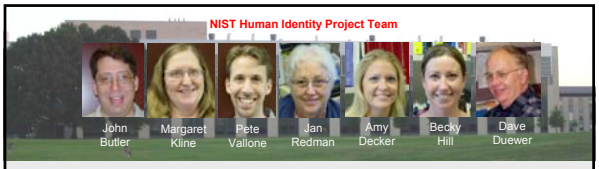


NIST Update

John M. Butler
and Human Identity Project Team
National Institute of Standards and Technology

SWGDAM
Fredericksburg, VA
January 8, 2008

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**
  - Standard Reference Materials
  - Standard Information Resources (STRBase website)
  - Interlaboratory Studies
- **Technology**
  - Research programs in SNPs, miniSTRs, Y-STRs, mtDNA, qPCR
  - Assay and software development, expert system review
- **Training Materials**
  - Review articles and workshops on STRs, CE, validation
  - PowerPoint and pdf files available for download

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

Outline

- SRM 2372 status
- Updated certificates for SRM 2391b and 2395
- Biomatrica stability study
- New autosomal STR loci
- Y-STR and autosomal SNP work
- Training workshops
- Other topics

SRM 2372 Now Available

- The NIST SRM Office began selling SRM 2372 Human DNA Quantitation Standard on **October 5, 2007**
- Cost is $316 per unit
- **>50 units in use already**

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

Requirements for NIST SRM 2372 Human DNA Quantitation Standard

Material must be fit for purpose:

- **Homogeneity** — Tested Random Samples
  - All tubes are the same
- **Stability** — Sarstedt Tubes (2.0 mL)
  - Will withstand shipping and normal storage
- **Recoverability** — Interlaboratory Study & Tube Study
  - What went in the tubes comes out
- **Traceability** — Analysis by Reference Spectrophotometer
  - Values assigned are traceable to the designated certification method.

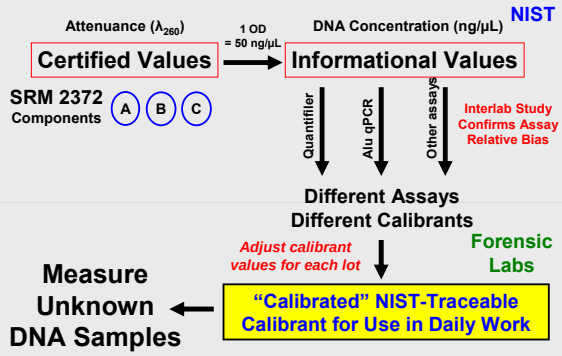
HAS II Certified Values of Decadic Attenuance for SRM 2372

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

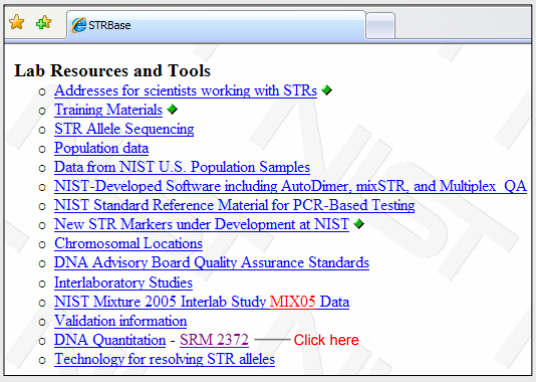
5 mL were required to fill 2 cuvettes per component, each run in duplicate (4 replicate measurements).

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

Overview of SRM 2372 Values and Use



Information on SRM 2372 Now on STRBase



Additional Information

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.

SRM 2391b and 2395 Certificate Updates

- **SRM 2391b** (Autosomal STR Loci)
  - **MiniFiler examined** (allele dropout with component 8 and D16S539)
  - **Additional Loci: 26 new miniSTR loci**
  - Demonstrating extended stability (new quantitation data and no significant degradation to existing components)
- **SRM 2395** (Y-STR and Y-SNP Loci)
  - **Yfiler loci sequenced** (DYS635 now included)
  - **Additional Loci: 20 new Y-STR loci**
  - Demonstrating extended stability (new quantitation data and no significant degradation to existing components)

Final Documents are Now in Review…Information to be Posted on STRBase and Registered Users will be Notified of Certificate Updates

Technology: Research Programs

- **DNA stability studies** – Biomatrica tests
- **miniSTRs** – new STR loci and megaplex
- **Y-chromosome STRs** – worldwide Yfiler studies
- **SNPs** – comparison to STRs; efforts with AIMs
- **Rapid PCR** – to speed multiplex amplification
- mtDNA
- qPCR for DNA quantitation
- Variant allele characterization and sequencing
- Software tools
- Expert System review
- Assay development with collaborators

DNA Storage Study with Biomatrica

DNA SampleMatrix

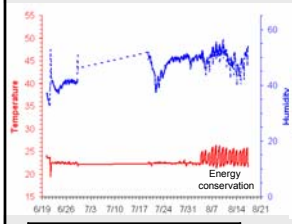
- Preservation of genomic and plasmid DNA at room temperature
- **Biomatrica SampleGuard™** is a novel sample storage medium ideal for (dry) shipping and long-term storage of DNA at room temperature.
- Eliminates the need to send samples overnight in costly dry ice containers

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

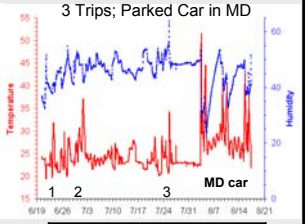
Storage Conditions for 56 days

NIST Office ambient



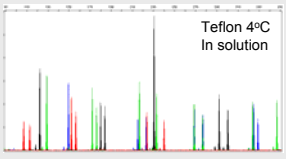
office	% Rh	° C
Max	56.1	26.4
Min	32.6	19.4
Median	48.1	22.4
Avg	46.5	22.9

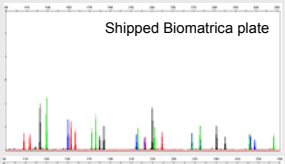
Shipped MD → CA → MD
3 Trips; Parked Car in MD



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

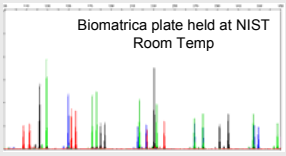
56 day Identifiler Profiles





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

miniSTRs

Advantages

- Better success with degraded DNA (compared to larger PCR products present in commercial STR kits)
- Better success with low amounts of DNA (due to more efficient PCR amplification compared to larger PCR products)
- Better capacity for handling mixed DNA samples than SNPs (due to more alleles being possible)
- Concordance to STR loci in commercial kits is possible

Disadvantages

- Not all commonly used STRs can be made significantly smaller—thus **new loci will be needed**
- Cannot multiplex as many loci due to size constraints
- ~~No commercial kit available yet~~
- STR flanking region mutations may make results disconcordant (e.g., D13 and VWA deletions)

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, more autosomal or Y-STR 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
- 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**

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 **already available on STRBase**

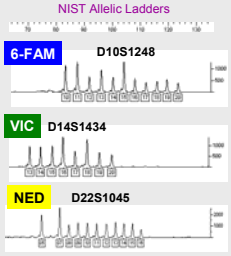
Assay Performance

- 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



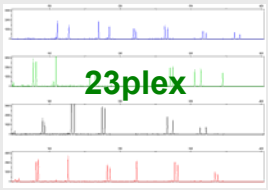
NC01 Loci

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

Single Megaplex

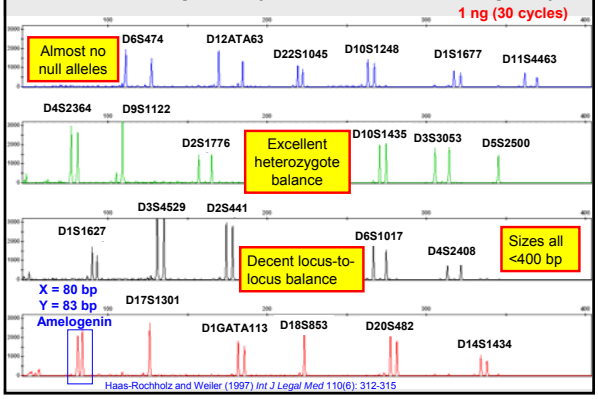
- So far **22 STRs and amelogenin** in single multiplex (Eventual goal to have all 26 loci)
- Multiple loci in four dye channels
- **Amplicons 70 to 400 bp**
  (No longer 'miniSTRs')
- Typically use 1 ng DNA
- **For reference samples**
  (a missing person's relatives)

"Autoplex" or "miniMegaplex"



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

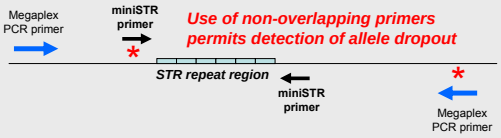
Evaluation of Autoplex (23plex)

- **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



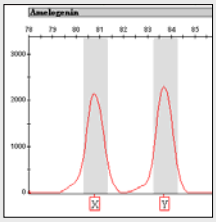
"Autoplex" vs miniSTRs
639 samples compared
Total types (639 x 22 loci): 14,058
28 types discordant (0.20%)*
99.80% concordance
*discordance not confirmed yet with sequencing

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

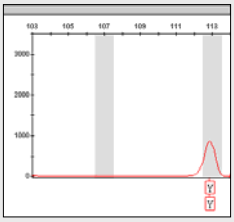
Conclusions: (1) Our PCR primers have been well-designed and have almost no primer binding site mutations. (2) Roughly half of dropout is from megaplex primers – flanking regions near STR repeat do not appear to have a higher level of mutation

Amelogenin X Null Allele

African American Male Sample



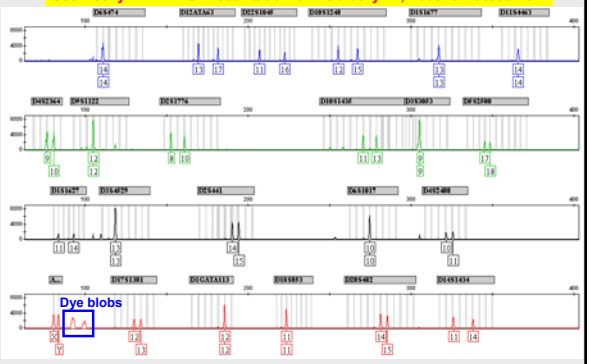
23plex Result



Identifiler Kit Result

ABI Control 007 with 23plex

See Becky Hill AAFS Presentation on February 21, 2008 for latest work



Smaller amelogenin amplicons used to avoid PET dye blobs

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.

Population Data on New STRs

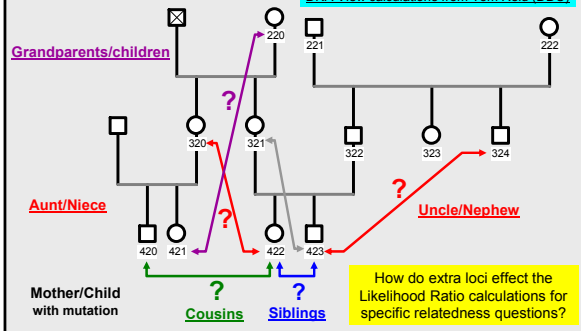
- **~660 samples** with three major U.S. populations on **all 26 autosomal STR loci**
  - Available on STRBase
    - **http://www.cstl.nist.gov/biotech/strbase/NISTpopdata/Allele_Frequencies_for_26miniSTRs.pdf**
- **>3,000 samples tested world-wide** (Spain, Italy, Japan, Malaysia, Korea) on **first 6 loci** (NC01 & NC02)
  - **D2, D10, D22 now recommended European loci**

Gill *et al.* (2006) *Forensic Sci Int* **156(2):** 242-244

Can these new STRs help in missing persons cases or other forms of relationship testing?

Extended Family Sample Testing

15 vs 37 STRs
DNA View calculations from Tom Reid (DDC)



Comparison of Likelihood Ratios

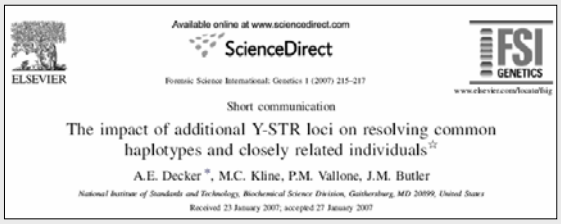
Relationship Examined	15 STRs (Identifiler, ID15)	ID15 + Autoplex 22 STRs = 37 loci (A37)
Mother/Child* (*with single mutation)	0.214	**5,200,000** Extra loci help…
Siblings	477	**113,000** Extra loci help…
Uncle/Nephew	824	**247,000** Extra loci help…
Cousins	0.45	**2.25**
Grandparents/ Grandchildren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

Need lineage markers like Y-STRs

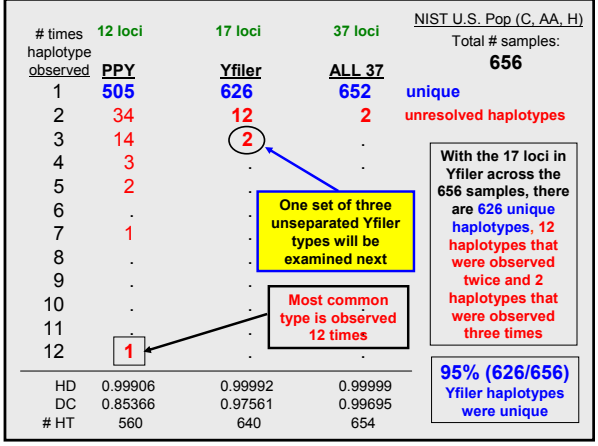
NIST Work with Additional Y-STR Loci

- Studies of Locus Variation
  - **37 Y-STRs** have been examined in all 665 NIST U.S. population samples and **92 Y-STRs** in a subset (32 C, 32 AA, 31 H) using previously published primers and 3-5plexes
- Analysis of Mutation Rates
  - **389 father/son pairs** with **17 Yfiler loci**
- Further characterization of SRM 2395 components
  - To enable calibration with additional Y-STRs
- Defining allele nomenclature on **144 Y-STRs**
  - To aid on-going genetic genealogy work

Are there advantages to typing additional loci beyond the PowerPlex Y 12 or the Yfiler 17 Y-STRs?


Available online at www.sciencedirect.com
ScienceDirect
ELSEVIER
FSI GENETICS
Forensic Science International: Genetics 1 (2007) 215–217
Short communication
The impact of additional Y-STR loci on resolving common haplotypes and closely related individuals☆
A.E. Decker *, M.C. Kline, P.M. Vallone, J.M. Butler
National Institute of Standards and Technology, Biochemical Science Division, Gaithersburg, MD 20899, United States
Received 23 January 2007; accepted 27 January 2007

Full 37 locus haplotypes available on STRBase:
http://www.cstl.nist.gov/biotech/strbase/NISTpopdata/HispanicsHaplotype37.pdf
http://www.cstl.nist.gov/biotech/strbase/NISTpopdata/CaucasiansHaplotype37.pdf
http://www.cstl.nist.gov/biotech/strbase/NISTpopdata/AfricanAmericansHaplotype37.pdf

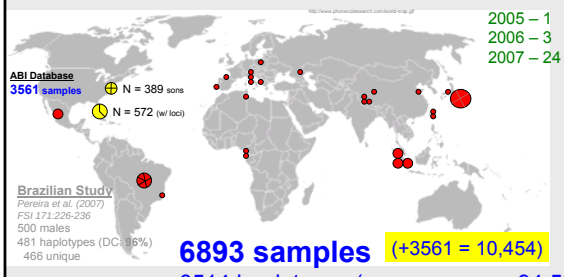


Lessons Learned from NIST Data Set

- Some Y-STRs that are more useful than others in sub-dividing common haplotypes (e.g., DYS576)
- You don't gain much by typing additional Y-STRs (most unresolved types only occur twice)
- **95% of 17 locus Yfiler haplotypes are unique**

Sources of Yfiler Worldwide Population Data

28 published population studies with Yfiler data



6893 samples (+3561 = 10,454)

6514 haplotypes (discrimination capacity 94.5%)

6257 unique haplotypes **(96.0% unique)**

Summaries of Recent Worldwide Yfiler Data

- **10,454 Yfiler profiles** now available
  - 3561 current Yfiler database + 6893 published data
- ~95% of the time a complete 17 locus Yfiler profile will be unique
- However, just like mtDNA, common types do exist so many of the remaining Yfiler haplotypes are shared (present in multiple individuals)

To Summarize…

Autosomal STRs

- **26 unlinked loci** have been characterized and we have developed multiple miniplexes and a megaplex (23plex)
- Additional loci show value with relationship testing
- **NIST SRM 2391b** will include information on additional autosomal STR loci

Y-Chromosome STRs

- Studies at NIST and worldwide show ~95% of observed 17 locus Yfiler profiles are unique
- Additional loci can help with common types
- **NIST SRM 2395** will include information on additional Y-STR loci

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

Promega Meeting Proceedings Paper


New Autosomal and Y-Chromosome STR Loci Butler *et al.*

New Autosomal and Y-Chromosome STR Loci:
Characterization and Potential Uses*

John M. Butler[1], Carolyn R. Hill[1], Amy E. Decker[1], Margaret C. Kline[1], Thomas M. Reid[2], and Peter M. Vallone[1]

[1]Biochemical Science Division, National Institute of Standards and Technology, Gaithersburg MD 20899
[2]DNA Diagnostics Center, Fairfield, OH 45014

http://www.cstl.nist.gov/biotech/strbase/pub_pres/Promega2007_NewSTRloci.pdf

- **42 page article** available on STRBase and Promega site
- Describes 26 miniSTR loci
- Covers 23plex STR assay
- Includes world-wide Yfiler data review

STRs vs SNPs Article


Forensic Sci Med Pathol (2007) 3:200–205
DOI 10.1007/s12024-007-0018-1

ORIGINAL PAPER

STRs vs. SNPs: thoughts on the future of forensic DNA testing

John M. Butler · Michael D. Coble · Peter M. Vallone

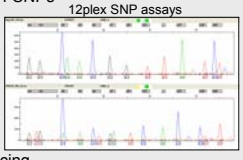
- Describes challenges with SNPs in terms of mixture detection and interpretation
- Most likely use of SNPs is as ancestry-informative markers (AIMs)

Butler *et al.* (2007) STRs vs SNPs: thoughts on the future of forensic DNA testing. *Forensic Science, Medicine and Pathology* 3:200-205.

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)
  - Performed Y-SNP typing
- Dr. Michael Coble (AFDIL)
  - mitochondrial control region sequencing
- Data currently under review

12plex SNP assays



Rapid PCR

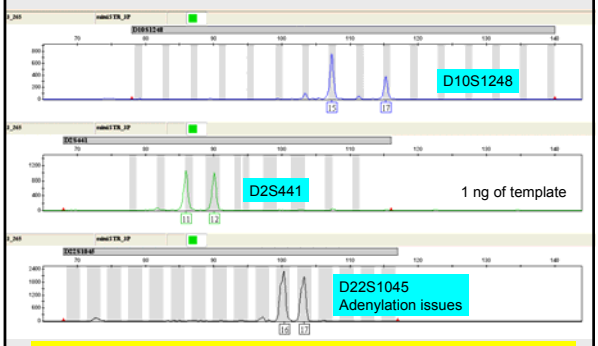
- Existing commercial STR typing kits are not optimized for rapid PCR
- Challenge for miniaturize STR typing platforms – since they are tied into the commercial kits/loci
- Fewer loci and smaller amplicon size favor rapid multiplex PCR
- We have well characterized miniSTR panels

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.

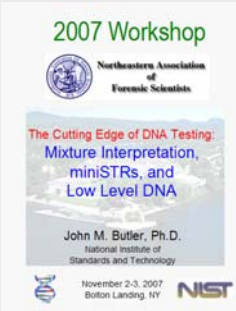
3plex

Training Workshops
and Other Topics

Training Workshops Since July 2007

- ISFG Meeting (**August 2007**, Copenhagen, Denmark)
  - **CE Fundaments and Troubleshooting**
  - **Validation**
- SAFS Meeting (**September 2007**, Atlanta, GA)
  - **Mixture Interpretation**
- Int. Symposium on Human Identification (Promega) Meeting (**October 2007**, Hollywood, CA)
  - **Validation**
- NEAFS Meeting (**November 2007**, Bolton Landing, NY)
  - **Mixture Interpretation**
  - **Low-copy Number DNA Issues**
  - **miniSTRs**

NEAFS Workshop on "The Cutting Edge of DNA Testing"



- 42 participants from 13 different labs
- **70 page handout from workshop available for download**
  (see training section of STRBase)
- Contains up-to-date references on mixture interpretation, miniSTRs, and LCN DNA analysis

http://www.cstl.nist.gov/biotech/strbase/pub_pres/NEAFS2007_CuttingEdgeDNA.pdf

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)

158 page handout prepared

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 Sgueglia (MA)
  - Angela Dolph (Marshall U./NIST)
  - Tim Kalafut (USACIL)

196 page handout prepared

Workshop Presenters


Ann Marie Gross
MN BCA


John M. Butler
NIST


George Carmody
Carleton University/
Statistical Consultant


Gary Shutler
Wash State Police
Crime Lab


Angie Dolph
Marshall University
(NIST Summer Intern)


Joanne B. Sgueglia
Mass State Police
Crime Lab


Tim Kalafut
US Army
Crime Lab

Morning Agenda - **Theory**

Background and Introductory Information
8:30 a.m. – 9:00 a.m. – John Butler

Survey Results on Numbers and Types of Casework Mixtures
9:00 a.m. – 9:15 a.m. – Ann Gross

Principles in Mixture Interpretation
9:15 a.m. – 10:15 a.m. – John Butler

***10:15 a.m. – 10:30 a.m.* BREAK**

Strategies for Mixture Deconvolution with Worked Examples
10:30 a.m. – 11:30 a.m. – John Butler

Different Approaches to Statistical Analysis of Mixtures
11:30 a.m. – 12:00 p.m. – George Carmody

***12:00 p.m. – 1:15 p.m.* LUNCH**

Afternoon Agenda – **Practical Application**

Real Case Example – Importance of Properly Stating Your Conclusions
1:15 p.m. – 1:30 p.m. – Gary Shutler

Variability between Labs in Approaches & Mixture Interlaboratory Studies
1:30 p.m. – 2:15 p.m. – John Butler

Validation Studies and Preparing Mixture Interpretation Guidelines
2:15 p.m. – 2:45 p.m. – Joanne Sgueglia

***2:45 p.m. – 3:00 p.m.* BREAK**

Testing of Mixture Software Programs
3:00 p.m. – 3:15 p.m. – Angela Dolph

DNA_DataAnalysis Software Demonstration
3:15 p.m. – 4:00 p.m. – Tim Kalafut

Training Your Staff to Consistently Interpret Mixtures
4:00 p.m. – 4:45 p.m. – Panel Discussion with Ann Gross, Gary Shutler, Joanne Sgueglia

***4:45 p.m. – 5:00 p.m.* – Questions and Answers as needed**

Upcoming Lawyer Training…

- NY State Prosecutors in West Point, NY
  - **March 5, 2008**
  - Will address "Emerging Issues" similar to NDAA talk in May 2007
- Defense Attorneys in Richmond, VA
  - **April 25, 2008**
  - Invited to address subject of mixture interpretation

Planned Promega 2008 Meeting Troubleshooting Workshop

- Title: **"Principles of Interpretation and Troubleshooting of Forensic DNA Typing Systems"**
- Instructors: **John Butler (NIST) and Bruce McCord (FIU)**
- Date: **October 16, 2008** with Promega Int. Symp. Human ID

The workshop will consist of three parts:
(1) a through examination of theoretical issues with capillary electrophoresis PCR amplification of short tandem repeat markers
(2) a discussion of how to properly set instrument parameters to interpret data (including mixtures), and
(3) **a review of specific problems seen by labs** submitting problematic data and commentary on possible troubleshooting solutions.

Seeking input of problems observed with CE systems

Forensic Science International: Genetics

http://www.fsigenetics.com/

Editor-in-Chief:
Angel Carracedo (Spain)
Associate Editors:
Peter M. Schneider (Germany)
John M. Butler (USA)

FSI: Genetics is a new journal dedicated exclusively to the field of forensic genetics. It has been launched in 2007 by Elsevier Publishers in affiliation with the International Society of Forensic Genetics. **All members of the ISFG receive a free subscription of this journal** (print and online version) as part of their membership benefits.

New ISFG Website

Contents of *FSI Genetics* March 2007 (first issue)

http://www.fsigenetics.com/current

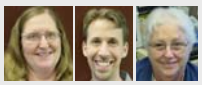
- Launching *Forensic Science International* daughter journal in 2007:*Forensic Science International: Genetics*
- DNA Commission of the International Society for Forensic Genetics (ISFG): Recommendations regarding the role of forensic genetics for disaster victim identification (DVI)
- Extended guidelines for mtDNA typing of population data in forensic science
- Towards unc
- A modular re mitochondria
- Forensic mit technology
- Coding regio
- MiniY-STR c
- The prevalen population
- Review artic
- **Internationa**

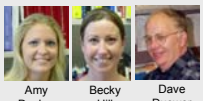
Thank you for your attention…

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


Margaret Kline | Pete Vallone | Jan Redman


Amy Decker | Becky Hill | Dave Duewer

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