ISHI Workshop on New Loci and Kits
October 10, 2013 (Atlanta, GA)
New Autosomal and Y-STR Loci and Kits: Making Data Driven Decisions

STRBase Resources & Additional Information

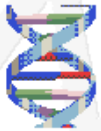
John M. Butler
NIST Office of Special Programs

NIST FORENSIC SCIENCES

NIST

NIST **STRBase** Website

Serving the Forensic DNA Community for >15 Years



Short Tandem Repeat DNA

Internet DataBase

NIST Standard Reference Database SRD 130 [Recent Updates]

Serving the forensic DNA and human identity testing communities for over 10 years... These data are intended to benefit research and application of short tandem repeat DNA markers to human identity testing. The authors are solely responsible for the information herein.
Please Rate Our Products and Services: http://tsapps.nist.gov/MSDSurvey/default.aspx?ID=5&DB=130

This database has been accessed 458551 *times since 10/02/97.* (Counter courtesy www.digits.com - see disclaimer)

Created by ***John M. Butler***
and Dennis J. Reeder (NIST Biochemical Science Division),
with invaluable help from Jan Redman, Christian Ruitberg and Michael Tung
Site creators' curriculum vitaes available using links above.

Partial support for the design and maintenance of this website is being provided by The National Institute of Justice through the NIST Office of Law Enforcement Standards.

General Information

- Purpose of STRBase/NAR 2001 Paper describing STRBase/Overview Presentation
- Publications and Presentations from NIST Human Identity Project Team
- NIJ-Funded Projects
- Training Materials
- Links to other web sites
- Glossary of commonly used terms

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

A Brief History of the STRBase Website

- Initial information was collected on STR markers while working on my PhD dissertation in 1993-1995
- Started a review article in 1996 while a NIST postdoc but wanted to create a dynamic rather than an out-of-date resource
- Created hundreds of individual web pages that were hyperlinked together
- **Website launched in July 1997** (discussed at ISHI 1997)
- Became a NIST Standard Reference Database (SRD 130) because of its high visibility
- **I continue to update the website** (via an HTML editor)…
- **I have more information than I have had time to upload** (i.e., there is additional information in development)

Core STRBase Information

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
- Mixture Interpretation
- Kinship Analysis
- miniSTRs (short amplicons)
- Null Alleles - discordance observed between STR kits
- STR Reference List - ***now 3687 references***

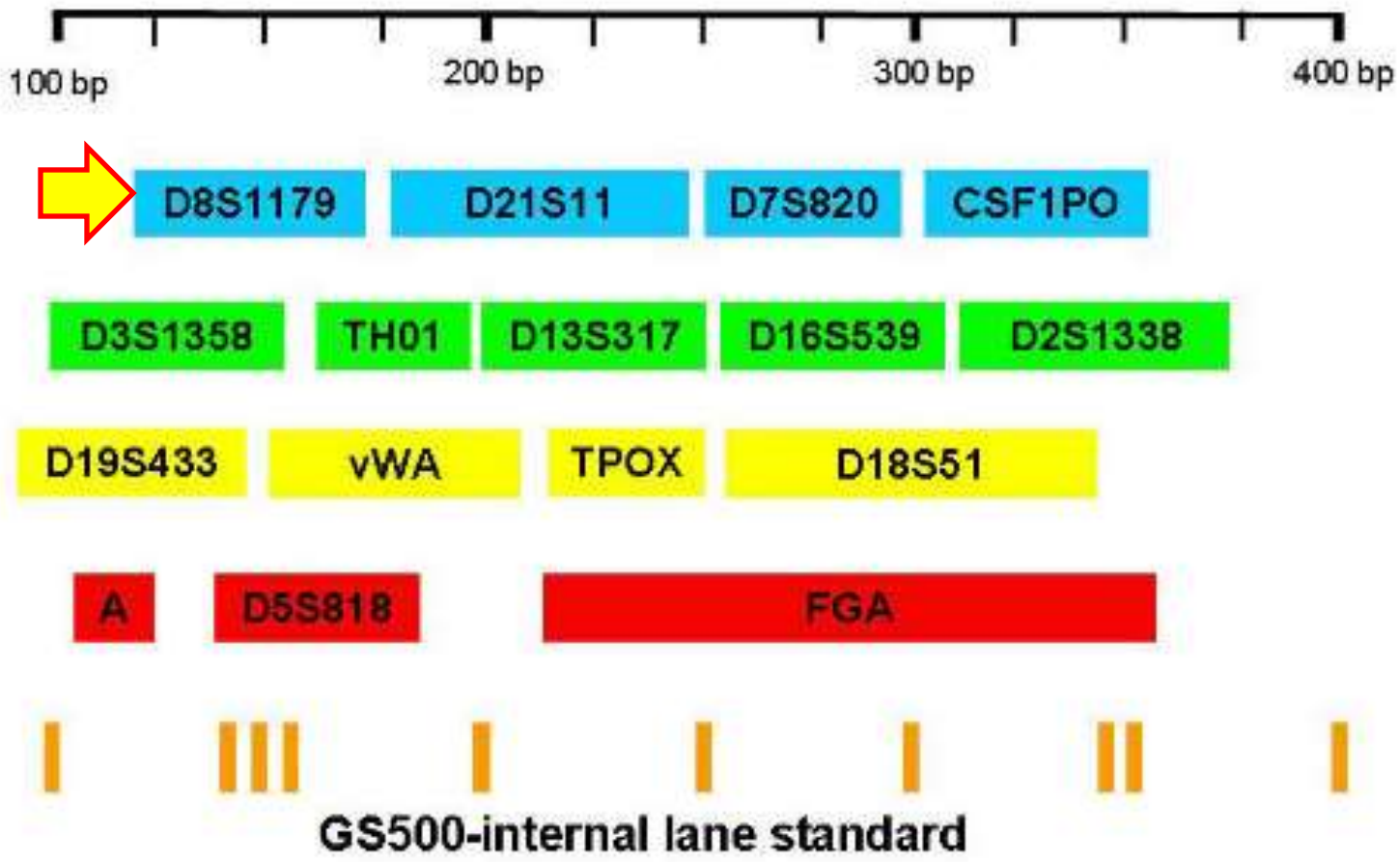
Multiplex STR Kit Information

STR Kits from Applied Biosystems (Foster City, CA)

- AmpF*ℓ*STR **Identifiler**: D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, VWA, TPOX, D1
- AmpF*ℓ*STR **Identifiler Direct**: D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, VWA, T
- AmpF*ℓ*STR **Identifiler Plus**: D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, VWA, TPO
- AmpF*ℓ*STR **NGM**: D10S1248, VWA, D16S539, D2S1338, Amelogenin, D8S1179, D21S11, D18S51, D22S1045, D19S433, TH01, FGA, D
- AmpF*ℓ*STR **NGM SElect**: D10S1248, VWA, D16S539, D2S1338, Amelogenin, D8S1179, D21S11, D18S51, D22S1045, D19S433, TH01
- AmpF*ℓ*STR **GlobalFiler**: D3S1358, VWA, D16S539, CSF1PO, TPOX, Yindel, Amelogenin,D8S1179, D21S11, D18S51, DYS391, D2S441, D2S1338
- AmpF*ℓ*STR **VeriFiler**: D10S1248, D1S1656, Amelogenin, D2S1338, D22S1045, D19S433, TH01, D2S441, D6S1043, D12S391
- AmpF*ℓ*STR **MiniFiler**: D13S317, D7S820, Amelogenin, D2S1338, D21S11, D16S539, D18S51, CSF1PO, FGA
- AmpF*ℓ*STR **Yfiler**: DYS456, DYS389I, DYS390, DYS389II, DYS458, DYS19, DYS385a/b, DYS393, DYS391, DYS439, DYS635, DYS392, Y
- AmpF*ℓ*STR **SGM Plus**: D3S1358, VWA, D16S539, D2S1338, Amelogenin, D8S1179, D21S11, D18S51, D19S433, TH01, FGA
- AmpF*ℓ*STR **Profiler Plus**: D3S1358, VWA, FGA, Amelogenin, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820
- AmpF*ℓ*STR **Profiler Plus ID**: D3S1358, VWA, FGA, Amelogenin, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820
- AmpF*ℓ*STR **COfiler** : D3S1358, D16S539, Amelogenin, TH01, TPOX, CSF1PO, D7S820
- AmpF*ℓ*STR **Sinofiler** *(available only in China)*: D8S1179, D21S11, D7S820, CSF1PO, D3S1358, D5S818, D13S317, D16S539, D2S1
- AmpF*ℓ*STR **Profiler**: D3S1358, VWA, FGA, Amelogenin, TH01, TPOX, CSF1PO, D5S818, D13S317, D7S820
- AmpF*ℓ*STR **SEfiler**: D3S1358, VWA, D16S539, D2S1338, Amelogenin, D8S1179, SE33, D19S433, TH01, FGA, D21S11, D18S51
- AmpF*ℓ*STR **SEfiler Plus**: D3S1358, VWA, D16S539, D2S1338, Amelogenin, D8S1179, SE33, D19S433, TH01, FGA, D21S11, D18S51
- AmpF*ℓ*STR **Green I** : Amelogenin, TH01, TPOX, CSF1PO
- AmpF*ℓ*STR **Blue**: D3S1358, VWA, FGA

http://www.cstl.nist.gov/strbase/multiplx.htm

AmpFℓSTR® Identifiler™



The schematic diagram illustrates the fluorescent dye label color and relative PCR product size ranges for the various STR loci present in this particular kit. *Click on the locus name to learn more about the STR marker of interest.*

http://www.cstl.nist.gov/strbase/kits/Identifiler.htm

STR Fact Sheet for D8S1179

D8S1179

Other Names	Chromosomal Location	GenBank Accession
D6S502 UniSTS: 83408	**8q24.13** Chr 8; 125.976 Mb (May 2004, NCBI build 35)	G08710; has 12 repeat units AF216671; has 13 repeat units

Repeat: [TATC] = GenBank top strand (called [TCTA] by FSS {375})

Reported Primers	Ref.	PCR Primer Sequences
Set 1	369	5' - TTTTTGTATTTCATGTGTACATTCG - 3' 5' - CGTAGCTATAATTAGTTCATTTTCA - 3'
Set 2	PE ABI	Profiler Plus (JOE labeled), SGM Plus (JOE labeled), Identifiler (6-FAM labeled)
Set 3	Promega	PowerPlex 2.1 (TMR labeled), PowerPlex 16 (TMR labeled) primer sequences 5'-**ATT**GCAACTTATATGTATTTTTGTATTTCATG-3' 5'-[TMR]-ACCAAATTGTGTTCATGAGTATAGTTTC-3'

PCR Product Sizes of Observed Alleles

Allele (Repeat #)	Set 1	Set 2	Set 3	Repeat Structure	Ref.
7	157 bp	123 bp	203 bp	$[TCTA]_7$	716
19	205 bp	171 bp	251 bp	$[TCTA]_2[TCTG]_2[TCTA]_{15}$	716
20	209 bp	175 bp	255 bp		*variant allele*

Allelic Ladders: Commercially available from **Promega** and **Applied Biosystems**

Common Multiplexes: PowerPlex 2.1, PowerPlex 16, Profiler Plus, SGM Plus, Identifiler

Mutation Rate: **0.14%**

http://www.cstl.nist.gov/strbase/str_D8S1179.htm

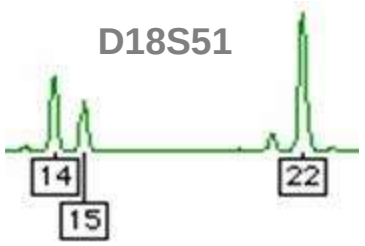
Information on Variant Alleles

- We collect contributions from all over the world where unusual results have been observed with STR data
- Enables laboratories to check if others have seen a specific variant allele or tri-allelic pattern
- Currently (as of Aug 29, 2013 update)

  676 variants at 43 loci

  344 tri-allelic patterns at 35 loci

Type 1 tri-allelic pattern



From **D2S1338 Variants Table** (http://www.cstl.nist.gov/strbase/var_D2S1338.htm)

Allele Designation	Allele Size	Instrument	Amp Kit*	Contributor	Verification/Conformation Method(s)	Notes	Frequency
11	290.61	ABI 310	ID	Cintia alves, IPATIMUP, Porto, Portugal	Re-extracted and re-amplified	Portuguese Caucasian sample	1 in 780

http://www.cstl.nist.gov/strbase/var_tab.htm

Autosomal STR Loci

Autosomal STR Kits

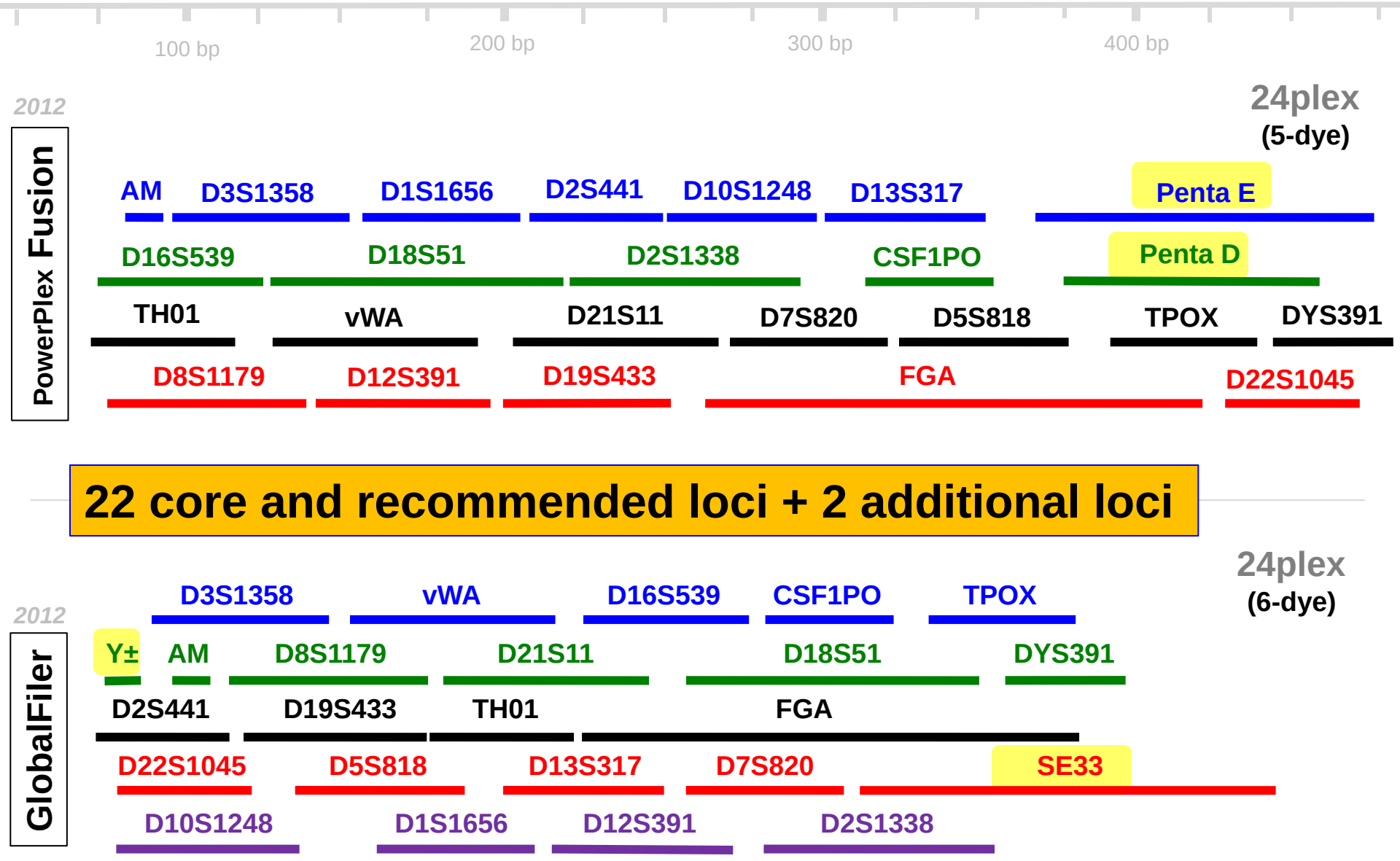
Chr	STR Locus	Repeat	Allele Range (Butler et al. 2012)	CODIS 13 (US 1997-present)	CODIS 20 (US future)	ESS 12 (EU 2009-present)
				required		
1q31	F13B	AAAT	6 to 11			
1q42	D1S1656	TAGA	10 to 19.3		■	■
2p25.3	**TPOX**	AATG	5 to 13	■		
2p14	D2S441	TCWA	8 to 17		■	■
2q35	D2S1338	TKCC	15 to 27		■	
3p21.31	**D3S1358**	TCTR	11 to 20	■	■	■
4q31.3	**FGA**	YTYY	16.2 to 43.2	■	■	■
5q23.2	**D5S818**	AGAT	7 to 15	■	■	
5q33.1	**CSF1PO**	AGAT	7 to 15	■	■	
6p24	F13A01	AAAG	3.2 to 17			
6q14	SE33	AAAG	6.3 to 36			
6q15	D6S1043	AGAY	8 to 26			
7q21.11	**D7S820**	GATA	6 to 14	■	■	
8p22	LPL	AAAT	7 to 15			
8q24.13	**D8S1179**	TCTR	8 to 18	■	■	■
9p13	Penta C	AAAAC	5 to 16			
10q26.3	D10S1248	GGAA	8 to 19		■	■
11p15.5	**TH01**	TCAT	5 to 11	■	■	■
12p13.31	**vWA**	TCTR	11 to 21	■	■	■
12p13.2	D12S391	AGAY	14 to 27		■	■
13q31.1	**D13S317**	TATC	8 to 15	■	■	
15q25	FESFPS	ATTT	5 to 14			
15q26.2	Penta E	AAAGA	5 to 25			
16q24.1	**D16S539**	GATA	5 to 15	■	■	
18q21.33	**D18S51**	AGAA	9 to 28	■	■	■
19q12	D19S433	WAGG	9 to 18.2		■	
21q21.1	**D21S11**	TCTR	24.2 to 39	■	■	■
21q22.3	Penta D	AAAGA	2.2 to 17			
22q12.3	D22S1045	ATT	8 to 19			■
Xp, Yp	Amelogenin	--	--		■	
Yq11.21	DYS391	TCTA	7 to 13		■	

Promega STR kits						
PowerPlex 16 (HS)	PowerPlex 18D	PowerPlex ESI/ESX 16	PowerPlex ESI/ESX 17	PowerPlex 21	PowerPlex CS7	**PowerPlex Fusion**
					■	
		■	■	■		■
■	■			■		■
		■	■			■
	■	■	■	■		■
■	■	■	■	■		■
■	■	■	■	■		■
■	■			■		■
■	■			■		■
					■	
			■			
				■		
■	■			■		■
					■	
■	■	■	■	■		■
					■	
		■	■	■		■
■	■	■	■	■		■
■	■	■	■	■		■
		■	■	■		■
■	■			■	■	
					■	
					■	
■	■	■	■	■		■
■	■	■	■	■		■
		■	■	■		■
■	■	■	■	■		■
					■	
		■	■	■		■
■	■	■	■	■		■
					■	
■	■	■	■	■		■

Life Technologies (ABI) STR kits										
Profiler Plus	COfiler	SGM Plus	SEfiler Plus	SinoFiler	MiniFiler	**Identifiler (Plus)**	VeriFiler	NGM	NGM SElect	**GlobalFiler**
							■	■	■	■
	■					■				■
							■	■	■	■
		■	■	■	■	■	■	■	■	■
■		■	■	■		■		■	■	■
■		■	■	■	■	■		■	■	■
	■			■	■	■				■
			■						■	■
				■			■			
■	■			■	■	■				■
■		■	■	■		■		■	■	■
							■	■	■	■
	■	■	■			■	■	■	■	■
■		■	■	■		■		■	■	■
				■			■	■	■	■
					■	■				■
	■	■	■	■	■	■		■	■	■
■		■	■	■	■	■		■	■	■
		■	■	■	■	■	■	■	■	■
							■	■	■	■
										■

Qiagen STR kits					
ESSplex	ESSplex SE	Hexaplex ESS	Nonaplex ESS	Decaplex SE	IDplex
■	■	■	■		
					■
■	■	■	■		
■	■			■	■
■	■		■	■	■
■	■		■	■	■
					■
					■
	■		■	■	
					■
■	■		■	■	■
■	■			■	■
■	■		■	■	■
■	■			■	■
■	■	■	■		
■	■		■	■	■
■	■			■	■
■	■	■	■		
■	■			■	■
■	■	■	■		
					■

STR Marker Layouts for New U.S. Kits

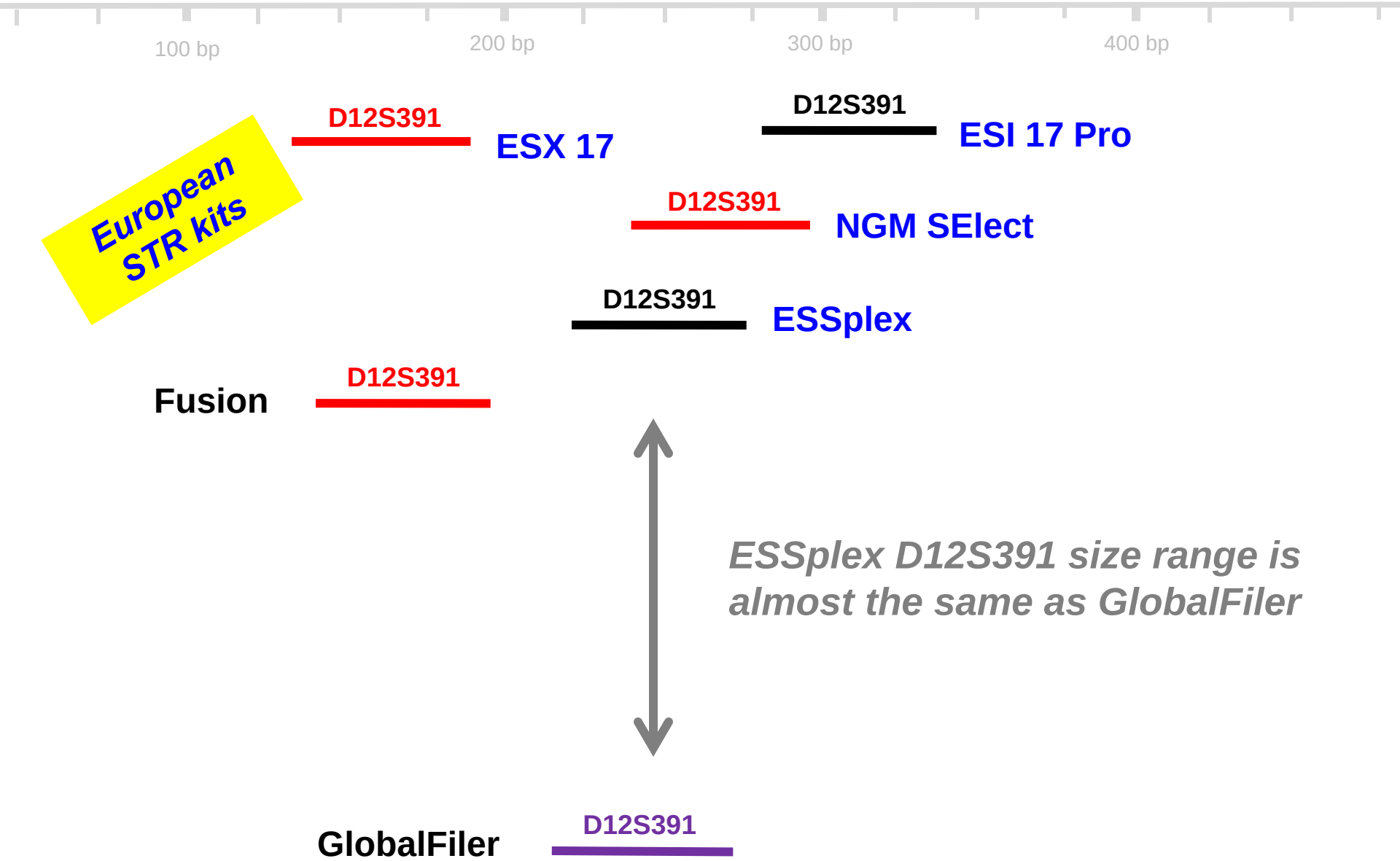


Information on “New” STR Loci

STR Locus	Chromosomal Location	Physical Position	Repeat Motif	Ladder Range
D1S1656	1q42	Chr 1 230.905 Mb	compound TAGA	10 to 19.3
D2S441	2p14	Chr 2 68.239 Mb	compound TCTA/TCAA	8 to 17
SE33	6q14 beta-actin related pseudogene	Chr 6 88.987 Mb	complex AAAG	6.3 to 36
D10S1248	10q26.3	Chr 10 131.093 Mb	simple GGAA	8 to 19
D12S391	12p13.2	Chr 12 12.450 Mb	compound AGAT/AGAC	**14 to 27**
D22S1045	22q12.3	Chr 22 37.536	simple ATT	8 to 19

Butler, J.M., & Hill, C.R. (2013) *Topics on Forensic DNA Analysis: Current Practices and Emerging Technologies* (CRC Press). Chapter 9. Biology and Genetics of New Autosomal STR Loci Useful for Forensic DNA Analysis, pp. 181-196

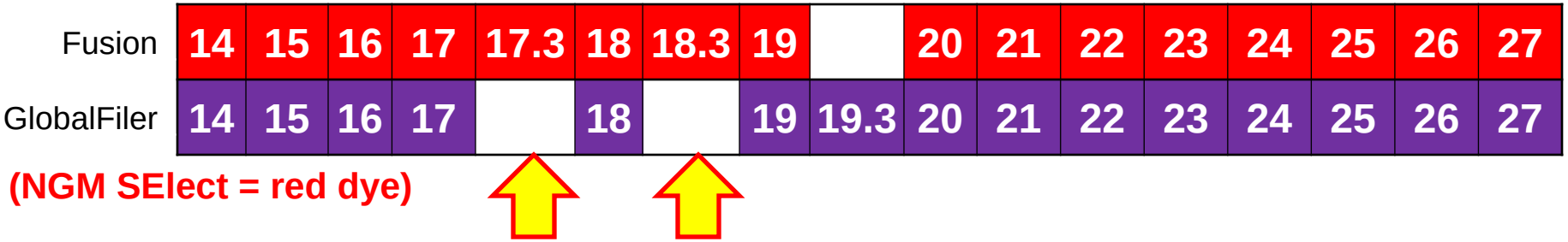
Relative Positions of D12S391



STR Locus **D12S391 "Variant" Alleles**

What is defined as a variant (or off-ladder) allele by a laboratory is typically based on alleles present in STR kit allelic ladder

Allelic Ladder Alleles



D12S391 variant alleles (126 total) reported so far in STRBase

(data provided based on **123 NGM SElect**, 1 ESI16, 1 NGM, and 1 PP21)

As of Feb 2013

Variant	# times		Variant	# times
16.1	1x		19.1	1x
17.1	2x		20.1	2x
17.3	**43x**		20.3	2x
18.1	3x		21.3	1x
18.3	**66x**		28	1x

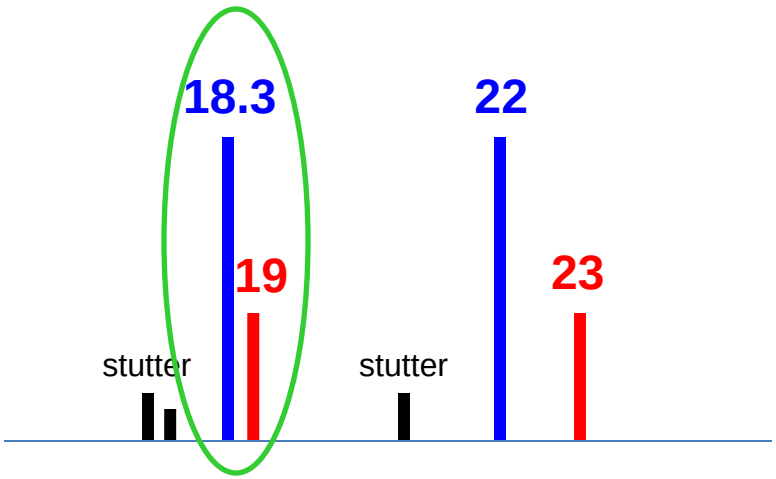
<u>1 tri-allele reported</u>

17,19,20

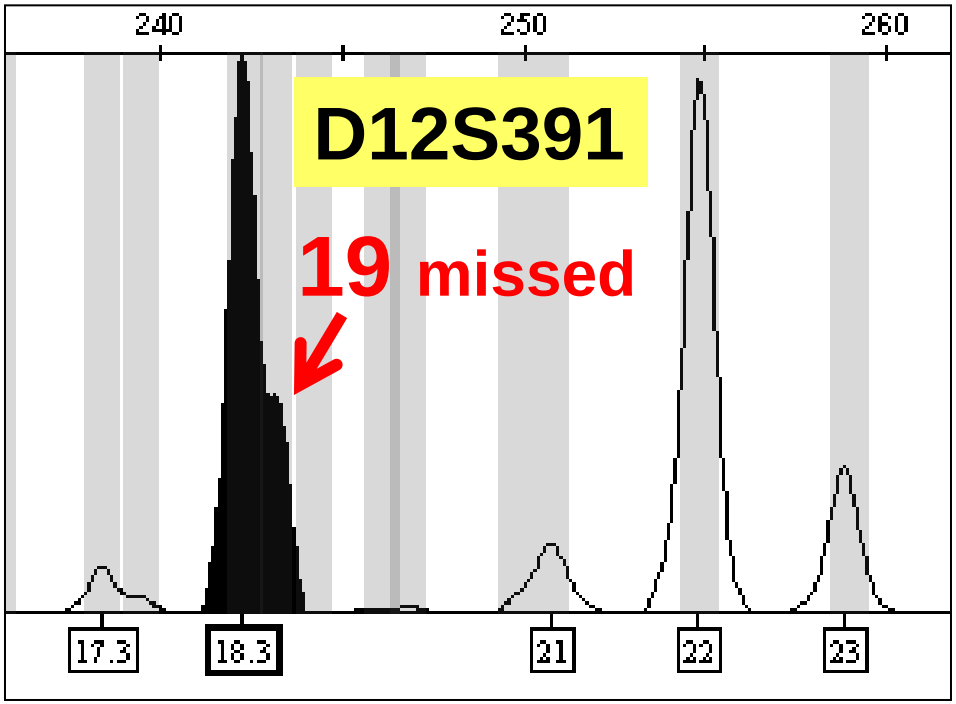
Sinofiler (China)

NIST SRM 2391c Component D

Provides a Single Base Resolution Challenge



ESSplex (Qiagen Investigator kit)



Resolution challenges exist with D12S391 alleles 18.3 and 19, which differ by a single nucleotide; resolution can be impacted by the size of the PCR products in the specific STR kit and electrophoresis conditions (especially run voltage and polymer concentration)

NIST U.S. Population Data

- We have analyzed **1036 unrelated samples** with **29 autosomal STRs and 23 Y-STRs** (all current STR and Y-STR kit loci)

- Becky Hill and Mike Coble have described this data set in their presentations

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

D12S391
NIST U.S. Allele Frequencies

From NIST 1036 data set (Butler et al. 2012 *Profiles in DNA*)

	Total		Populations, %			
Allele	#	%	AfAm	Asian	Cauc	Hisp
14	1	0.0	0.1			
15	105	5.1	7.7	4.1	3.2	4.4
16	84	4.1	6.7	1.0	2.2	4.2
17	258	12.5	16.7	8.2	12.7	7.6
17.1	3	0.1	0.4			
17.3	**26**	1.3	0.4		**2.1**	1.7
18	**432**	20.8	25.3	26.3	17.2	17.8
18.1	1	0.0	0.1			
18.3	**27**	1.3	0.4		**2.5**	1.3
19	**314**	15.2	14.8	17.5	12.5	18.9
19.1	7	0.3	0.9			0.2
19.3	**10**	0.5	0.4	0.5	0.4	0.6
20	**262**	12.6	10.4	19.6	11.1	15.5
20.1	2	0.1	0.3			
20.3	1	0.0				0.2
21	209	10.1	6.4	9.8	12.9	11.2
22	137	6.6	3.7	5.7	9.6	6.8
22.2	1	0.0				0.2
23	102	4.9	2.9	2.6	6.9	5.7
24	53	2.6	1.3	1.0	4.7	1.7
24.3	1	0.0		0.5		
25	24	1.2	0.9	1.5	1.7	0.6
26	7	0.3		1.0	0.3	0.6
27	5	0.2		0.5	0.1	0.6

Theoretical heterozygotes (2pq)

2 x 0.013 x 0.208 = **0.54%** (17.3,18)
2 x 0.013 x 0.152 = **0.40%** (18.3, 19)

Observed heterozygotes with a single nucleotide difference

9 out of 1036 = 0.87%

17, 17.1
17.3, 18 (3x)
18, 18.1
18.3, 19 (2x)
19, 19.1
19.3, 20

Hill, C.R., et al. (2013) U.S. population data for 29 autosomal STR loci. *Forensic Sci. Int. Genet.* 7: e82-e83

Variant STR Allele Sequencing

Margaret Kline

Main Points:

- **STR allele sequencing has been provided free to the community** for the past ten years thanks to NIJ-funding
- Article provides primer sequences (outside of all known kit primers) for 23 autosomal STRs & 17 Y-STRs and full protocol for gel separations and sequencing reactions
  - 111 normal and variant alleles sequenced (at 19 STR & 4 Y-STRs)
  - 17 null alleles sequenced (with impact on various STR kit primers)

Contents lists available at ScienceDirect

Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsig

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

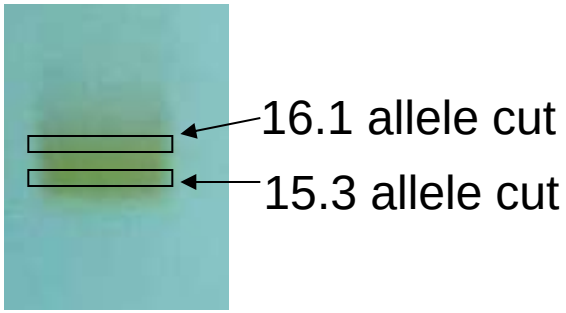
Presentations/Publications:

- FSI Genetics article (Aug 2011) and numerous talks

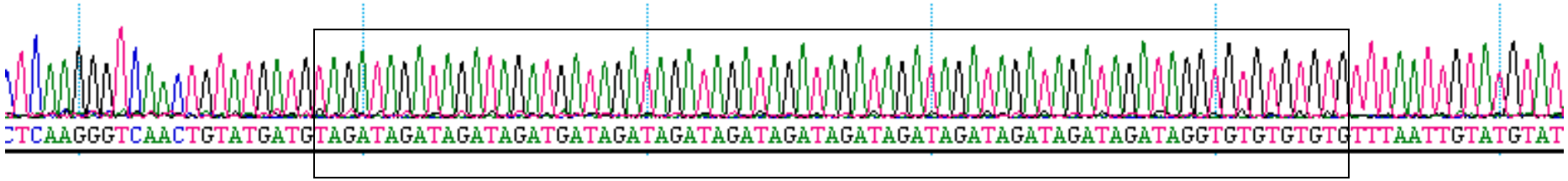
D1S1656 Variants

Submitted by Kerstin Montelius
Analyzed by Margaret Kline (May 11, 2011)

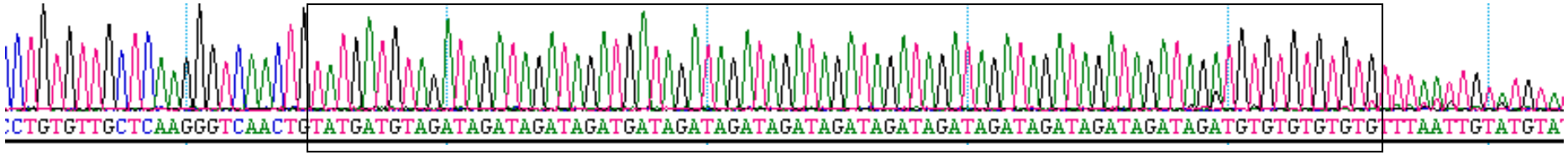
Silver-stained gel



Allele 15.3: $[TAGA]_4$ TGA $[TAGA]_{10}$ TAGG $[TG]_5$

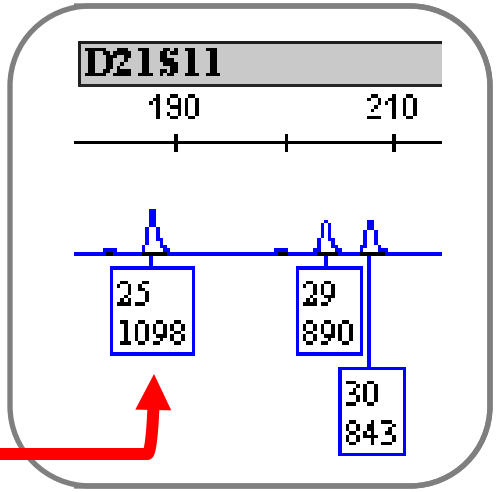


Allele 16.1: $[TAGA]_4$ TGA $[TAGA]_{11}$ $[TG]_6$

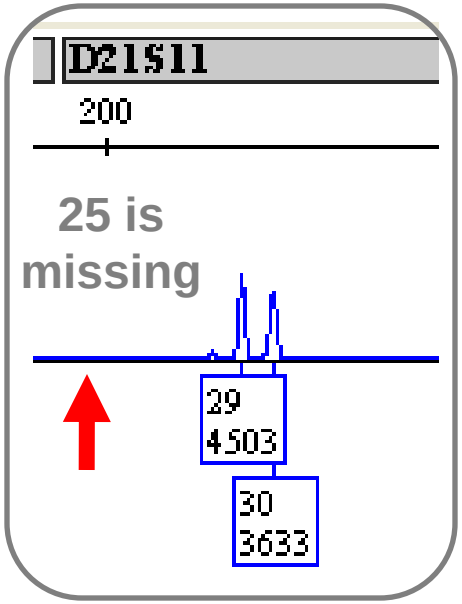


How Do You Characterize Your Tri-Allelic Patterns?

Identifiler

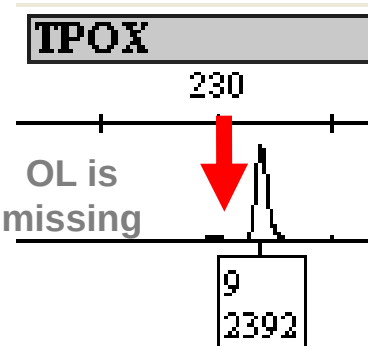


PowerPlex 16 HS

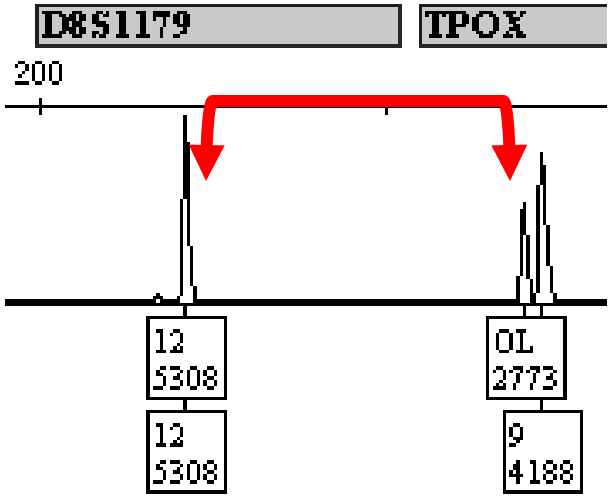


You re-amplify it…
It's Reproducible!

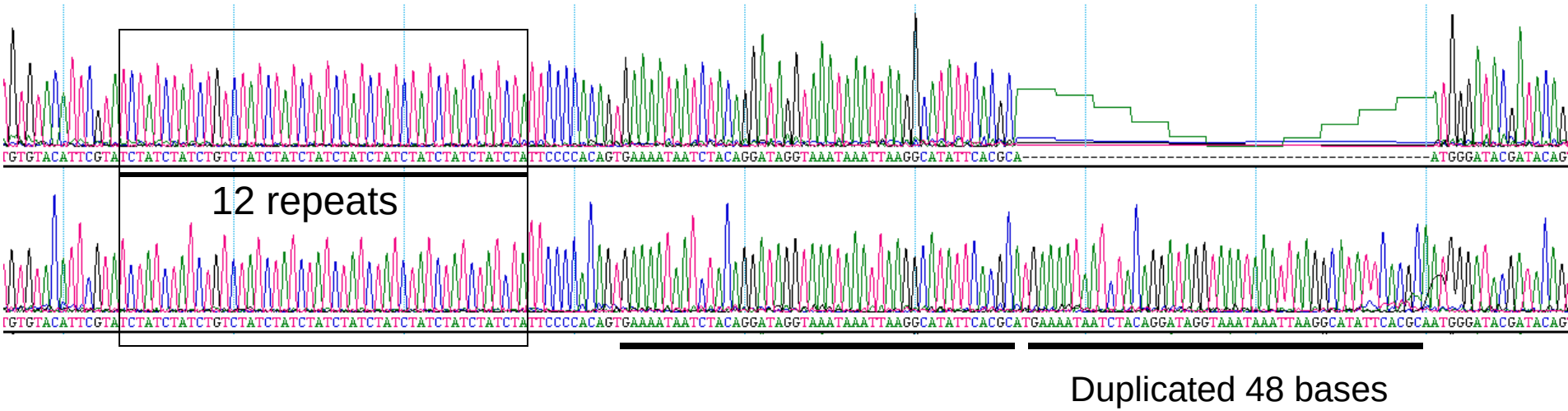
Check STRBase…
It has never been observed before!



A New Large D8S1179 Allele is Discovered – with "24" repeats!
(sequence analysis shows duplication in flanking region)



D8S1179 12,“24”



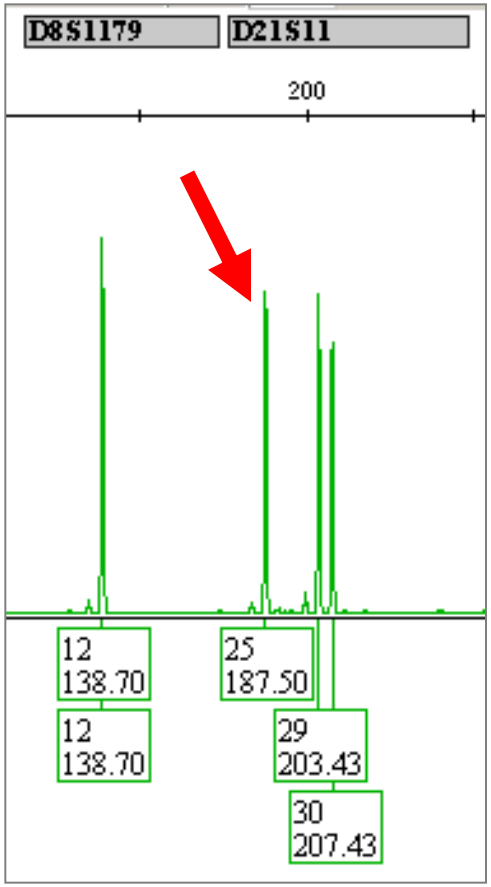
Allele 12 : $[TCTA]_2$ TCTG $[TCTA]_9$

Allele “24” : $[TCTA]_2$ TCTG $[TCTA]_9$ **duplication of the 48 bases 10 bases downstream of the repeat**

Result with This Large D8S1179 Allele

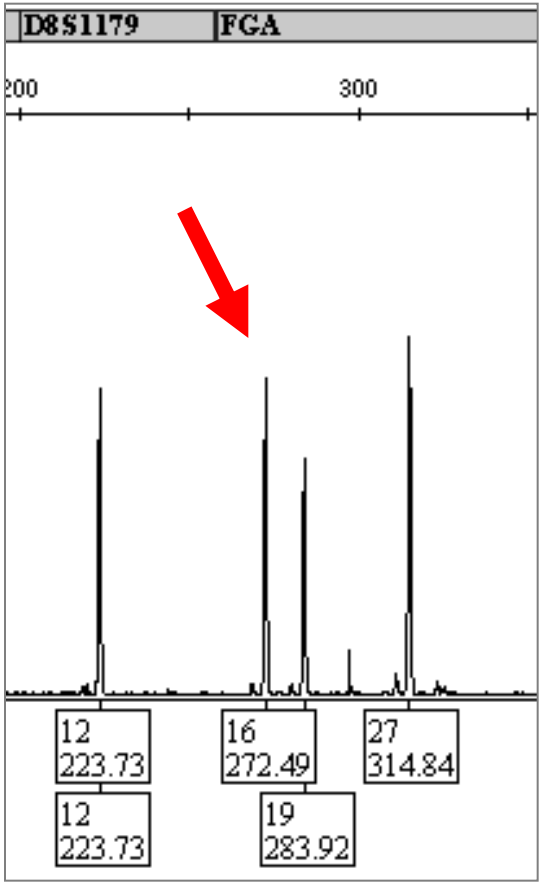
Using European STR Kits

NGM SElect



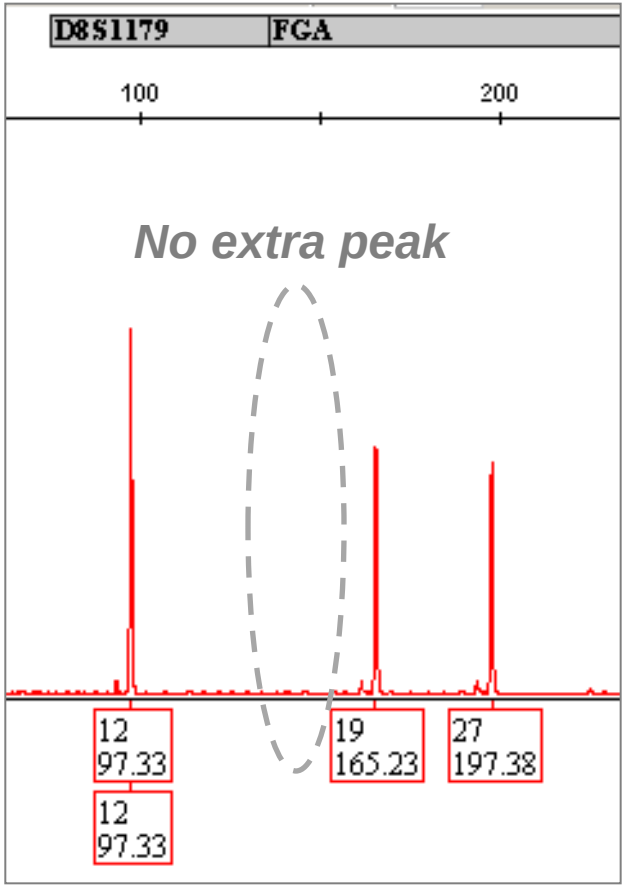
False D21S11 tri-allele

PP ESX 17



False FGA tri-allele

PP ESI 17



Reverse primer internal to duplicated flanking region

Comparison of Allelic Ladder Alleles

D1S1656

Fusion	9	10	11	12	13	14	14.3	15	15.3	16	16.3	17	17.3	18	18.3	19	19.3	20.3
GlobalFiler	9	10	11	12	13	14	14.3	15	15.3	16	16.3	17	17.3		18.3		19.3	20.3

D8S1179

Fusion			7	8	9	10	11	12	13	14	15	16	17	18	19
GlobalFiler	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19

D16S539

Fusion	4	5	6	7	8	9	10	11	12	13	14	15	16
GlobalFiler		5			8	9	10	11	12	13	14	15	

DYS391

Fusion	5	6	7	8	9	10	11	12	13	14		16
GlobalFiler			7	8	9	10	11	12	13			

More Allelic Ladder Allele Comparisons

D2S441

Fusion	8	9	10	11	11.3	12	13	14	15	16	17
GlobalFiler	8	9	10	11	11.3	12	13	14	15	16	17

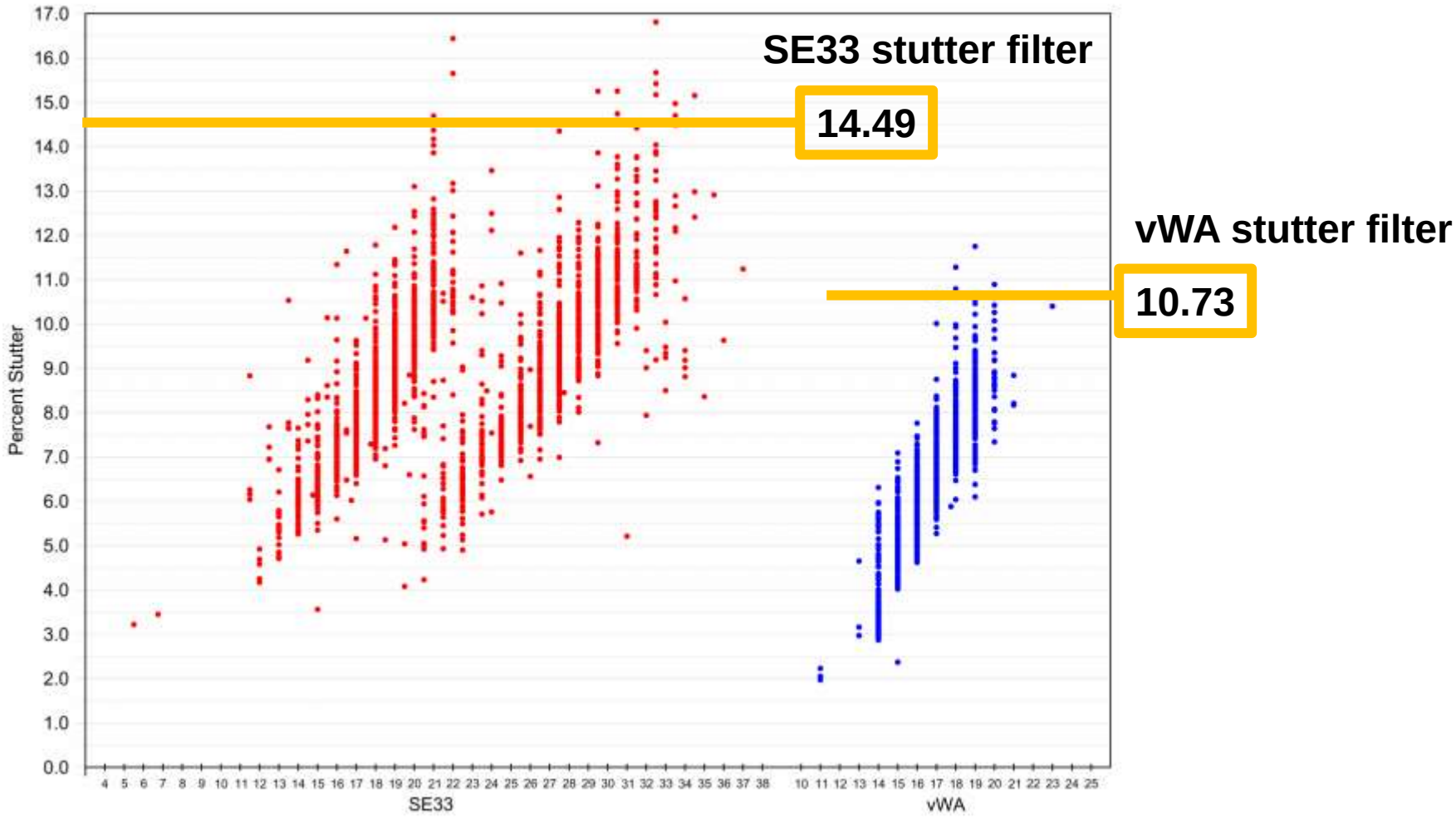
D10S1248

Fusion	8	9	10	11	12	13	14	15	16	17	18	19
GlobalFiler	8	9	10	11	12	13	14	15	16	17	18	19

D22S1045

Fusion	7	8	9	10	11	12	13	14	15	16	17	18	19	20
GlobalFiler		8	9	10	11	12	13	14	15	16	17	18	19	

Stutter Observations vs Stutter Filters



Data from GlobalFiler Kit User Manual, p. 79

Recent NIST Publications on “New” STR Loci

1. Hill, C.R., Duewer, D.L., Kline, M.C., Sprecher, C.J., McLaren, R.S., Rabbach, D.R., Krenke, B.E., Ensenberger, M.G., Fulmer, P.M., Stort, D.R., Butler, J.M. (2011) Concordance and population studies along with stutter and peak height ratio analysis for the PowerPlex® ESX 17 and ESI 17 Systems. *Forensic Sci. Int. Genet.* 5(4): 269-275.

2. O’Connor, K.L., Hill, C.R., Vallone, P.M., Butler, J.M. (2011) Linkage disequilibrium analysis of D12S391 and vWA in U.S. population and paternity samples. *Forensic Sci. Int. Genet.* 5(5): 538-540.

3. Butler, J.M., Hill, C.R., Kline, M.C., Bastisch, I., Weirich, V., McLaren, R.S., Storts, D.R. (2011) SE33 variant alleles: sequences and implications. *Forensic Sci. Int. Genet.: Suppl. Ser.* 3: e502-e503.

4. Butler, J.M. and Hill, C.R. (2012) Biology and genetics of new autosomal STR loci useful for forensic DNA analysis. *Forensic Sci. Rev.* 24(1): 15-26.

5. Butler, J.M., Hill, C.R., Coble, M.D. (2012) Variability of new STR loci and kits in U.S. population groups. *Profiles in DNA*. Available at http://www.promega.com/resources/articles/profiles-in-dna/2012/variability-of-new-str-loci-and-kits-in-us-population-groups/.

6. Coble, M.D., Hill, C.R., Butler J.M. (2013) Haplotype data for 23 Y-chromosome markers in four U.S. population groups. *Forensic Sci. Int. Genet.* 7: e66-e68.

7. Hill, C.R., Duewer, D.L., Kline, M.C., Coble, M.D., Butler, J.M. (2013) U.S. population data for 29 autosomal STR loci. *Forensic Sci. Int. Genet.* 7: e82-e83.

8. Butler, J.M. and Hill, C.R. (2013) Biology and genetics of new autosomal STR loci useful for forensic DNA analysis. Chapter 9 in Shewale, J. (ed.), *Forensic DNA Analysis: Current Practices and Emerging Technologies*. Taylor & Francis/CRC Press: Boca Raton. pp. 181-198.

Additional Information Needed/Planned

- **Mutation rate information** to aid kinship analysis
  - More father/son studies are needed with D12S391, D1S1656, D2S441, D10S1248, and D22S1045
- A complete summary of **flanking region variation** and null alleles produced from primer binding site mutations
- Future plans for STRBase: listing of **full sequences for detected STR alleles** (repeats and flanking regions) to aid next-generation sequencing efforts
  - Will enable nomenclature and classification of sub-allele variation for STR markers

Summary

- The U.S. forensic DNA community will soon expand to additional STR loci and new kits are now available to help with this effort
- New information is being developed at NIST, published, and added to STRBase to aid understanding of these additional STR loci
- STRBase can be a model for other forensic disciplines in sharing information with the forensic science community

Acknowledgments

$ National Institute of Justice and NIST OLES

Becky Hill and Mike Coble (NIST Applied Genetics Group)
Jeff Nye (Michigan State Police)
Angelo Della Manna (Alabama DFS)

Contact info:

john.butler@nist.gov

+1-301-975-4049

Final version of this presentation will be available at:
http://www.cstl.nist.gov/strbase/NISTpub.htm