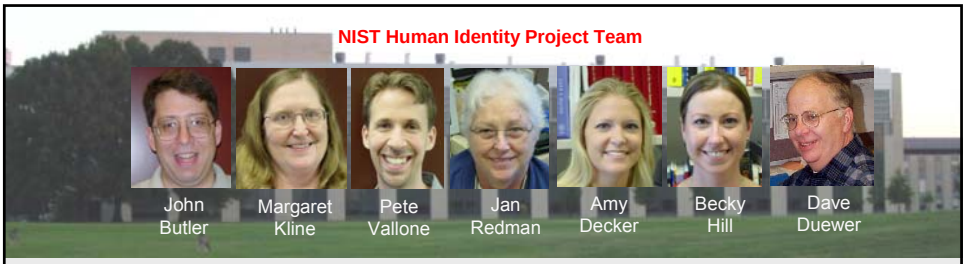


NIST Update

Dr. Peter M. Vallone
and Human Identity Project Team
National Institute of Standards and Technology

CODIS Conference
San Francisco, CA
October 29, 2007

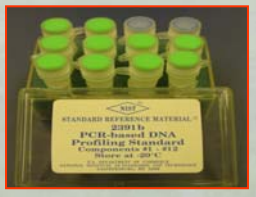
Our Team Mission Statement

- The NIST Human Identity Project Team is trying **to lead the way in forensic DNA**… through research that helps bring traceability and technology to the scales of justice.

NIST History and Mission

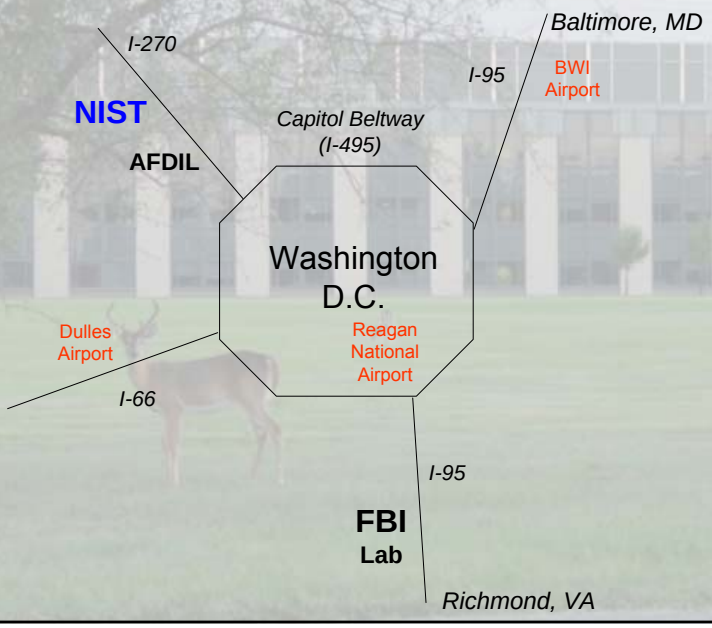
- National Institute of Standards and Technology (NIST) was created in 1901 as the National Bureau of Standards (NBS). The name was changed to NIST in 1988.
- NIST is **part of the U.S. Department of Commerce** with a mission to develop and promote measurement, standards, and technology to enhance productivity, facilitate trade, and improve the quality of life.
- NIST supplies over 1,300 Standard Reference Materials (SRMs) for industry, academia, and government **use in calibration of measurements**.
- **NIST defines time for the U.S.**

$573 for 3 jars



DNA typing standard

Location of NIST (near Washington, DC)



National Institute of Justice
The Research, Development, and Evaluation Agency of the U.S. Department of Justice

Current Areas of NIST Effort with Forensic DNA

- **Standards** http://www.cstl.nist.gov/biotech/strbase/
  - Standard Reference Materials
  - Standard Information Resources (STRBase website)
  - Interlaboratory Studies
- **Technology**
  - Research programs in SNPs, miniSTRs, Y-STRs, mtDNA, qPCR
  - Assay and software development
- **Training Materials**
  - Review articles and workshops on STRs, CE, validation
  - PowerPoint and pdf files available for download

Outline

- SRM 2372
- STRBase updates
- Biomatrica stability study
- MiniFiler concordance study
- New autosomal STR loci
- Upcoming workshops
- Other

SRM 2372 Now Available

- The NIST SRM Office began selling SRM 2372 Human DNA Quantitation Standard on October 5, 2007
- Cost will be $316.00 per unit

SRM 2372
Human DNA Quantitation Standard

Components

A: Male/single donor/RNased/NIST
B: Female/multiple donors/NIST
C: Mixture/male & female/commercial

Quantities supplied:

110 µL of Human Genomic DNA ≈ 50ng/µL

Certification

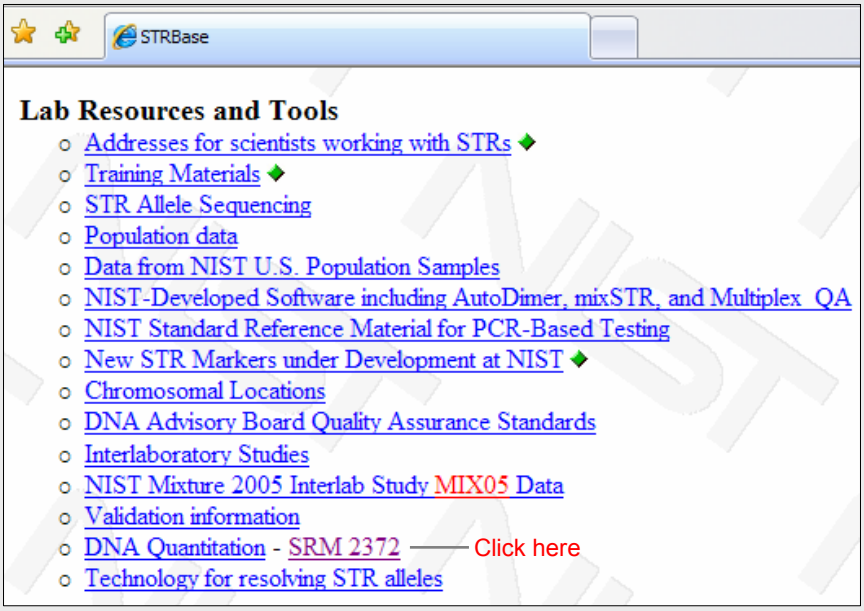
Decadic Attenuance (Absorbance) by a US National Reference Spectrophotometer
Homogeneity by a Cary 100 Bio Spectrophotometer
Validation of conventional [DNA] by Interlaboratory Study and NIST qPCR studies

HAS II Certified Values of Decadic Attenuance for SRM 2372

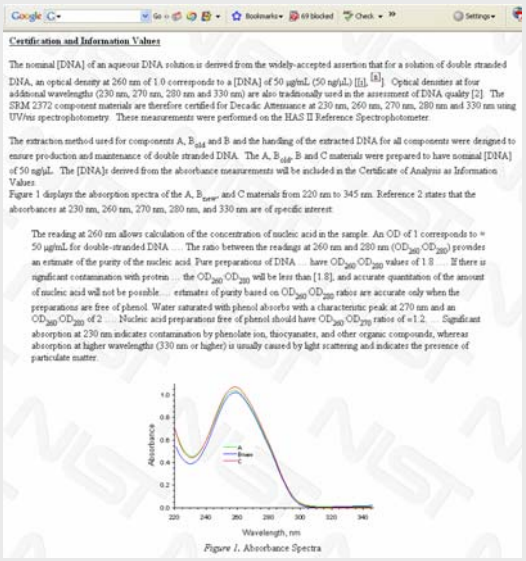
Component	260 nm	error at 260nm	Nominal [DNA], ng/µL
A	1.049	± 0.025	52.5
B	1.073	± 0.030	53.6
C	1.086	± 0.028	54.3

The nominal DNA concentration was estimated *Using 1 OD = 50 ng/µL double stranded DNA.* ***We do not know the uncertainty in this conversion.***

Information on SRM 2372 Now on STRBase



Additional Information



Certification and Information Values

The nominal [DNA] of an aqueous DNA solution is derived from the widely-accepted assertion that for a solution of double stranded DNA, an optical density at 260 nm of 1.0 corresponds to a [DNA] of 50 µg/mL (50 ng/µL) [1]. [2] Optical densities at four additional wavelengths (230 nm, 270 nm, 280 nm and 330 nm) are also traditionally used in the assessment of DNA quality [2]. The SRM 2372 component materials are therefore certified for Decadic Attenuance at 230 nm, 260 nm, 270 nm, 280 nm and 330 nm using UV/vis spectrophotometry. These measurements were performed on the HAS II Reference Spectrophotometer.

The extraction method used for components A, B_{dd4} and B and the handling of the extracted DNA for all components were designed to ensure production and maintenance of double stranded DNA. The A, B_{dd4}, B and C materials were prepared to have nominal [DNA] of 50 ng/µL. The [DNA]t derived from the absorbance measurements will be included in the Certificate of Analysis as Information Values.

Figure 1 displays the absorption spectra of the A, B_{new}, and C materials from 220 nm to 345 nm. Reference 2 states that the absorbances at 230 nm, 260 nm, 270 nm, 280 nm, and 330 nm are of specific interest.

The reading at 260 nm allows calculation of the concentration of nucleic acid in the sample. An OD of 1 corresponds to ≈ 50 µg/mL for double-stranded DNA. … The ratio between the readings at 260 nm and 280 nm (OD_{260}/OD_{280}) provides an estimate of the purity of the nucleic acid. Pure preparations of DNA … have OD_{260}/OD_{280} values of 1.8. … If there is significant contamination with protein … the OD_{260}/OD_{280} will be less than [1.8], and accurate quantitation of the amount of nucleic acid will not be possible. … estimates of purity based on OD_{260}/OD_{280} ratios are accurate only when the preparations are free of phenol. Water saturated with phenol absorbs with a characteristic peak at 270 nm and an OD_{260}/OD_{280} of 2. … Nucleic acid preparations free of phenol should have OD_{260}/OD_{270} ratios of ≈1.2. … Significant absorption at 230 nm indicates contamination by phenolate ion, thiocyanates, and other organic compounds, whereas absorption at higher wavelengths (330 nm or higher) is usually caused by light scattering and indicates the presence of particulate matter.

Figure 1. Absorbance Spectra

Supplemental data for SRM 2372 can be found on STRBase

Includes information on the production and characterization of the materials:

Homogeneity study

Interlaboratory study

Quantifiler, Alu, CFS assays

DNA standard calibration

http://www.cstl.nist.gov/biotech/strbase/srm2372.htm

Example of Calibrant Value Assignment

Standard	1		2		3		4	
Dilution	[DNA]	SD	[DNA]	SD	[DNA]	SD	[DNA]	SD
10x	105	3.2	122	1	126	5.8	256	10.1
50x	105	3.3	122	7.3	145	0.8	272	7.8
100x	99	6.2	113	11.6	138	0.5	270	10.5
200x	100	1.7	137	18.5	137	3.9	311	3.7
Average	102		123		136		277	
Stated	200		200		200		260	
Deviation	-49%		-38%		-32%		6%	

The table above is a summary of the results using Component A as the calibrant.

DNA Storage Study with Biomatrica

DNA SampleMatrix

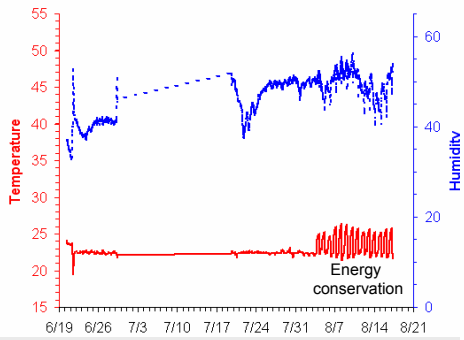
- Preservation of genomic and plasmid DNA at room temperature
- **Biomatrica SampleGuard™** is a novel sample storage medium ideal for (dry) shipping and long-term storage of DNA at room temperature.
- Eliminates the need to send samples overnight in costly dry ice containers

Experimental

- Margaret Kline (NIST)
- Prepare a plate of DNA extracts with varying concentrations (0.05, 0.25, and 1 ng/μL)
- Sample plates mailed back and forth from NIST and Biomatrica (CA)
- Monitor temperature and relative humidity
- Samples quantitated by qPCR and STR profiles obtained using Identifiler

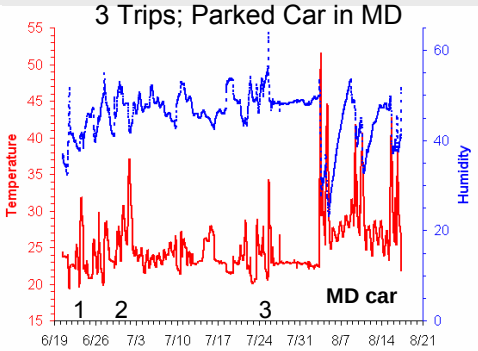
Storage Conditions for 56 days

NIST Office ambient



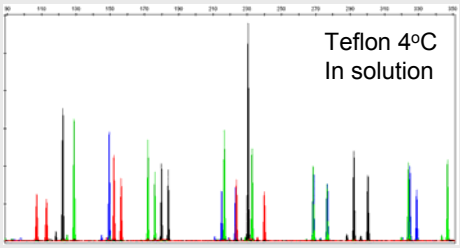
office	% Rh	° C
Max	56.1	26.4
Min	32.6	19.4
Median	48.1	22.4
Avg	46.5	22.9

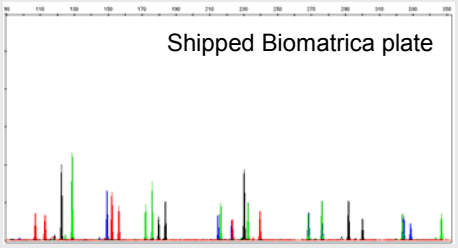
Shipped MD → CA → MD
3 Trips; Parked Car in MD



ship	% Rh	° C
Max	63.9	**51.6**
Min	23.1	19.4
Median	47.0	23.8
Avg	45.6	25.1

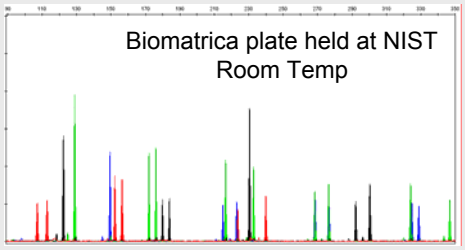
56 day Identifiler Profiles





250 pg amplified (5 μL of 0.05 ng/μL)

- Teflon stored DNA exhibited higher peak heights than the Biomatrica plates
- The NIST ambient Biomatrica plate had higher peak heights than the Shipped matrix plate
- The shipped plate had been exposed to excessive temperatures



All samples were successfully typed

STRBase Updates

Expanded NIJ Projects Section

Projects

33 different projects are described

[Human DNA Quantitation] [Mitochondrial DNA] [Y Chromosome] [Compromised DNA Evidence] [Miniaturization and Automation] [General Tools and Information] [Non-Human DNA] [Alternative Forensic DNA Markers]

Alphabetical Listing of Projects

ABI 3100 performance with various STR typing systems (April 2001-June 2003)

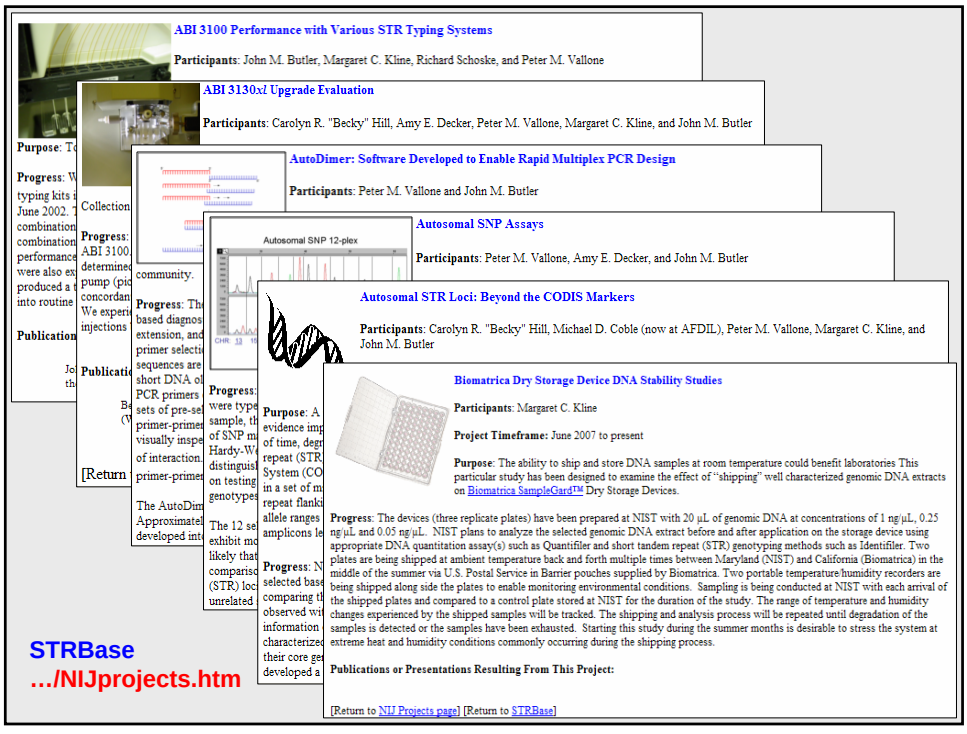
ABI 3130xl upgrade evaluation (Sept 2005-May 2006)

AutoDimer: software to enable rapid multiplex PCR design (2000-2005) [see also software.htm]

Autosomal SNP loci (July 2002-present)

Autosomal STR loci: beyond the CODIS markers (Jan 2004-present) [see also newSTRs.htm]

Biomatrica dry storage device DNA stability studies (June 2007-present)



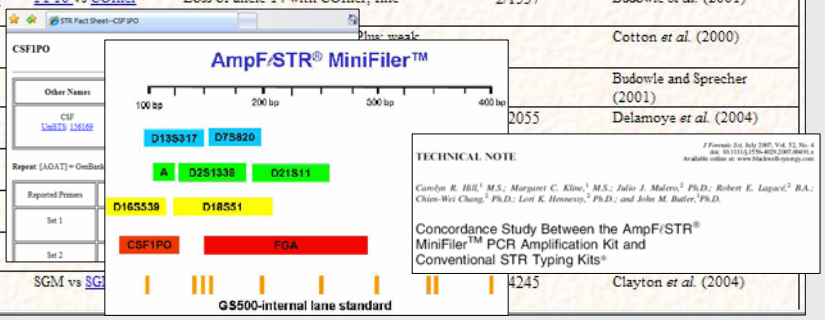
New Null Allele Section on STRBase

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

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 PP16	MF: 11,11 and ID: 11,11.1 One base insertion in Identifiler amplicon outside of MiniFiler and PP16 primers	1/1308	Hill *et al.* (2007)
CSF1PO	PP16 vs COfiler	Loss of allele 14 with COfiler; fine	2/1537	Budowle *et al.* (2001)
FGA		Plus: weak		Cotton *et al.* (2000)
FGA				Budowle and Sprecher (2001)
FGA			2055	Delamoye *et al.* (2004)
FGA				
FGA				
TH01				
TH01	SGM vs SG		4245	Clayton *et al.* (2004)

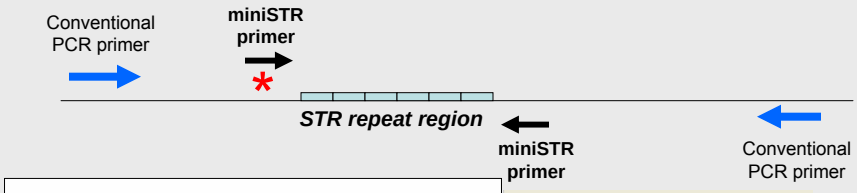


TECHNICAL NOTE

Concordance Study Between the AmpF/STR® MiniFiler™ PCR Amplification Kit and Conventional STR Typing Kits*

MiniFiler Concordance Study

Concordance Studies Reveal Potential Primer Binding Site Mutations with Different Primer Sets

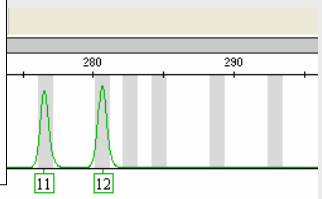


Carolyn R. Hill,[1] M.S.; Margaret C. Kline,[1] M.S.; Julio J. Mulero,[2] Ph.D.; Robert E. Lagacé,[2] B.A.; Chien-Wei Chang,[2] Ph.D.; Lori K. Hennessy,[2] Ph.D., and John M. Butler,[1] Ph.D.

Concordance Study Between the AmpFℓSTR® MiniFiler™ PCR Amplification Kit and Conventional STR Typing Kits*

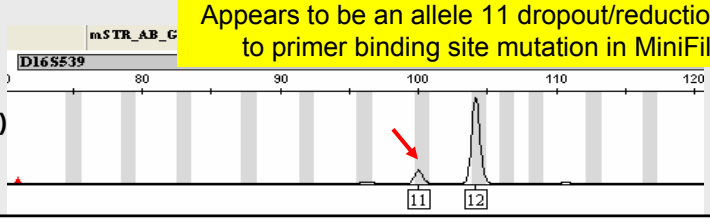
[1]National Institute of Standards and Technology, Biochemical Science Division, 100 Bureau Drive, Mail Stop 8311, Gaithersburg, MD 20899.

[2]Applied Biosystems, 850 Lincoln Centre Drive, Foster City, CA 94404.



Appears to be an allele 11 dropout/reduction due to primer binding site mutation in MiniFiler

MiniFiler (beta-test)

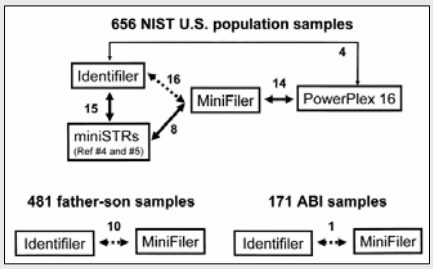


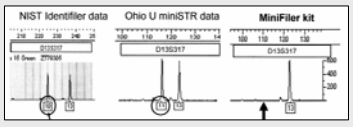
TECHNICAL NOTE

J Forensic Sci, July 2007, Vol. 52, No. 4
doi: 10.1111/j.1556-4029.2007.00491.x
Available online at: www.blackwell-synergy.com

Carolyn R. Hill,[1] M.S.; Margaret C. Kline,[1] M.S.; Julio J. Mulero,[2] Ph.D.; Robert E. Lagacé,[2] B.A.; Chien-Wei Chang,[2] Ph.D.; Lori K. Hennessy,[2] Ph.D.; and John M. Butler,[1] Ph.D.

Concordance Study Between the AmpFℓSTR® MiniFiler™ PCR Amplification Kit and Conventional STR Typing Kits*





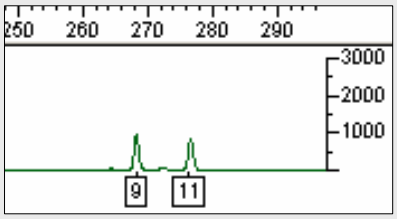
	Locus	Ethnicity	Source	MiniFiler	Identifiler	PP16
1	CSF1PO	H	IBB	11,11	11, "11.1"	11,11
2	D7S820	AA	IBB	8,11	8,"9.3"	8,11
3	D13S317	H	IBB	11,11	9,11	9,11
4	D13S317	H	IBB	13,13	9,13	9,13
5	D13S317	H	IBB	14,14	9,14	9,14
6	D13S317	AA	IBB	11,11	9,11	9,11
7	D13S317	AA	IBB	12,12	8,12	8,12
8	D13S317	AA	IBB	11,11	8,11	8,11
9	D13S317	AA	IBB	13,13	10,13	10,13
10	D13S317	AA	IBB	11,11	9,11	9,11
11	D13S317	AA	IBB	12,12	9,12	9,12
12	D13S317	AA	DDC	10,10	9,10	
13	D13S317	C	IBB	12,12	9,12	9,12
14	D13S317	C	DDC	11,11	10,11	
15	D13S317	C	DDC	8,8	8,10	
16	D13S317	A	DDC	12,12	10,12	
17	D16S539	AA	DDC	9,9	9,11	
18	D16S539	AA	IBB	12,12	11,12	11,12
19	D16S539	AA	MLN	11,11	9,11	9,11
20	D16S539	AA	DDC	14,14	11,14	11,14
21	D16S539	AA	DDC	9,9	9,11	9,11
22	D16S539	AA	DDC	13,13	11,13	
23	D16S539	AA	DDC	12,12	11,12	
24	D16S539	AA	DDC	12,12	11,12	
25	D16S539	AA	DDC	9,9	9,12	
26	D16S539	A	ABI	11,11	10,11	
27	D18S51	H	IBB	13,15	15,15	13,15

Hill, C.R., Kline, M.C., Mulero, J.J., Lagace, R.E., Chang, C.-W., Hennessy, L.K., Butler, J.M. (2007) Concordance study between the AmpFISTR MiniFiler PCR Amplification Kit and conventional STR typing kits. *J. Forensic Sci.* 52(4): 870-873.

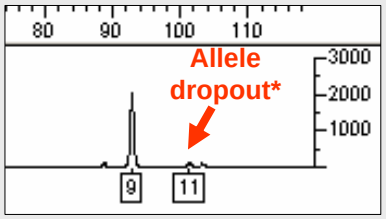
SRM 2391b Genomic 8 with D16S539

All allele calls with MiniFiler for CSF1PO, D7S820, D13S317, D18S51, D21S11, FGA, and D16S539 (with the exception noted below) ***match previously certified values.***

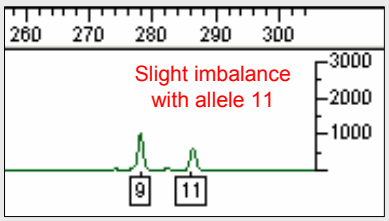
Identifiler



MiniFiler



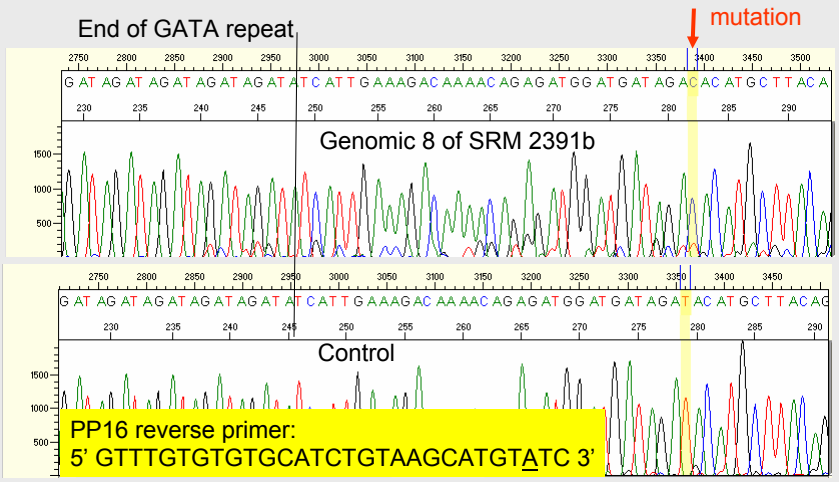
PowerPlex 16



Due to primer binding site mutation

D16S539 SRM 2391b Genomic 8

T→C mutation 34 bp downstream of the repeat



Position of the T→C probably affects the reverse primer of Minifiler and is the 3rd base found the 3' end of the Reverse PP16 primer. This could explain the imbalance of the allele seen when using PP16.

New Autosomal STR Loci

Why consider new STR loci?

Aren't the Current STR Loci Good Enough?

- Depends on the question being asked…
- For general forensic matching of evidence to suspect, the 13 CODIS STR loci are sufficient
- For other human identity/relationship testing questions, additional autosomal loci can be beneficial or even necessary

How Would Additional STR Loci Be Useful?

- **Databases**: More loci to help resolve relatives in growing national DNA databases (UK went from 6 to 10 STRs in 1999; future Pan-European database will include >10 loci)
- **Casework**: Obtaining additional information with degraded DNA samples (miniSTRs); rapid screening of multiple crime scene samples
- **Identity/Relationship Testing**: Kinship analysis, parentage testing, complex criminal paternity, **missing persons/mass disasters**, immigration testing

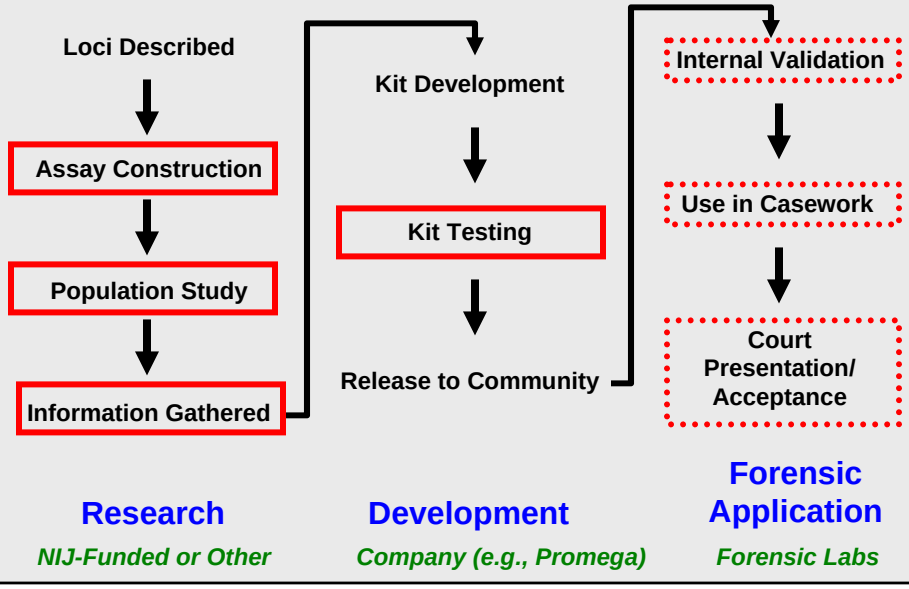
Call for More Loci
in Situations Involving Relatives

- **Missing Persons** and Disaster Victim Identification (kinship analysis)
- Immigration Testing (often limited references)
  - Recommendations for 25 STR loci (*Karlsson et al.*)
- Deficient Parentage Testing
  - often needed if only one parent and child are tested

Relationship testing labs are being pushed to answer more difficult genetic questions…and **we want to make sure the right tools are in place**

Steps in Adopting Genetic Markers

Role of the NIST Human Identity Project Team



What are important characteristics to consider in new loci?

Primary Characteristics in New STRs

- Genomic position
  - Adequate spacing from other (and current) loci to enable product rule use with autosomal markers
- Avoid known disease genes or linkage
  - To protect privacy concerns
- Polymorphic content (high heterozygosity)
  - More variable markers mean less can be used to reach desired rarity in full profile

Valuable Characteristics in New STRs

- Span/Range of observed alleles
  - Impacts electrophoretic real-estate
  - Narrow range makes differential amplification less likely
- 'Clean' flanking region
  - To enable primer design near repeat (miniSTRs)
- Mutation rate known when trying to address multi-generational questions

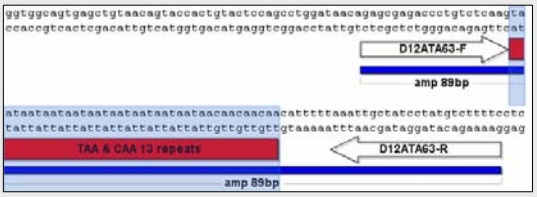
Steps We Use in Characterizing New Loci

- ✓ Select genetic loci
- ✓ Design primers – optimize multiplex assay
- ✓ Type population samples to examine variation
- ✓ Sequence alleles to establish nomenclature
- ✓ Develop bins and panels for genotyping
- ✓ Construct allelic ladders
- ✓ Evaluate RMP or ability to separate common types
- ✓ Perform mutation rate studies
- ✓ Perform concordance studies (when applicable)
- ✓ Calibrate genotypes with NIST SRM components
- ✓ Work with companies/collaborators
- ✓ Publish details on loci and assays

Characterization of New Autosomal Loci

(miniSTR **D12ATA63**)

GenBank accession AC009771; positions 55,349..55,437



[FAM] – GAGCGAGACCCTGTCTCAAG
GGAAAAGACATAGGATAGCAATTT

Chr 12 106.825 Mb
(12q23.3)

Trinucleotide
[TAA][CAA] repeat
76 -106 bp
Alleles 9 -19

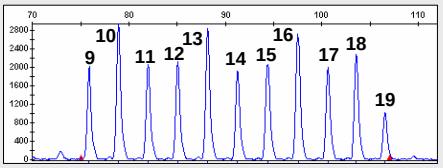
Allele	Caucasian (N = 260)	African Am (N = 259)	Hispanic (N = 140)
9	--	--	0.0036
10	0.0019	0.0154	0.0036
11	0.1385	0.1525	
12	0.2154	0.100	
13	0.0173		0.0286
14		3340	0.2214
		0.0772	0.0714
	0.2981	0.1004	**0.2643**
17	0.0981	0.0521	0.0679
18	0.0096	0.0058	0.0071
19	0.0019	0.0058	0.0036

~660 U.S. population samples

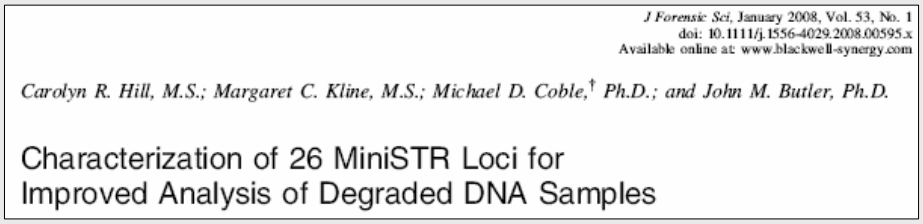
Heterozygosity Values

U.S. Caucasian	**0.842**
African American	**0.788**
U.S. Hispanic	**0.879**

D12ATA63 Allelic Ladder



To Appear in Jan 2008 Issue of *J. Forensic Sci.*



J Forensic Sci, January 2008, Vol. 53, No. 1
doi: 10.1111/j.1556-4029.2008.00595.x
Available online at: www.blackwell-synergy.com

Carolyn R. Hill, M.S.; Margaret C. Kline, M.S.; Michael D. Coble,† Ph.D.; and John M. Butler, Ph.D.

Characterization of 26 MiniSTR Loci for Improved Analysis of Degraded DNA Samples

- Primer sequences, GeneMapper bins and panels, genotypes on common samples, and allele frequency information **for the 26 loci are currently available on STRBase**

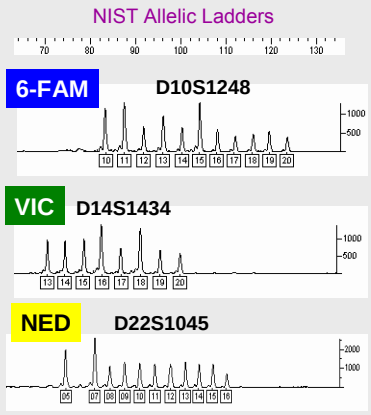
Assay Performance

- Our multiplex assays are designed to perform similarly to commercial kits
  - PCR Reaction (buffer, fluorescent dyes, volume)
  - PCR thermal cycling conditions
  - Work robustly on 0.5 to 1 ng of template DNA (or lower)
- Multiple miniplexes and a single megaplex developed to study **26 autosomal STRs**

Multiple Miniplexes

- **26 characterized loci** divided into nine 3plexes
- One locus per dye color
- Allelic ladders created
- **Amplicons <140 bp**
- miniSTRs
- Work with 100 pg DNA
- **For degraded samples**
  (bones in missing persons cases)

NC = Non-CODIS or non-core



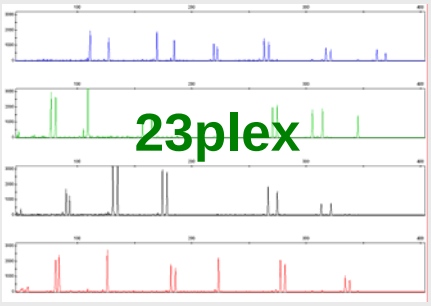
NC01 Loci

See Dixon et al. (2006) *Forensic Sci. Int.* 164: 33-44.

Single Megaplex

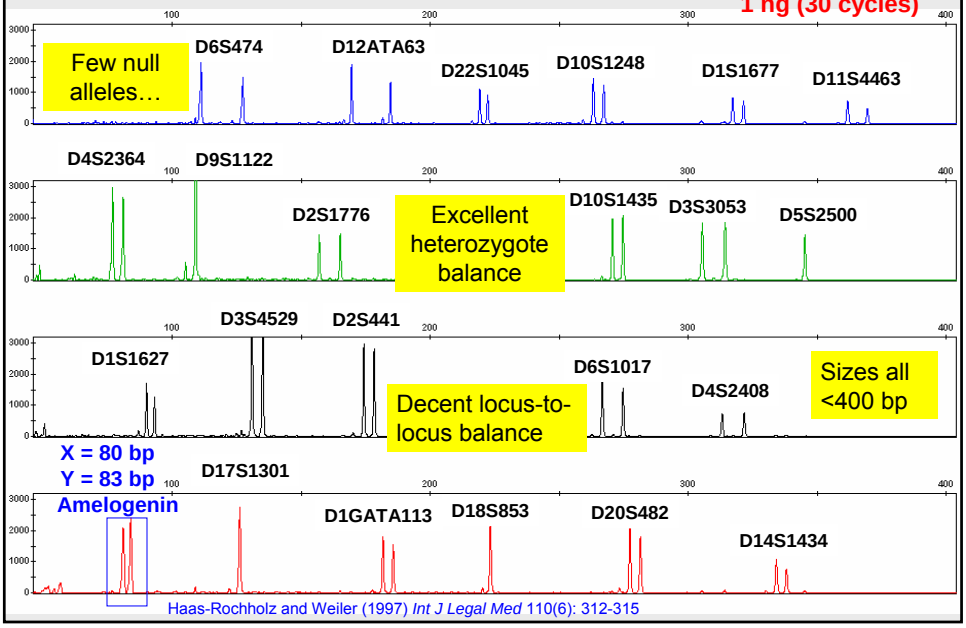
- So far **22 STRs and amelogenin** in single multiplex (Eventual goal to have all 26 loci)
- Multiple loci in four dye channels
- **Amplicons 70 to 400 bp**
  (No longer 'miniSTRs')
- Typically use 1 ng DNA
- **For reference samples**
  (a missing person's relatives)

"Autoplex"



All loci unlinked from core (CODIS) STRs

NIST "Autoplex" (Autosomal STR 23plex)



Haas-Rochholz and Weiler (1997) *Int J Legal Med* 110(6): 312-315

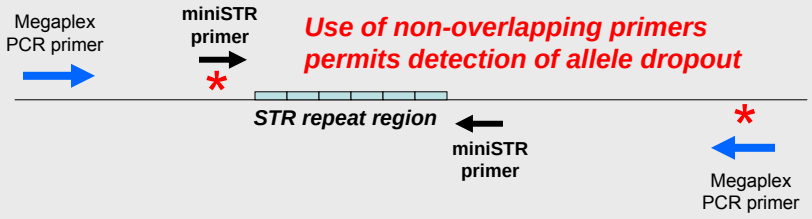
Evaluation of Autoplex (23plex)

- **660 U.S. population samples**
  - U.S. Caucasian, African American, Hispanic
  - **Concordance testing** compared to miniSTR results
- **790 father/son samples**
  - U.S. Caucasian, African American, Hispanic, Asian
  - **Mutation rate determination**
- 12 samples for **extended family testing**

>1450 samples examined so far
(multiple primer batches prepared)

Concordance Study to Check for Null Alleles

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



"Autoplex" vs miniSTRs

639 samples compared
Total types (639 x 22 loci): 14,058
28 types discordant (0.20%)*

99.80% concordance

*discordance not confirmed yet with sequencing

Identifiler vs MiniFiler

1308 samples compared
Total types (1308 x 8 loci): 10,464
27 types discordant (0.26%)

99.74% concordance

Hill et al. (2007) JFS 52(4): 870-873

Conclusions: (1) Our PCR primers have been well-designed and have very few primer binding site mutations. (2) Roughly half of dropout is from megaplex primers – flanking regions near STR repeat do not appear to have a higher level of mutation

Mutation Rates Measured for New STRs

- **395 father/son pairs** (790 samples total)
- 22 STR loci examined
- 8690 allelic transfers
- Only **6 mutations** were observed in total

- **0.069%**
- (2-3 times less than typical 0.2% for common STRs)

Mutation rates generally track with heterozygosity (locus variability)

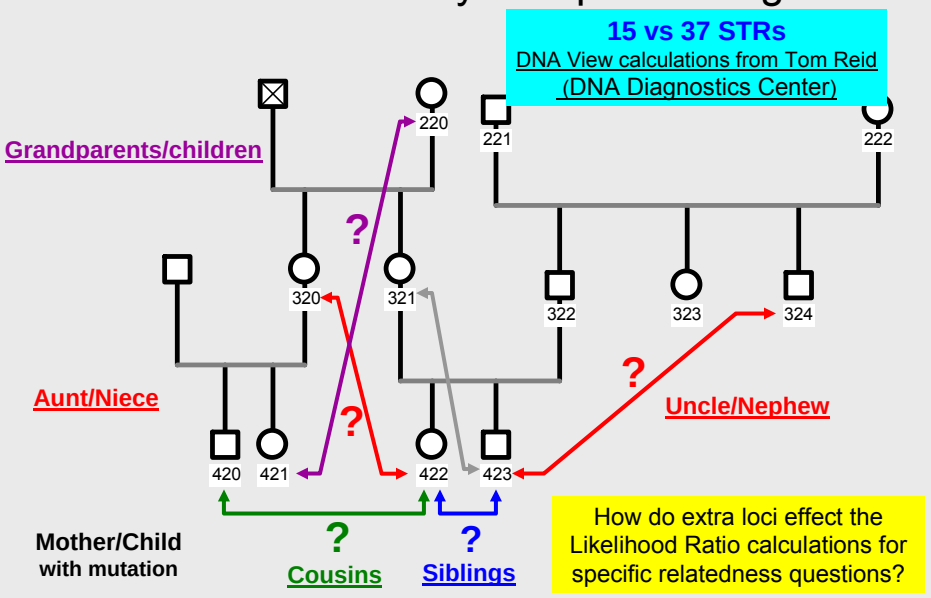
Locus	Mutation Rate
SE33	0.64%
FGA	0.28%
D18S51	0.22%
…	…
TPOX	0.01%

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

Conclusions: Mutation rates are lower than commonly used STRs likely due to selection of loci for miniSTR application with tighter allele ranges, more moderate heterozygosities, and more stable flanking regions.

Effect of additional loci on likelihood ratio calculations

Extended Family Sample Testing



Comparison of Likelihood Ratios

Relationship Examined	**15 STRs** (Identifiler, ID15)	ID15 **+ Autoplex 22** STRs = **37 loci** (A37)
Mother/Child* (*with single mutation)	0.214	**5,200,000** Extra loci help…
Siblings	477	**113,000** Extra loci help…
Uncle/Nephew	824	**247,000** Extra loci help…
Cousins	0.45	**2.25**
Grandparents/ Grandchildren	0.53	**1.42**

Conclusions: Longer distance multi-generational questions cannot usually be solved with additional autosomal STRs…

Rapid PCR

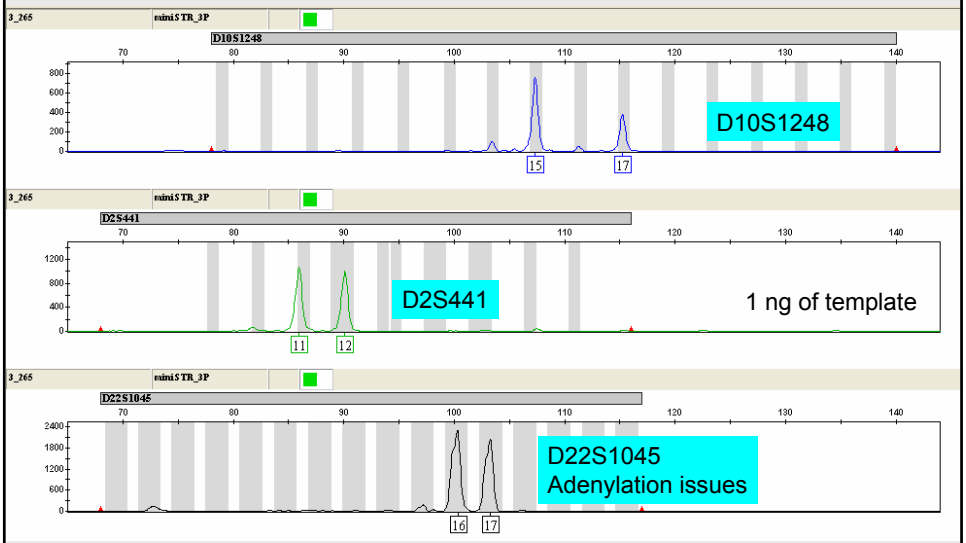
- Existing commercial STR typing kits are not optimized for rapid PCR
- Challenge for miniaturize STR typing platforms – since they are tied into the commercial kits/loci
- Fewer loci and smaller amplicon size favor rapid multiplex PCR
- We have well characterized miniSTR panels

Informal collaborations with:
Dr. Michael Gaitan (NIST) – microwave thermal heating
Dr. Eugene Tan (Network Biosystems) – chip platforms

Rapid Thermal Cycling

- Evaluate faster polymerases
- Test with miniSTRs
  - primer concentrations can be adjusted and PCR primer sequences are known
- Use standard cycler (GeneAmp 9700), tubes, …
- Examine shortened dwell times and adenylation soak
- Study limitations in terms of PCR amplification speed when examining multiplex STR assays

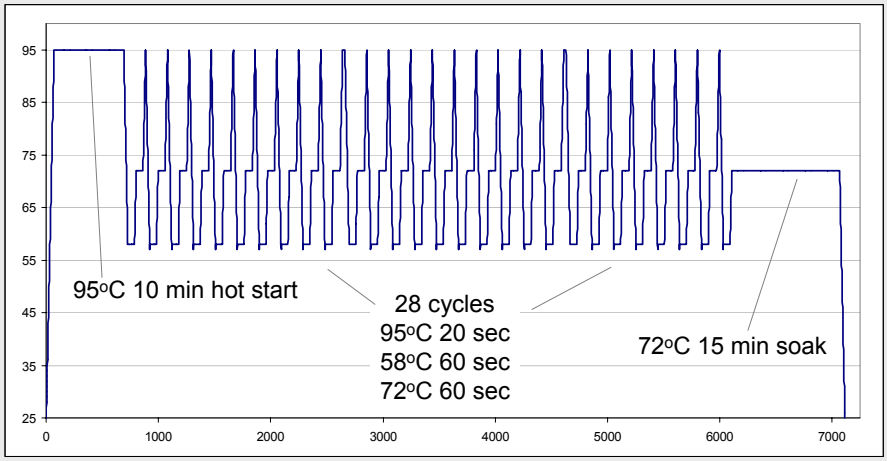
Rapid PCR 28 cycles in 36 minutes on a AB 9700



Further results will be presented at AAFS meeting Feb 23, 2008 Washington D.C.

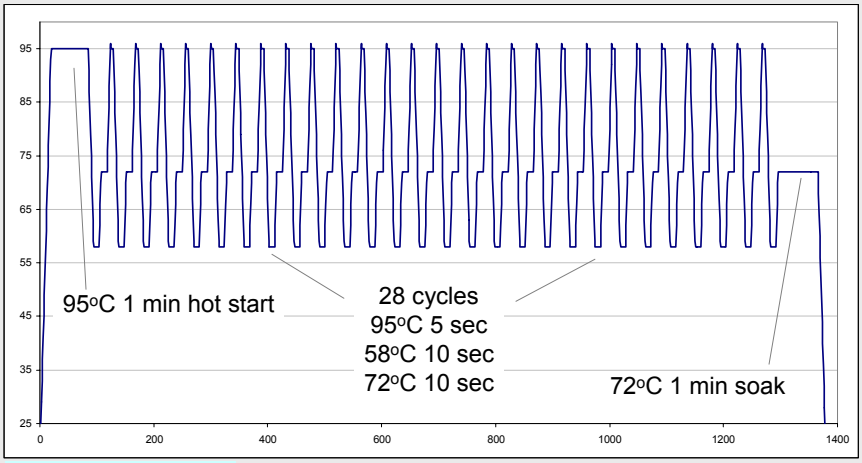
3plex

Standard Cycling on a AB 9700



Ramp Rate 1°C/sec

Rapid Cycling on a AB 9700



Ramp Rate 4°C/sec

SNP Work

- Working with Dr. Manfred Kayser (Netherlands)
  - Set of Ancestry Informative Markers (AIMs)
  - NIST developed assays for typing 34 SNPs
  - Typed over 600 + of our samples
- Dr. Peter deKnijff (Netherlands)
  - Performing Y SNP typing
- Dr. Michael Coble (AFDIL)
  - mitochondrial control region sequencing
- Data currently under review

12plex SNP assays

Training Workshops Planned

Training Workshops Planned

- NEAFS Meeting (November 2-3, 2007 Bolton Landing, NY)
  - Mixture Interpretation (JMB)
  - Low-copy Number DNA Issues (JMB)
  - miniSTRs (JMB)
- AAFS (February 18-19, 2008)
  - Real-Time PCR DNA Quantitation (PMV)
  - Mixture Interpretation (JMB)

qPCR Workshop

- AAFS (February 18th, 2008)
  - Human DNA Quantification Using Real-Time PCR Assays
  - Peter Vallone (NIST)
  - Margaret Kline (NIST)
  - Eric Buel (Vermont)
  - Jan Nicklas (Vermont)
  - Marie Allen (Uppsala)
  - Mark Timken (CA DOJ)
  - David Foran (Michigan State)
  - Melanie Richard (CFS – Toronto)
  - Toni Diegoli (AFDIL)

Mixture Interpretation Workshop

- AAFS (February 19, 2008)
  - **DNA Mixture Interpretation:** Principles and Practice in Component Deconvolution and Statistical Analysis
  - John Butler (NIST)
  - Ann Gross (MN)
  - George Carmody (Carleton U.)
  - Gary Shutler (WA)
  - Joanne Sguelia (MA)
  - Angela Dolph (Marshall U./NIST)
  - Tom Overson (retired USACIL)

Forensic Science Review Article

Anal. Chem. **2007,** *79,* 4365–4384

***Analytical Chemistry* (June 15, 2007 issue)**

Forensic Science

T. A. Brettell*

Department of Chemical and Physical Sciences, Cedar Crest College, 100 College Drive, Allentown, Pennsylvania 18104-6196

J. M. Butler

Biochemical Science Division, National Institute of Standards and Technology, Gaithersburg, Maryland 20899-8311

J. R. Almirall

Department of Chemistry and Biochemistry and International Forensic Research Institute, Florida International University, University Park, Miami, Florida 33199

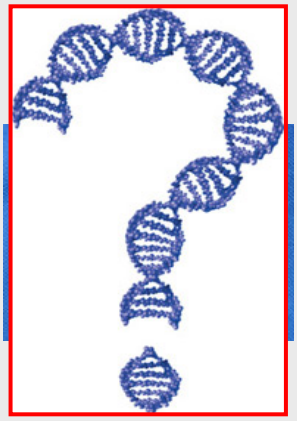
560 references covering articles published in 2005-2006
181 articles on forensic DNA analysis

Brettell, T.A., Butler, J.M., Almirall, J.R. (2007) Forensic science. *Anal. Chem.* 79: 4365-4384.

Thank you for your attention…

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

Questions?



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

peter.vallone@nist.gov

301-975-4872


John Butler


Margaret Kline


Jan Redman


Amy Decker


Becky Hill


Dave Duewer

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

Collaborators

Mike Coble (now AFDIL) – early miniSTR work

Tom Reid (DDC) - father/son samples