National CODIS Conference

November 15, 2010 – Salt Lake City, Utah

NIST Update

John M. Butler

NIST Human Identity Project Team

National Institute of Standards and Technology

Gaithersburg, Maryland

NIST Human Identity Project Teams
within the Applied Genetics Group

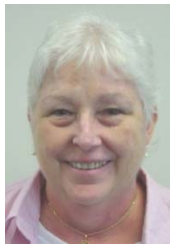
Forensic DNA Team


John Butler


Mike Coble


Becky Hill


Margaret Kline


Jan Redman

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

DNA Biometrics Team


Pete Vallone


Erica Butts


Kristen Lewis O'Connor

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

Data Analysis Support


Dave Duewer

In March 2010, **Mike Coble returned to NIST** after 4 years at AFDIL

Amy Decker left for AFDIL in Nov 2009

New Staff and Projects

Erica Butts – DNA extraction

Kristen Lewis - kinship analysis

Since November 2009…

- **47 presentations** to the forensic DNA community

- **16 publications**
  - Assisting with PP16HS developmental validation
  - ESI/ESX 17 European STR kit concordance
  - Rapid PCR of commercial kits
  - Room temperature DNA sample storage
  - Low template DNA testing
  - Concordance testing strategies
  - Variant allele sequencing primers
  - SE33 variation in U.S. samples
  - Evaluation of D12/vWA independence
  - Assessing self-declared ancestry in U.S. samples
  - Cell line authentication with STRs

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

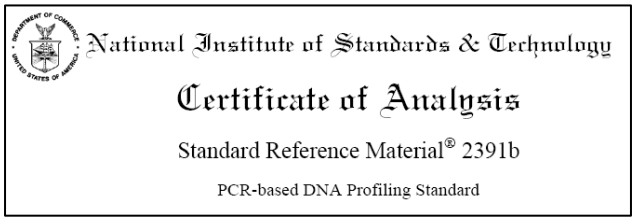
Presentation Outline

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

Standard Reference Materials (SRMs)

http://www.nist.gov/srm

Traceable standards to ensure accurate and comparable measurements between laboratories

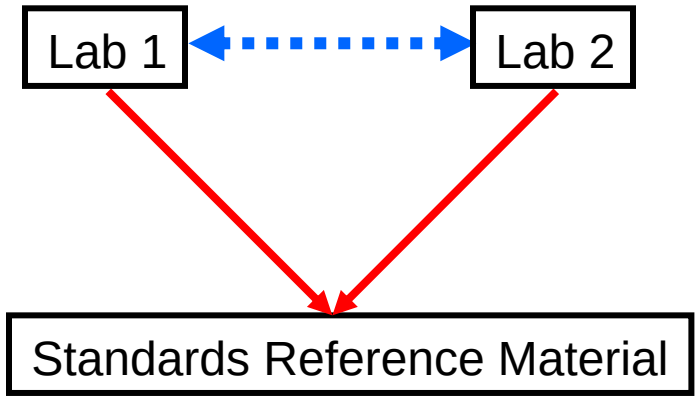

National Institute of Standards & Technology

Certificate of Analysis

Standard Reference Material® 2391b

PCR-based DNA Profiling Standard

SRM 2391b – autosomal STRs
SRM 2392 &-I – mtDNA sequencing
SRM 2395 – Y-STRs
SRM 2372 – DNA quantitation
SRM 2394 – mtDNA heteroplasmy
SRM 2399 – Fragile X



Calibration with SRMs enables confidence in comparisons of results between laboratories

Helps meet ISO 17025 needs

for traceability to a national metrology institute

2003: NIST SRM 2391b

Driven primarily by commercial kit loci…

National Institute of Standards & Technology

Certificate of Analysis

Standard Reference Material® 2391b

PCR-based DNA Profiling Standard

This Standard Reference Material (SRM) is intended primarily for use in the standardization of forensic and paternity quality assurance procedures for Polymerase Chain Reaction (PCR)-based genetic testing and for instructional law enforcement or non-clinical research purposes. This SRM can also be used for quality assurance when assigning values to in-house control materials. It is not intended for any human or animal clinical diagnostic use. Note that SRM 2391b is slightly modified from SRM 2391, in that there is more emphasis on Short Tandem Repeats (STRs) and less emphasis on D1S80 [1,2] reflecting the growing interest and utility of STRs [3 to 14]. Additional information on each STR locus can be found at a NIST-sponsored database on the internet: http://www.cstl.nist.gov/biotech/strbase [14].

This SRM is composed of well-characterized human deoxyribonucleic acid (DNA) in two forms: genomic DNA and DNA to be extracted from cells spotted onto filter paper. A unit of the SRM is composed of 12 frozen components packaged in one box. See the section in this certificate entitled *Description of Components* for a complete listing of the components.

Certified Values: The SRM is certified for genetic loci of forensic interest that were commercially available at the time of production. Genetic types for these loci can be found in Tables 1, 2, and 3. The tables are organized as follows: Table 1 lists the genetic types for the Federal Bureau of Investigation's (FBI's) CODIS (COmbined DNA Index System) core STR loci; Table 2 lists additional STR loci of interest; and Table 3 lists the genetic types for D1S80, AmpliType® PM + HLADQA1, and Amelogenin.

Expiration of Certification: The certification of this SRM is valid until **31 December 2008**, provided the SRM is handled and stored in accordance with the instructions given in this certificate. However, the certification is invalid if the SRM is contaminated or otherwise modified.

Maintenance of SRM Certification: NIST will monitor this SRM over the period of its certification. If substantive technical changes occur that affect the certification before the expiration of certification, NIST will notify the purchaser. Return of the attached registration card will facilitate notification.

Storage: Store frozen at a temperature of -20 °C. **DO NOT** use a self-defrosting freezer because periodic cycling of temperatures may cause shortened shelf life of this SRM.

The overall direction and coordination of the technical activities leading to certification were under the chairmanship of J.M. Butler of the NIST Biotechnology Division.

Analytical determination and technical measurements leading to the certification of this SRM were performed by M.C. Kline and J.W. Redman of the NIST Biotechnology Division.

The support aspects involved in the preparation, certification, and issuance of this SRM were coordinated through the NIST Standard Reference Materials Group by C.S. Davis.

Vincent Vilker, Acting Chief
Biotechnology Division

Gaithersburg, MD 20899
Certificate Issue Date: 06 December 2002

John Rumble, Jr., Chief
Measurement Services Division

SRM 2391b — Page 1 of 7

2. Certified Values for Additional STR Loci

F13B	FES/FPS	LPL	Penta D	Penta E	D2S1338	D19S433
10,10	12,12	10,11	10,15	7,12	17,23	13,16.2
8,10	10,11					16
9,10	11,12					4
6,9	10,13					3
8,9	11,13					14
9,10	11,11	10,12	9,12	12,14	25,25	12,14
6,8	11,11*	11,12	3.2,11	12,16	17,22	13,15.2
6,8	10,11	9,11	8,9	5,10	22,22	12.2,15
8,10	10,12	11,12	12,12	12,13	19,23	14,15
8,8	11,11	10,12	8,12	11,11	23,23	13,14
8,10	10,12	11,12	12,12	12,13	19,23	14,15
8,8	11,11	10,12	8,12	11,11	23,23	13,14

48 autosomal STRs
characterized across
12 DNA samples

NIST Standard Reference Material (SRM) for Forensic DNA Testing

SRM 2391b (2003-2011)

- **48 autosomal STR loci** with certified values
- **10 liquid genomic DNA** components + **2 punches** (cells on 903 paper)
- All single source samples
- 4 males + 6 females
- 9947A & 9948 included

SRM 2391c (2011-future)

- **23 autosomal STR loci and 17 Y-STRs** certified
- **4 liquid genomic DNA** components + **2 punches** (cells on **FTA** & 903 paper)
- 5 single source + 1 mixture
- 3 males + 2 females (unique)
- All new samples
  - no 9947A or 9948

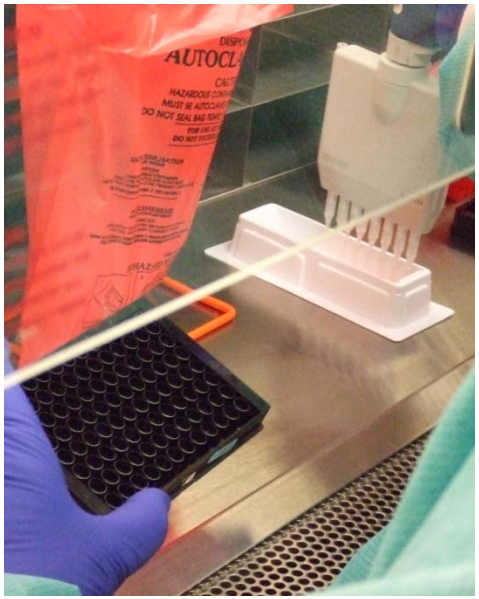
SRM 2391c to replace SRM 2391b and SRM 2395 (price reduction)

SRM Production Process for Preparing Cells on FTA or 903 Paper

Required >200 million cells (43 mL of media) to spot 2688 paper punches

Paper is punched and placed into a sterile 96 well tray

Cell suspension is stirred to keep homogeneous



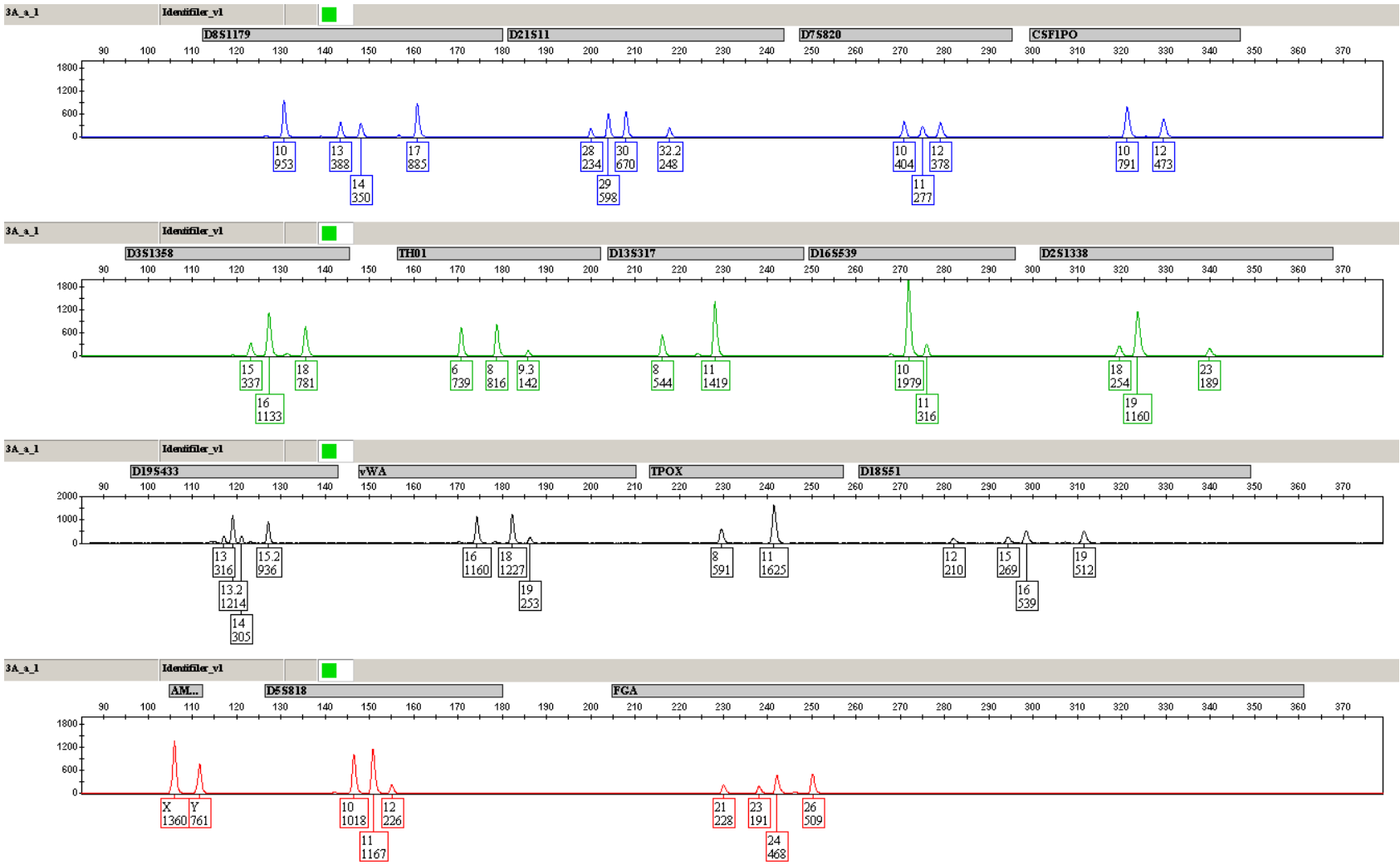
8-channel pipette is used to load cell plates and spot paper punch

Punches are first air-dried and then stored in a desiccator

Each punch, containing hopefully a similar amount of cells, is then placed into a tube and packaged with the other SRM 2391c components

Making a Mixture for SRM 2391c

Carefully considering allele combinations & mixture ratios



Additional Information on SRM 2391c

- Liquid genomic DNA components
  - Considering **50 µL volume with ~2 ng/µL** concentration (will not be certified for DNA quantity)
  - Mixture will be 3 parts male, 1 part female (total ~2 ng/µL)
  - For production purposes, we will **need 140 µg** of each DNA sample
  - PFA (Teflon) tubes to reduce DNA binding to walls
- Paper punches (6 mm diameter)
  - Enables multiple punches from a single spot
  - Theoretically **400 ng of DNA per punch** (recovery will depend on extraction efficiency)
- Will have sequence information or multiple STR kit confirmation results for every certified allele call
- **Will verify performance on every commercially available STR typing kit**

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)

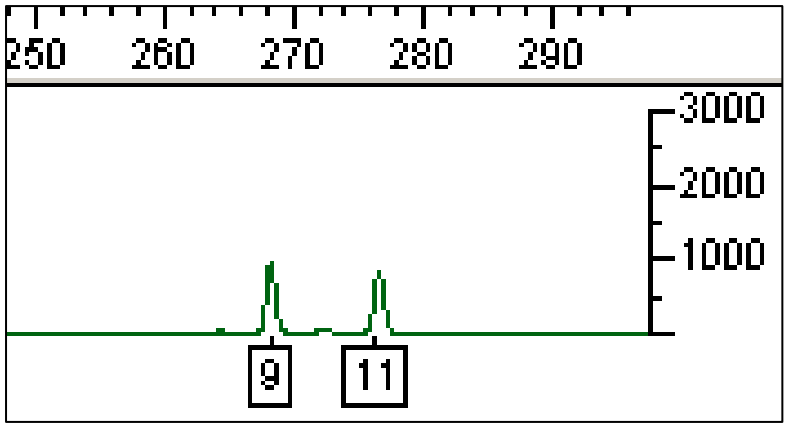
~1/3 of all STR kits were released in the last year

STR Kit Concordance Testing

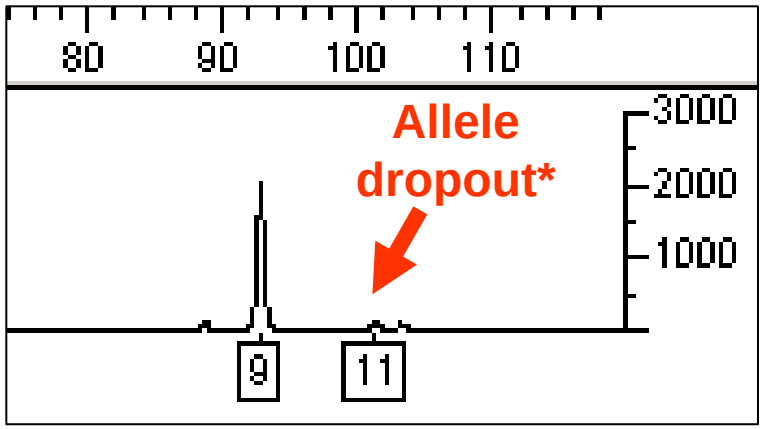
- Many of these STR kits have different primer sequences for amplifying the same STR locus
- Need to analyze the same DNA samples with different STR typing kits looking for differences
- In some rare cases, allele dropout may occur due to mutations in primer binding regions

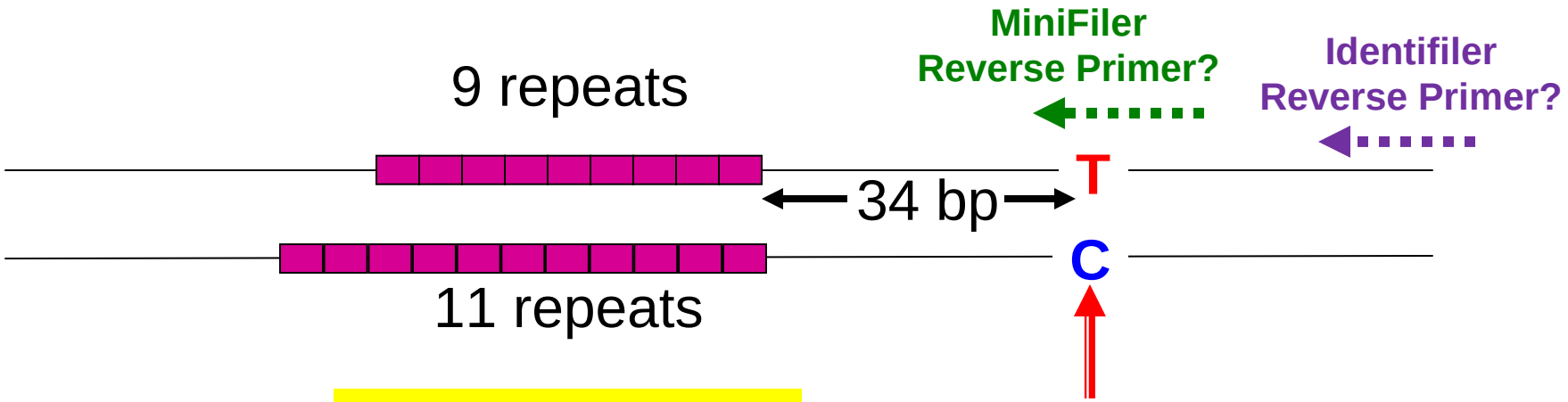
SRM 2391b Genomic 8 with D16S539

Identifiler



MiniFiler





Type 9T,11C

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

NIST Pipeline for STR Kit Analysis

Work by Becky Hill and Dave Duewer

- Concordance testing with standard samples
  - Sequence analysis of any null alleles to understand differences
- Locus characteristics
  - Heterozygote peak height ratios
  - Stutter percentages (including allele-specific)
- Allele frequencies for all new loci
  - Across U.S. Caucasian, Hispanic, African American, and Asian
- Probability of identity for different locus sets

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

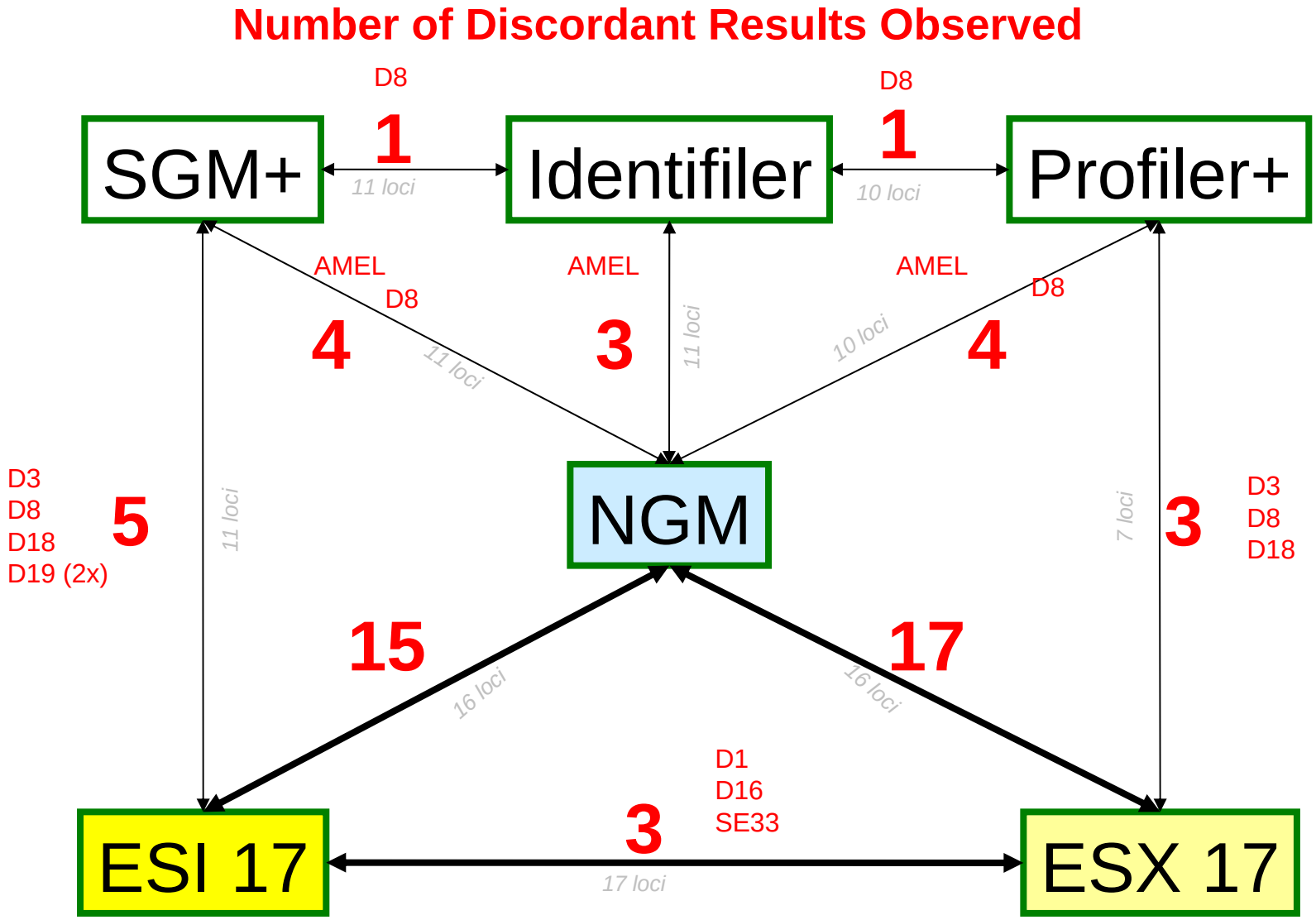
Kit Concordance Comparisons

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%
SGM-NGM	1436	11	15,796	4	99.975%
ID-NGM	1449	11	15,939	3	99.981%
ProPlus-NGM	1427	10	14,270	4	99.972%
SGM-ESI	1436	11	15,796	5	99.968%
ProPlus-ESX	1427	7	9,989	3	99.970%
ESI-NGM	1449	16	23,184	15	99.935%
ESX-NGM	1449	16	23,184	17	99.927%
ESI-ESX	1455	17	24,735	3	99.988%
		TOTAL	**172,959**	**56**	**99.970%**

172,959 comparisons
56 total differences
99.97% concordance

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

Concordance Testing Summary



See also Hill, C.R., et al. (2010) Strategies for concordance testing. *Profiles in DNA (Promega)*, 13(1). Available at http://www.promega.com/profiles/1301/1301_08.html

Characterization of New STR Loci

- **23 loci now present in commercial STR kits**
  - 13 CODIS loci plus **D2S1338** (40 alleles), **D19S433** (36 alleles), **Penta D** (50 alleles), **Penta E** (54 alleles), **D2S441** (22 alleles), **D10S1248** (13 alleles), **D22S1045** (14 alleles), **D12S391** (51 alleles), **D1S1656** (25 alleles), and **SE33** (171 alleles)

- Chromosomal location
- Repeat structure and sequence
- U.S. population samples
- Literature surveys to gather all known alleles

23 STR loci present in STR kits

STR Locus	Alleles Observed	Genotypes Observed	H(obs)	P_I (all samples) n = 1426
SE33	58	341	0.9383	0.0063
Penta E*	20	113	0.8779	0.0175
D2S1338	13	73	0.8752	0.0221
D1S1656	17	99	0.8871	0.0229
D18S51	23	102	0.8696	0.0263
D12S391	24	120	0.8654	0.0279
FGA	29	111	0.8702	0.0299
Penta D*	16	70	0.8733	0.0360
D21S11	32	98	0.8331	0.0399
D19S433	16	83	0.8100	0.0534
D8S1179	11	48	0.7966	0.0553
vWA	11	42	0.8000	0.0624
D16S539	9	30	0.7812	0.0723
D13S317	9	30	0.7749	0.0724
D7S820	12	35	0.7826	0.0745
TH01	9	27	0.7518	0.0752
D2S441	14	46	0.7777	0.0807
D10S1248	12	41	0.7812	0.0828
D3S1358	11	31	0.7489	0.0904
D22S1045	11	45	0.7567	0.0935
D5S818	9	34	0.7225	0.1057
CSF1PO	10	33	0.7567	0.1071
TPOX	10	30	0.6830	0.1351

Rank ordered
by their variability
(P_I = probability of identity)

Better for mixtures (more alleles seen)

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

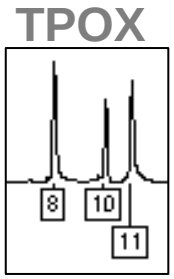
Better for kinship (low mutation rate)

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* ◆

Tri-Allelic Patterns



Tri-Allelic Patterns

- Tri-alleles are Copy Number Variants (CNVs) in the human genome detected as three peaks at a single locus rather than the expected single (homozygous) or double (heterozygous) peak

- Observed at a rate of ~1 in every 1,000 DNA profiles with some loci having a higher rate

- With a million DNA profiles going into NDIS each year, **collectively CODIS DNA databasing labs will see approximately 1,000 tri-alleles this next year**

Slide from Steven Myers, CA DOJ Data from Missouri Highway Patrol DNA Lab

Frequency of Tri-Allelic Patterns

- Database Size:

  69,000

- Overall Average Occurrence:

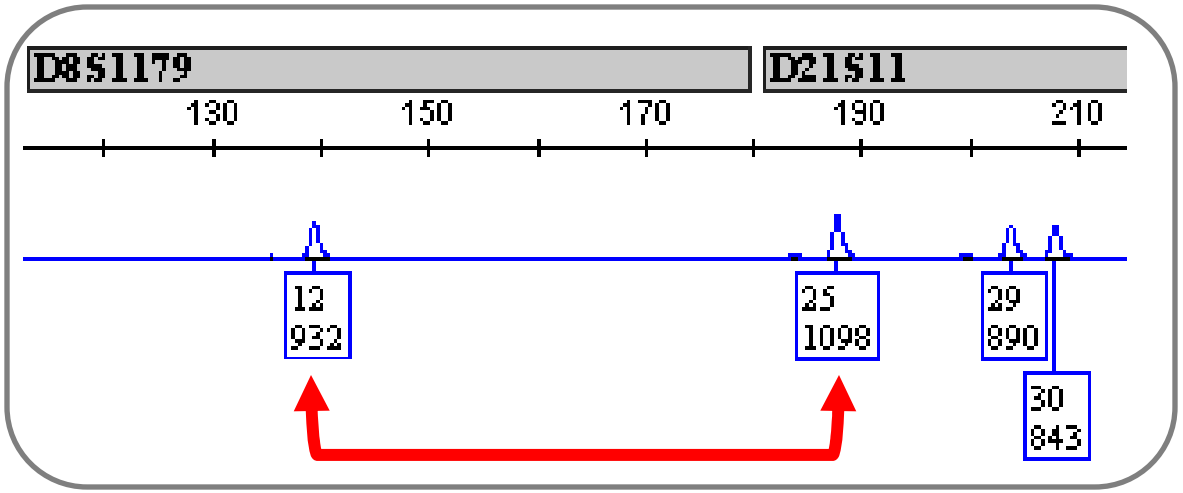
  1 in 1,000

Note:
This is Steven's summary of Missouri's data. You won't find this table on STRBase.

Locus	Observations	1 in...
D3S1358	2	35,000
VWA	10	6,900
FGA	11	6,300
D8S1179	2	35,000
D21S11	9	7,700
D18S51	3	23,000
D5S818	1	69,000
D13S317	4	17,000
D7S820	0	
D16S539	3	23,000
TH01	0	
TPOX	9	7,700
CSF1PO	1	69,000
Penta D	3	23,000
Penta E	10	6,900
Combined	68	1,000

How Do You Characterize Your Tri-Allelic Patterns?

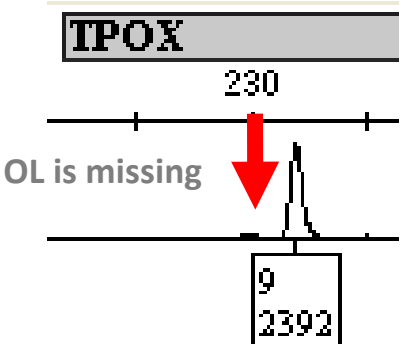
Identifiler



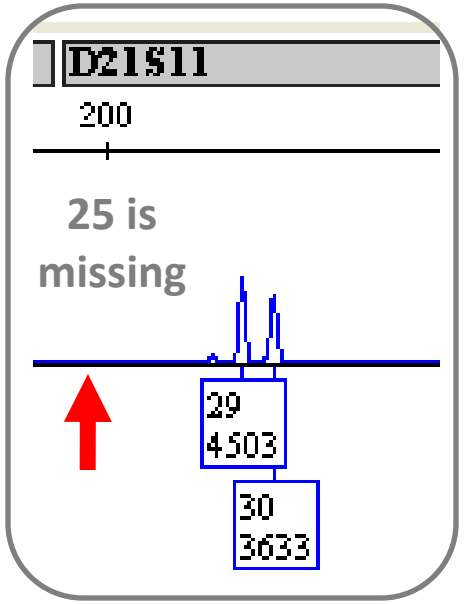
You re-amplify it…
It's Reproducible!

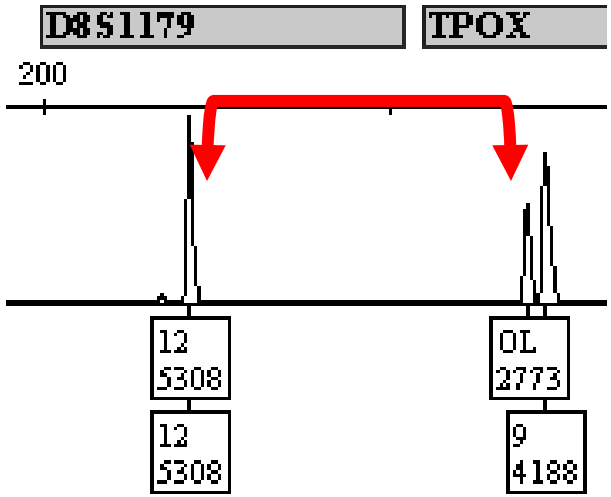
Check STRBase…
It has never been observed before!

A New Large D8S1179 Allele is Discovered – with either 23 or 24 repeats! (sequence analysis will be done soon)



PowerPlex 16 HS





D8S1179

All Previously Known Alleles

Many alleles sequences are not known

We just set the new world record for the largest D8 allele (23 or 24)

Allele (Repeat #)	Promega PowerPlex 16	ABI Identifiler	Repeat Structure $[TCTR]_n$	Reference
6	199 bp	119 bp	Not published	STRBase
7	203 bp	123 bp	$[TCTA]_7$	Griffiths *et al.* (1998)
8	207 bp	127 bp	$[TCTA]_8$	Barber and Parkin (1996)
9	211 bp	131 bp	$[TCTA]_9$	Barber and Parkin (1996)
10	215 bp	135 bp	$[TCTA]_{10}$	Barber and Parkin (1996)
10.1	216 bp	136 bp	Not published	STRBase
10.2	217 bp	137 bp	Not published	STRBase
11	219 bp	139 bp	$[TCTA]_{11}$	Barber and Parkin (1996)
12	223 bp	143 bp	$[TCTA]_{12}$	Barber and Parkin (1996)
12.1	224 bp	144 bp	Not published	STRBase
12.2	225 bp	145 bp	Not published	STRBase
12.3	226 bp	146 bp	Not published	STRBase
13 (a)	227 bp	147 bp	$[TCTA]_1[TCTG]_1[TCTA]_{11}$	Barber and Parkin (1996)
13 (b)	227 bp	147 bp	$[TCTA]_2[TCTG]_1[TCTA]_{10}$	**Kline *et al.* (2010)**
13 (c)	227 bp	147 bp	$[TCTA]_1[TCTG]_1TGTA[TCTA]_{10}$	**Kline *et al.* (2010)**
13 (d)	227 bp	147 bp	$[TCTA]_{13}$	**Kline *et al.* (2010)**
13.1	228 bp	148 bp	Not published	STRBase
13.2	229 bp	149 bp	Not published	STRBase
13.3	230 bp	150 bp	Not published	STRBase
14	231 bp	151 bp	$[TCTA]_2[TCTG]_1[TCTA]_{11}$	Barber and Parkin (1996)
14.1	232 bp	152 bp	Not published	STRBase
14.2	233 bp	153 bp	Not published	STRBase
15	235 bp	155 bp	$[TCTA]_2[TCTG]_1[TCTA]_{12}$	Barber and Parkin (1996)
15.1	236 bp	156 bp	Not published	STRBase
15.2	237 bp	157 bp	Not published	STRBase
15.3	238 bp	158 bp	Not published	STRBase
16	239 bp	159 bp	$[TCTA]_2[TCTG]_1[TCTA]_{13}$	Barber and Parkin (1996)
16.1	240 bp	160 bp	Not published	STRBase
17	243 bp	163 bp	$[TCTA]_2[TCTG]_2[TCTA]_{13}$	Barber and Parkin (1996)
17.1	244 bp	164 bp	Not published	STRBase
17.2	245 bp	165 bp	Not published	STRBase
18	247 bp	167 bp	$[TCTA]_2[TCTG]_1[TCTA]_{15}$	Barber and Parkin (1996)
19	251 bp	171 bp	$[TCTA]_2[TCTG]_2[TCTA]_{15}$	Griffiths *et al.* (1998)
20	255 bp	175 bp	Not published	**STRBase**

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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

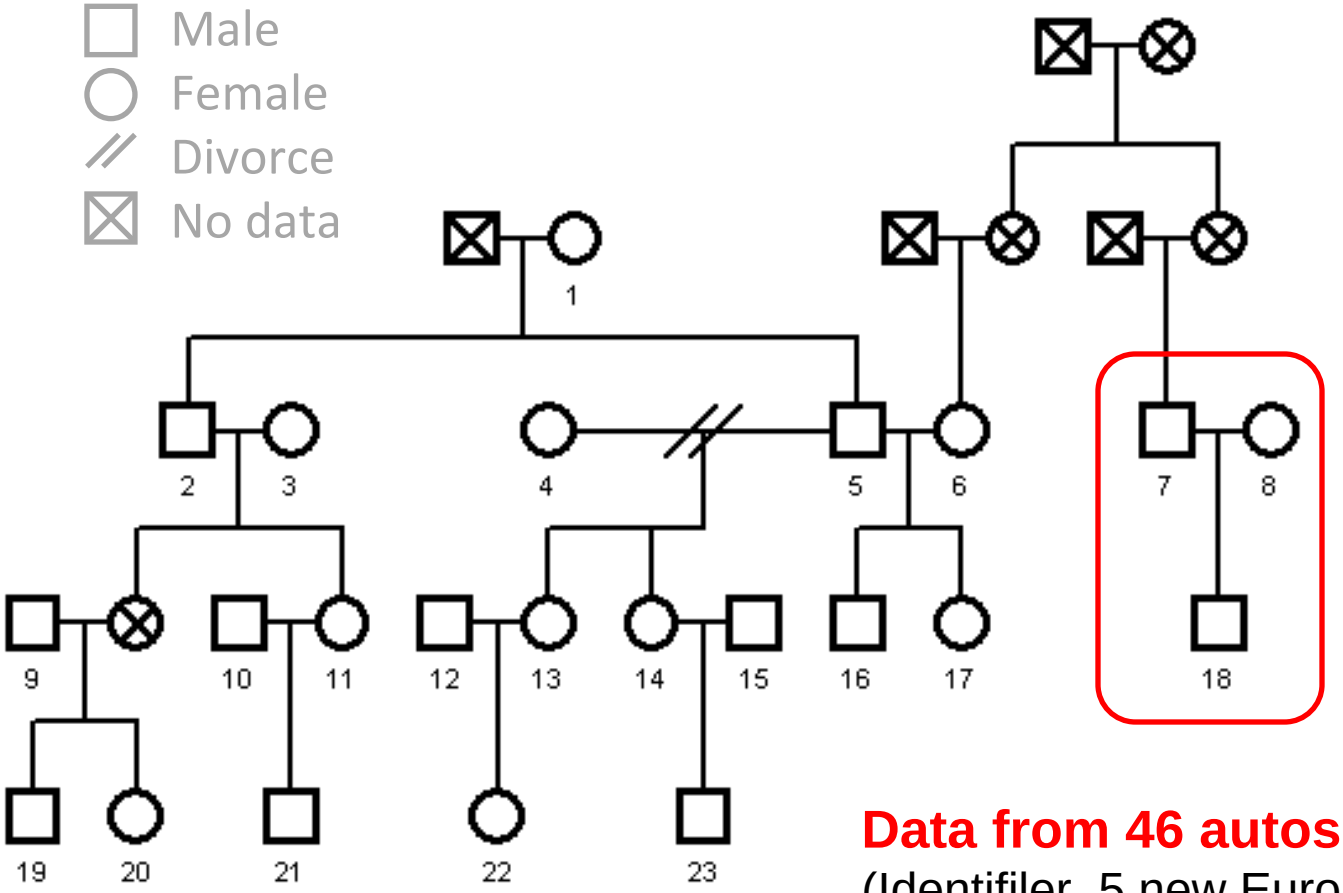
Work by Kristen Lewis O'Connor, NIST NRC Postdoc

(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

Rapid DNA

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

How Fast Can We Go?

Steps Involved

Better chemistry has potential to lead to ability to routinely obtain results in < 1 hour with commercially available instruments

Collection

Extraction → **Direct PCR (new enzymes & master mix to overcome PCR inhibitors from blood)**

Quantitation

Amplification → **Rapid PCR (new enzymes & thermal cyclers)**

Separation/ Detection — **Improved CE systems (ABI 3500?)**

Data Interpretation — **Expert system software**

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

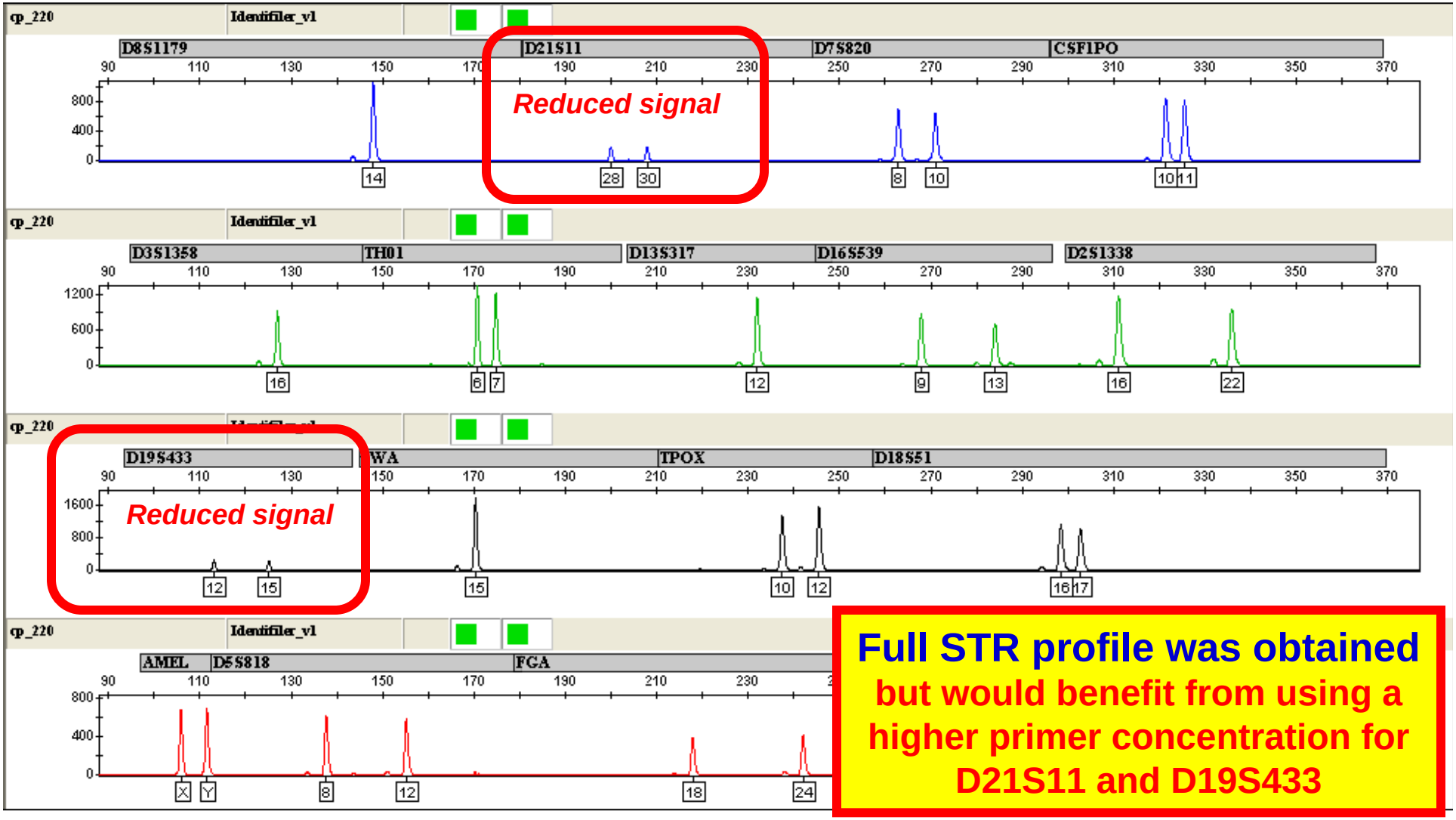
Rapid and Direct PCR

- 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)

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

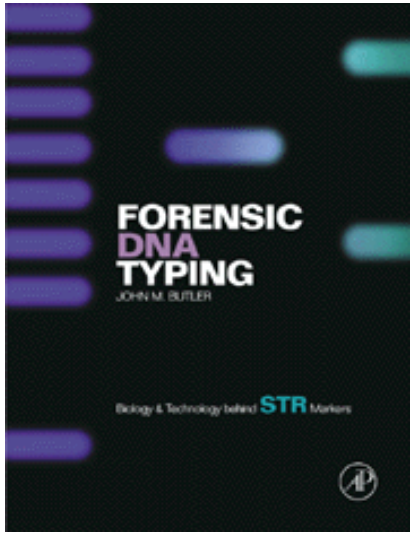
Planning for ~200 people

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)

The Expansion of *Forensic DNA Typing*

1st Edition

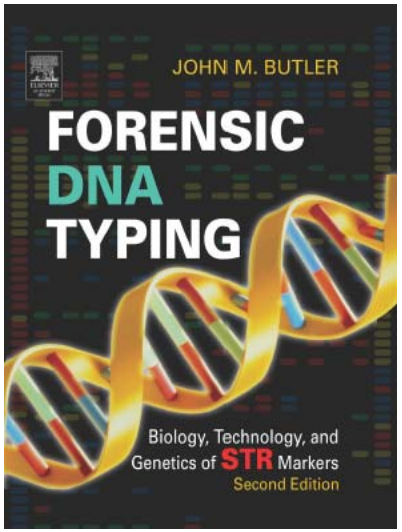


Jan 2001

335 pp.

17 chapters

2nd Edition



Feb 2005

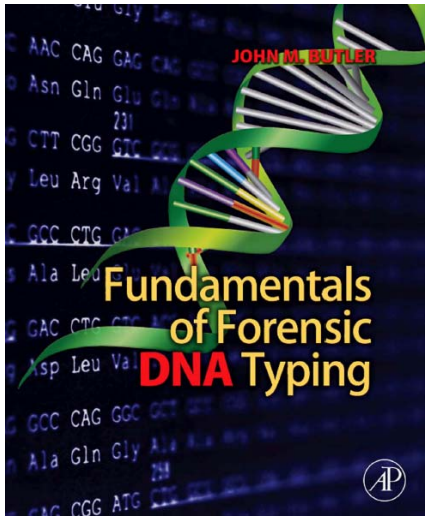
688 pp.

24 chapters

Chinese Translation (2007) Y. Hou, translator

Japanese Translation (2009) Y. Fukuma, translator

3rd Edition



Sept 2009

Fundamentals
18 chapters (520 pp.)

Advanced Topics
25 chapters (~800 pp.)

Planned for Oct 2011

New Materials in *Advanced Topics* book

Planned release date: October 2011

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

Overview of NIST Efforts

- **C**oncordance Testing of STR Kits
- **O**ther Genetic Markers & Software
- **D**NA Biometrics (rapid PCR)
- **I**nternational Impact (European loci/kits)
- **S**TRBase Resources and SRMs

The NIST Human Identity Project Team

(Forensic DNA & DNA Biometrics)

Applied Genetics

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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