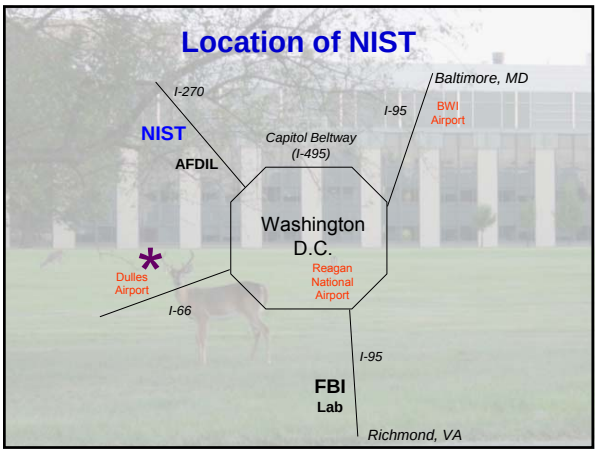
NIST Update

John M. Butler
and the Human Identity Project Team

National CODIS Conference
November 2, 2009
Reston, VA

Location of NIST



Presentation Outline

- Team Members and Outputs for the Past Year
- **Standards**
  - SRM 2391c: plans for next reference material
- **Technology**
  - Rapid PCR for DNA biometrics
  - New STR loci, assays, and kits evaluated
  - Variant alleles cataloged in STRBase
  - Low template DNA studies
- **Training**
  - Workshops and STRBase information available
  - New book: ***Fundamentals of Forensic DNA Typing***

NIST Human Identity Project Team

...Bringing traceability and technology to the scales of justice...

Becky Hill, John Butler, Margaret Kline, Amy Decker (aka Elvis), Pete Vallone


Jan Redman


Erica Butts


Dave Duewer

Funding from the **National Institute of Justice (NIJ)** through NIST Office of Law Enforcement Standards and the **FBI S&T Branch** for DNA Biometrics projects

Communication with the Community

Since the Nov 2008 CODIS Conference…

	Totals	John	Pete	Margaret	Becky	Amy
Presentations	**51**	32	8	4	4	3
Posters	**8**	2	3	1	1	1
Workshops	**11**	11	1			1
Totals	**70**	45	12	5	5	5

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

Applied Genetics

APPLIED GENETICS Group

Major Programs Currently Underway

- **Forensic DNA**
  - New loci and assays (26plex)
  - **STR kit testing**
  - Ancestry SNP assays
  - **Low-template DNA studies**
  - Mixture interpretation
  - STR nomenclature
  - **Variant allele cataloging** and sequencing
  - Expert systems review
  - Training workshops to forensic DNA laboratories
  - Validation information and **software tools**
  - **Textbook** – 3rd ed. (2 vol.)
- **Clinical Genetics**
  - CMV SRM
  - Huntington's SRM
- **Ag Biotech**
  - "universal" GMO detection/ quantitation (35S promoter)
- **DNA Biometrics**
  - **Rapid PCR** methods
  - Efforts to standardize testing of future portable DNA systems
  - Kinship analysis
- **Cell Line Authentication**

Looking for a Ph.D. to Expand Our Team

- **We are currently seeking a Ph.D. scientist to help with our forensic DNA and clinical DNA efforts**
- Please email me if you or someone you know may be interested: john.butler@nist.gov

Standards

NIST SRM 2391b will need to be replaced within the next year

SRM	Name	FY06	FY07	FY08	FY09	Avg	Remaining	Current $*
2372	Human DNA Quantitation Std	0	0	160	147	153.5	1,078	$372
2390	DNA Profiling	2	0	1	0	0.8	3	$833
2391B	PCR-Based DNA Profiling	86	81	125	140	108	107	$811
2392	Mitochondrial DNA Sequencing	8	6	0	12	6.8	165	$883
2392-I	Mitochondrial DNA Sequencing (Human HL-60 DNA)	6	32	20	19	19.3	176	$365
2395	Human Y-Chromosome DNA Profiling	34	39	72	88	58.3	136	$383

*As of Oct 7, 2009

Considering preparing DNA in different forms:
3 liquid samples
2 swabs
1 paper punch

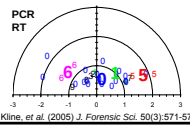
Plan to certify both autosomal and Y-STRs on SRM 2391c components

http://www.cstl.nist.gov/biotech/strbase/pub_pres/Promega2009poster_SRM2391c.pdf

SRM 2372:
Human DNA Quantitation Standard

Do NOT use Component C with Quantifiler Duo

- Released in Oct 2007
  - >300 units in use as of October 2009
- **Used by more than 110 forensic laboratories worldwide**
- Manuscript describing production published in *Anal. Bioanal. Chem.*
- **Serves to adjust qPCR calibrants supplied by manufacturers and adjust for assay-specific bias**



Kline, *et al.* (2005) *J. Forensic Sci.* 50(3):571-578

Technology

How fast can we go?
How large of a multiplex can we build?
Are there better loci to improve DNA testing?
Can we speed up validation of new STR kits?
How low can we go in terms of sensitivity?

Rapid PCR work published in *FSI Genetics* (Dec 2008)

Full STR profiles in 36 minutes (instead of 3 hour PCR)

Complete concordance of STR allele calls (for 60 samples) between the rapid and standard thermal cycling protocols were observed although there was incomplete adenylation at several of the loci examined and some PCR artifacts were detected. Using less than **750 pg of template DNA and 28 cycles, STR peaks for all loci were above a 150 relative fluorescent unit (RFU) detection threshold** with fully adequate inter-locus balance and heterozygote peak height ratios of greater than 0.84.

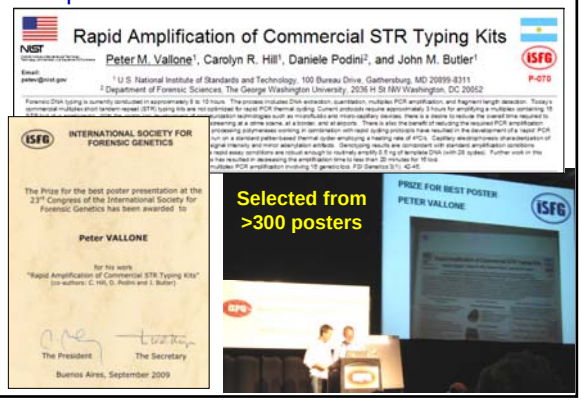
Pete Vallone has described additional work on rapid PCR in two recent posters

"Rapid Amplification of Commercial STR Typing Kits"

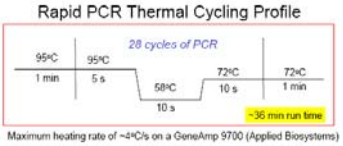
- **International Society of Forensic Genetics (ISFG)** meeting (Buenos Aires, Argentina), September 16-17, 2009
- **20th International Symposium on Human Identification** (Las Vegas, NV), October 13-14, 2009

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

Rapid PCR Work wins ISFG Poster Contest



Further Rapid PCR Work

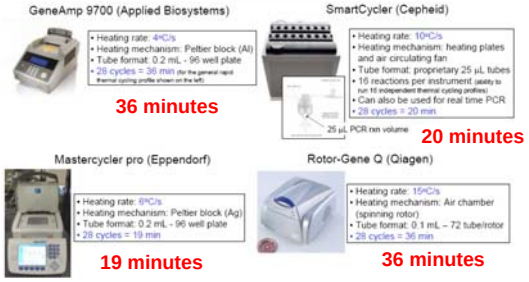


- **Much shorter hold times at each temperature**
- **Faster ramp rates between temperatures**

- **Examination of different enzyme mixes**
  - 0.5 x master mix PyroStart (Fermentas) ($0.14/rxn)
  - 0.5 x master mix Premix Ex Taq (Takara) ($0.22/rxn)
  - 0.25 µL = 1.25 units of SpeedStar (Takara) ($1.09/rxn)
- **Evaluation of additional kits**
  - Identifiler, PP16, Yfiler, MiniFiler and Promega S5
- **Testing thermal cyclers with faster ramp rates**

Four Thermal Cyclers Being Evaluated

How fast can we run 28 cycles?



http://www.cstl.nist.gov/biotech/strbase/pub_pres/VallonePromega2009poster.pdf

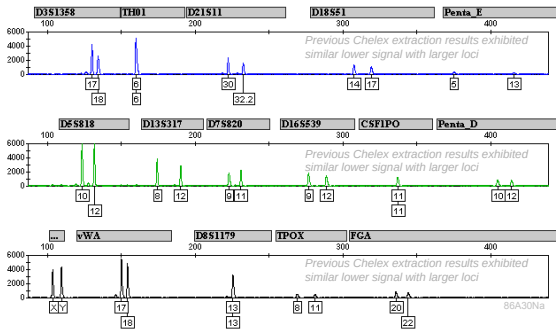
How Fast Can We Go?

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**

Direct PCR (no DNA extraction) using PP16 HS from a 23 year old blood stain (room temperature storage)



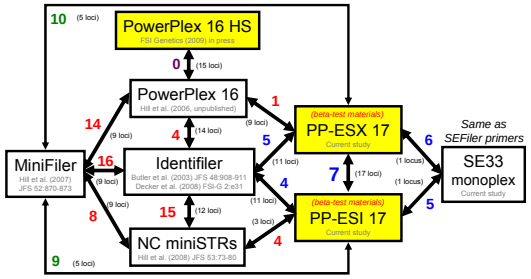
1.2 mm punch (untreated blood stain card S&S 903) and PP16 HS (28 cycles)

NIST Studies with New STR Kits

- Over the past year, our NIST team has worked with Promega to evaluate their new STR kits
  - **PowerPlex ESX 17 & ESI 17** - with new European loci
  - **PowerPlex 16 HS** – with new enzyme & buffer system
- **Concordance studies**, population data analysis, and additional validation information
- Plan to do similar studies with Applied Biosystems on their NGM and other new kits

Summary of Allele Discordance Observed

Number of Discordant Results Observed between Various STR Assays



Comparison made with 186 samples
Comparisons made with ~660 samples
Comparisons made with ~1120 samples
Comparisons made with ~1440 samples

Features of These New STR Kits

- **Improved sensitivity** ("turbo-charged engines")
  - New PCR buffer and polymerase master mix
  - Better fluorescent dye labels (5-dye chemistry)
- **Greater tolerance for PCR inhibitors**
  - New PCR buffer and polymerase master mix
- **Different primer sequences** for amplifying core STRs
  - **Requires concordance checks** to confirm no null alleles
- **Additional STR loci** with high heterozygosities to improve power of discrimination for entire profile
  - Addresses requirements for extended European Standard Set

PowerPlex® ESI 17 Population Data (N=1443)

Marker	Number of Alleles	Theoretical Genotypes	Genotypes Observed	Heterozygosity	PIC
Amelogenin	2	3	3	--	--
TH01	8	36	25	0.7479	0.7572
D3S1358	11	66	31	0.7493	0.7305
D22S1045	11	66	45	0.7548	0.7318
D2S441	15	120	47	0.7729	0.7499
D16S539	9	45	30	0.7791	0.7650
D10S1248	12	78	41	0.7805	0.7460
D8S1179	11	66	48	0.7971	0.7961
vWA	11	66	42	0.7999	0.7866
D19S433	16	136	83	0.8089	0.7984
D21S11	28	406	95	0.8296	0.8293
D12S391	24	300	120	0.8650	0.8651
FGA	29	435	111	0.8691	0.8598
D18S51	23	276	103	0.8698	0.8699
D2S1338	13	91	73	0.8726	0.8821
D1S1656	17	153	101	0.8837	0.8806
SE33	**58**	1711	**343**	**0.9377**	0.9426

SE33 (58 alleles observed)

343 genotypes observed
Heterozygosity = 0.9377

Allele	Total #	Total %	Af Am	Asian	Cauc	Hisp
6.3	2	0.1	0.2			
7	11	0.4	0.3		0.5	0.4
8	4	0.1	0.2			0.3
10.2	31	1.1	1.1		1.5	1.0
11	9	0.3	1.0			
11.2	85	2.9	5.1	0.2	2.5	2.4
12	10	0.3	0.4		0.4	0.3
13	102	3.5	3.9	1.2	3.9	3.9
13.2	8	0.3	0.3			0.7
14	144	5.0	4.8	4.7	4.0	6.7
14.2	5	0.2	0.3		0.1	0.1
15	2	0.1				0.3
15.2	205	7.1	9.3	4.0	6.2	7.3
16	1	0.0	0.1			
16.2	5	0.2	0.1		0.2	0.3
16.3	268	9.3	12.1	5.0	7.2	**11.0**
17	1	0.0			0.1	
17.2	250	8.7	**12.4**	6.2	6.6	8.0
17.3	8	0.3		0.2	0.4	0.4
18	216	7.5	10.9	9.2	5.4	4.8
18.3	20	0.7	0.3	1.2	1.1	0.3
19	108	3.7	4.6	6.7	2.4	2.7
19.2	48	1.7	1.1	1.7	2.4	1.3
20	42	1.5	1.3	1.7	1.5	1.3
20.2	65	2.3	0.4	3.2	3.8	1.9
21	12	0.4	0.6	1.0	0.2	0.1
21.2	91	3.2	2.2	4.2	4.3	2.1
22	1	0.0			0.1	
22.2	74	2.6	1.3	6.2	2.2	2.5
23	109	3.8	2.6	6.9	4.0	3.1
23.2	1	0.0	0.1			
24	163	5.6	6.1	5.2	4.3	7.1
24.2	1	0.0				0.1
25	225	7.8	4.3	**10.4**	**9.5**	8.6
25.2	2	0.1				0.3
26	2	0.1	0.1	0.2		
27	180	6.2	4.4	7.9	7.4	6.1
27.2	2	0.1	0.1		0.1	
28	1	0.0		0.2		
28.2	147	5.1	2.7	5.7	6.3	6.3
28.3	1	0.0		0.2		
29	1	0.0				0.1
29.2	111	3.8	1.6	3.2	5.8	4.6
29.3	3	0.1	0.1		0.2	
30	52	1.8	1.5	2.5	2.2	1.3
30.2	1	0.0			0.1	
31	25	0.9	0.4	0.7	1.3	0.9
31.2	2	0.1			0.1	0.1
32	11	0.4	0.3		0.5	0.4
32.2	9	0.3	0.3		0.7	
33	1	0.0			0.1	
33.2	1	0.0	0.1			
34	2	0.1	0.2			
34.2						
35						
36						

Software Tools to Support STR Kit Evaluation and Validation Studies

New NIST Software Tools
Developed by Dave Duewer (NIST)

From NIST STRBase Website:

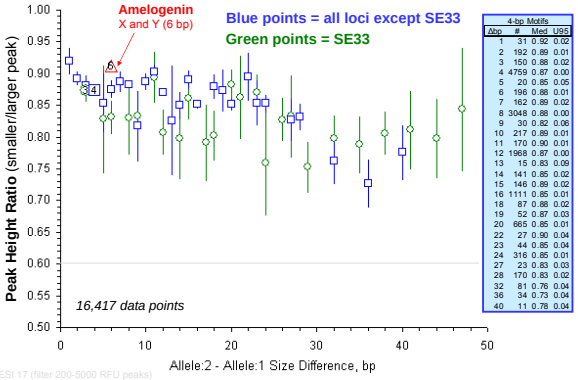
http://www.cstl.nist.gov/biotech/strbase/tools/STR_MatchSamples.xls

STR_MatchSamples
- An Excel-based tool developed to aid comparison of STR genotypes from two or more data sets.

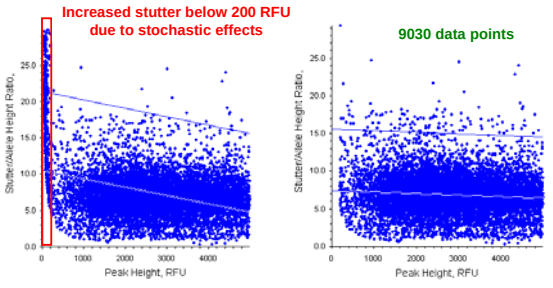
Tools under development
(to aid validation studies)
- Peak height ratio
- Inter-locus balance
- Stutter percentages
- Allele frequency

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

Peak Height Ratio as a Function of Allele Spread



PowerPlex® ESI 17 Stutter Ratios
by Peak Height across All Loci



Data filter applied
>50 RFU and <5000 RFU

Data filter applied
>200 RFU and <5000 RFU

Trinucleotide **D22S1045**
Allele-Specific Stutter Percentages

ESX 17

Allele	Size	Stutter #	Stutter Median
10	84.5	21	1.8
11	87.4	134	3.0
12	90.4	37	4.2
14	96.4	51	7.2
15	99.4	165	8.9
16	102.4	120	10.5
17	105.5	105	14.7
	Avg	633	7.2
	SD		4.6

633 data points

Avg + 3SD
21.0%

ESI 17

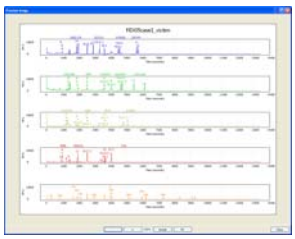
Allele	Size	Stutter #	Stutter Median
10	308.7	22	1.9
11	311.8	98	2.8
12	314.8	32	4.5
14	321.0	36	6.1
15	324.0	150	9.9
16	327.1	94	9.8
17	330.1	95	14.2
	Avg	527	7.0
	SD		4.4

527 data points

Avg + 3SD
20.2%

OSIRIS Software for STR Typing
Open Source Independent Review and Interpretation System

- Being developed at NCBI (NIH) by a team led by Lisa Forman
- Input: .fsa files
- Output: CODIS CMF
- Files are fully editable with audit trail
- Currently works with Identifiler, PP16, ProPlus, COfiler
- **NIST has supplied test data and feedback on performance**



Free download available at NCBI website:
http://www.ncbi.nlm.nih.gov/projects/SNP/osiris/

Variant Alleles

524 Variant Alleles on STRBase

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

524 total variants reported as of 10/26/2009

New Addition

[click on loci listed below for details]

Core STR Loci (363)	Other Common STR Loci (122)	Y-STR Loci (39)
• CSF1PO (20) • FGA (103) • TH01 (19) • TPOX (17) • VWA (13) • D3S1358 (21) • D5S818 (15) • D7S820 (26) • D8S1179 (21) • D13S317 (17) • D16S539 (21) • D18S51 (41) • D21S11 (32)	• D2S1338 (23) • D19S433 (27) • Penta D (37) • Penta E (30) • F13A01 (1) • FES/FPS (1) • F13B • LPL • SE33 (1) • D1S1677 (1) • D14S1434 (1)	• DYS19 (2) • DYS389I (2) • DYS389II (1) • DYS390 (2) • DYS391 • DYS392 (4) • DYS393 (1) • DYS385 a/b (16) • DYS438 (2) • DYS439 (4) • DYS437 (3) • DYS448 • DYS456 • DYS458 (2) • DYS635 (1) • Y-GATA-H4

Many New Y-STR Variants Being Reported by Missouri State Highway Patrol

DYS439 Variants

At time of submission had run over 41,000 samples!

To contribute to this table, click here

Allele Designation	Allele Size (bp)	Instrument	Amp Kit*	Contributor	Verification/Conformation Method(s)	Notes	Frequency
7 (<8)	194.26	ABI 3130xl	PPY	Jackie Johnson, MO State Hwy Patrol	redo sample		1 in 41635
10.1	207.20	ABI 3130xl	PPY	Jackie Johnson, MO State Hwy Patrol	redo sample		2 in 41635
11.1	211.22	ABI 3130xl	PPY	Jackie Johnson, MO State Hwy Patrol	redo sample		1 in 41635
16 (>15)	230.44	ABI 3130xl	PPY	Jackie Johnson, MO State Hwy Patrol	redo sample		1 in 41635

189 Tri-Allelic Patterns on STRBase

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

189 total patterns reported as of 10/20/2009

[click on loci listed below for details]

Core STR Loci (165)	Other Common STR Loci (23)	Y-STR Loci (1) duplications or triplications
• CSF1PO (7) • FGA (26) • TH01 (3) • TPOX (15) • VWA (20) • D3S1358 (7) • D5S818 (7) • D7S820 (1) • D8S1179 (11) • D13S317 (9) • D16S539 (8) • D18S51 (26) • D21S11 (19)	• D2S1338 (3) • D19S433 (3) • Penta D (6) • Penta E (11) • F13A01 • FES/FPS (1) • F13B • LPL • SE33	• DYS19 • DYS389I • DYS389II • DYS390 • DYS391 • DYS392 • DYS393 • DYS385 a/b • DYS438 • DYS439 • DYS437 • DYS448 • DYS456 (1) • DYS458 • DYS635/GATA-C4 • Y-GATA-H4

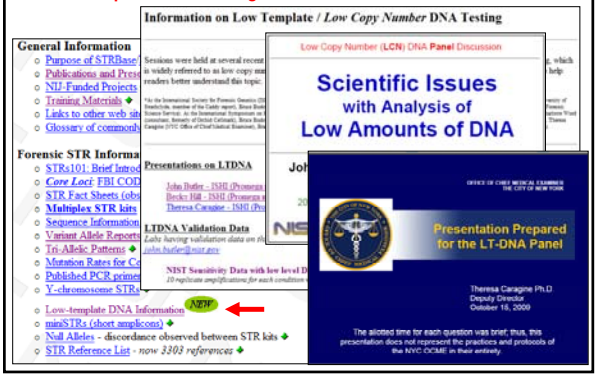
Low-Level DNA Studies

New Section of STRBase on This Issue

- Recently launched webpage
  - **http://www.cstl.nist.gov/biotech/strbase/LTDNA.htm**
  - Low-template DNA = LTDNA (not LCN!)
- The LTDNA section includes:
  - **Presentations from the Promega LCN Panel**
  - **Validation data from our sensitivity studies** to illustrate problems and consensus profile solution to low levels of DNA testing
  - **Literature listing of pertinent articles** to help explain the issues involved in this topic

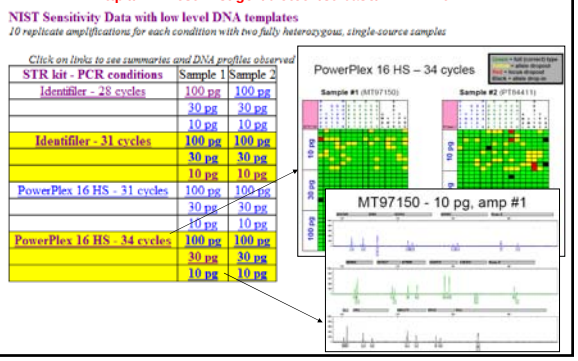
New STRBase Website on LT-DNA (LCN)

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



Complete Set of NIST Sensitivity Data Available on New LT-DNA Website

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

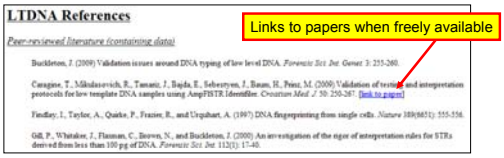


Literature Listing on LT-DNA (LCN)

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

Subdivided into categories

- Peer-reviewed literature *(containing data)*
- Reports *(evaluating the methodology)*
- Review articles *(commenting on other's data)*
- Non-peer reviewed literature *(representing the authors' opinions only)*

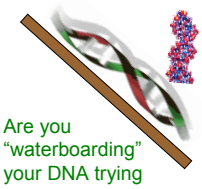


Framing the Issues

- Forensic science methods often **must work close to the edge** of a technique due to the limited nature of the evidence
  - perpetrators are usually not willing to go back and add more biological material to a crime scene…
- **Validation studies** are performed in order to **define the limits of a technique**
  - sensitivity studies to determine at what point a lab cannot obtain reliable results anymore

We would always like improved sensitivity to enable results where ever possible

"Enhanced Interrogation" Techniques to Improve Sensitivity



Are you "waterboarding" your DNA trying to get more information from the sample?

- **Increased PCR cycle number**
  With 100% efficiency:
  - 28 cycles = 67 million copies
  - 31 cycles = 1 billion copies (x16)
  - 34 cycles = 4 billion copies (x64)
- Reduced volume PCR
- Sample desalting (e.g., MinElute) prior to CE
- Extended CE injections

Requires validation to determine appropriate thresholds for reliability

Low Template DNA Testing

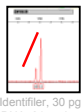
- **Every lab faces samples with low template DNA**
  - Do you choose to attempt an "enhanced interrogation technique" such as increasing the cycle number, desalting samples, etc.?
  - **Next generation kits coming from manufacturers are capable of greater sensitivity – will they be misused without appropriate caution and validation?**
- **At what point do you draw a line and not attempt to analyze data below this line?**
  - A certain amount of input DNA (based on what data?)
  - A pre-determined stochastic threshold (based on what data?)

Stochastic (Random) Effects with Low [DNA]

When Combined with Higher Sensitivity Techniques

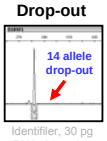
*Loss of True Signal (**False Negative**)*

Heterozygote Peak Imbalance



Identifiler, 30 pg DNA, 31 cycles

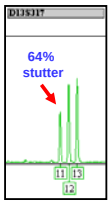
Allelic **Drop-out**



Identifiler, 30 pg DNA, 31 cycles

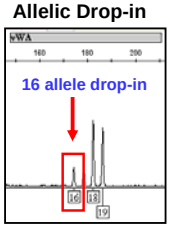
*Gain of False Signal (**False Positive**)*

Higher Stutter



Identifiler, 10 pg DNA, 31 cycles

Allelic Drop-in



Identifiler, 10 pg DNA, 31 cycles

Early Work on Replicate Testing with Low Levels of DNA

© 1996 Oxford University Press — Nucleic Acids Research, 1996, Vol. 24, No. 16 3189–3194

Reliable genotyping of samples with very low DNA quantities using PCR

Pierre Taberlet*, Sally Griffin, Benoit Goossens, Sophie Questiau, Valérie Manceau, Nathalie Escaravage, Lisette P. Waits and Jean Bouvet

Laboratoire de Biologie des Populations d'Altitude, CNRS UMR 5553, Université Joseph Fourier, BP 53, 38041 Grenoble Cedex 9, France

Received May 1, 1996; Revised and Accepted July 2, 1996

Replicate testing introduced (up to 7 times) to account for allele drop-out and avoid miscalling allele drop-in

ELSEVIER — Forensic Science International 112 (2000) 17–40 — Forensic Science International — www.elsevier.com/locate/forsciint

An investigation of the rigor of interpretation rules for STRs derived from less than 100 pg of DNA

Peter Gill[a,*], Jonathan Whitaker[a], Christine Flaxman[a], Nick Brown[a], John Buckleton[b]

[a]Forensic Science Service, Priory House, Gooch Street North, Birmingham B5 6QQ, UK
[b]ESR, Private Bag 92021, Auckland, New Zealand

Received 9 December 1999; received in revised form 12 February 2000; accepted 15 February 2000

In conjunction with interpretation rules, duplication of observed alleles in replicates was shown to correctly define the original sample

Comparison of Approaches

What "LCN Labs" Are Doing

Replicate Amplification with Consensus Profile

Low amount of DNA examined

↓ *Stochastic effects*

Amplification #1
Amplification #2
Amplification #3

Consensus Profile Developed
(from repeated alleles observed)

Interpretation Rules Applied
(based on validation experience)
e.g., specific loci may dropout more

Result can be and usually is Reliable & Reproducible

Single Amplification

Low amount of DNA examined

↓ *Stochastic effects*

Amplification #1
(only a single test)

Result can be Unreliable

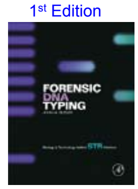
Individual results may vary but a consensus profile is reproducible (based on our experience with sensitivity studies and replicate amplifications)

Impact of "Unreliable" Results

- Allele drop-out can be dealt with using moderate stringency searches in CODIS algorithms
  - a homozygote "14" would hit to a heterozygote "11,14"
- **Allele drop-in is most problematic for DNA database searches**
  - **this can be corrected for with replicate testing and consensus profiles to eliminate incorrect alleles**

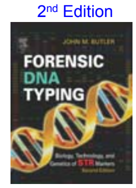
The Expansion of *Forensic DNA Typing*

1st Edition



Jan 2001
335 pp.
17 chapters

2nd Edition

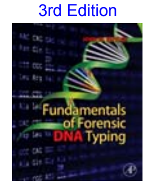


Feb 2005
688 pp.
24 chapters

Chinese Translation (2007) Y. Hou, translator

Japanese Translation (2009) Y. Fukuma, translator

3rd Edition



Sept 2009

Fundamentals
18 chapters (504 pp.)

Advanced Topics
25 chapters (~600 pp.)

Planned for Spring 2011

Improved Reference Format

***Forensic DNA Typing* (2nd Edition)**

Full list of authors but no article title

Lazaruk, K., Walsh, P.S., Oaks, F., Gilbert, D., Rosenblum, B.B., Menchen, S., Scheibler, D., Wenz, H.M., Holt, C. and Wallin, J. (1998) *Electrophoresis*, 19, 86–93.

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***Fundamentals* (3rd Edition)**

Subdivided by subject with article title provided

Instrument Platforms

ABI 373 and 377

Frazier, R. R. E., et al. (1996). Validation of the Applied Biosystems Prism™ 377 automated sequencer for forensic short tandem repeat analysis. *Electrophoresis*, 17, 1550–1552.

Fregeau, C. J., et al. (1999). Validation of highly polymorphic fluorescent multiplex short tandem repeat systems using two generations of DNA sequencers. *Journal of Forensic Sciences*, 44, 133–166.

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>1500 references total
(>600 new since 2nd edition)

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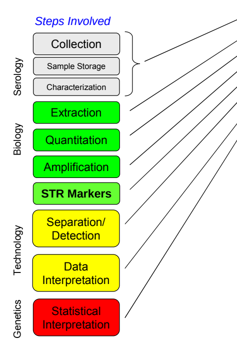
Butler, J. M., et al. (2004). Forensic DNA typing by capillary electrophoresis using the ABI Prism 310 and 3100 genetic analyzers for STR analysis. *Electrophoresis*, 25, 1397–1412.

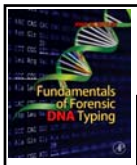
Lazaruk, K., et al. (1998). Genotyping of forensic short tandem repeat (STR) systems based on sizing precision in a capillary electrophoresis instrument. *Electrophoresis*, 19, 86–93.

Chapters Re-ordered to Reflect DNA Testing Process



***Fundamentals of Forensic DNA Typing* (2009)**

References are provided at the end of each chapter by subtopic (but without direct citation within the text).



Written as Part of My Job at NIST
(no royalties to be received)

Fundamentals of Forensic DNA Typing

John M. Butler

National Institute of Standards and Technology
Gaithersburg, Maryland, USA

Contribution of the National Institute of Standards and Technology, 2010

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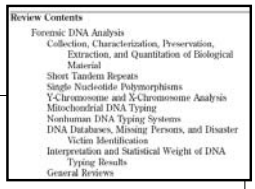
Entire book was subjected to NIST review process for approval prior to publication

Forensic Science Review Article

June 15, 2009 issue of *Analytical Chemistry*



Review Contents
Forensic DNA Analysis
Collection, Characterization, Preservation, Extraction, and Quantitation of Biological Material
Short Tandem Repeats
Single Nucleotide Polymorphisms
Y-Chromosome and X-Chromosome Analysis
Mitochondrial DNA Typing
Nonhuman DNA Typing Systems
DNA Databases, Missing Persons, and Disaster Victim Identification
Interpretation and Statistical Weight of DNA Typing Results
General Reviews

Anal. Chem. **2009**, *81*, 4695–4711

Forensic Science

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2009 review article covers 160 DNA articles published in 2007-2008

Overview of NIST Efforts

Communication with the Community

Other Genetic Markers & Software

DNA Biometrics (rapid PCR)

International Impact (European loci/kits)

STRBase Resources and SRMs

Thank you for your attention!

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Margaret Kline
STR allele sequencing

Jan Redman
Variant allele cataloging

Becky Hill
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Amy Decker
Mixtures & Y-STRs

Pete Vallone
Rapid PCR, SNPs, & DNA Biometrics

Erica Butts
DNA Biometrics

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