

NIST Research Update

Michael Coble

Peter M. Vallone, Margaret C. Kline, Amy E. Decker, Janette W. Redman, Becky Hill, David L. Duewer, John Butler

April 4, 2005

EDNAP Meeting – Glasgow, Scotland

NIST Human Identity Project Team



John Butler (Project Leader)
Pete Vallone
Margaret Kline
Jan Redman
Amy Decker
Mike Coble
Dave Duewer
Becky Hill (new hire)


Funding:
Interagency Agreement between National Institute of Justice and NIST Office of Law Enforcement Standards



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


Current Areas of NIST Research Effort

- **Standard Information Resources** (STRBase information, training materials/review articles, validation standardization, calibration datasets)
- **Interlaboratory Studies** (Real-time PCR, mixture interpretation)
- **Resources for “Challenging Samples”** (miniSTRs for degraded DNA)
- **Information on New Loci** (Y-Chromosome, new STRs)



Standard Information Resources

STRBase, training materials, variant allele sequencing etc.




STRBase Updates
(since July 2004)

- Validation section
- miniSTR section
- Y-chromosome information (multiplexes & databases)
- Population data summary & OmniPop program download (courtesy of Brian Burritt)
- Reference Sequences for Commonly Used STR Markers

More minor additions

- Additional commercial STR kit schematics (Yfiler, PowerPlex Y)
- Published Promega primers (added PP16)
- Additional NIST publications/presentations (14 new talks, 12 new papers)
- Additional variant alleles & scientist addresses

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



NEAFS Workshop Slide Handouts

Handouts available as downloadable pdf files from <http://www.cstl.nist.gov/biotech/strbase/NISTpub.htm#NEAFSworkshop>


2 day workshop with **>500 slides** describing STRs and CE (ABI 310 and ABI 3100)

NEAFS CE-DNA Workshop (Butler and McCord) Sept 29-30, 2004

Capillary Electrophoresis in DNA Analysis

STR Analysis

NEAFS Workshop
Mystic, CT
September 29-30, 2004
Dr. John M. Butler
Dr. Brian R. McCord



Outline for Workshop

- Introductions
- STR Analysis
- Introduction to CE and ABI 310
- Data Interpretation
- Additional Topics – Real-time PCR and miniSTRs
- Higher Throughput Approaches
- Troubleshooting the ABI 310 (Participant Roundtable)
- Additional Topics – Y-STRs, validation, accuracy
- Review and Test

Review Article on STRs and CE

pdf available from <http://www.cstl.nist.gov/biotech/strbase/NISTpub.htm>

Electrophoresis 2004, 25, 1397-1412

Review

John M. Butler¹
Eric Basi²
FedERICA Crivellente^{3*}
Bruce R. McCord³

Forensic DNA using the ABI PRISM for STR anal

DNA typing with short applications including such as the ABI PRISM for many laboratories including sample preparation results using CE system in the context of throughput and ease

Contents

1	Introduction	1397
1.1	General aspects	1397
1.2	Early work with CE	1400
2	Sample preparation and injection	1401
3	Sample separation	1402
3.1	The polymer separation matrix	1403
3.2	The buffer	1403
3.3	The capillary	1404
4	Sample detection	1405
5	Software used	1406
5.1	Assessing resolution of DNA separations	1406
5.2	Applications of forensic DNA testing	1407
6	Forensic casework	1407
6.1	DNA databasing	1408
6.2	Increasing sample throughput	1408
7	Capillary array electrophoresis systems	1408
7.1	Microchip CE systems	1409
7.2	Future methods for DNA typing with STR markers	1410
7.3	References	1410
8		

FORENSIC DNA TYPING

JOHN M. BUTLER

Biology and Technology behind STR Markers - Second Edition

John M. Butler

Listed on amazon.com

Published February 2005

ACADEMIC PRESS Forensic Science

Validation Standardization Efforts

Presentation at Promega meeting (October 2004)

<http://www.cstl.nist.gov/biotech/strbase/validation.htm>

We have been contacted by NFSTC with the desire to collaborate on validation standardization—they do not plan to produce validation kits now but rather have a workbook to help members of the community with validation...

Can Validation be Standardized?

Validation Standardization Questionnaire (conducted June-August 2004)

Statements from survey responders...
Over 86% (45/52) said yes

Those who responded "no" said

- to some degree it can be, however, validation is specific to the platform, kits, ...
- a start-up lab should do much more than an experienced lab...
- validation builds on previous work by lab or published data
- parts of it can be standardized; I don't think the non-probative cases could be, and
- only in a general way, as with the SWGDAM guidelines. The uniqueness of each new procedure would make standardization difficult.

Our Conclusion...
to a certain extent it can...but everyone will always have a different comfort level...and inflexible, absolute numbers for defined studies will not likely be widely accepted

New Validation Homepage on STRBase

<http://www.cstl.nist.gov/biotech/strbase/validation.htm>

Validation Information to Aid Forensic DNA Laboratories

Validation Summary Sheets

We are initiating an effort to catalog literature. The purpose of this effort is to list the number of samples tested, and the number of samples analyzed by forensic DNA laboratories. SWGDAM Revised Validation Guidelines are documented and summarized:

Kit, Assay, or Instrument	Ref	How?
PowerPlex Y	102	102
Profiler Plus	102	102
COiler	102	102
AmplifSTR Blue	102	102
AmplifSTR Green 1	102	102

Other information and conclusions

Validation Summary Sheet for PowerPlex Y

Study Completed (17 studies done)	Description of Samples Tested (performed in 7 labs and Promega)	# Run
Single Source (Concordance)	5 samples x 8 labs	40
Mixture Ratio (male:female)	6 labs x 2 M:F mixture series x 11 ratios (1:0, 1:1, 1:10, 1:50, 1:100, 0.5:300, 0.25:300, 0.125:300, 0.0625:300, 0.03300 ng M:F)	132
Mixture Ratio (male:male)	6 labs x 2 MM mixtures series x 11 ratios (1:0, 19:1, 9:1, 5:1, 2:1, 1:1, 1:2, 1:5, 1:9, 1:19, 0:1)	132
Sensitivity	7 labs x 2 series x 6 amounts (1/0.5/0.25/0.125/0.06/0.03)	84
Non-Human	24 animals	24
NIST SRM	6 components of SRM 2395	6
Precision (ABI 3100 and ABI 377)	10 ladder replicates + 10 sample replicated + 8 ladders + 8 samples for 377	36
Non-Probative Cases	65 cases with 102 samples	102
Stutter	412 males used	412
Peak Height Ratio	N/A (except for DYS385 but no studies were noted)	
Cycling Parameters	5 cycles (28/27/26/25/24) x 8 punch sizes x 2 samples	80
Annealing Temperature	5 labs x 5 temperatures (54/58/60/62/64) x 1 sample	25
Reaction volume	5 volumes (50/25/15/12.5/6.25) x 5 amounts + 5 concentrations	50
Thermal cycler test	4 models (480/2400/9600/700) x 1 sample + 3 models x 3 sets x 12 samples	76
Male-specificity	2 females x 1 titration series (0-500 ng female DNA) x 5 amounts each	10
TaqGold polymerase titration	5 amounts (1.382, 0.692, 0.346, 0.173, 0.087) x 4 quantities (10, 50, 250, 13 ng DNA)	20
Primer pair titration	5 amounts (0.5x/0.75x/1.5x/3x/6x) x 4 quantities (10, 50, 250, 13 ng DNA)	20
Magnesium titration	5 amounts (1.1, 2.5, 5.1, 7.5, 15 mM Mg) x 4 quantities (10, 50, 250, 13 ng DNA)	20
Krenke et al. (2005) Forensic Sci. Int. 148: 1-14		TOTAL SAMPLES EXAMINED 1269

Laboratory Internal Validation Summaries

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

We invite updates to this table. Please contact John Butler <john.butler@nist.gov> if you would like to add a summary of your laboratory's validation studies with a particular forensic DNA test, instrument, or software program. Please submit information in a standard format summarizing the studies conducted, a description of sample run, and the number of samples examined using the downloadable Excel file [click here]

Summaries of Validation Studies Conducted in Individual Laboratories (not published in the literature)

Kit, Assay or Instrument	Laboratory	Submitter
PowerPlex 16 Kit with ABI 310	Pennsylvania State Police	Christina Tomasz
Quantifiler with ABI 7900	Alabama Department of Forensic Sciences	Angelo Trilla Mascias

Soliciting Information on Studies Performed by the Community

Study Category	Description of Samples Run with Comments on Volume	# of Samples	# of Laboratories
Single Source (Concordance)	8 samples (8 samples concordance x 200 samples each of population concordance study)	200	100
Mixtures	48	45	10
Mixture Ratio	1 sample x 11 ratios (1:10, 1:8, 1:4, 1:1, 1:1, 1:1, 1:1, 1:1, 1:1, 1:1, 1:1, 1:1) x 2 reactions (500 reactions)	22	33
Sensitivity	5 samples x 5 amounts (5000, 500, 50, 5, 1) x 5 replicates x 2 probes (40000-40000000)	55	33
Non-Human	11 animals	11	0
NIST SRM 2391a	12 components	12	12
Precision (ABI 310)	(5 samples x 10 reactions each) x 10 reactions of allele ladders	60	60
Non-Probable Cases	5 cases x 4 samples each (evidence EP37/AR200/AR200)	20	20
Stutter	200 samples (data used from population samples)	60	0
Peak Height Ratio	200 samples (data used from population samples)	60	0
Cycling Parameters	14 samples x 2 different cycle numbers (2002) x 2 reaction times (35 seconds)	56	0
Annealing Temperature	3 samples x 4 concentrations (2.0, 2.5, 3.0, 3.5) x 5 temperatures (55/55/55/55/55)	60	0
Proficiency	8 sets x 4 samples per set	36	12
Substrate	9 common substrates x 1 sample each	9	0
Environment	5 conditions (cold/dry/dark/low humidity) x 6 time points (1:1, 1:2, 1:3, 1:4, 1:5, 1:6)	30	0
Various Issues	Bone, hair, teeth, semen, perspiration, urine, blood, semen, vaginal fluid (minimum of one sample each)	9	0
TOTAL SAMPLES RUN		633	200

Goals of this Validation Standardization Project

- To help the community gain a better understanding of the validation process and how others have implemented validation in their labs so that validation in one's own lab may be performed more quickly
- To help with establishing uniformity throughout the field to aid auditors in their inspections

NIST QA/QC Software

Tool being developed by Dave Duewer for STR Process Control

Tracks Kit size standard in samples

Will be available soon for beta-testing; still working on user's manual (and will need NCBI file conversion program to be more easily accessible)

X	Y
103	436
104	569

This software does not perform genotyping.
It merely permits a view of analytical parameters over time.

Variant Allele Sequencing

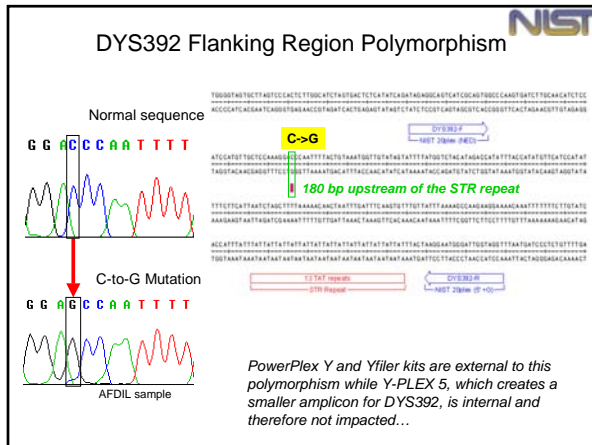
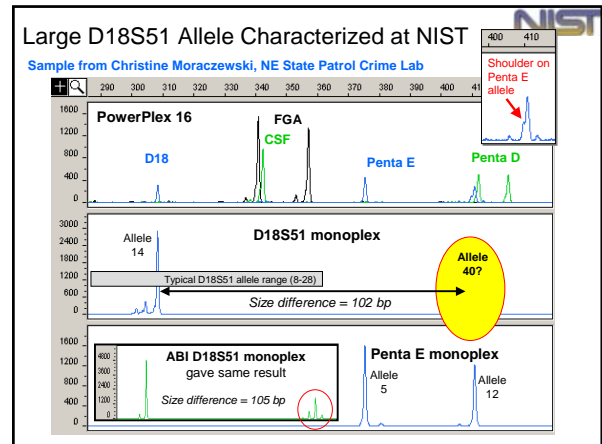
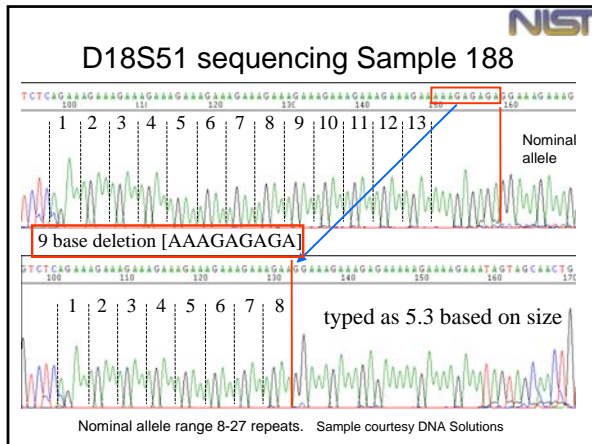
- Recent examples:
 - D18 null alleles
 - D18 large allele
 - DYS392 variant
- AAFS talk (Feb 26, 2005) by Margaret Kline on sequencing methods and applications
- We are happy to sequence unusual variant alleles for laboratories

Extreme D18S1 Variants

Range 258 – 396 bp

Samples amplified with Identifier. Nominal range 8 - 28
Small D18 allele just outside of the TPOX allele range.
Large D18 is 46 bp larger than the D18 allele range.

Gel Separation Of D18 Variant Alleles



Analysis of Common STR Variant Alleles

- We have monoplex primers for all common STR loci and kits
- We have sequencing primers that bind outside of STR kit primer sequence positions to enable view of polymorphic nucleotides that cause primer binding site mutations
- NIJ has funded us to characterize STR variants for the forensic DNA community

D16S539 (bottom strand)

Interlaboratory Studies

DNA Quantitation (2004) – in press (May issue JFS)

Mixture Interpretation (2005) – under evaluation

Mixture Interpretation Interlab Study (MIX05)

- Only involves interpretation of data
- As of early March, ~97 labs are enrolled for participation (22 from overseas) – Data are currently being evaluated.
- Four mock cases supplied with "victim" and "evidence" electropherograms (GeneScan .fsa files – that can be converted for Mac or GeneMapper; gel files MAC & NT made available to FMBIO labs)
- Data available with Profiler Plus, COfiler, SGM Plus, PowerPlex 16, Identifiler, PowerPlex 16 BIO (FMBIO) kits
- Summary of results with involve training materials to illustrate various approaches to solving mixtures

Perpetrator Profile(s) ??

Along with reasons for making calls and any stats that would be reported

NIST

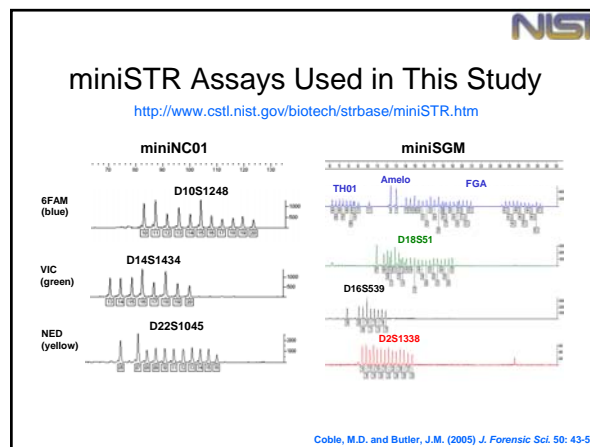
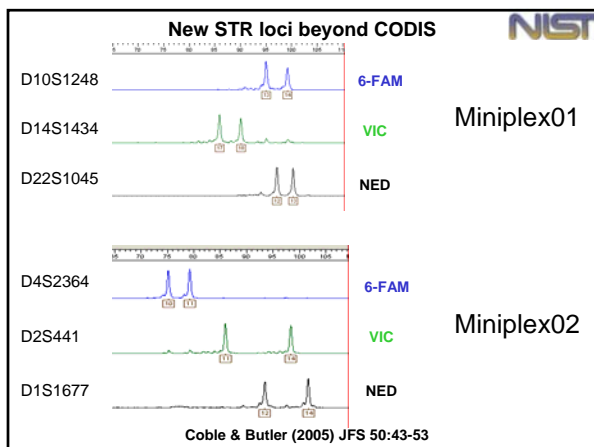
Resources for Challenging Samples

Degraded DNA and Mixtures

NIST

Degraded DNA work

- ENFSI study participation
 - compared STRs, miniSTRs, and autosomal SNPs on same set of degraded DNA samples provided by Peter Gill
- miniSTR website
 - <http://www.cstl.nist.gov/biotech/strbase/miniSTR.htm>
- New miniSTR loci published
 - http://www.cstl.nist.gov/biotech/strbase/pub_pres/Coble2005miniSTR.pdf
- SNP markers and assays
 - <http://www.cstl.nist.gov/biotech/strbase/SNP.htm>
- Performance of miniSTRs on shed hairs
 - Mike Coble spoke at AAFS (Feb 25, 2005)



NIST

Recovered Volumes from DNA Extractions – Sample 02

Sample	Recovered Volume (µL)	Approx. Quantity (ng/µL)	Approx. Final Conc. (ng/µL)	Sample	Recovered Volume (µL)	Approx. Quantity (ng/µL)	Approx. Final Conc. (ng/µL)
02 blood - day 0	22	3.8		02 saliva - day 0	17	6.45	
02 blood - day 0	26	4.36	5.161	02 saliva - day 0	17	17.74	8.952
02 blood - day 0	22	7.47		02 saliva - day 0	24	4.5	
02 blood - week 2	31	0.741		02 saliva - week 2	22	0.104	
02 blood - week 2	21	0.884	0.921	02 saliva - week 2	26	0.04	
02 blood - week 2	16	1.32		02 saliva - week 2	21	0.029	0.057
02 blood - week 8	37	0.188		02 saliva - week 8	26	0.01	
02 blood - week 8	25	0.237	0.249	02 saliva - week 8	17	0.015	0.013
02 blood - week 8	21	0.372		02 saliva - week 8	22	0.014	
02 blood - week 16	29	1.16		02 saliva - week 12	33	0.004	
02 blood - week 16	25	0.224	0.455	02 saliva - week 12	34	0.006	0.034
02 blood - week 16	38	0.968		02 saliva - week 12	27	0.106	
Reagent Blank	18	0	0.000	Reagent Blank	42	0	0.000

ENFSI Degraded DNA Collaborative Study

NIST

Summary of Results for Sample 02 Blood (Weeks 2, 8, 16)

	Week 2		Week 8		Week 16	
	SGM+	miniSGM	SGM+	miniSGM	SGM+	miniSGM
Amelo	++	++	Amelo	++	Amelo	++
TH01	++	++	TH01	++	TH01	++
FGA	failed	++	FGA	failed	FGA	failed
D18	drop out	drop out	D18	failed	D18	failed
D16	++	++	D16	failed	D16	++
D2	++	++	D2	failed	D2	++
	<u>miniNC01</u>		<u>miniNC01</u>		<u>miniNC01</u>	
D10	++		D10	++	D10	++
D14	++		D14	++	D14	++
D22	++		D22	++	D22	++

ENFSI Degraded DNA Collaborative Study

PCR Product Size Reduction Improves Recovery of STR Information from Telo-gen hairs

Int J Legal Med (2001) 114:269-273
 Hellmann, et al. (2001) Int. J. Legal Med. 114(4-5): 269-273
 © Springer-Verlag 2001

TECHNICAL NOTE

First use of miniSTRs for typing hair shafts

A. Hellmann · U. Rohleder · H. Schmitter · M. Wittig
STR typing of human telogen hairs – a new approach

108 bp size reduction

160 bp size reduction

Fig. 2 Typing efficiency (%) of single telogen hairs using vs-primer pairs (TH01)vs, n = 29) in comparison to primer pairs supplied by the AmpFSTR Green I PCR Amplification kit (TH01)gk, n = 48 + 36 from preliminary experiments) for the HUMTH01 locus

Fig. 4 Typing efficiency (%) of single telogen hairs using vs-primer pairs (TPOX)vs, n = 49) in comparison to primer pairs supplied by the AmpFSTR Green I PCR Amplification kit (TPOX)gk, n = 48 + 36 from preliminary experiments) for the HUMTPOX locus

DNA Quantitation with Real-Time PCR

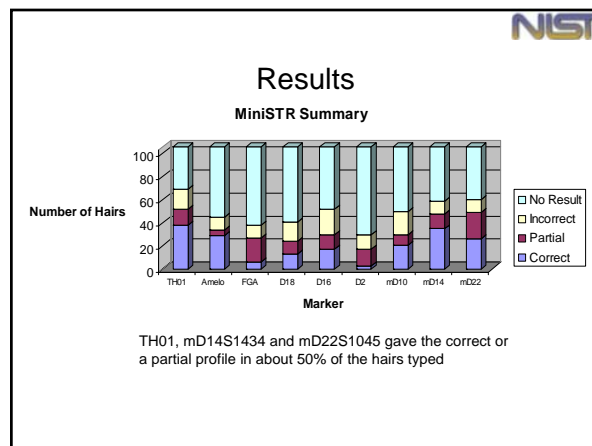
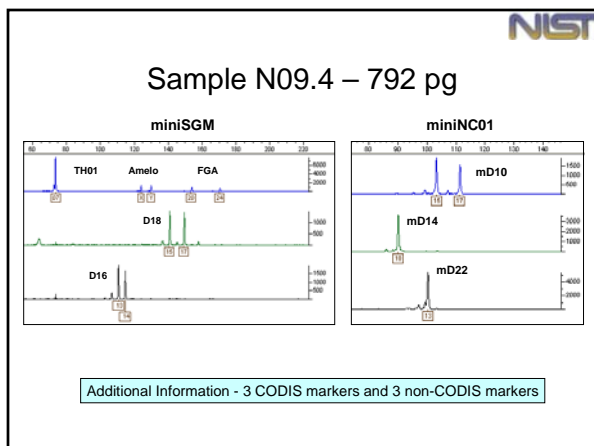
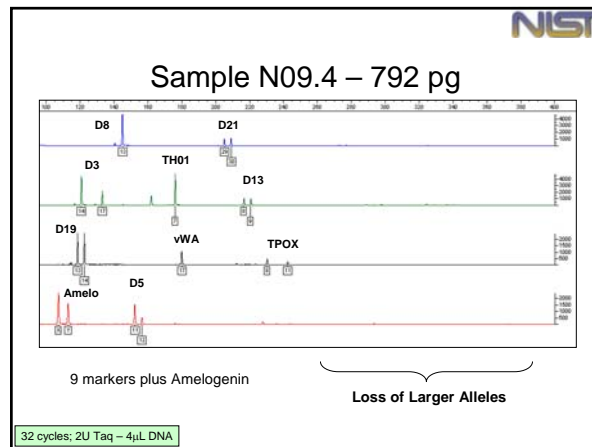
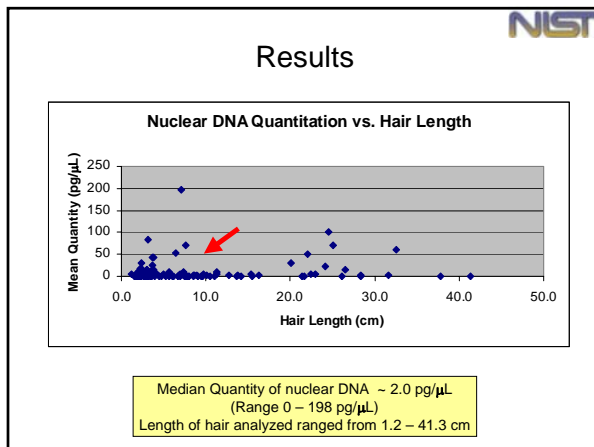
ABI 7500

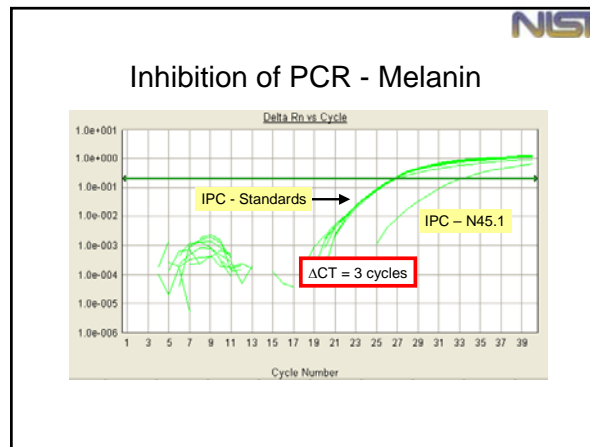
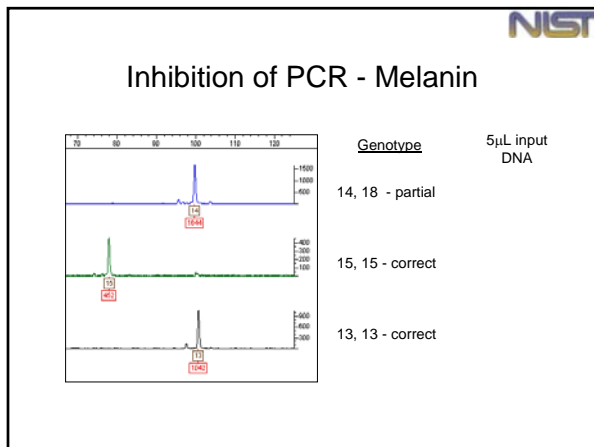
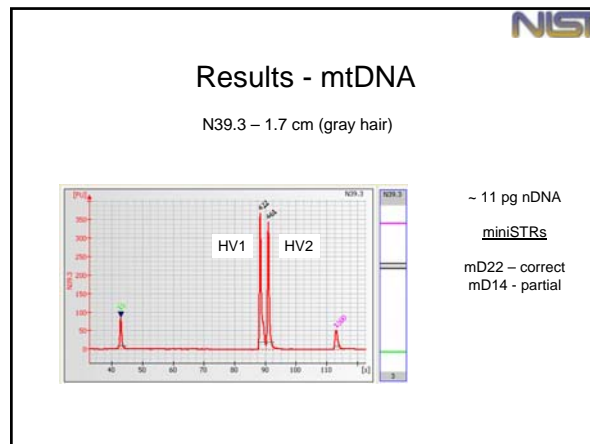
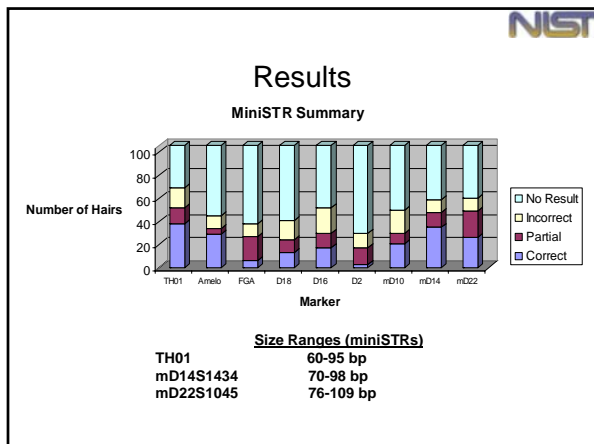
Quantifier assay

Standards

Internal Positive Control

Can Now Examine Low Levels of Nuclear DNA...





Recent Publications on miniSTRs

- Butler, J.M., Shen, Y., McCord, B.R. (2003) The development of reduced size STR amplicons as tools for analysis of degraded DNA. *J. Forensic Sci* 48(5): 1054-1064.
- Chung, D.T., Drabek, J., Opel, K.L., Butler, J.M., McCord, B.R. (2004) A study on the effects of degradation and template concentration on the efficiency of the STR multiplex primer sets. *J. Forensic Sci.* 49(4): 733-740.
- Drabek, J., Chung, D.T., Butler, J.M., McCord, B.R. (2004) Concordance study between multiplex STR assays and a commercial STR typing kit. *J. Forensic Sci.* 49(4): 859-860.
- Coble, M.D. and Butler, J.M. (2005) Characterization of new miniSTR loci to aid analysis of degraded DNA., *J. Forensic Sci.*, in press. (January 2005 issue)

<http://www.cstl.nist.gov/biotech/strbase/miniSTR.htm>
<http://www.cstl.nist.gov/biotech/strbase/miniSTR/timeline.htm>

Information on New Loci

Autosomal SNPs, Y-Chromosome

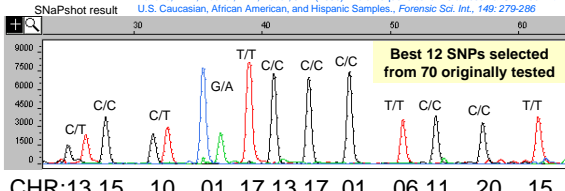
Standard U.S. Population Dataset

<http://www.cstl.nist.gov/biotech/strbase/NISTpop.htm>
 260 Caucasians, 260 African Americans, 140 Hispanics, 3 Asians = **663 males**

Genetic Markers	Loci Examined	Publications
Common STRs	Identifier kit 15 STRs (CODIS + D2S1338 & D19S433)	Butler et al. (2003) JFS
miniSTRs	All CODIS loci except D3S1358	Drabek et al. (2004) JFS
New autosomal STRs	New 6 loci for miniSTRs	Coble et al. (2005) JFS
Autosomal SNPs	70 C/T SNPs (Orchid panel)	Vallone et al. (2004) FSI
Common Y-STRs	22 loci (27 regions) Yfiler concordance study	Schoske et al. (2004) FSI <i>Data in ABI Yfiler database</i>
New Y-STRs	27 additional loci	Butler et al., in press FSI
Y-SNPs	50 loci spanning haplogroups A-R	Vallone et al. (2004) JFS
mtDNA	LINEAR ARRAY and coding mtSNPs Full control regions by AFDIL	Kline et al. (2005) JFS <i>inclusion in EMPOP</i>

NIST Autosomal 12plex SNP Assay

Vallone, P.M., Decker, A.E., Butler, J.M. (2005) Allele frequencies for 70 autosomal SNP loci with U.S. Caucasian, African American, and Hispanic Samples. *Forensic Sci. Int.*, 149: 279-296



12plex PCR followed by 12-plex ASPE
 Fragments separated on a ABI 3100 in 35 minutes
 A Genotyper macro has been developed to type data
 The 12plex assay has been run on over 600 samples
 Works well on 1-2 ng of template
 Sensitivity studies are underway along with degraded DNA

New Y-STR Loci, Issues, and Assays

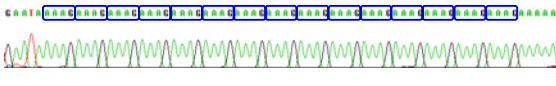
- Updates on Y-chromosome information
 – http://www.cstl.nist.gov/biotech/strbase/y_strs.htm
- Testing on 27 new Y-STR loci
 – Butler, J.M., Decker, A.E., Vallone, P.M., Kline, M.C. (2005) Allele frequencies for 27 Y-STR loci with U.S. Caucasian, African American, and Hispanic samples, *in press FSI*
- Chromosomal duplication issues
 – Butler, J.M., Decker, A.E., Kline, M.C., Vallone, P.M. (2005) Chromosomal duplications along the Y-chromosome and their potential impact on Y-STR interpretation, *in press JFS*

New Y-STR Loci, Issues, and Assays

- Updates on Y-chromosome information
 – http://www.cstl.nist.gov/biotech/strbase/y_strs.htm
- Testing on 27 new Y-STR loci
 – Butler, J.M., Decker, A.E., Vallone, P.M., Kline, M.C. (2005) Allele frequencies for 27 Y-STR loci with U.S. Caucasian, African American, and Hispanic samples, *in press FSI*
- Chromosomal duplication issues
 – Butler, J.M., Decker, A.E., Kline, M.C., Vallone, P.M. (2005) Chromosomal duplications along the Y-chromosome and their potential impact on Y-STR interpretation, *in press JFS*

DYS576

15 AAAG repeats



Allele	Combined Freq (N = 659)	Cau freq (N = 261)	Afr Am freq (N = 258)	Hisp freq (N = 140)
13	0.0030	0.0038	0.0039	0.0000
14	0.0273	0.0115	0.0426	0.0286
15	0.1047	0.0421	0.1977	0.0500
16	0.1745	0.1762	0.2016	0.1214
17	0.2640	0.2635	0.2209	0.3071
18	0.2822	0.3257	0.2403	0.2786
19	0.1077	0.1188	0.0698	0.1571
20	0.0288	0.0307	0.0194	0.0429
21	0.0076	0.0077	0.0039	0.0143

Butler et al. (2005) in press FSI

Our Recent Y-Chromosome Work

[pdf files available at http://www.cstl.nist.gov/biotech/strbase/NISTpub.htm](http://www.cstl.nist.gov/biotech/strbase/NISTpub.htm)

- Schoske, R., Vallone, P.M., Kline, M.C., Redman, J.W., Butler, J.M. (2004) High-throughput Y-STR typing of U.S. populations with 27 regions of the Y chromosome using two multiplex PCR assays, *Forensic Sci. Int.* 139: 107-121.
- Vallone, P.M. and Butler, J.M. (2004) Multiplexed assays for evaluation of Y-SNP markers in U.S. populations. *Progress in Forensic Genetics 10*, Elsevier Science: Amsterdam, The Netherlands, International Congress Series 1261, 85-87.
- Butler, J.M. and Schoske, R. (2004) Forensic value of the multi-copy Y-STR marker DYS464. *Progress in Forensic Genetics 10*, Elsevier Science: Amsterdam, The Netherlands, International Congress Series 1261, 278-280.
- Butler, J.M. and Schoske, R. (2004) Duplication of DYS19 flanking regions in other parts of the Y chromosome. *Int. J. Legal Med.*, 118: 178-183.
- Vallone, P.M. and Butler, J.M. (2004) Y-SNP typing of U.S. African American and Caucasian samples using allele-specific hybridization and primer extension. *J. Forensic Sci.* 49(4): 723-732.
- Butler, J.M., Decker, A.E., Kline, M.C., Vallone, P.M. (2005) Chromosomal duplications along the Y-chromosome and their potential impact on Y-STR interpretation. *J. Forensic Sci.*, in press.
- Butler, J.M., Decker, A.E., Vallone, P.M., Kline, M.C. (2005) Allele Frequencies for 27 Y-STR Loci with U.S. Caucasian, African American, and Hispanic Samples. *Forensic Sci. Int.*, in press.
- Butler, J.M. and Schoske, R. (2005) U.S. population data for the multi-copy Y-STR locus DYS464. *J. Forensic Sci.*, in press.

Mitochondrial DNA Work

- Evaluation of Roche LINEAR ARRAY screening assay. Kline et al. (2005) JFS 50: 377-385
- Comparison of LINEAR ARRAY resolution to control region sequencing performed by AFDIL
- Collaboration with AFDIL (Tom Parsons) for developing coding SNP assays using SNaPshot

Coble, M.D., Just, R.S., O'Callaghan, J.E., Letmanyi, I.H., Peterson, C.T., Irwin, J.A., Parsons, T.J. (2004) Single nucleotide polymorphisms over the entire mtDNA genome that increase the power of forensic testing in Caucasians. *Int. J. Legal Med.*, 118: 137-146.

Vallone, P.M., Just, R.S., Coble, M.D., Butler, J.M., Parsons, T.J. (2004) A multiplex allele-specific primer extension assay for forensically informative SNPs distributed throughout the mitochondrial genome. *Int. J. Legal Med.*, 118: 147-157.

Acknowledgements

NIST Project Team:

- John Butler
- Pete Vallone
- Margaret Kline
- Jan Redman
- Amy Decker
- Becky Hill
- Dave Duewer

Funding:

Interagency Agreement between
National Institute of Justice and
NIST Office of Law Enforcement
Standards

michael.coble@nist.gov

This presentation available as pdf file from
<http://www.cstl.nist.gov/biotech/strbase/NISTpub.htm>