EDNAP and 34th ENFSI DNA WG Meeting
April 6-8, 2011 – Brussels, Belgium

NIST Update

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National Institute of Standards and Technology
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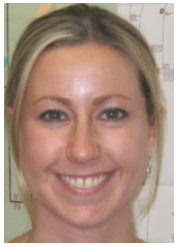
NIST Human Identity Project Teams
within the Applied Genetics Group

Manuel **Fonde**vila Alvarez

Forensic DNA Team


John Butler


Mike Coble

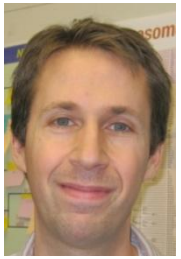

Becky Hill


Margaret Kline

Data Analysis Support


Dave Duewer

DNA Biometrics Team


Pete Vallone


Erica Butts


Kristen Lewis O'Connor

Funding from the **National Institute of Justice (NIJ)** through NIST Office of Law Enforcement Standards

Funding from the **FBI S&T Branch** through NIST Information Access Division

Workshops & Textbooks

Concordance & LT-DNA

Software Tools & Data Analysis

ABI 3500 & DNA Extraction

Mixtures, mtDNA & Y

SRM work, variant alleles & Cell Line ID

Rapid PCR & Biometrics

D12/vWA & Kinship Analysis

NIJ National Institute of Justice

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

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001-301-975-4049

DEPARTMENT OF JUSTICE FEDERAL BUREAU OF INVESTIGATION

Since April 2010…

- **43 presentations** and **4 workshops** to the forensic DNA community

- **12 publications**
  - Assisting with PP16HS developmental validation
  - ESI/ESX 17 European STR kit concordance
  - Room temperature DNA sample storage
  - Low template DNA testing
  - Concordance testing strategies
  - Variant allele sequencing primers
  - Evaluation of D12/vWA independence (and erratum)
  - Assessing self-declared ancestry in U.S. samples
  - Cell line authentication with STRs

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

Presentation Outline

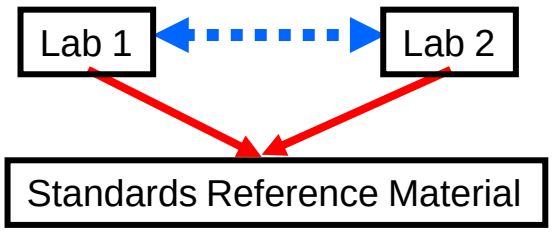
- **SRM 2391c** to be available mid-2011
- **STR kit concordance studies**
- **New STR loci** characterized
- **New STRBase sections**: LT-DNA, mixtures, kinship
- **Kinship analysis support**
- **Rapid and direct DNA testing**
- **Training workshops** & information
- *Advanced Topics in Forensic DNA Typing* (3rd edition)

- **Linkage disequilibrium study: D12S391 and vWA (separate presentation)**

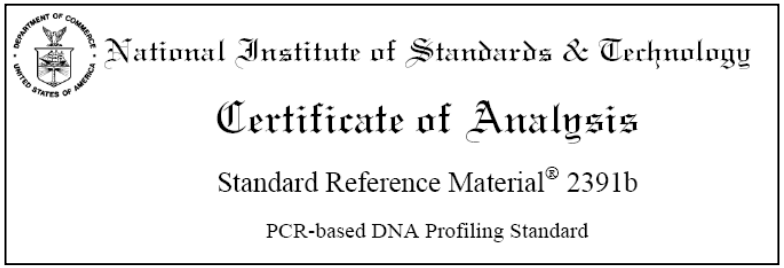
Standard Reference Material (SRM) 2391c

http://www.nist.gov/srm

Traceable standards to ensure accurate and comparable measurements between laboratories



Calibration with SRMs enables confidence in comparisons of results between laboratories


National Institute of Standards & Technology

Certificate of Analysis

Standard Reference Material® 2391b

PCR-based DNA Profiling Standard

SRM 2391b
48 autosomal STRs characterized across 12 DNA samples

SRM 2391c Details

- 6 components
- **4 liquid genomic DNA** components (**PFA tubes**) + **2 punches** (cells on **FTA** & 903 paper)
- **Certified values: 23 autosomal STR loci and 16 Y-STRs (all loci in kits)** either through sequencing alleles or examining multiple STR kits
- **Reference values:** 26 autosomal STRs (NIST 26plex + FFFL)
- 5 single source + **1 mixture**
- 3 males + 2 females (unique)
- All new samples
  - no 9947A or 9948
- **Will be available in mid-2011**

STR Kits Tested with SRM 2391c

Applied Biosystems (12)
Identifiler
Identifiler Plus
NGM
NGM SElect
COfiler
Profiler
Profiler Plus
Profiler Plus ID
SGM Plus
SEfiler Plus
MiniFiler
Yfiler

Promega (9)
PowerPlex 16
PowerPlex 16 HS
PowerPlex Y
PowerPlex ESX 17
PowerPlex ESI 17
PowerPlex ES
PowerPlex S5
PowerPlex Y
FFFL

Qiagen (2)
ESSplex
IDplex

NIST assays
26plex
miniSTRs

Alleles sequenced:
SE33
D12S391
D1S1656
Penta D
Penta E
D8S1115

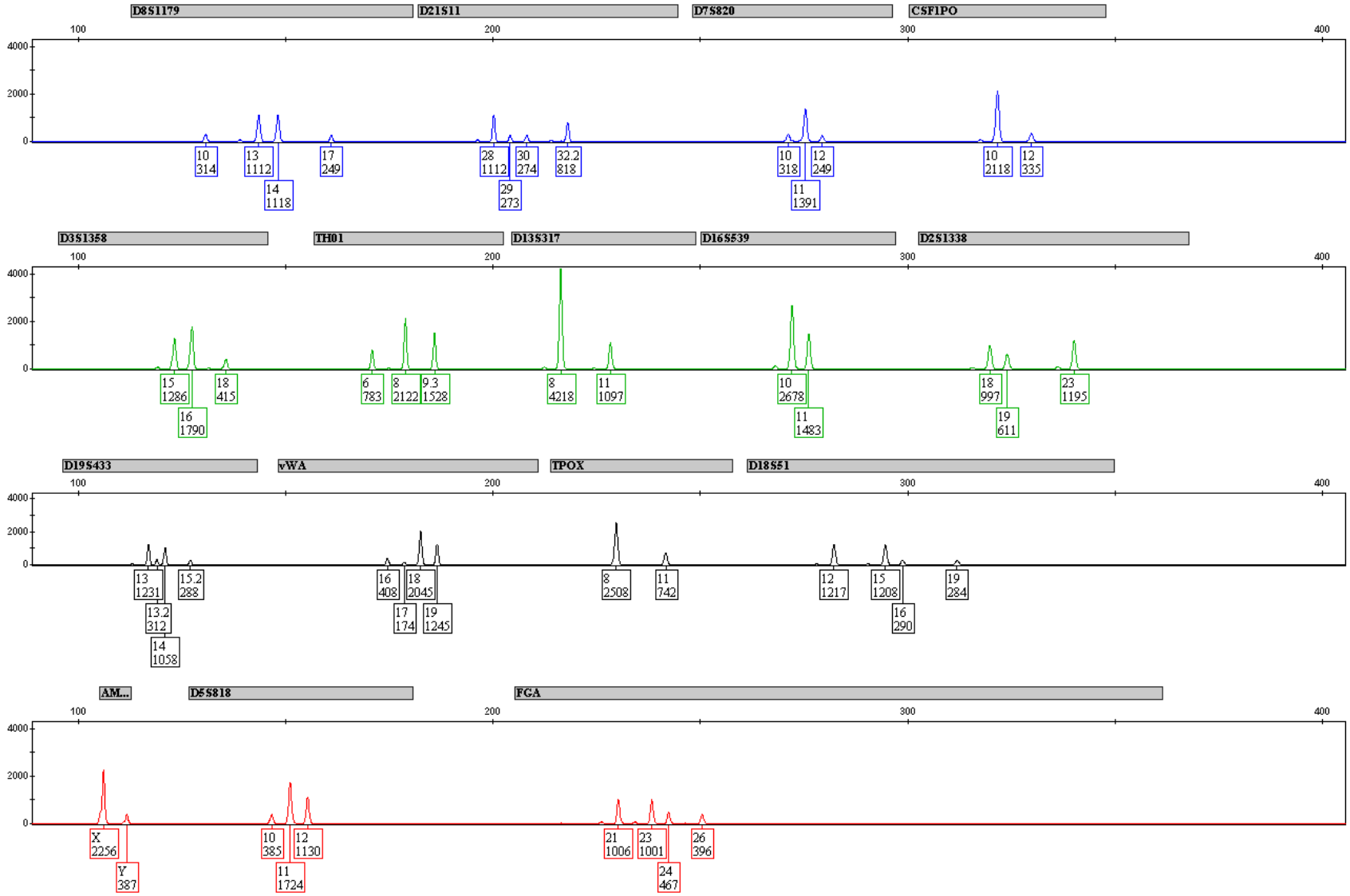
23 commercial STR kits examined

NIST developed 26plex and miniplexes

No discordant results observed on SRM 2391c samples

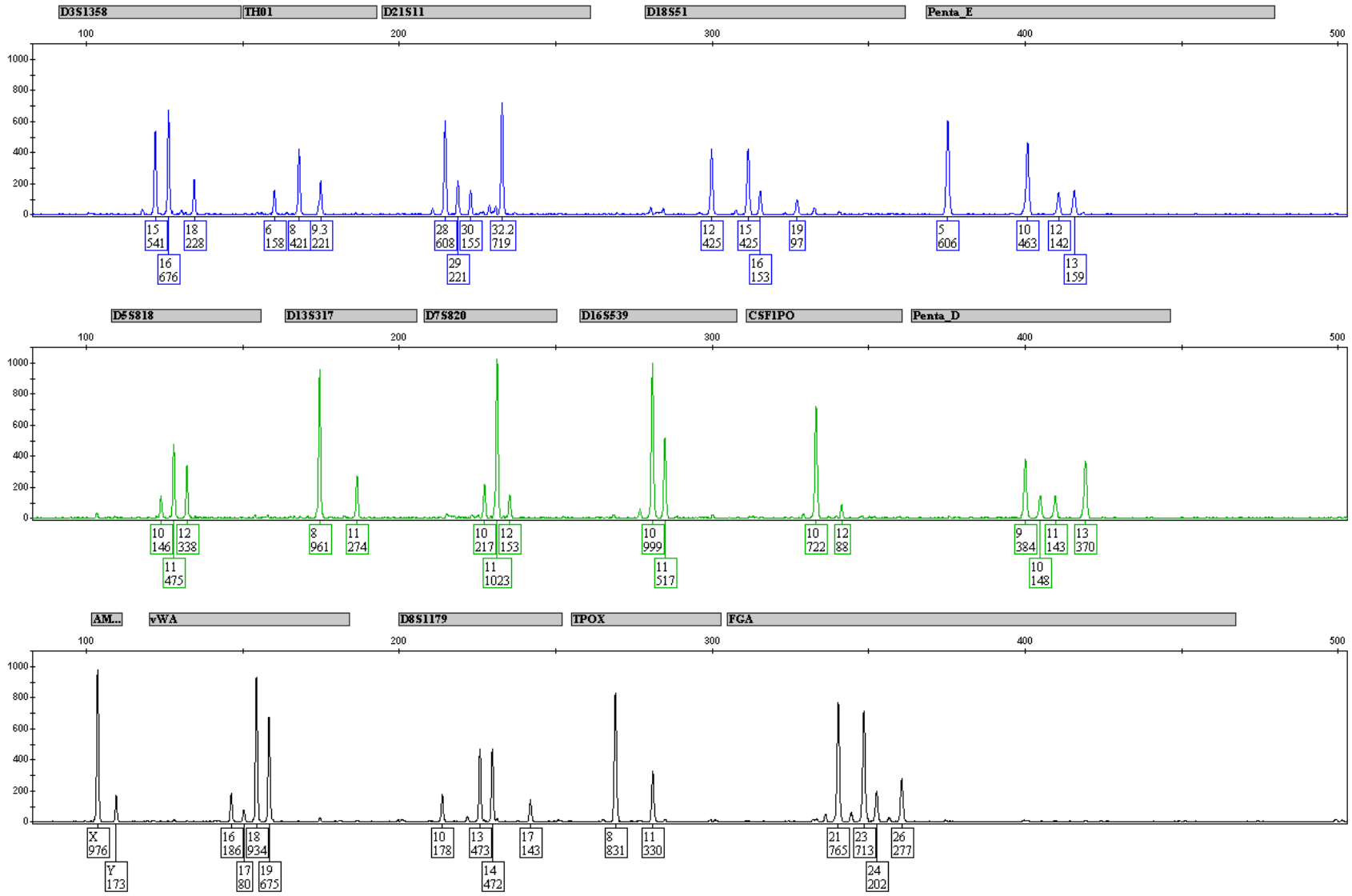
SRM 2391c Component D (mixture)

Identifiler Plus (1 ng total)



SRM 2391c Component D (mixture)

PowerPlex 16 HS (1 ng total)



Commercially Available STR Kits

Applied Biosystems (17)

- ~~AmpFlSTR Blue (1996)~~
- ~~AmpFlSTR Green I (1997)~~
- Profiler (1997)
- Profiler Plus (1997)
- COfiler (1998)
- SGM Plus (1999)
- **Identifiler** (2001)
- Profiler Plus ID (2001)
- ~~SEfiler (2002)~~
- Yfiler (2004)
- MiniFiler (2007)
- SEfiler Plus (2007)
- Sinofiler (2008) – China only
- **Identifiler Direct** (2009)
- NGM (2009)
- **Identifiler Plus** (2010)
- NGM SElect (2010)

Promega Corporation (13)

- PowerPlex 1.1 (1997)
- PowerPlex 1.2 (1998)
- PowerPlex 2.1 (1999)
- **PowerPlex 16** (2000)
- PowerPlex ES (2002)
- PowerPlex Y (2003)
- PowerPlex S5 (2007)
- **PowerPlex 16 HS** (2009)
- PowerPlex ESX 16 (2009)
- PowerPlex ESX 17 (2009)
- PowerPlex ESI 16 (2009)
- PowerPlex ESI 17 (2009)
- PowerPlex 18D (2010)

Qiagen (2010)

Primarily selling kits in Europe

Due to patent restrictions cannot sell in U.S.

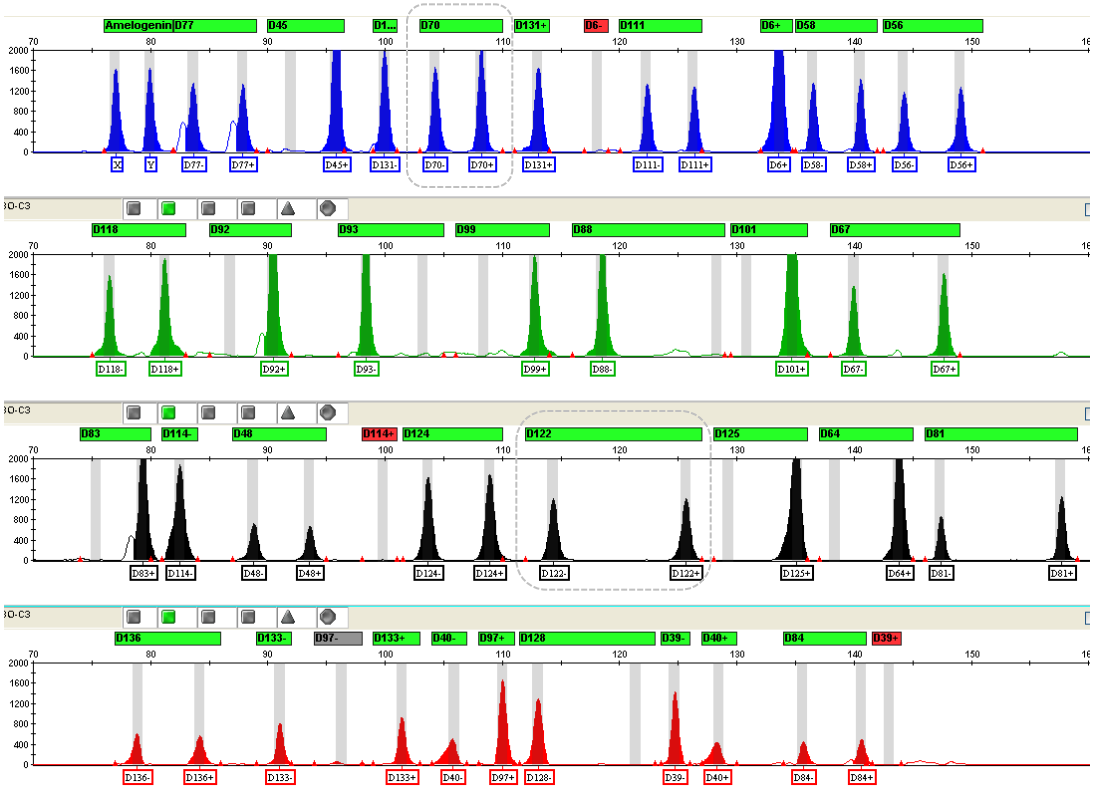
- ESSplex
- ESSplex SE
- Decaplex SE
- IDplex
- Nonaplex ESS
- Hexaplex ESS
- HD (Chimera)
- Argus X-12
- Argus Y-12
- DIPlex (30 indels)

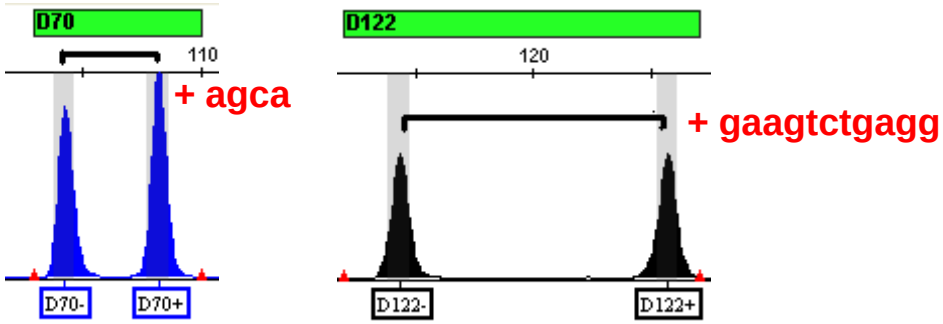
~1/3 of all STR kits were released in the last two years

DIPlex Insertion/Deletion Assay (Qiagen kit)

- Bi-allelic length polymorphisms with properties like SNPs
- PCR/CE detection properties like STRs
- 30 In/Dels (‘-’ or ‘+’ allele)
- Short amplicons (75-160 bp)
- Sensitive to ~100 pg with 30 cycle PCR
- Kits kindly provided by Qiagen

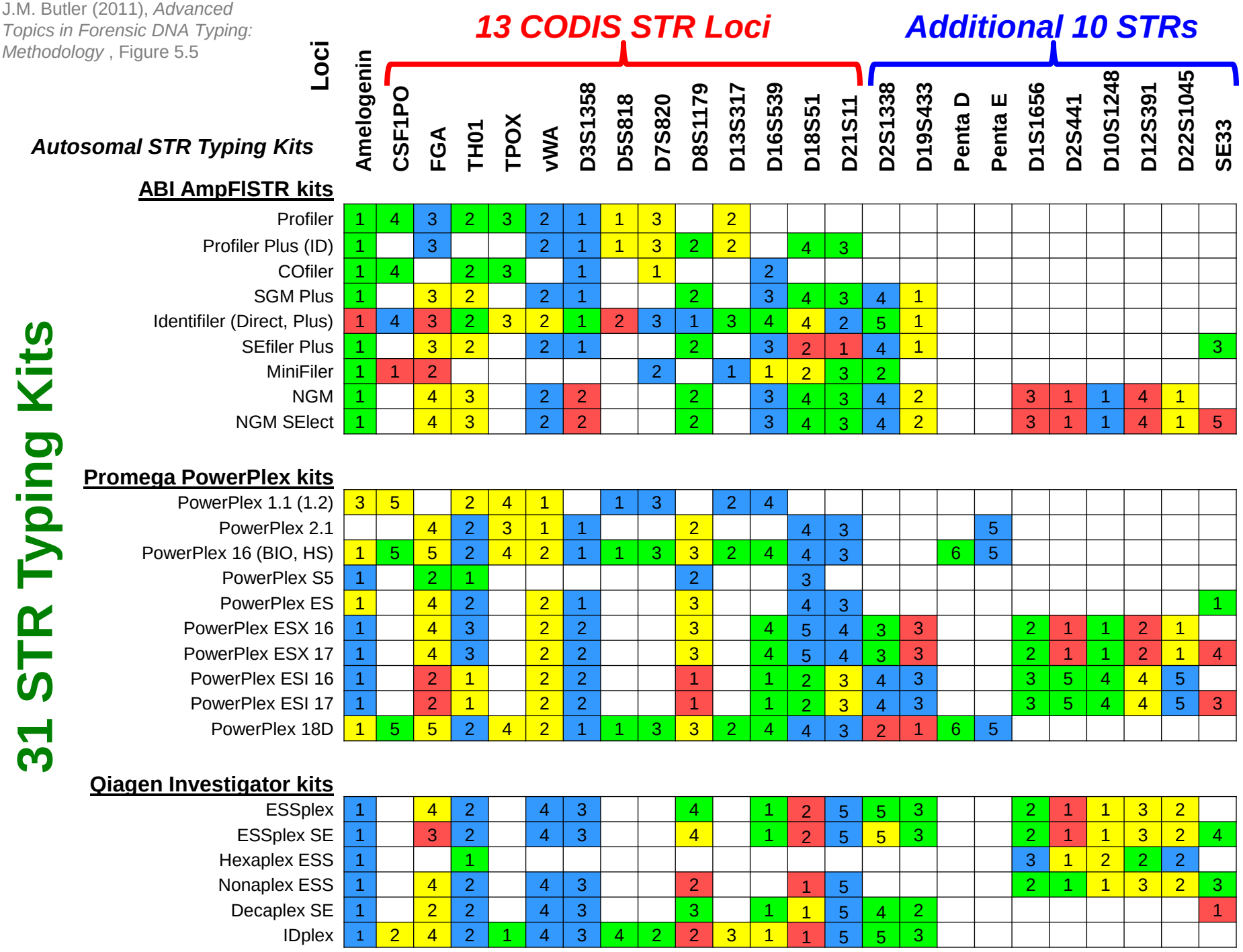
- Work performed by Manuel **Fonde**vila Alvarez (Santiago de Compostela, SPAIN), guest researcher at NIST



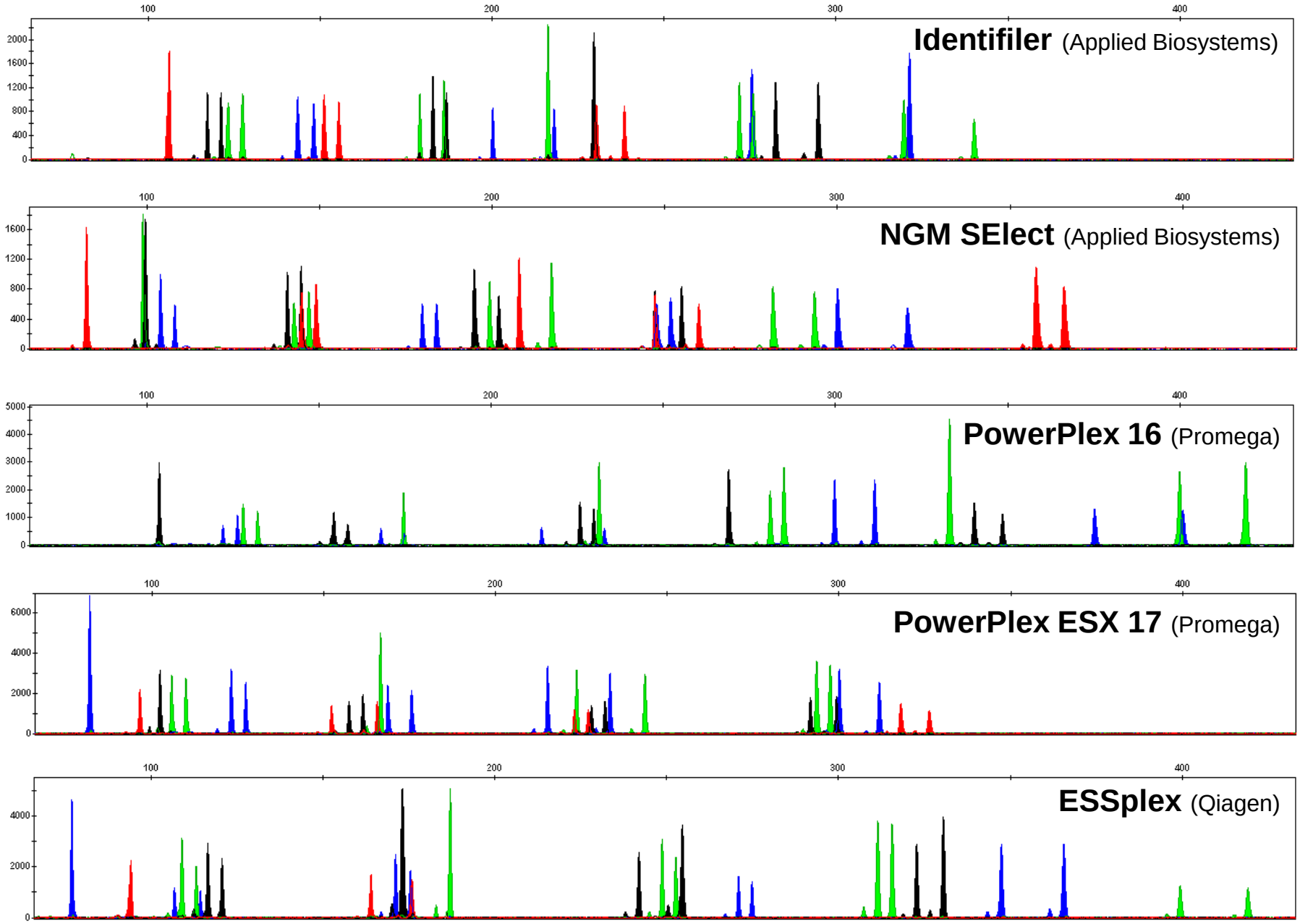


Heterozygous alleles with different insertion lengths

J.M. Butler (2011), *Advanced Topics in Forensic DNA Typing: Methodology* , Figure 5.5



Same DNA Sample Tested with Five STR Kits



STR Kit Concordance Testing

Profiles in DNA Article Published April 2010

Article Type: Feature

Volume 13 No. 1, April 2010

Strategies for Concordance Testing

Carolyn R. Hill, Margaret C. Kline, David L. Duewer and John M. Butler
National Institute of Standards and Technology, Biochemical Science Division, Gaithersburg, Maryland, USA

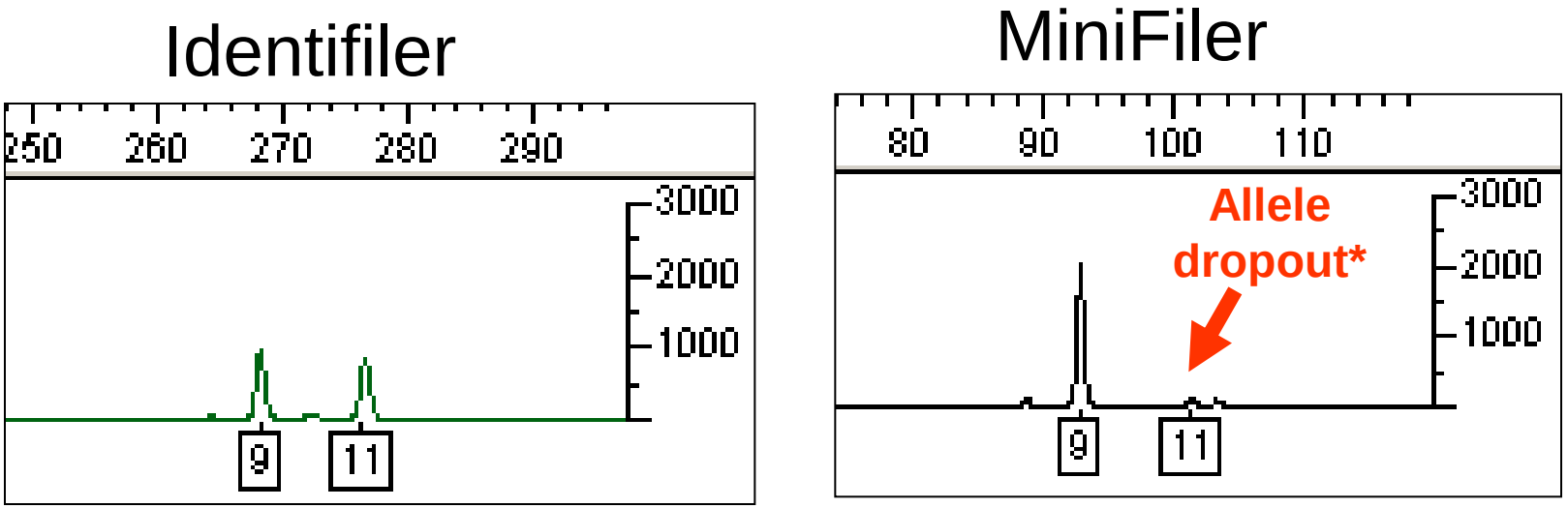
Concordance evaluatio
or "null alleles" present
commercial short tand
markers available to th
kits because the primer
(PCR) product sizes. W
may occur due to primer-binding-site mutations that affect one set of primers but not another.

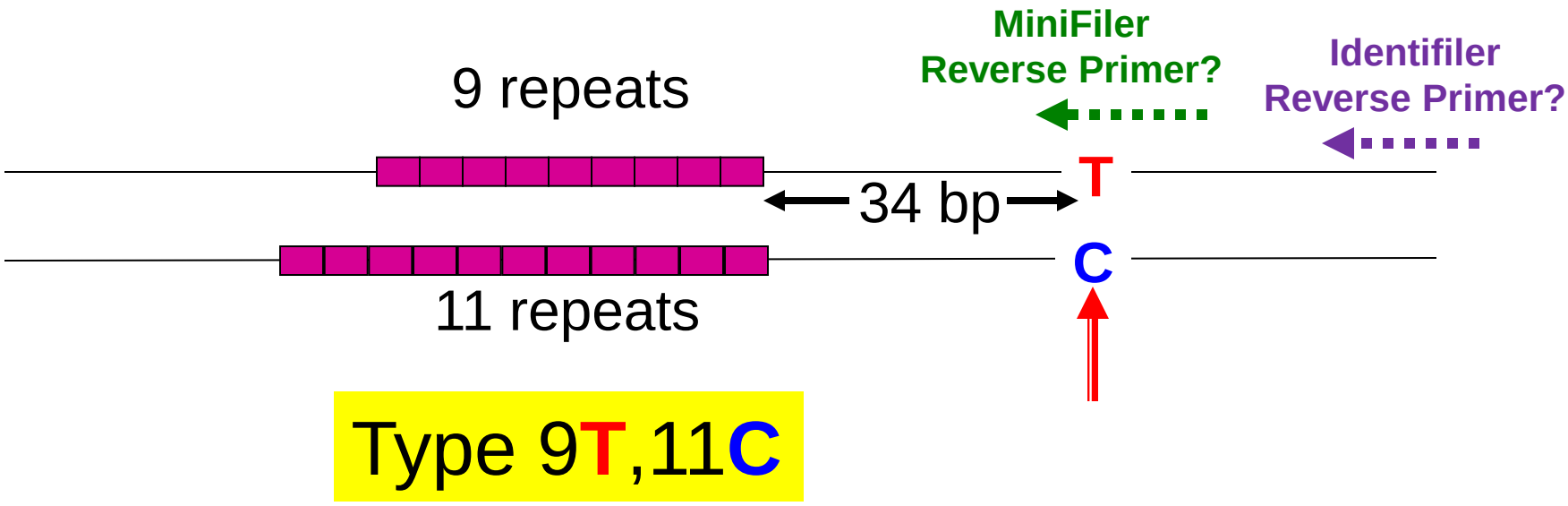
4 S's of Concordance Testing

Standard samples (data on same samples)
Software (to check data concordance)
Sequencing (to understand null alleles)
STRBase (sharing with the community)

http://www.promega.com/profiles/1301/1301_08.html

SRM 2391b Genomic 8 with D16S539





Type 9T,11C

Summary of NIST Samples Evaluated

- **U.S. Population Samples** (**657 samples**)
  - Previously studied with Identifiler, MiniFiler, Yfiler, PP16, miniSTRs, and many additional assays *(>200,000 allele calls)*
  - 260 African Americans, 260 Caucasians, 140 Hispanics, and 3 Asians

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

- **U.S. Father/Son pairs** (**786 samples**)
  - Previously studied with Identifiler, MiniFiler, Yfiler
  - ~**100 fathers/100 sons for each group**: African Americans, Caucasians, Hispanics, and Asians

- **NIST SRM 2391b** PCR DNA Profiling Standard (**12 samples**)
  - Components 1-10 (includes 9947A and 9948): *well characterized*
  - ABI 007 and K562

Total number of samples = 1455

1443 population samples

Kit Concordance Comparisons

Kits compared	Samples	Loci compared	Comparisons	# Differences	Concordance (%)
SGM-ID	1436	11	15,796	1	99.994
ID-ProPlus	1427	10	14,270	1	99.993
ID-IDplex	669	16	10,704	19	99.822
ID-PP16	662	14	9,268	4	99.957
ID-MiniFiler	1308	9	11,772	27	99.771
SGM-NGM	1436	11	15,796	4	99.975
ID-NGM				3	99.981
ProPlus-NGM				4	99.972
SGM-ESI				5	99.968
ProPlus-ESX				3	99.970
ESI-ESX				15	99.939
ESI-ESSplex	1445	16	23,120	29	99.875
ESX-ESSplex	1445	16	23,120	30	99.870
ESI-NGMSElect	715	17	12,155	17	99.860
ESX-NGMSElect	715	17	12,155	7	99.942
ESS-NGMSElect	663	17	11,271	17	99.849
		TOTAL	240,156	186	99.923

240,156 comparisons
186 total differences
99.92% concordance

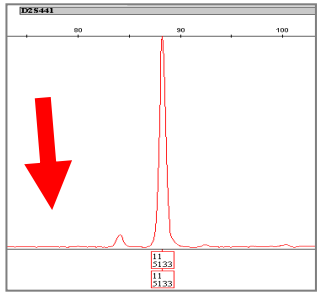
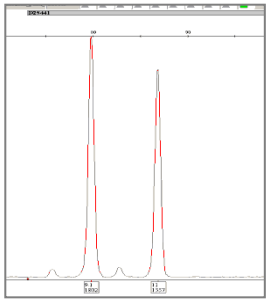
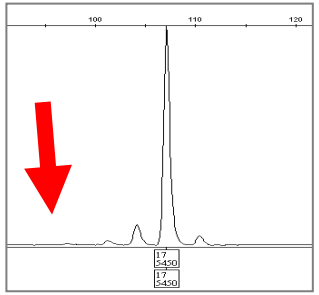
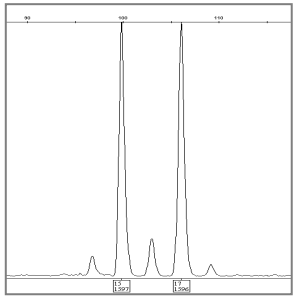
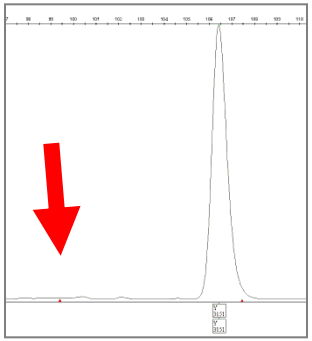
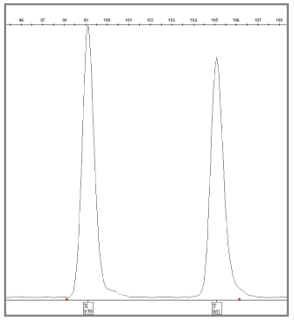
*Kits (except Identifiler) were kindly provided by **Applied Biosystems, Promega, and Qiagen** for concordance testing performed at NIST*

NGM SElect

D2S441, D22S1045, Amel, and SE33

Confirmation Genotyping

Extra (Degenerate) Primers Added with NGM SElect

	NGM (original)		NGM SElect	
D2S441 9.1 allele missing in 9 Asians		**11,11**		**9.1,11**
D22S1045 15 allele missing in 4 samples		**17,17**		**15,17**
Amelogenin X allele missing in 3 samples		**Y,Y**		**X,Y**

PowerPlex18D Study
New Promega Kit for **Direct** & **Rapid** PCR

- 15 STRs present in Promega PP16 + 2 Identifiler loci
  - **D2S1338 & D19S433**
- Initial testing with 50 anonymous blood samples
  - Blood stored on FTA and 903 paper
- Concordance typing performed with PP16HS and Identifiler
- All comparisons concordant except for

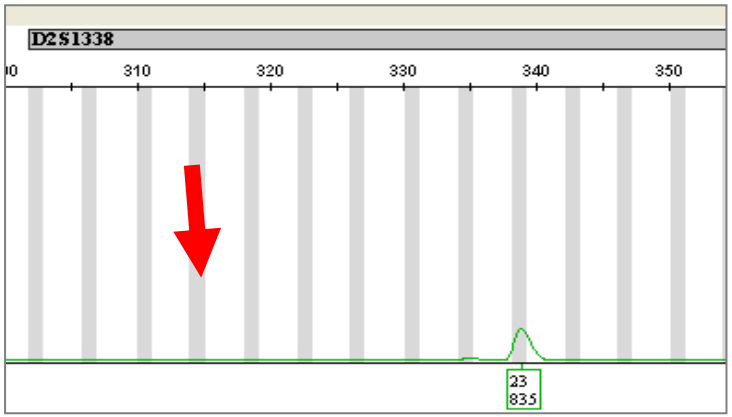
  One sample at D2S1338 (null allele)
  - **PP18D = 17,23**
  - **Identifiler = 23,23**

Thermal Cycling Protocol[1]	
96°C for 2 minutes, then:	
94°C for 10 seconds 60°C for 1 minute for 27 cycles, then:	~1.5 h
60°C for 20 minutes	
4°C soak	

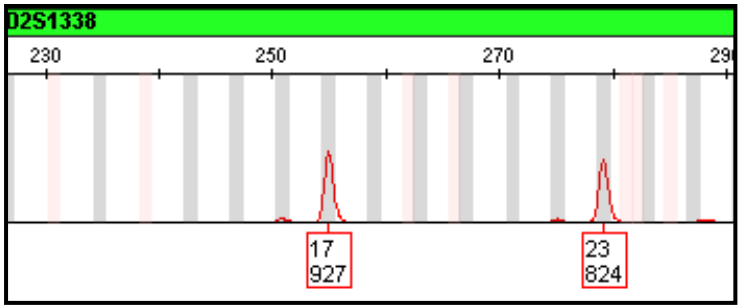
PP18D work performed by Peter Vallone and Erica Butts

D2S1338 Discordance

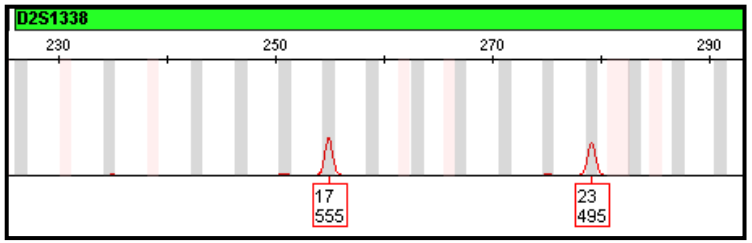
Identifiler: **23,23**



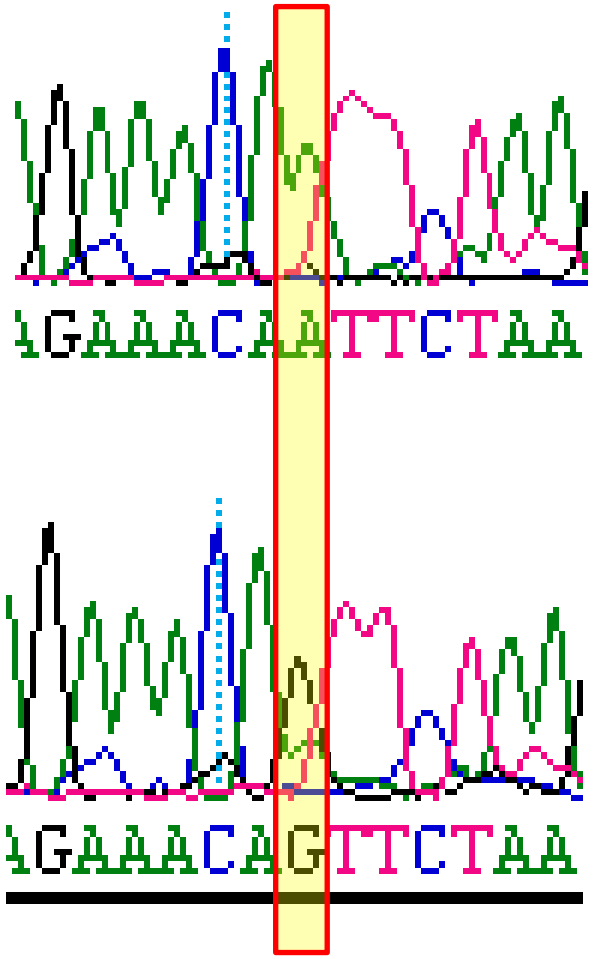
PP18D FTA: **17,23**



PP18D 903: **17,23**



G→A 173 bp downstream of repeat impacts ABI D2S1338 reverse primer in allele 17



Allele 17: $[TGCC]_6$ $[TTCC]_{11}$

G →A 173 bp downstream

Allele 23: $[TGCC]_7$ $[TTCC]_{13}$ GTCC $[TTCC]_2$

T →G 35 bp downstream

SE33 Differences

NGM Select/PP ESX 17 vs PP ESI 17

SE33 Seq Differences

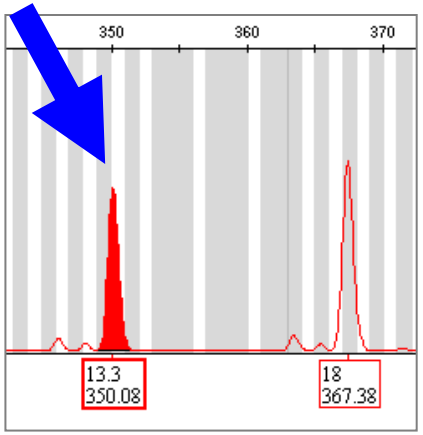
- Total African American samples tested:
  - 46 Blood samples
  - 258 Population samples
  - 190 Father/Son samples

494 AA samples total

- 12 seq variations found out of 494 samples

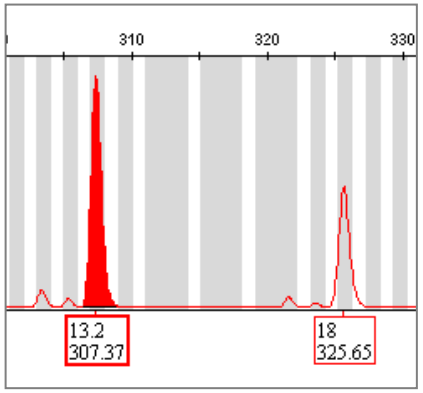
2.43% NIST AA samples exhibit ESI difference

Impact of SE33 Primer Positions



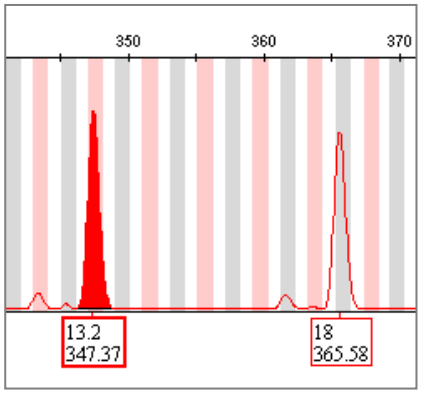
PowerPlex **ESI 17** (30 cycles)

“13.3”,18



PowerPlex **ESX 17** (30 cycles)

13.2,18



NGM SElect (29 cycles)

13.2,18

The 10 STR Loci Beyond the CODIS 13

STR Locus	Location	Repeat Motif	Allele Range*	# Alleles*
D2S1338	2q35	TGCC/TTCC	10 to 31	40
D19S433	19q12	AAGG/TAGG	5.2 to 20	36
Penta D	21q22.3	AAAGA	1.1 to 19	50
Penta E	15q26.2	AAAGA	5 to 32	53
D1S1656	1q42	TAGA	8 to 20.3	25
D12S391	12p13.2	AGAT/AGAC	13 to 27.2	52
D2S441	2p14	TCTA/TCAA	8 to 17	22
D10S1248	10q26.3	GGAA	7 to 19	13
D22S1045	22q12.3	ATT	7 to 20	14
SE33	6q14	AAAG‡	3 to 49	**178**

5 new European loci

**Allele range and number of observed alleles from Appendix 1, J.M. Butler (2011) Advanced Topics in Forensic DNA Typing: Methodology; ‡SE33 alleles have complex repeat structure*

25 Alleles Reported in the Literature for **D1S1656**

15 NIST observed alleles circled in red

Allele (Repeat #)	Promega ESX 17	Promega ESI 17	ABI NGM	Repeat Structure $[TAGA]_4[TGA]_{0-1}[TAGA]_nTAGG[TG]_5$	Reference
8	133 bp	222 bp	171 bp	$[TAGA]_8[TG]_5$	Phillips *et al.* (2010)
9	137 bp	226 bp	175 bp	$[TAGA]_9[TG]_5$	Phillips *et al.* (2010)
10 (a)	141 bp	230 bp	179 bp	$[TAGA]_{10}[TG]_5$	Lareu *et al.* (1998)
10 (b)	141 bp	230 bp	179 bp	$[TAGA]_{10}TAGG[TG]_5$	Phillips *et al.* (2010)
11	145 bp	234 bp	183 bp	$[TAGA]_{11}[TG]_5$	Lareu *et al.* (1998)
12 (a)	149 bp	238 bp	187 bp	$[TAGA]_{12}[TG]_5$	Lareu *et al.* (1998)
12 (b)	149 bp	238 bp	187 bp	$[TAGA]_{11}TAGG[TG]_5$	Lareu *et al.* (1998)
13 (a)	153 bp	242 bp	191 bp	$[TAGA]_{12}TAGG[TG]_5$	Lareu *et al.* (1998)
13 (b)	153 bp	242 bp	191 bp	$[TAGA]_{13}[TG]_5$	Phillips *et al.* (2010)
13.3	156 bp	245 bp	194 bp	$[TAGA]_1TGA[TAGA]_{11}TAGG[TG]_5$	Phillips *et al.* (2010)
14 (a)	157 bp	246 bp	195 bp	$[TAGA]_{13}TAGG[TG]_5$	Lareu *et al.* (1998)
14 (b)	157 bp	246 bp	195 bp	$[TAGA]_{14}[TG]_5$	Phillips *et al.* (2010)
14.3	160 bp	249 bp	198 bp	$[TAGA]_4TGA[TAGA]_9TAGG[TG]_5$	Phillips *et al.* (2010)
15	161 bp	250 bp	199 bp	$[TAGA]_{14}TAGG[TG]_5$	Lareu *et al.* (1998)
15.3	164 bp	253 bp	202 bp	$[TAGA]_4TGA[TAGA]_{10}TAGG[TG]_5$	Lareu *et al.* (1998)
16	165 bp	254 bp	203 bp	$[TAGA]_{15}TAGG[TG]_5$	Lareu *et al.* (1998)
16.3	168 bp	257 bp	206 bp	$[TAGA]_4TGA[TAGA]_{11}TAGG[TG]_5$	Lareu *et al.* (1998)
17	169 bp	258 bp	207 bp	$[TAGA]_{16}TAGG[TG]_5$	Lareu *et al.* (1998)
17.1	170 bp	259 bp	208 bp	Not published	Schröer *et al.* (2000)
17.3	172 bp	261 bp	210 bp	$[TAGA]_4TGA[TAGA]_{12}TAGG[TG]_5$	Lareu *et al.* (1998)
18	173 bp	262 bp	211 bp	$[TAGA]_{17}TAGG[TG]_5$	Phillips *et al.* (2010)
18.3	176 bp	265 bp	214 bp	$[TAGA]_4TGA[TAGA]_{13}TAGG[TG]_5$	Lareu *et al.* (1998)
19	177 bp	266 bp	215 bp	Not published	Asamura *et al.* (2008)
19.3	180 bp	269 bp	218 bp	$[TAGA]_4TGA[TAGA]_{14}TAGG[TG]_5$	Lareu *et al.* (1998)
20.3	184 bp	273 bp	222 bp	Not published	Gamero *et al.* (2000)

from Appendix 1, J.M. Butler (2011) Advanced Topics in Forensic DNA Typing: Methodology

NIST **U.S. Population Allele Frequencies**

D1S1656 (15 different alleles)

15 different alleles

Allele	African American (N = 341)	Caucasian (N = 361)	Hispanic (N = 236)
10	0.01433	0.00277	0.00630
11	0.04871	0.07756	0.02731
12	0.06304	0.11773	0.08824
13	0.10029	0.06648	0.11555
14	**0.25788**	0.07895	0.11765
14.3	0.00716	0.00277	0.00420
15	0.15616	**0.14820**	0.13866
15.3	0.03009	0.05817	0.05042
16	0.11032	0.13573	**0.17437**
16.3	0.10029	0.06094	0.05462
17	0.02865	0.04709	0.04202
17.3	0.05014	0.13296	0.14496
18	0.00287	0.00554	0.00630
18.3	0.02436	0.05125	0.02521
19.3	0.00573	0.01385	0.00420

N = 938

(only unrelated samples used; fathers removed from this sample set)

< 5/2N

D1S1656 Characteristics

- **15 alleles** observed
- **92 genotypes** observed
- **>89% heterozygotes** (heterozygosity = 0.8934)
- **0.0220 Probability of Identity** (P_I)

$$P_I = \sum (genotype\ \ frequencies)^2$$

These values have been calculated for all 23 STR loci across the U.S. population samples examined

Loci sorted on Probability of Identity (P_I) values

STR Locus	Alleles Observed	Genotypes Observed	Het. (obs)	P_I value N = 938
SE33	53	292	0.9360	0.0069
Penta E*	20	114	0.8799	0.0177
D2S1338	13	68	0.8785	0.0219
D1S1656	15	92	0.8934	0.0220
D18S51	21	91	0.8689	0.0256
D12S391	23	110	0.8795	0.0257
FGA	26	93	0.8742	0.0299
Penta D*	16	71	0.8754	0.0356
D21S11	25	81	0.8358	0.0410
D19S433	16	76	0.8124	0.0561
D8S1179	11	45	0.7878	0.0582
vWA	11	38	0.8060	0.0622
D7S820	11	32	0.8070	0.0734
TH01	8	24	0.7580	0.0784
D16S539	9	28	0.7825	0.0784
D13S317	8	29	0.7655	0.0812
D10S1248	12	39	0.7825	0.0837
D2S441	14	41	0.7772	0.0855
D3S1358	11	30	0.7569	0.0873
D22S1045	11	42	0.7697	0.0933
CSF1PO	9	30	0.7537	0.1071
D5S818	9	34	0.7164	0.1192
TPOX	9	28	0.6983	0.1283

23 STR Loci present in STR kits

rank ordered by their variability

Better for mixtures (more alleles seen)

There are several loci more polymorphic than the **current CODIS 13 STRs**

Better for kinship (low mutation rate)

New STRBase Sections

Forensic STR Information

- STRs101: Brief Introduction to STRs
- ***Core Loci***: FBI CODIS Core STR Loci and European Core Loci
- STR Fact Sheets (observed alleles and PCR product sizes)
- **Multiplex STR kits**
- Sequence Information (annotated)
- Variant Allele Reports
- Tri-Allelic Patterns
- Mutation Rates for Common Loci
- Published PCR primers
- Y-chromosome STRs
- Low-template DNA Information *Updated*
- Mixture Interpretation *NEW*
- Kinship Analysis *NEW*
- miniSTRs (short amplicons)
- Null Alleles - discordance observed between STR kits
- STR Reference List - *now 3400 references*

G Model
FSIGEN-645; No. of Pages 4
ARTICLE IN PRESS

Forensic Science International: Genetics xxx (2010) xxx–xxx

STR Allele Sequencing Has Been Provided
Free to the Community for the Past Ten Years
Thanks to NIJ-Funding

Short communication

STR sequence analysis for characterizing normal, variant, and null alleles

Margaret C. Kline *, Carolyn R. Hill, Amy E. Decker [1], John M. Butler

National Institute of Standards and Technology, 100 Bureau Drive, M/S 8312, Gaithersburg, MD 20899, USA

111 normal and variant alleles **sequenced (at 19 STR & 4 Y-STRs)**
17 null alleles **sequenced (with impact on various STR kit primers)**

Provides primer sequences **for 23 autosomal STRs & 17 Y-STRs**
Provides full protocol for gel separations and sequencing reactions
Primer positions are outside of all known kit primers

Kline, M.C., et al. (2010) STR sequence analysis for characterizing normal, variant, and null alleles, Forensic Sci. Int. Genet. doi:10.1016/j.fsigen.2010.09.005

NIST Efforts with Kinship Analysis

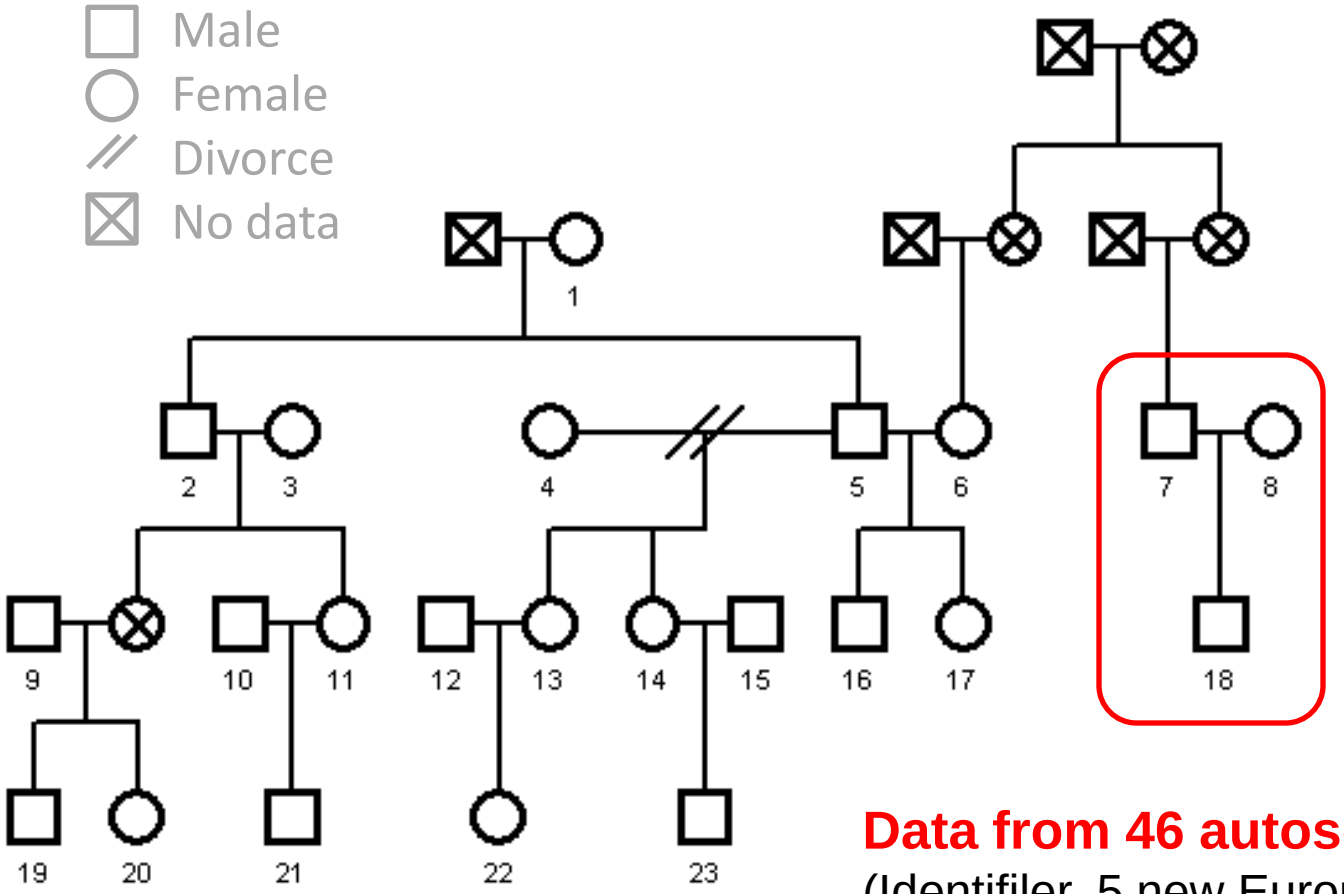
Work by Kristen Lewis O'Connor, NIST NRC Postdoc

(PhD research with Bruce Weir at University of Washington on familial search issues)

- Provide technical expertise and advice to DHS and other federal agencies as needed
- Examine impact of additional STR loci (and other genetic markers) on addressing specific kinship questions
- Simulate likelihood ratio distributions with different sets of STR loci and different potential relationships
- Examine different software programs (and develop approaches for lab validation including investigating possible standard data sets for software testing)

http://www.cstl.nist.gov/biotech/strbase/pub_pres/OConnor-Promega2010-Additional-Loci-Kinship.pdf

NIST Standard Reference Family Pedigree

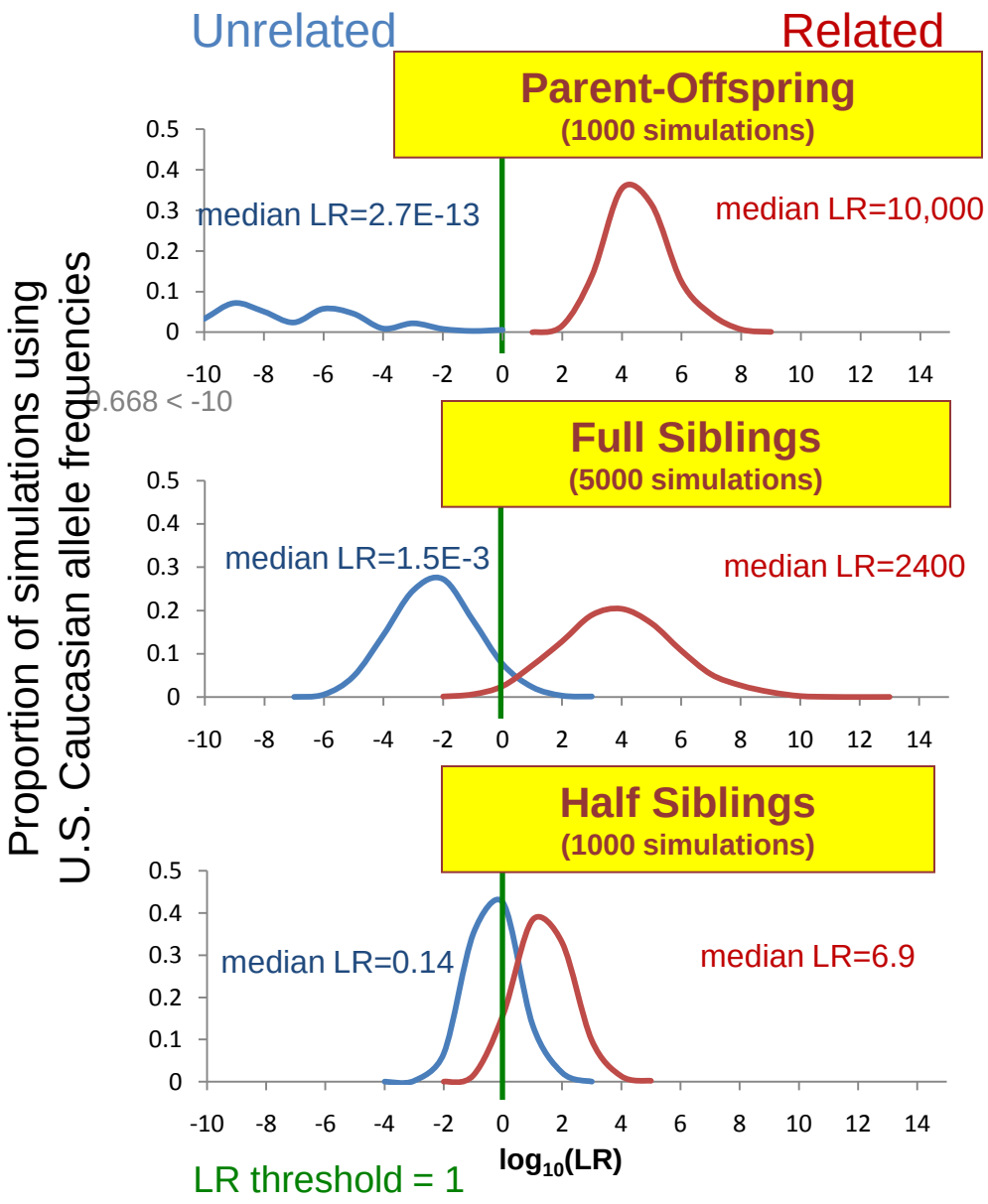


Paternity Trio Individuals 7,8,18	
Locus	**PI Formula (AABB Appendix 8)**
D8S1179	1
D21S11	9
D7S820	8
CSF1PO	13
D3S1358	14
TH01	8
D13S317	2
D16S539	3
vWA	7
TPOX	15
D18S51	4
D5S818	4
FGA	mutation

Data from 46 autosomal STRs
(Identifiler, 5 new European loci, SE33, NIST 26plex) **and 17 Y-STRs** (Yfiler)

Data available for testing software programs:
http://www.cstl.nist.gov/biotech/strbase/kinship.htm

How do 13 loci perform for kinship analysis?



The degree of overlap corresponds with possible values for false positive or false negative results.

Parent-offspring comparisons:

No overlap between unrelated and related LR distributions

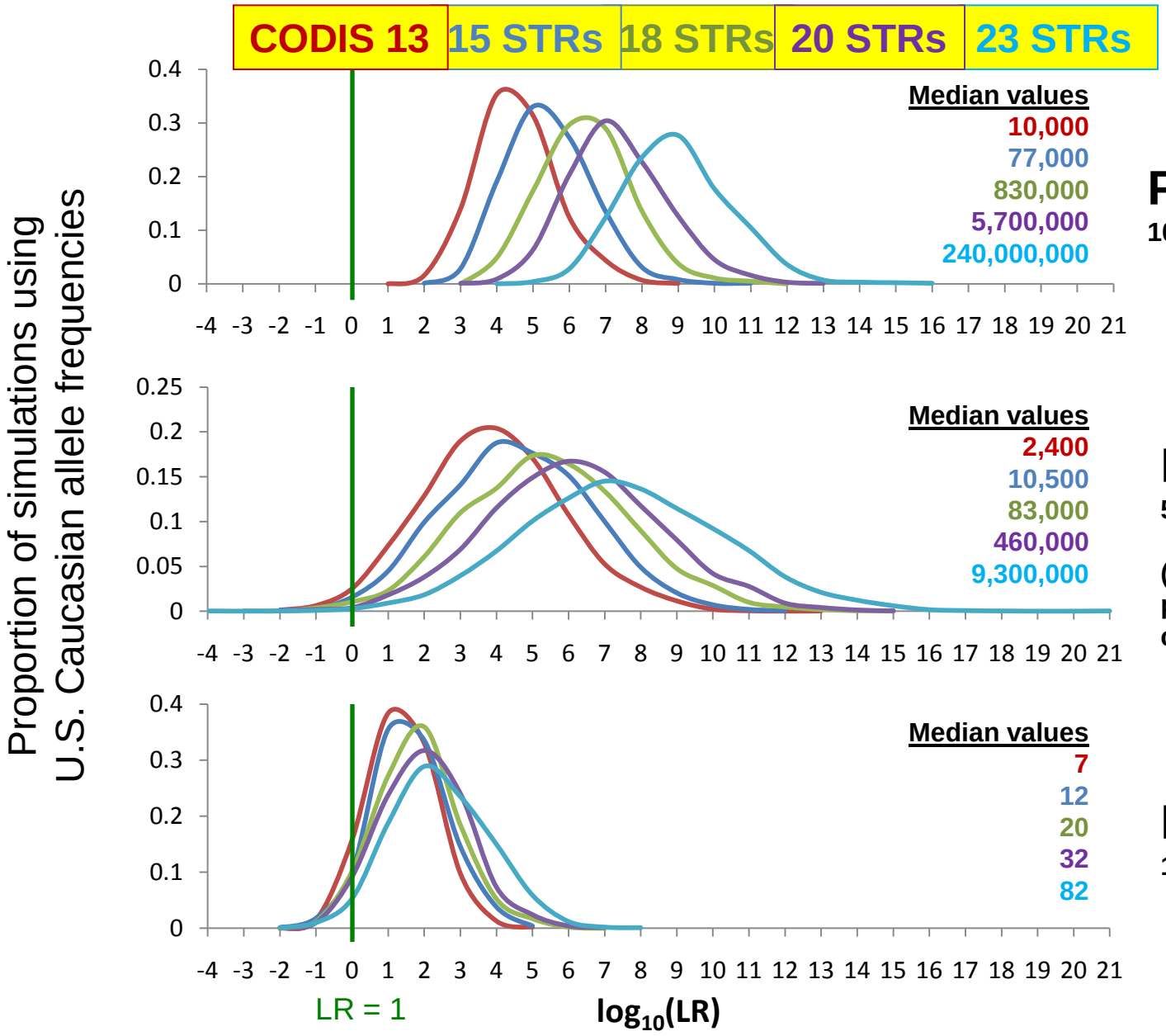
Full sibling comparisons:

False positive rate = 0.027
False negative rate = 0.033

Half sibling comparisons:

False positive rate = 0.155
False negative rate = 0.168

Do additional loci improve kinship determination?



Parent-offspring
1000 simulations

Full siblings
5000 simulations

(additional simulations performed for smoother curves)

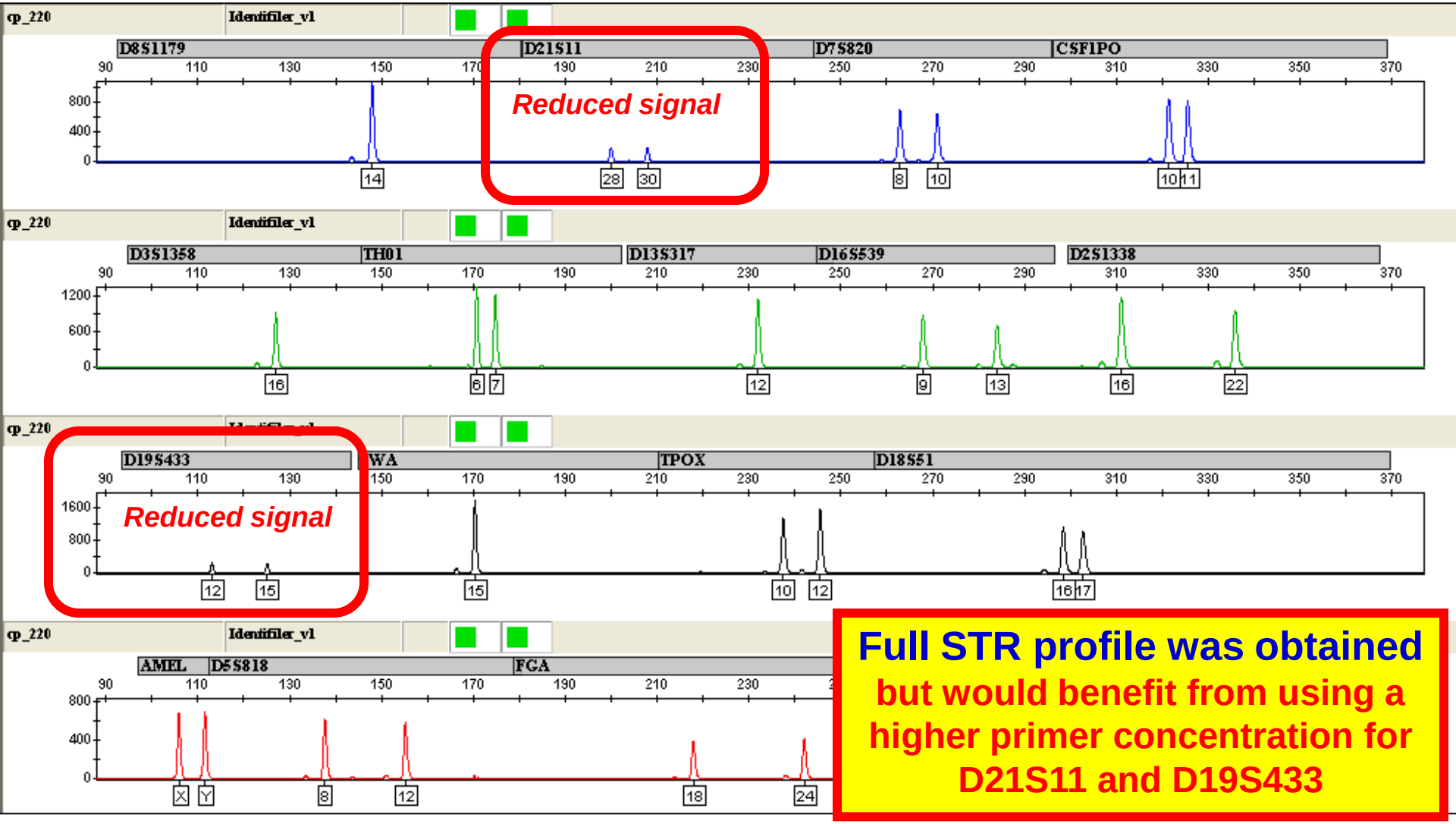
Half siblings
1000 simulations

Work by Pete Vallone and Erica Butts (FBI-funded)

Rapid and Direct PCR

- Performing research on reducing the total time required for STR typing
  - Focusing on the multiplex amplification of commercial STR kits with faster polymerases and thermal cyclers
  - Single-source reference samples (sensitivity > 200 pg)
- Testing rapid DNA typing devices as they become available
- Exploring direct PCR protocols with FTA and 903 papers

20 Minute PCR Amplification
on Cepheid Cycler



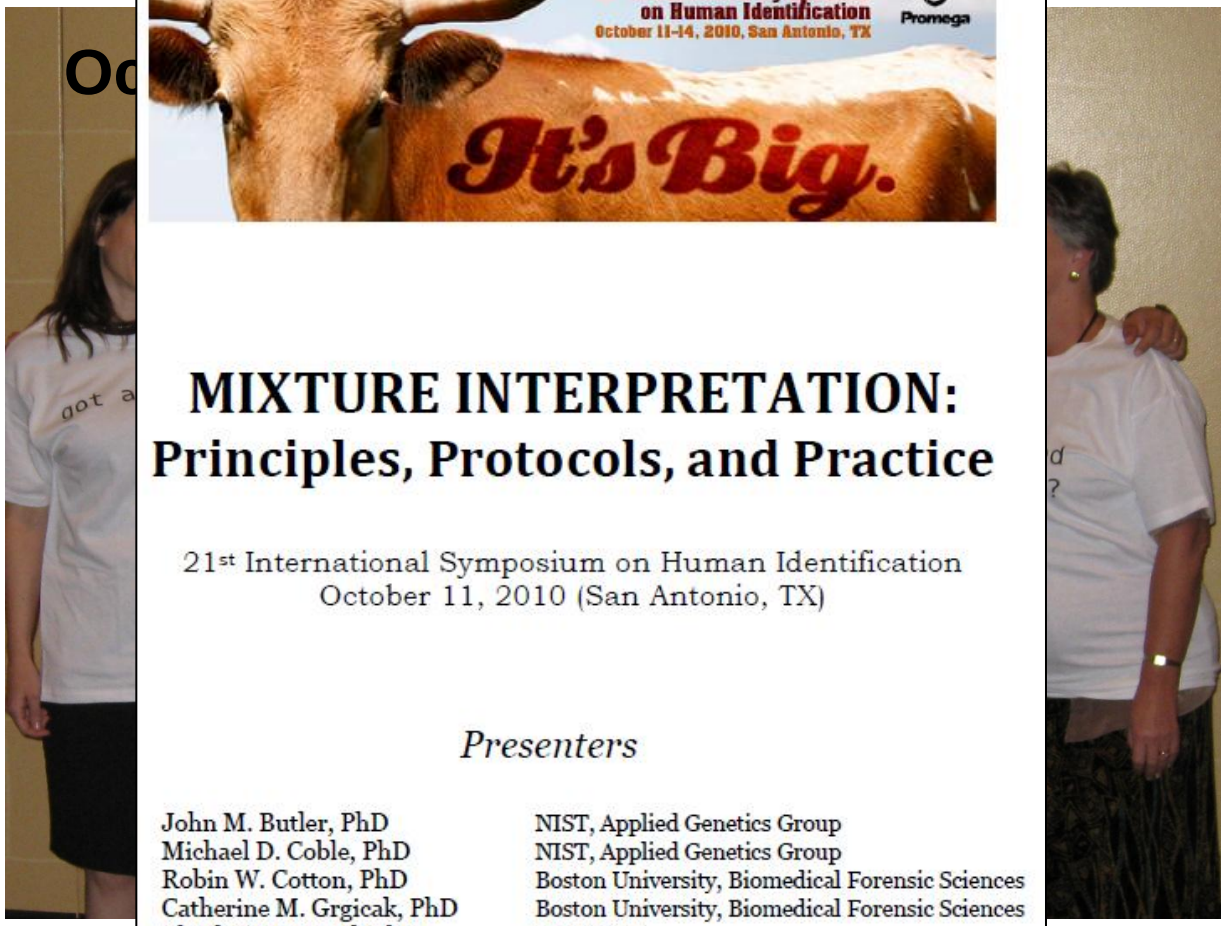
Full STR profile was obtained
but would benefit from using a higher primer concentration for D21S11 and D19S433

Using fast cycler and new DNA polymerases

28 cycles, Identifiler STR kit, 1 ng of DNA

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)

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

~220 people attended

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)

Upcoming Workshops

- ISFG (August 30, 2011)
  - **CE Fundamentals and Troubleshooting**

- Int. Symp. Human Ident. (October 3, 2011)
  - **Mixture Interpretation**

- Int. Symp. Human Ident. (October 6, 2011)
  - **Troubleshooting Laboratory Systems**

Open Letter to Applied Biosystems on Concerns with ABI 3500

- **3/14/11 - emailed ~900 forensic DNA scientists** (SWGDAM, forens-dna, ENFSI, EDNAP) inviting them to sign onto a letter that will be sent to Applied Biosystems expressing concern with ABI 3500
- **Very positive response with 101 who agreed to sign the letter**
- Letter was sent March 31 to the president of ABI and scientists involved with the ABI 3500
- **Community will be notified of ABI's response**

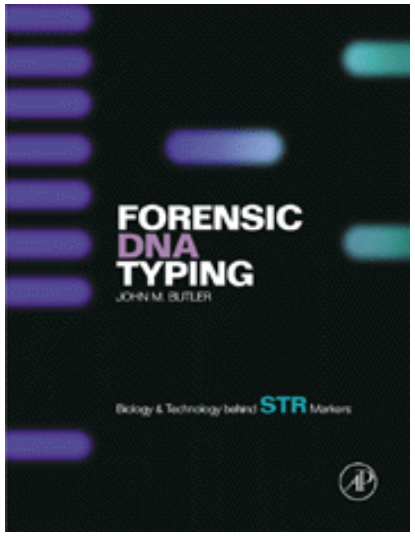
Concerns Expressed in Open Letter

- RFID tags
- New .hid file structure requires new software
- Short shelf life of reagents

Hopefully a change will result…

Forensic DNA Typing Textbook

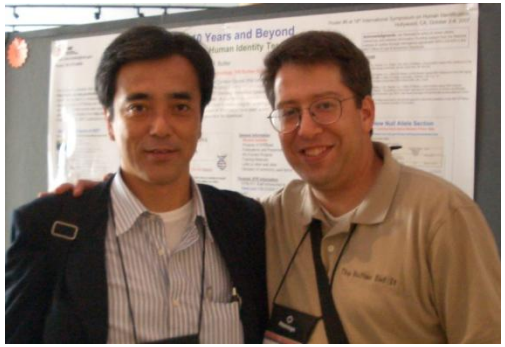
1st Edition



Jan 2001

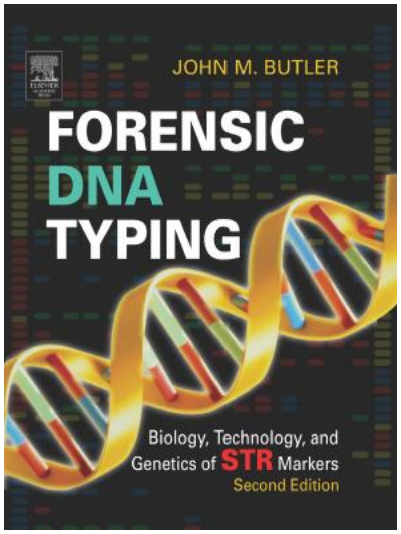
335 pp.

17 chapters



With Y. Fukuma
(Japanese translator)

2nd Edition



Feb 2005

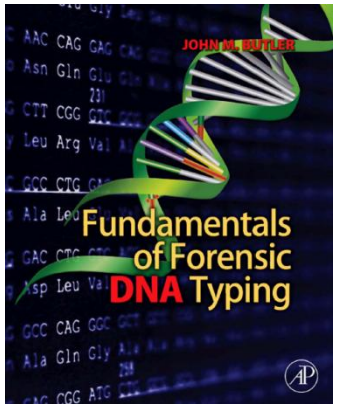
688 pp.

24 chapters

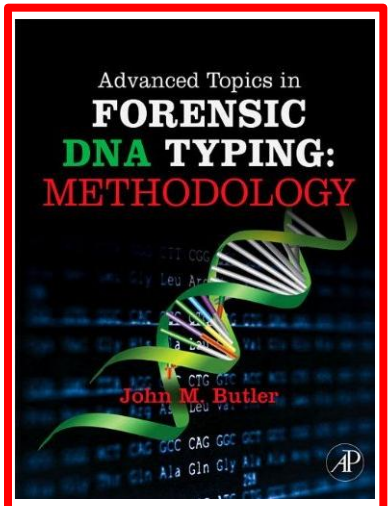
Now available in **Chinese**
(Yiping Hou)

Japanese in preparation
(Yoshiya Fukuma)

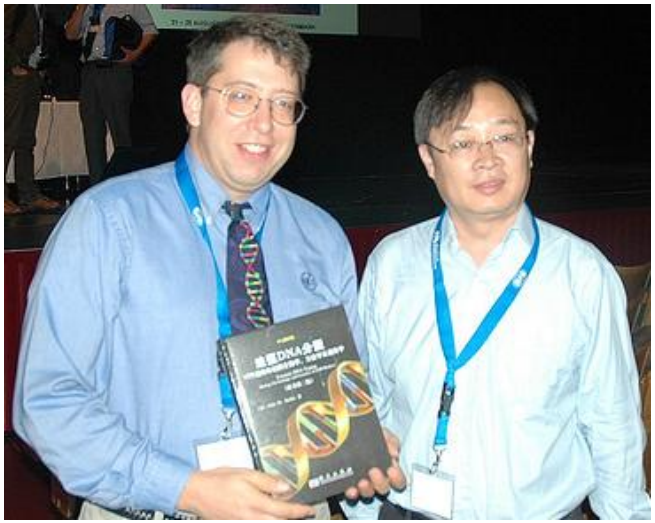
3rd Edition



Sept 2009

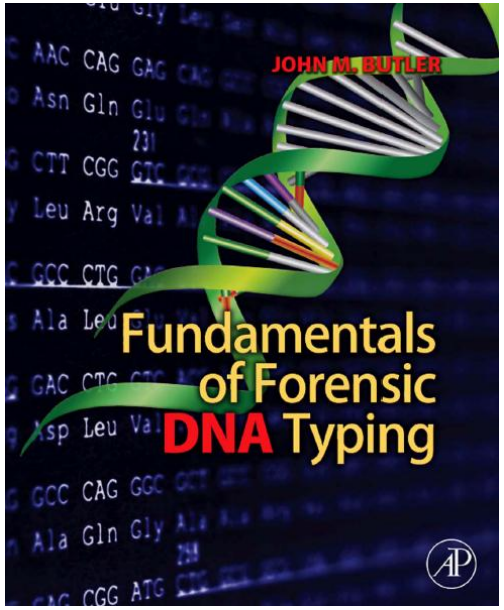


Sept 2011



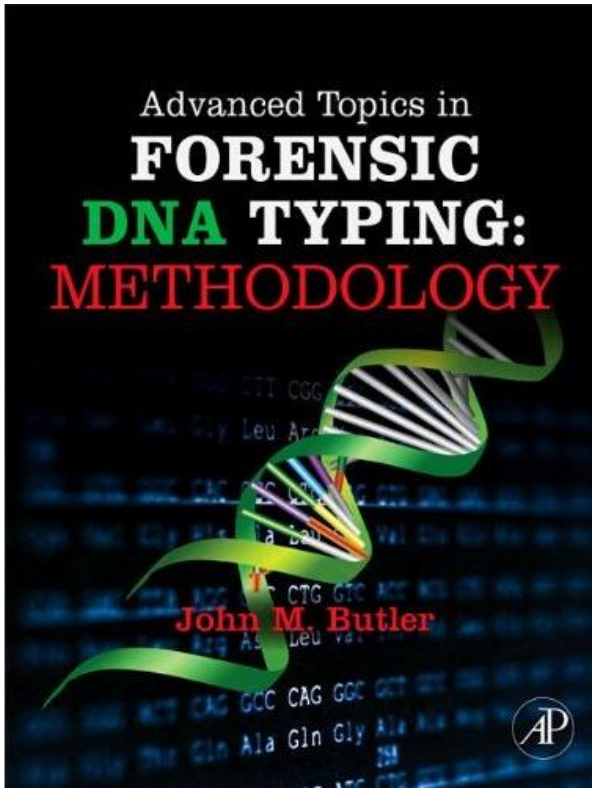
With Y. Hou (Chinese translator)

3rd Edition is Three Volumes



Sept 2009

~500 pages



Sept 2011

~700 pages

Advanced Topics in
Forensic
DNA Typing:
INTERPRETATION

Fall 2012

~400 pages

New Materials in *Advanced Topics* book

Planned release date: September 2011

- Will cite >1500 new references (>2800 ref. total)
- New chapter on legal aspects
  - expert witness prep, perspectives from lawyers
- New chapter on X-chromosome markers
- Extensive updates on LCN, Y-STRs, miniSTRs, mtDNA, SNPs, non-human DNA, and database issues
- Coverage of all the new STR kits
- Listing of all known STR alleles for all 23 kit loci

Thank you for your attention

Acknowledgments: Applied Biosystems, Promega, and Qiagen for STR kits used in concordance studies

Contact Information

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

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