EDNAP and 32th ENFSI DNA WG Meeting
April 13-15, 2010 – The Hague, The Netherlands

NIST Update

John M. Butler
and the NIST Human Identity Project Teams
National Institute of Standards and Technology
Gaithersburg, Maryland USA

APPLIED GENETICS Group

Applied Genetics

Major Programs Currently Underway

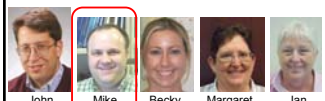
- **Forensic DNA**
  - New loci and assays (26plex)
  - **STR kit testing**
  - Ancestry SNP assays
  - **Low-template DNA studies**
  - Mixture interpretation
  - STR nomenclature
  - **Variant allele cataloging** and sequencing
  - Expert systems review
  - Training workshops to forensic DNA laboratories
  - 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**

Topics to Address

- NIST Team Members and Projects
- SWGDAM STR Interpretation Guidelines
- Concordance studies with ESX/ESI and NGM kits
- Potential linkage with D12S391 and vWA
- Cell line authentication using STR markers
- Low template DNA work
- Rapid PCR & DNA biometrics work
- *Fundamentals* book published *& Advanced Topics* book underway

NIST Human Identity Project Teams
within the Applied Genetics Group

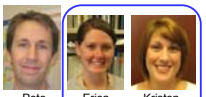
Forensic DNA Team



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

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

Data Analysis Support

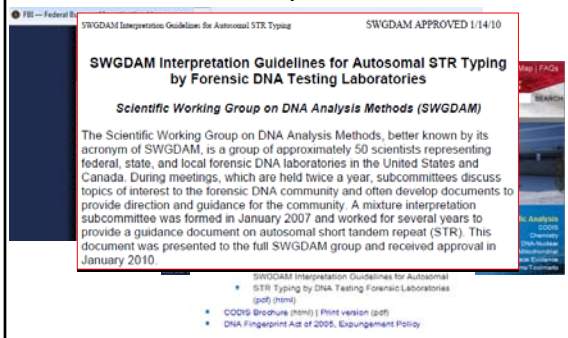
Dave Duewer

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

New Staff and Projects
Erica Butts – DNA extraction
Kristen Lewis - kinship analysis

Amy Decker left for AFDIL in Nov 2009

SWGDAM STR Interpretation Guidelines Completed & Released



SWGDAM Interpretation Guidelines for Autosomal STR Typing — SWGDAM APPROVED 1/14/10

SWGDAM Interpretation Guidelines for Autosomal STR Typing by Forensic DNA Testing Laboratories

Scientific Working Group on DNA Analysis Methods (SWGDAM)

The Scientific Working Group on DNA Analysis Methods, better known by its acronym of SWGDAM, is a group of approximately 50 scientists representing federal, state, and local forensic DNA laboratories in the United States and Canada. During meetings, which are held twice a year, subcommittees discuss topics of interest to the forensic DNA community and often develop documents to provide direction and guidance for the community. A mixture interpretation subcommittee was formed in January 2007 and worked for several years to provide a guidance document on autosomal short tandem repeat (STR). This document was presented to the full SWGDAM group and received approval in January 2010.

http://www.fbi.gov/hq/lab/html/codis_swgdam.pdf

All Statistical Approaches Are Considered

Table 1 – Suitable Statistical Analyses for DNA Typing Results
The statistical methods listed in the table cannot be combined into one calculation. For example, combining RMP at one locus with a CPI calculation at a second locus is not appropriate. However, an RMP may be calculated for the major component of a mixture and a CPE/CPI for the entire mixture (as referred to in section 4.6.2).

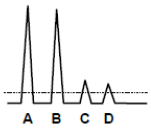
Category of DNA Typing Result	RMP	CPE/CPI	LR (1)
Single Source	✔		✔
Single Major Contributor to a Mixture	✔		✔
Multiple Major Contributors to a Mixture	✔ (2)	✔ (2)	✔
Single Minor Contributor to a Mixture	✔	✔ (3)	✔
Multiple Minor Contributors to a Mixture	✔ (2)	✔ (3)	✔
Indistinguishable Mixture	✔ (1)	✔	✔

(1) Restricted or unrestricted
(2) Restricted
(3) All potential alleles identified during interpretation are included in the statistical calculation

http://www.fbi.gov/hq/lab/html/codis_swgdam.pdf

Restricted vs Unrestricted

Are relative peak heights considered?



Unrestricted

All combinations of alleles are deemed possible (relative peak height differences are not utilized)

AB + AC + AD + BC + BD + CD

Restricted

Based on relative peak heights, alleles are paired only where specific combinations of alleles are deemed possible

AB + ~~AC~~ + ~~AD~~ + ~~BC~~ + ~~BD~~ + CD

Figure 1. Illustration of "restricted" versus "unrestricted" approaches based on relative peak heights (using an assumption of two donors with all peaks above the stochastic threshold).

http://www.fbi.gov/hq/lab/html/codis_swgdam.pdf

Evaluation of New European STR Loci

- U.S. population data collected using multiple kits
  - Examined **U.S. population data from 1443 individuals** (Caucasian, African American, Hispanic, Asian)
  - **PowerPlex ESX 17 & ESI 17 Systems (Promega)**
  - **AmpFlSTR NGM Kit (Applied Biosystems)**
- Linkage analysis of vWA and D12S391
  - Located 6.3 Mb apart on chromosome 12
  - With unrelated individuals, no significant linkage in agreement with Phillips, C., et al. (2010)
  - **With related individuals, linkage observed**
  - Recommending use of diplotypes with relatives – see Lewis, K.E., et al. (submitted)

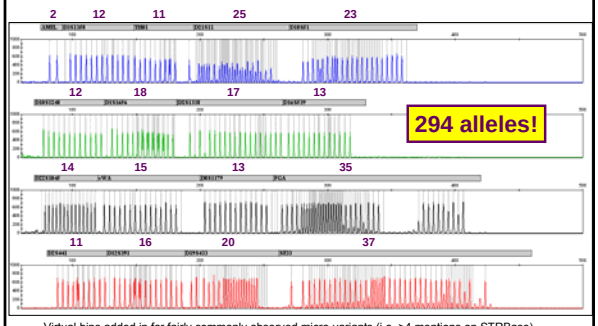
STR Loci Present in Commercial Kits

U.S.			Europe			
PP16	Identifiler	MiniFiler	ESX/ESI17	NGM	SEfiler	SGM Plus
TPOX	TPOX					
CSF1PO	CSF1PO	CSF1PO				
D5S818	D5S818					
D7S820	D7S820	D7S820				
D13S317	D13S317	D13S317				
FGA	FGA	FGA	FGA	FGA	FGA	FGA
vWA	vWA		vWA	vWA	vWA	vWA
D3S1358	D3S1358		D3S1358	D3S1358	D3S1358	D3S1358
D8S1179	D8S1179		D8S1179	D8S1179	D8S1179	D8S1179
D18S51	D18S51	D18S51	D18S51	D18S51	D18S51	D18S51
D21S11	D21S11	D21S11	D21S11	D21S11	D21S11	D21S11
TH01	TH01		TH01	TH01	TH01	TH01
D16S539	D16S539	D16S539	D16S539	D16S539	D16S539	D16S539
	D2S1338	D2S1338	D2S1338	D2S1338	D2S1338	D2S1338
	D19S433		D19S433	D19S433	D19S433	D19S433
			D12S391	D12S391		
			D1S1656	D1S1656		
			D2S441	D2S441		
			D10S1248	D10S1248		
			D22S1045	D22S1045		
			SE33		SE33	
Penta D						
Penta E						

U.S. is looking to expand the core loci (18-20 total)
to provide more international overlap

New STR Kits: Analysis and Concordance

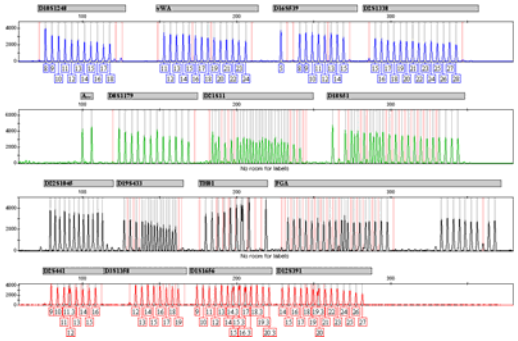
PowerPlex® ESX 17 Allelic Ladders



Virtual bins added in for fairly commonly observed micro-variants (i.e. >4 mentions on STRBase)

ESX/ESI 17 kits provided by Promega Corporation

AmpFlSTR® NGM Allelic Ladders



NGM kits provided by Applied Biosystems

Summary of NIST Samples Evaluated

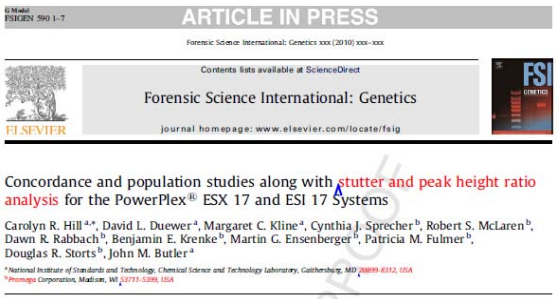
- **U.S. Population Samples** (**657 samples**)
  - Previously studied with Identifiler, MiniFiler, Yfiler, PP16, miniSTRs, and many additional assays *(>200,000 allele calls)*
  - 260 African Americans, 260 Caucasians, 140 Hispanics, and 3 Asians

    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 attempted = 1455

1443 samples with complete profiles

FSI Genetics Forthcoming Article on PowerPlex ESX 17 and ESI 17 Systems



G Model
FSIGEN 590 1–7

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

ELSEVIER

Concordance and population studies along with stutter and peak height ratio analysis for the PowerPlex® ESX 17 and ESI 17 Systems

Carolyn R. Hill [a,*], David L. Duewer [a], Margaret C. Kline [a], Cynthia J. Sprecher [b], Robert S. McLaren [b], Dawn R. Rabbach [b], Benjamin E. Krenke [b], Martin G. Ensenberger [b], Patricia M. Fulmer [b], Douglas R. Storts [b], John M. Butler [a]

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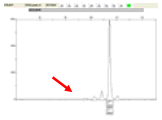
[b] Promega Corporation, Madison, WI 53711-5399, USA

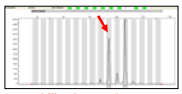
D22S1045 Discordance

ESX 17 (prototype) = 17,17

NGM = 17,17

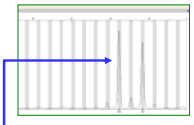


NIST NC01 = 15,17

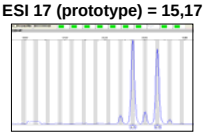


Destabilized some (but uses lower annealing temperature with fewer amplicons in multiplex)

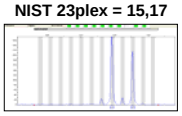
ESX 17 (final) = 15,17



ESI 17 (prototype) = 15,17



NIST 23plex = 15,17

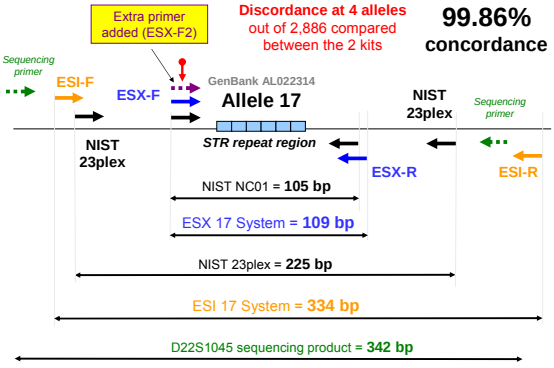


NIST PT84195

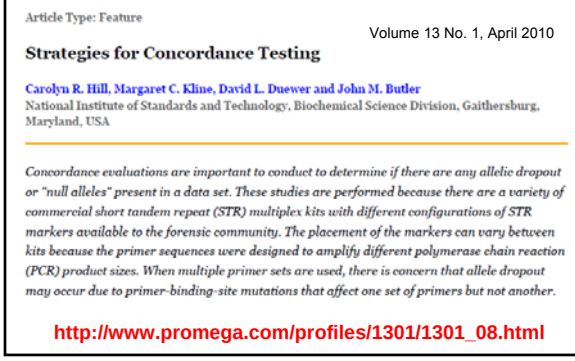
G→T 15 bp upstream impacting forward primer binding with ESX17

Promega added additional primer to correct issue

D22S1045 Relative PCR Primer Positions



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

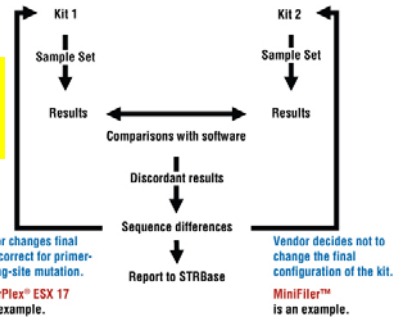
Concordance evaluations are important to conduct to determine if there are any allelic dropout or "null alleles" present in a data set. These studies are performed because there are a variety of commercial short tandem repeat (STR) multiplex kits with different configurations of STR markers available to the forensic community. The placement of the markers can vary between kits because the primer sequences were designed to amplify different polymerase chain reaction (PCR) product sizes. When multiple primer sets are used, there is concern that allele dropout may occur due to primer-binding-site mutations that affect one set of primers but not another.

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

Strategies for Concordance Testing

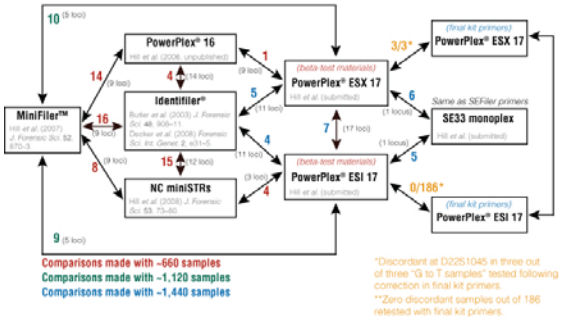
the four S's of concordance studies

Standard samples
Software
Sequencing
STRBase



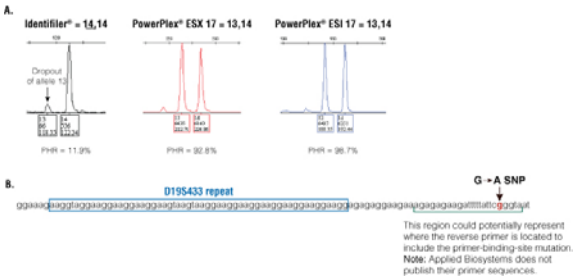
http://www.promega.com/profiles/1301/1301_08.html

Concordance Comparisons



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

D19S433 Example Discordance



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

New NIST Software Tools

Developed by Dave Duewer (NIST)

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

STR_MatchSamples

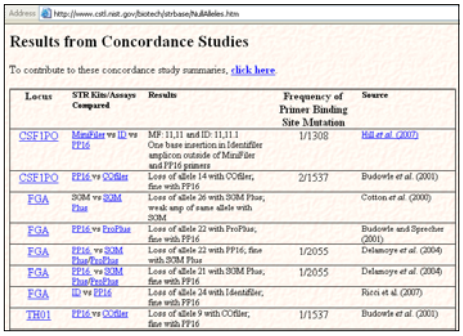
- An Excel-based tool developed to aid comparison of STR genotypes from two or more data sets.

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

STRBase Null Alleles Page



Results from Concordance Studies

To contribute to these concordance study summaries, click here

Locus	STR Kits/Assays Compared	Results	Frequency of Primer Binding Site Mutation	Source
CSF1PO	MiniFiler vs ID vs FP16	MF: 11,11 and ID: 11,11.1 One base insertion in Identifiler amplicon outside of MiniFiler and FP16 primers	1/1308	Hill et al. (2007)
CSF1PO	FP16 vs COfiler	Loss of allele 14 with COfiler, fine with FP16	2/1537	Budowle et al. (2001)
FGA	30M vs 30M Plus	Loss of allele 26 with 30M Plus, weak amp of same allele with 30M		Cotton et al. (2000)
FGA	FP16 vs ProPlus	Loss of allele 22 with ProPlus, fine with FP16		Budowle and Sprecher (2001)
FGA	FP16 vs 30M Plus/ProPlus	Loss of allele 22 with FP16, fine with 30M Plus	1/2055	Delamoye et al. (2004)
FGA	FP16 vs 30M Plus/ProPlus	Loss of allele 21 with 30M Plus, fine with FP16	1/2055	Delamoye et al. (2004)
FGA	ID vs FP16	Loss of allele 24 with Identifiler, fine with FP16		Ricci et al. (2007)
TH01	FP16 vs COfiler	Loss of allele 9 with COfiler, fine with FP16	1/1537	Budowle et al. (2001)

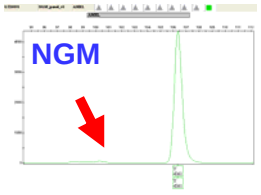
http://www.cstl.nist.gov/biotech/strbase/NullAlleles.htm

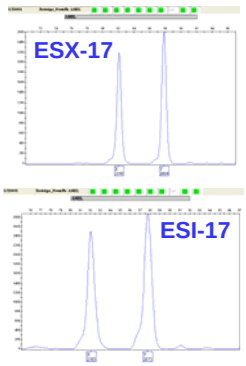
Concordance Testing with NGM Kit

- NGM results compared to ESX/ESI kits with **657 unrelated individuals** (NIST U.S. population set)
- NGM and ESX/ESI 17 are **fully concordant with NIST SRM 2391b** certified values (including D2S441, D10S1248, D22S1045, D1S1656, D12S391)
- **NGM null alleles**:
  - AMEL X (2/657)
  - D18S51 (1/657)
  - D22S1045 (3/657)

Amelogenin X Null Allele

Observed in 2/657 samples tested so far

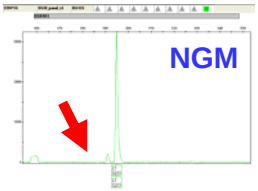


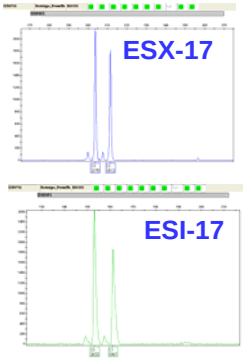


Correct type = X,Y

D18S51 Null Allele

Observed in 1/657 samples tested so far



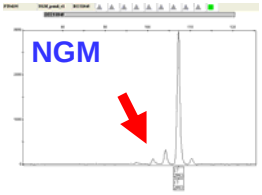


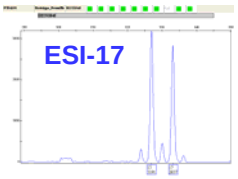
Correct type = 13,15

D22S1045 Null Allele

Observed in 3/657 samples tested so far

Final ESX 17 kit has an extra primer to enable correct typing





Correct type = 15,17

How Fast Can We Go?

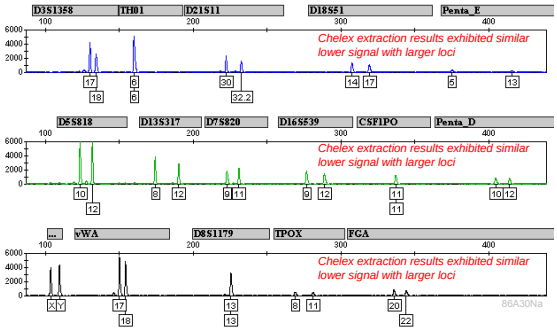
Steps Involved

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)

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

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

Forensic Science International: Genetics

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

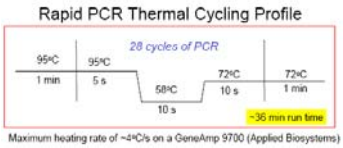
Short communication

Demonstration of rapid multiplex PCR amplification involving 16 genetic loci☆

Peter M. Vallone*, Carolyn R. Hill, John M. Butler

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.

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?

GeneAmp 9700 (Applied Biosystems)

- Heating rate: 4°C/s
- Heating mechanism: Peltier block (Al)
- Tube format: 0.2 mL - 96 well plate
- 28 cycles = 36 min

36 minutes

SmartCycler (Cepheid)

- Heating rate: 10°C/s
- Heating mechanism: heating plates and air circulating fan
- Tube format: proprietary 25 µL tubes
- 16 reactions per instrument
- Can also be used for real time PCR
- 28 cycles = 20 min

25 µL PCR rxn volume

20 minutes

Mastercycler pro (Eppendorf)

- Heating rate: 6°C/s
- Heating mechanism: Peltier block (Ag)
- Tube format: 0.2 mL - 96 well plate
- 28 cycles = 19 min

19 minutes

Rotor-Gene Q (Qiagen)

- Heating rate: 15°C/s
- Heating mechanism: Air chamber (spinning rotor)
- Tube format: 0.1 mL – 72 tube/rotor
- 28 cycles = 36 min

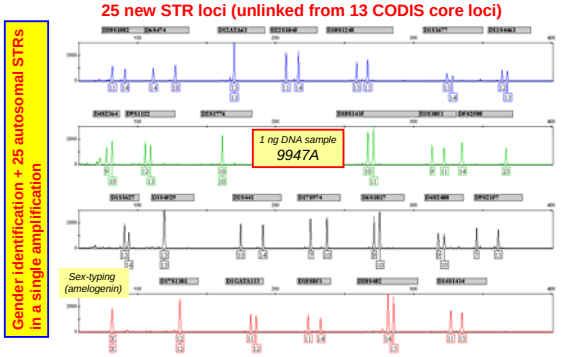
36 minutes

http://www.cstl.nist.gov/biotech/strbase/pub_pres/ValloneePromega2009poster.pdf

NIST 26plex published in *J. Forensic Sci.* (Sept 2009)

25 new STR loci (unlinked from 13 CODIS core loci)

Gender identification + 25 autosomal STRs in a single amplification



Hill, C.R., et al. (2009) A new STR 26plex assay for human identity testing. *J. Forensic Sci.* 54: 1008-1015

Primer sequences and GM bins & panels available: http://www.cstl.nist.gov/biotech/strbase/str26plex.htm

Authentication of Cell Lines Using STRs

- Working with the ATCC (American Type Culture Collection) to develop standards for testing human cell lines using STR markers
- NCBI (National Center for Biotechnology Information) will soon have a STR database for authenticating human cell lines
- Examining the minimum number of STR markers to separate human cell lines from one another
- Have observed DNA quantitation issues with cell lines particularly Quantifiler (hTERT target)

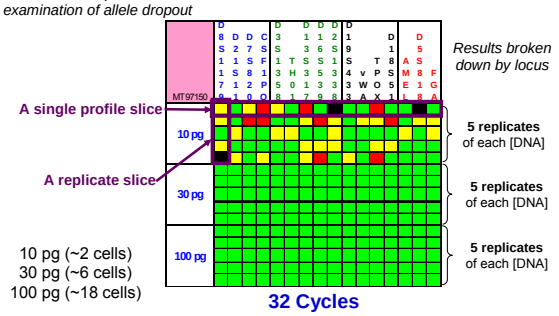
Experimental Design to Study LT-DNA Issues

- Pristine DNA Samples
  - 2 single-source samples
  - **heterozygous for all loci tested** (permits peak height ratio studies)
- **Low DNA Template Amounts**
  - Dilutions made after DNA quantitation against NIST SRM 2372
  - **100 pg, 30 pg, and 10 pg** (1 ng tested for comparison purposes)
- Replicates
  - **5 separate PCR reactions** for each sample
- STR Multiplex Kits
  - **Identifiler Plus and PowerPlex 16 HS** (half-reactions)
- **Increased Cycle Number**
  - Identifiler Plus (**29 cycles and 32 cycles**; 28 for 1 ng)
  - PowerPlex 16 HS (**31 cycles and 34 cycles**; 30 for 1 ng)

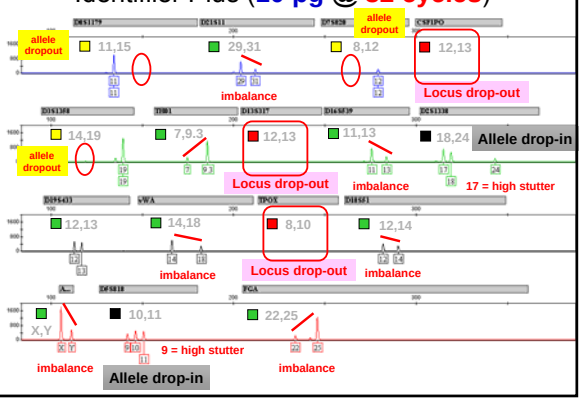
Sensitivity Comparison

Green = full (correct) type
Yellow = allele dropout
Red = locus dropout
Black = drop-in

Tested sample is heterozygous *(possesses 2 alleles) at every locus, which permits an examination of allele dropout*



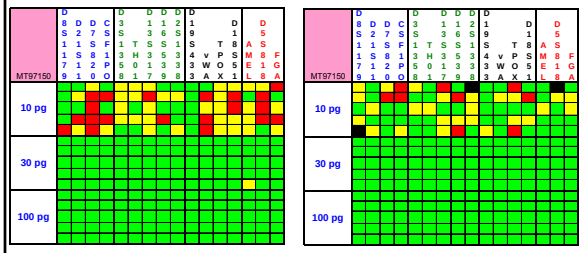
Identifiler Plus (10 pg @ 32 cycles)



Impact of Three More PCR Cycles
Identifiler Plus

Green = full (correct) type
Yellow = allele dropout
Red = locus dropout
Black = drop-in

*Full type = both alleles above 50 RFU
(does not account for peak imbalance)



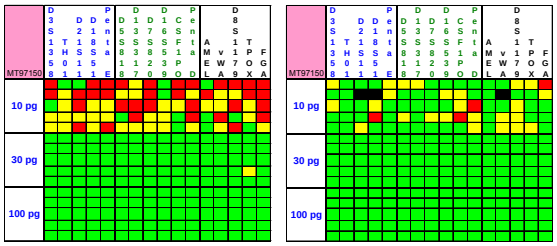
29 Cycles | 32 Cycles

33% vs. 53% full profiles

38% improvement with 3 extra cycles

Sensitivity & Performance
PowerPlex 16 HS

Green = full (correct) type
Yellow = allele dropout
Red = locus dropout
Black = drop-in

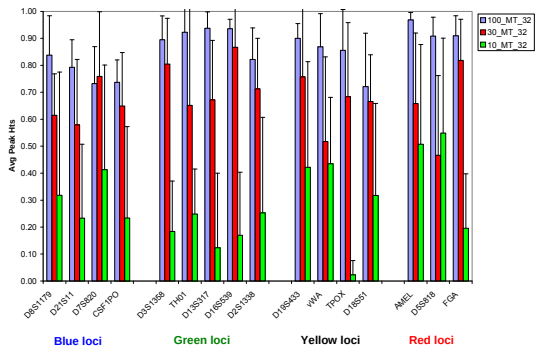


31 Cycles | 34 Cycles

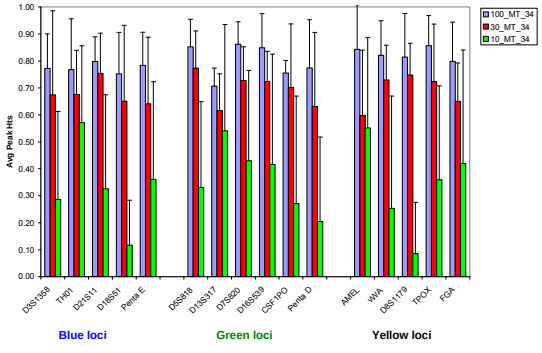
16% vs. 60% full profiles

73% improvement with 3 extra cycles

Peak Height Ratio: Identifiler Plus, 32 cyc

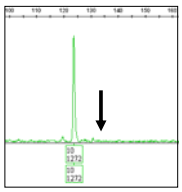


Peak Height Ratio: PP16HS, 34 cyc

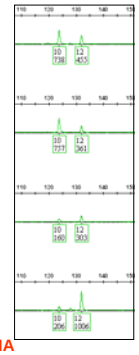


D5S818 replicates with 3 extra cycles

False Homozygote with 1272 RFUs, well above any stochastic thresholds



Allele "12" drop-out



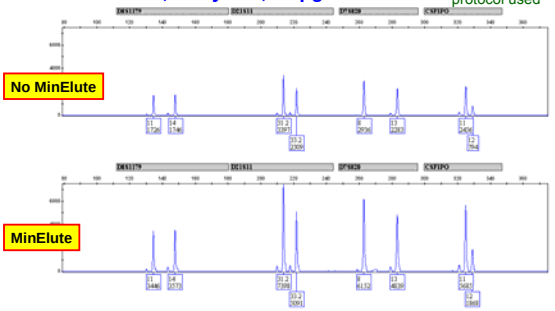
*Any combination of 3/5 replicates gives the correct genotype (10,12)

PowerPlex 16 HS, 34 cycles, 10 pg DNA

MinElute PCR Purification Kit

*96 well plates with vacuum protocol used

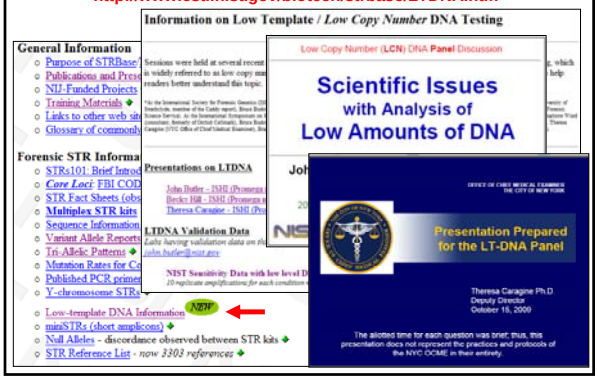
Identifiler Plus, 32 cycles, 30 pg



Signal Improvement: ~50% ~54% ~52% ~57%

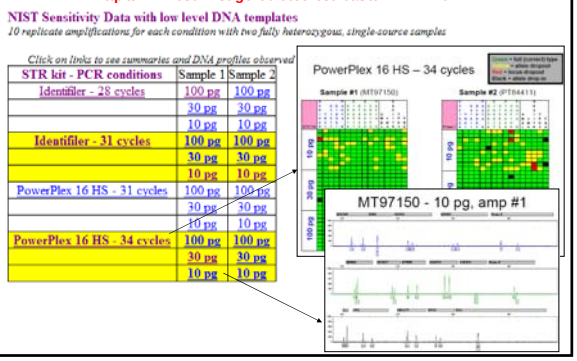
New STRBase Website on LT-DNA (LCN)

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

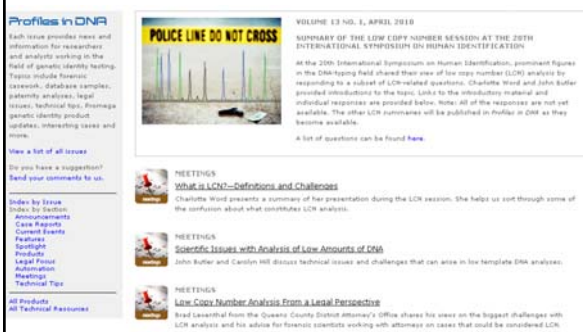


LT-DNA Conclusions

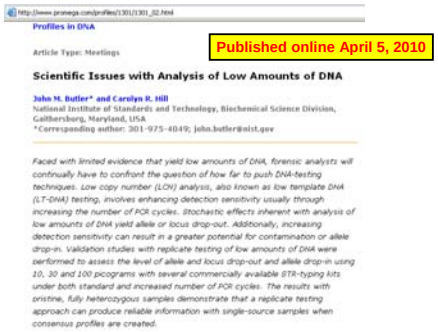
- The results with pristine full heterozygous samples demonstrate **that replicate testing can produce reliable information with single source samples at low levels of DNA when consensus profiles are created**.
- Identifiler Plus with 32 cycles and PowerPlex 16 HS with 34 cycles were comparable in performance with low-level DNA analysis.
- With 3 extra cycles, there was better recovery at 10 pg of DNA using both kits including less allelic and full locus drop-out. However, there is a greater potential for allele drop-in or high stutter.
- MinElute PCR Purification Kits were successful in significantly increasing the signal for LT-DNA PCR products and resulted in extra peaks being called at 10 pg DNA samples.

Profiles in DNA (April 2010)

http://www.promega.com/profiles/



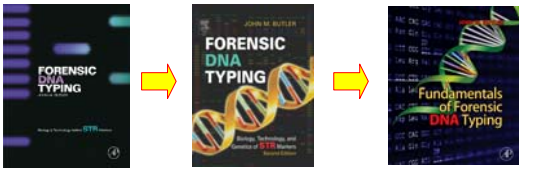
Our LT-DNA Article in *Profiles in DNA*



Published online April 5, 2010

***Based on LT-DNA studies performed in Fall 2009**

The Expansion of *Forensic DNA Typing*



Jan 2001
335 pp.
17 chapters

Feb 2005
688 pp.
24 chapters

Chinese Translation (2007) Y. Hou, translator

Japanese Translation (2009) Y. Fukuma, translator

Sept 2009

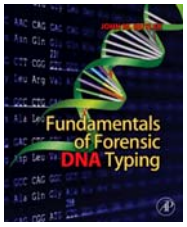
Fundamentals
18 chapters (504 pp.)

Advanced Topics
25 chapters (~600 pp.)

Planned for Spring 2011

The New Book…

3rd Edition, Volume 1



Sept 2009

504 pp.

- **Selection of basic information from previous editions** to aid students, lawyers, and scientists understand fundamentals of forensic DNA
- **Updated information** (cites >600 new references since 2nd edition was written in 2004)
- **Improved reference format**
  - by topic with title included
- **43 new figures, 17 new tables, 26 new D.N.A. boxes, and numerous new website links**
- **New chapters** on historical methods (Ch. 3) and future trends (Ch. 18)
- **New information** on DNA databases (Ch. 12), quality assurance (Ch. 13), & lineage markers (Ch. 16)
- **New order of chapters** to reflect process of DNA typing (Ch. 4-11)
- **Glossary with >400 key words**

Volume 2, *Advanced Topics of Forensic DNA Typing*, is expected in Spring 2011

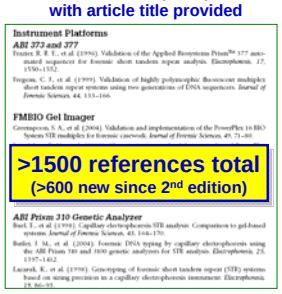
Improved Reference Format

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

Full list of authors but no article title

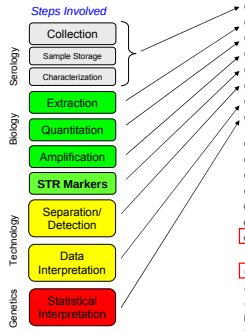
***Fundamentals* (3rd Edition)**

Subdivided by subject with article title provided



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

Chapters Re-ordered to Reflect DNA Testing Process

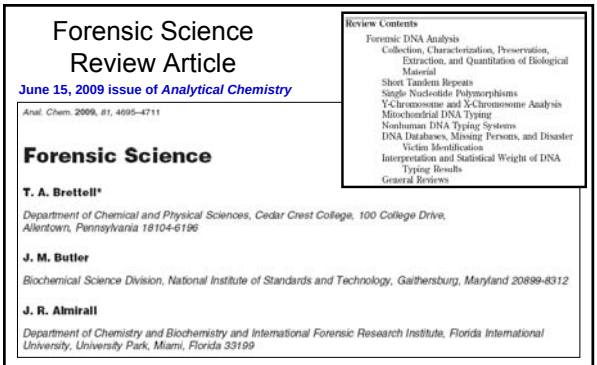


***Fundamentals of Forensic DNA Typing* (2009)**

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

Forensic Science Review Article

June 15, 2009 issue of *Analytical Chemistry*



Anal. Chem. **2009**, *81*, 4695–4711

Forensic Science

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Review Contents

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

Training Workshops Conducted in 2009

Individual Forensic DNA Laboratories

Sorenson Forensics

AFDIL | Harris Co. ME, Houston PD, TX DPS | New York City | Wisconsin | Utah

Scientific Conferences

Universities

FIU Florida International University | Towson University | The George Washington University | UAlbany | IONA | Bowie State University | Northeast Regional Forensic Institute | University of Virginia

Overview of NIST Efforts

EDNAP

- **E**valuation of new European loci
- **D**NA Biometrics (rapid PCR)
- **N**ew STR Kits: Analysis and Concordance
- **A**uthentication of Cell Lines
- **P**rojects with Low Template DNA

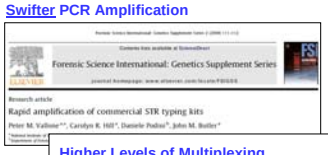
The Future of Forensic DNA

is Similar to the Olympic Motto of
"Swifter, Higher, Stronger"

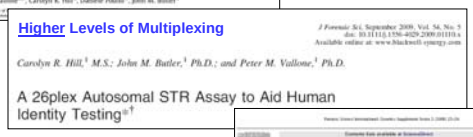
Resources **Training** **Action**

NIST Publications in 2009 Demonstrating "Swifter, Higher, Stronger" DNA Analysis

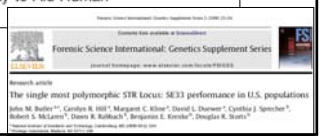
Swifter PCR Amplification



Higher Levels of Multiplexing



Stronger Powers of Discrimination



The NIST Human Identity Project Team

(Forensic DNA & DNA Biometrics)

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

DNA Extraction Efficiency | Software Tools & Data Analysis | Variant alleles & Cell Line ID | STRBase Support

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

john.butler@nist.gov
001-301-975-4049

Questions?