
- For Locus 3 declared 23,27 major contributor
- Calculated single source major statistic (RMP)

Example 4



- For Locus 2 declared 7,11 major contributor
- Allele 9 is below analytical threshold
- Could be 7 and 11 homozygotes, could be 7,X; 11,X; …
- Determining major is problematic

Example 4



- For Locus 3 declared 23,27 major
- Could be 23 homozygote and 27 homozygote, and other combinations
- Note that in this mixture evidence supports that major is degrading and minor is equivalent across loci

US v S5

2. A mixture of at least two people was obtained from the swab from back of left hand and fingers and swab from palm side left hand and fingers (Item 1_2).

[redacted] (Item 26J) cannot be excluded as a possible contributor to this mixture. The probability of selecting an unrelated individual at random having an STR profile which would be included as a contributor to the mixture obtained from the swab from back of left hand and fingers and swab from palm side left hand and fingers (Item 1_2) is approximately[1]:

Approximate Frequency	Population Database
1 in 765	African-American
1 in 2,430	US Caucasian
1 in 3,660	US Hispanic

[redacted] Item 27.1) cannot be excluded as a possible contributor to this mixture. The probability of selecting an unrelated individual at random having an STR profile which would be included as a contributor to the mixture obtained from the swab from back of left hand and fingers and swab from palm side left hand and fingers (Item 1_2) is approximately[1]:

Approximate Frequency	Population Database
1 in 140	African-American
1 in 349	US Caucasian
1 in 782	US Hispanic

Numbers are different!

US v S7

- Item 1; at least 3 people
- Potential allele dropout D21S11, D7S820, CSF1PO

Not Unique to One Lab

UNCLASSIFIED

Based on the typing results from the amelogenin locus (for sex determination), male DNA[2] is present in the DNA obtained from specimens Q1, Q2, Q3, and K1 (SCOTT).

The STR typing results for specimen Q1 indicate the presence of DNA from two or more individuals. Specimen K1 [redacted] cannot be excluded[3] as a potential contributor to this mixture. Based on the STR typing results,[4] the probabilities of inclusion calculated for specimen Q1 are approximately:

1 in 2 from the African American population
1 in 2 from the Caucasian population
1 in 2 from the Southeastern Hispanic population
1 in 2 from the Southwestern Hispanic population

The STR typing results for specimen Q2 indicate the presence of DNA from three or more individuals. A major contributor can be discerned from the DNA obtained from specimen Q2 and is suitable for matching purposes. Specimen K1 [redacted]) is excluded as a potential major contributor of the DNA recovered from Q2; however, specimen K1 [redacted]) cannot be excluded[3] as a potential minor contributor to this mixture. Based on the STR typing results,[4] the probabilities of inclusion calculated for the mixture of DNA obtained from specimen Q2 are approximately:

1 in 2 from the African American population
1 in 3 from the Caucasian population
1 in 3 from the Southeastern Hispanic population
1 in 6 from the Southwestern Hispanic population

The STR typing results for specimen Q3 indicate the presence of DNA from three or more individuals. Specimen K1 [redacted]) cannot be excluded[3] as a potential contributor to this mixture. Based on the STR typing results,[4] the probabilities of inclusion calculated for specimen Q3 are approximately:

1 in 17 from the African American population
1 in 11 from the Caucasian population
1 in 9 from the Southeastern Hispanic population
1 in 9 from the Southwestern Hispanic population

The DNA typing results obtained from the tested specimens are not eligible for entry into the Combined DNA Index System (CODIS). These results will be maintained by the FBI Laboratory for possible future comparisons.

No other nuclear DNA examinations were conducted.

Mixture Case

Sample	Barcode	Run	P*	D3S1358	vWA	FGA	AMEL	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820
9947A	FC110512	A2374_1	M	14,15	17,18	23,24	X	13	30	15,19	11	11	10,11
Negative	AMPBLANK	A2374_1	M	-	-	-	-	-	-	-	-	-	-
QB-1an Neat	00YSD	A2374_1	M	-	-	-	-	-	-	-	-	-	-
Q1-1an Neat	00YSA	A2374_1	M	(15),(16),(17)	17	-	X,Y	11,15	30,(31)	-	8,(12),(13)	(12)	-
			m	-	(13),(15),(19)	-	-	13,14	-	-	(11)	-	-
Q2-1an Neat	00YSB	A2374_1	M	15,16,17,(18)	17,18	20,21	X,Y	10,14	30,32.2	16,17	11,12	11,12	(9),10
			m	-	(16),(19)	(20.2),(25),(27)	-	11,12,(13),15	(29),(31)	(12),(15)	(8),(13)	-	-
Q3-1an Neat	00YSC	A2374_1	M	17	16,17	20,20.2,21,25	X,Y	11,12,13,15	29,30,31,32.2	15,16,20	11	12	8,(9),10,(11)
			m	15,16,18	(19)	(27)	-	-	-	(17)	8,12,13	9,(11)	-

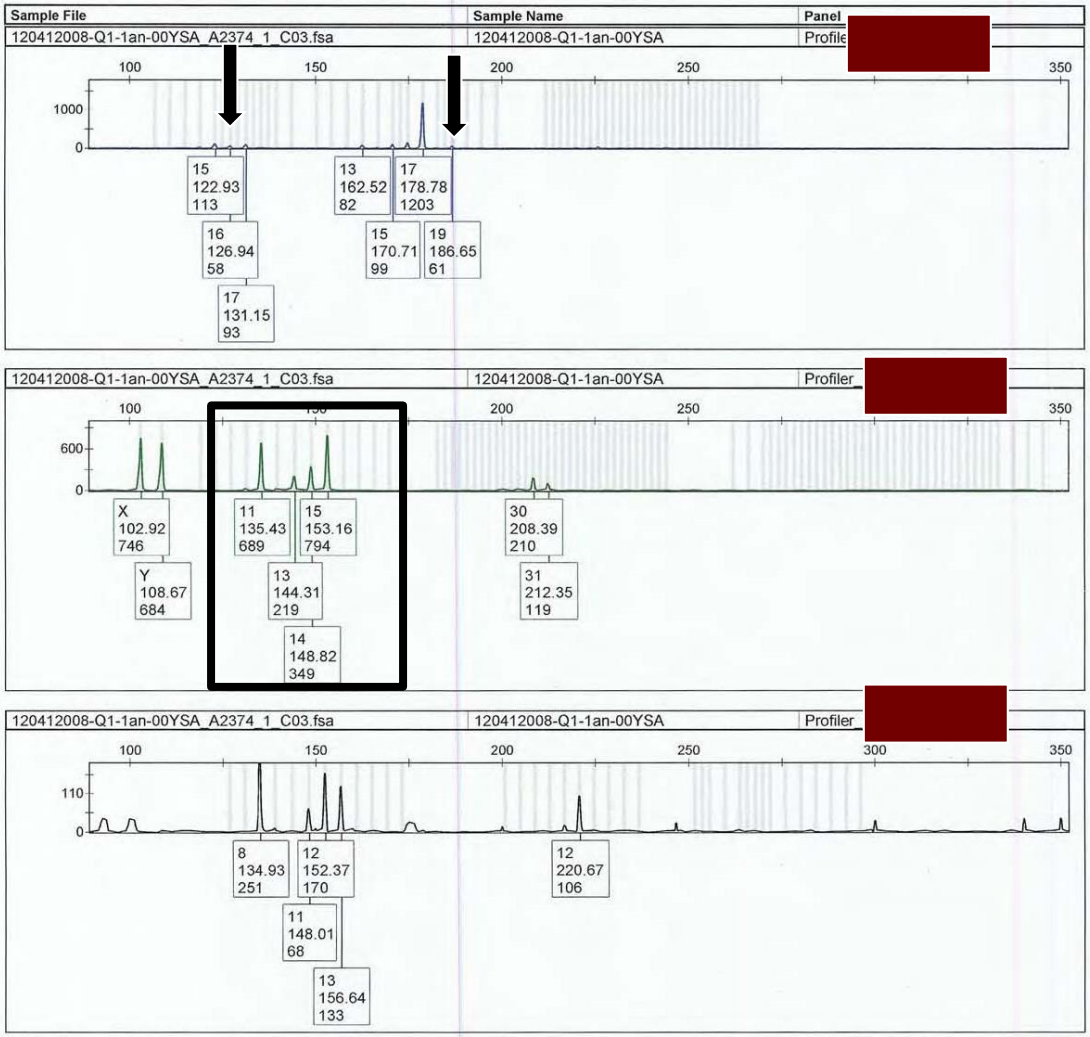
Sample	Barcode	Run	P*	D3S1358	vWA	FGA	AMEL	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820	D16S539	TH01	TPOX	CSF1PO	D2S1338	D19S433
9947A	FC000015	A2376_1	M	14,15	17,18	23,24	X	13	30	15,19	11	11	10,11	11,12	8,9.3	8	10,12	19,23	14,15
Negative	AMPBLANK	A2376_1	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
KB-1an Neat	00YQV	A2376_1	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
K1-1an Neat	00YQU	A2376_1	M	16	17,19	0,27	X,Y	15	30,31	16,17	13	11,12	9	12,14	7,8	8,11	12	17,24	14

Results

The STR typing results for specimen Q1 indicate the presence of DNA from two or more individuals. Specimen K1 [redacted] cannot be excluded[3] as a potential contributor to this mixture. Based on the STR typing results,[4] the probabilities of inclusion calculated for specimen Q1 are approximately:

1 in 2 from the African American population
1 in 2 from the Caucasian population
1 in 2 from the Southeastern Hispanic population
1 in 2 from the Southwestern Hispanic population

7.4.2.2.1.1 For questioned specimens, allelic peaks < 200 RFU may only be used for purposes of exclusion and/or to establish the presence of a mixture of DNA. A question specimen that displays a locus at which a peak(s) exhibits a height of < 200 RFU may have underwent stochastic amplification and/or allele drop out due to insufficient DNA template copy number.



- If two contributors, then favors exclusion
- If three contributors,
  then need to consider drop out potential

Presence of DNA from two or more contributors

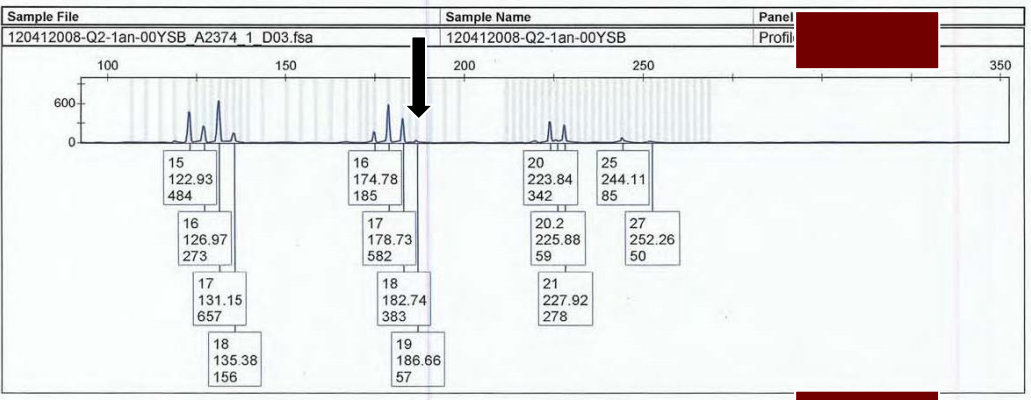
If two, then excluded
If three, then additive effects and drop out issues

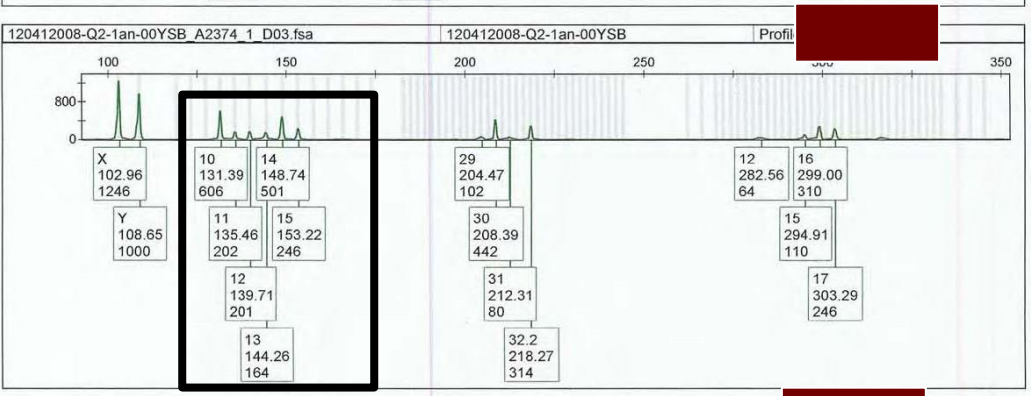
Sample	Barcode	Run	P*	D3S1358	vWA	FGA	AMEL	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820	D16S539	TH01	TPOX	CSF1PO	D2S1338	D19S433
9947A	FC000015	A2376_1	M	14,15	17,18	23,24	X	13	30	15,19	11	11	10,11	11,12	8,9.3	8	10,12	19,23	14,15
Negative	AMPBLANK	A2376_1	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
KB-1an Neat	00YQV	A2376_1	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
K1-1an Neat	00YQU	A2376_1	M	16	17,19	0,27	X,Y	15	30,31	16,17	13	11,12	9	12,14	7,8	8,11	12	17,24	14

Results

The STR typing results for specimen Q2 indicate the presence of DNA from three or more individuals. A major contributor can be discerned from the DNA obtained from specimen Q2 and is suitable for matching purposes. Specimen K1 [redacted] is excluded as a potential major contributor of the DNA recovered from Q2; however, specimen K1 [redacted] cannot be excluded[3] as a potential minor contributor to this mixture. Based on the STR typing results,[4] the probabilities of inclusion calculated for the mixture of DNA obtained from specimen Q2 are approximately:

1 in 2 from the African American population
1 in 3 from the Caucasian population
1 in 3 from the Southeastern Hispanic population
1 in 6 from the Southwestern Hispanic population

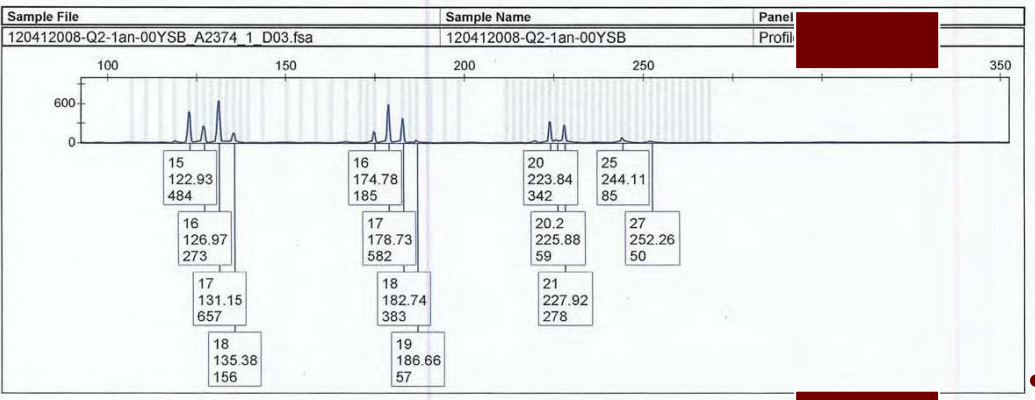


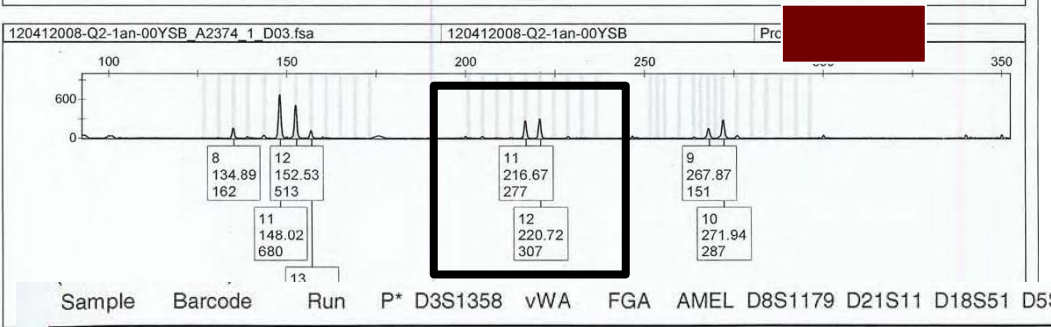


- If three contributors, then favors exclusion
- If four contributors,
  then drop out potential

If three, then excluded at D8

Sample	Barcode	Run	P*	D3S1358	vWA	FGA	AMEL	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820	D16S539	TH01	TPOX	CSF1PO	D2S1338	D19S433
9947A	FC000015	A2376_1	M	14,15	17,18	23,24	X	13	30	15,19	11	11	10,11	11,12	8,9.3	8	10,12	19,23	14,15
Negative	AMPBLANK	A2376_1	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
KB-1an Neat	00YQV	A2376_1	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
K1-1an Neat	00YQU	A2376_1	M	16	17,19	20,27	X,Y	15	30,31	16,17	13	11,12	9	12,14	7,8	8,11	12	17,24	14





- Four random individuals would be selected and all carry only an 11 allele, only a 12 allele or both 11 and 12 alleles

- Caucasian population - 0.02407
  African American population - 0.07270
  SE Hispanic population - 0.006762
  SW Hispanic population - 0.0009464

- Low probabilities - allele drop out at the D13S317 locus is highly probable under four person scenario

Sample	Barcode	Run	P*	D3S1358	vWA	FGA	AMEL	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820	D16S539	TH01	TPOX	CSF1PO	D2S1338	D19S433
9947A	FC000015	A2376_1	M	14,15	17,18	23,24	X	13	30	15,19	11	11	10,11	11,12	8,9.3	8	10,12	19,23	14,15
Negative	AMPBLANK	A2376_1	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
KB-1an Neat	00YQV	A2376_1	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
K1-1an Neat	00YQU	A2376_1	M	16	17,19	20,27	X,Y	15	30,31	16,17	13	11,12	9	12,14	7,8	8,11	12	17,24	14

Take Home Message

- Interpretation may be carried in a blind application manner
- Allele drop out is important to interpretation but may not be addressed well
- Stats can be overstated for the qualitative statements that accompany interpretation
- There also are examples that if the rules were not so blindly followed better value could have been obtained
  - Not using the major contributor information – just calling inconclusive
- Education/training essential
- Case review important and necessary

Moving Forward

- Need to determine generally accepted practices
- Need to determine if generally accepted was scientifically accepted
- Need to address SWGDAM “not retroactive” statement
- Need to address discovery and Brady issues
- Need to differentiate policy from science issues

Moving Forward

- Need to determine magnitude of problem
- Need education and training
- Need a plan
- Need a team (include practitioners)

ACKNOWLEDGMENTS

#1

- Tamyra Moretti
- Tony Onorato
- Courtney Head
- Dixie Peters
- Lynn Garcia
- Christina Capt

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