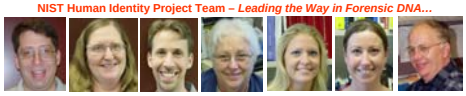
NIST Human Identity Project Team – *Leading the Way in Forensic DNA…*



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

NIST Human Identity Team Projects

John M. Butler, Ph.D.
National Institute of Standards and Technology

EDNAP and 26th ENFSI DNA Working Group Meeting

April 17-20, 2007
Krakow, Poland

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

Some Workshops Conducted This Past Year

- **qPCR workshop by Vallone and Orrego** (July 2006)
  slides available on STRBase
  – **http://www.cstl.nist.gov/biotech/strbase/qPCRworkshop.htm**
- **LCN workshop by Butler, Caragine, and Gill** (May 2006)
  Butler slides available on STRBase
  – **http://www.cstl.nist.gov/biotech/strbase/training.htm**
  Peter Gill's talk covered LoComatioN software (see *Forensic Sci. Int.* 2007, 116: 128-138)
- **Y-STR and mtDNA workshop by Butler and Coble** (Nov 2006)
  >600 slides available on STRBase
  – **http://www.cstl.nist.gov/biotech/strbase/YmtDNAworkshop.htm**

Training Workshops Planned

- ISFG Meeting (August 2007, Copenhagen, Denmark)
  – **CE Fundaments and Troubleshooting**
  – **Validation**
- SAFS Meeting (September 2007, Atlanta, GA)
  – **Mixture Interpretation**

Profiles in DNA (Promega Corporation), vol. 9(2), pp. 3-6

PROFILES IN DNA

VALIDATION

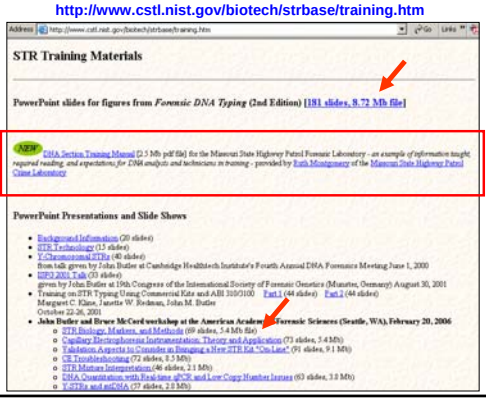
http://www.promega.com/profiles/902/ProfilesInDNA_902_03.pdf

Debunking Some Urban Legends Surrounding Validation Within the Forensic DNA Community

By John Butler
National Institute of Standards and Technology, Gaithersburg, Maryland, USA

Training Resources on STRBase…

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



Technology: NIST Research Programs

- miniSTRs
- Y-chromosome STRs
- mtDNA
- SNPs
- qPCR for DNA quantitation
- DNA stability studies
- Variant allele characterization and sequencing
- Software tools
- Expert System review
- Assay development with collaborators

Steps in Applying Forensic DNA Technology

Role of the NIST Human Identity Project Team

Loci Described
Assay Construction
Population Study
Information Gathered
STRBase website

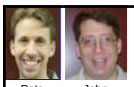
Kit Development
Kit Testing
Release to Community

Internal Validation
Use in Casework
Court Presentation/ Acceptance

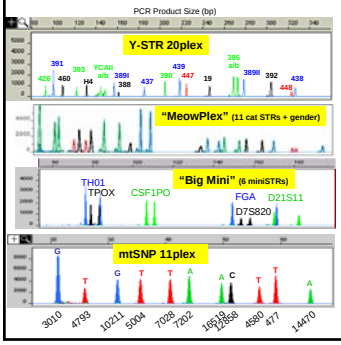
Research — *NIJ-Funded or Other*
Development — *Company (e.g., ABI)*
Forensic Application — *Forensic Labs*

Assay Development with Collaborators

(Usually Other NIJ-Funded Researchers)



Pete Vallone — John Butler



- **Y-STR 20plex** (Mike Hammer and Alan Redd)
  - Butler et al. (2002) FSI
- **Cat STRs** (Marilyn Raymond and Victor David)
  - Butler et al. (2002) Profiles in DNA
  - Raymond et al. (2005) JFS
- **miniSTRs** (Bruce McCord)
  - Butler et al. (2003) JFS
- **mtDNA coding region SNPs** (AFDIL)
  - Vallone et al. (2004) IJLM
- Others: **Dog STRs, ancestry SNPs, phenotype SNPs, additional autosomal STRs...**

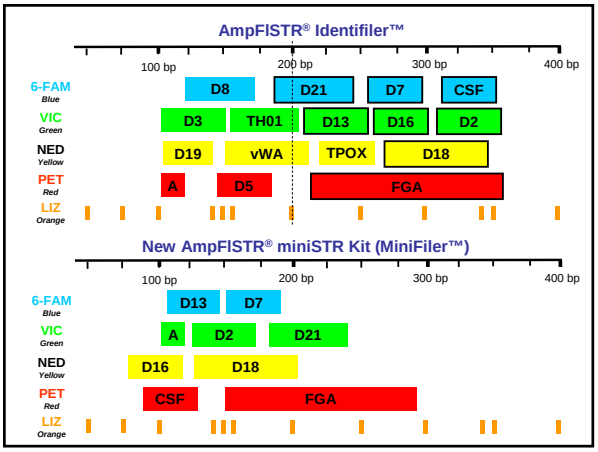
Becky Hill — Mike Coble — John Butler

miniSTRs, MiniFiler, and Non-CODIS (NC) Loci

No longer at NIST (AFDIL Research Section Chief since April 2006)

- **MiniFiler:** concordance study with ABI (Hill *et al. J. Forensic Sci., in press*)
- **New Non-CODIS (NC) Loci: 26 STR loci with allele sizes below 140 bp and good heterozygosities (above TPOX level)** tested on NIST **665 U.S. population samples; physically unlinked** to the 13 CODIS core loci; **article submitted** regarding primer sequences and locus characterization including population statistics
- **SRM 2391b components are being certified** through sequencing for D10S1248, D2S441, D22S1045; for reference purposes, genotypes for standard samples (9947A, 9948, 007, K562) are available on STRBase

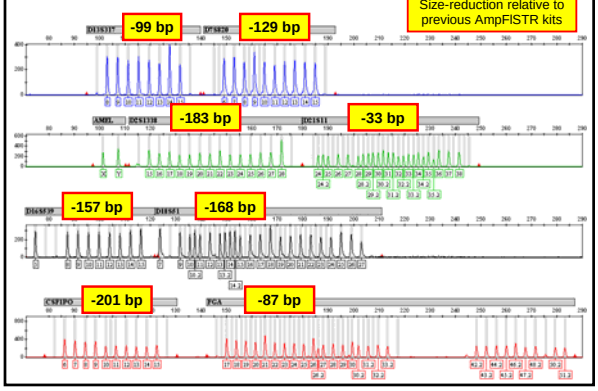
http://www.cstl.nist.gov/biotech/strbase/newSTRs.htm



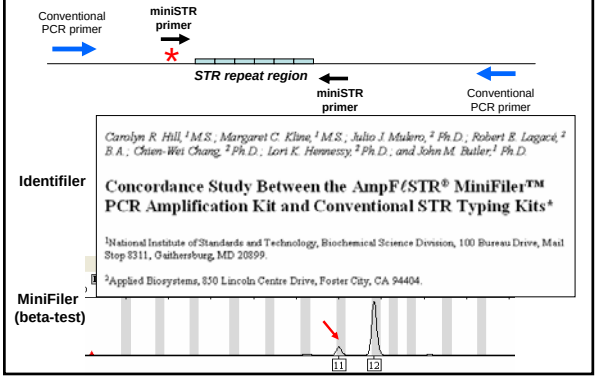
MiniFiler Allelic Ladders

(Beta-test materials)

Size-reduction relative to previous AmpFlSTR kits



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

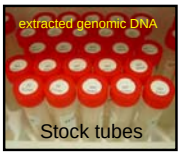


Standard U.S. Population Dataset

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

260 Caucasians, 260 African Americans, 140 Hispanics, 3 Asians = **663 males**

DNA extracted from whole blood (anonymous; self-identified ethnicities) received from Interstate Blood Bank (Memphis, TN) and Millennium Biotech Inc. (Ft. Lauderdale, FL)



To date: (>120,000 allele calls)

Identifiler (15 autosomal markers + Amelogenin) (10,608)
Roche Linear Arrays (HV1/HV2 10 regions) (6,630)
Y STRs 22 loci—27 amplicons (17,388)
Y STRs 27 new loci (14,535)
Yfiler kit 17 loci (11,237)
MiniFiler kit (5,248)
Y SNPs 50 markers on sub-set of samples (11,498)
Orchid 70 autosomal SNPs on sub-set (13,230)
miniSTR testing-new loci and CODIS concordance (9,228)
Ancestry informative SNPs (15,840)
New miniSTR loci – for 26 loci, 17,238 genotypes
mtDNA full control region sequences by AFDIL

Genotypes with various human identity testing markers

Summary of Samples Typed with ABI MiniFiler kit at NIST and ABI

- Primarily only population samples examined – no extensive sensitivity or degraded DNA tests were performed

1,308 samples **Allele concordance = 10,437/10,464 = 99.7%**

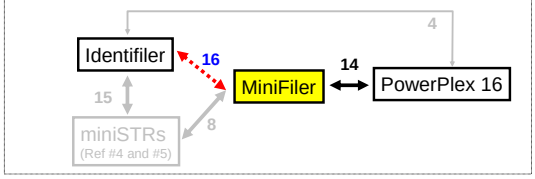
- **656 NIST U.S. population samples**
  - 260 Caucasian, 253 African American, 140 Hispanic, 3 Asian
  - Previously examined with **Identifiler; also with PowerPlex 16**
  - Also tested with Butler *et al.* (2003) **published miniSTR primers**
  - http://www.cstl.nist.gov/biotech/strbase/NISTpop.htm
- **481 father-son pairs**
  - 184 Caucasian, 196 African American, 101 Asian samples (provided by paternity testing company DDC)
  - Previously examined with **Identifiler**
- **171 samples from Applied Biosystems**

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., in press.*

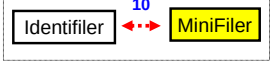
MiniFiler Concordance Study

27 Discordant Calls

656 NIST U.S. population samples



481 father-son samples



171 ABI samples

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., in press.*

Partial Summary of Discordant Calls

27 Discordant Calls **0.26 % discordance** (primarily D13, D16) **10,464 genotype comparisons** (1,308 samples x 8 loci)

	Locus	Ethnicity	MiniFiler	Identifiler	Genetic Variation
1	CSF1PO	H	11,11	11, "**11.1**"	One base insertion in Identifiler amplicon outside of MiniFiler and PP16 primers
2	D7S820	AA	8,11	8,"**9.3**"	5 base deletion in Identifiler amplicon outside of MiniFiler and PP16 primers
3	D13S317	H	**11**,11	9,11	4 base deletion in the reverse MiniFiler primer binding region
10	D13S317	AA	**11**,11	9,11	*(same as sample #3)*
11	D13S317	AA	**12**,12	9,12	*(same as sample #3)*
13	D13S317	C	**12**,12	9,12	*(same as sample #3)*
18	D16S539	AA	**12**,12	11,12	A → G SNP in MiniFiler primer binding site
19	D16S539	AA	**11**,11	9,11	*(same as sample #18)*
20	D16S539	AA	**14**,14	11,14	*(same as sample #18)*
21	D16S539	AA	9,**9**	9,11	*(same as sample #18)*
26	D16S539	A	**11**,11	10,11	G → A SNP in MiniFiler primer binding site
27	D18S51	H	13,15	**15**,15	Allele 13 C → T SNP in Identifiler primer binding site

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., in press.*

Apparent Null Alleles Observed During Concordance Studies

New Section of STRBase (launched to track MiniFiler discordance and allele dropout frequency):
http://www.cstl.nist.gov/biotech/strbase/NullAlleles.htm

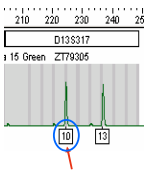
Locus	STR Kits/Assays Compared	Results	Frequency of Primer Binding Site Mutation	Source
CSF1PO	MiniFiler vs ID vs PP16	MF: 11,11 and ID: 11,11.1 One base insertion in Identifiler amplicon outside of MiniFiler and PP16 primers	1/1308	Hill *et al.* (2007)
CSF1PO	PP16 vs COfiler	Loss of allele 14 with COfiler, fine with PP16	2/1537	Budowle *et al.* (2001)
FGA	SGM vs SGM Plus	Loss of allele 26 with SGM Plus; weak amp of same allele with SGM		Cotton *et al.* (2000)
FGA	PP16 vs ProPlus	Loss of allele 22 with ProPlus; fine with PP16		Budowle and Sprecher (2001)
TH01	PP16 vs COfiler	Loss of allele 9 with COfiler, fine with PP16	1/1537	Budowle *et al.* (2001)
TH01	SGM vs SGM Plus	Loss of allele 6 with SGM Plus; fine with SGM	1/4045	Clayton *et al.* (2004)
VWA	PP1.1 vs ProPlus	Loss of allele 19 with ProPlus; fine with PP1.1	2/1483	Kline *et al.* (1998) and Walsh (1998)
VWA	PP16 vs ProPlus	Loss of alleles 15 and 17 with ProPlus; fine with PP16	2/1537	Budowle *et al.* (2001)
VWA	ID vs miniplexes	Loss of alleles 12, 13, and 14 with miniplex assay; fine with ID	9/532	Drabek *et al.* (2004)

Examination of **D13S317** Concordance:

African American sample ZT79305

Drabek, J., Chung, D.T., Butler, J.M., McCord, B.R. (2004) Concordance study between miniplex STR assays and a commercial STR typing kit. *J. Forensic Sci.* 49(4): 859-860.

NIST Identifiler data

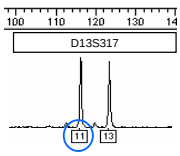


Really "11-1" allele

10,13

Reverse primer is outside deletion

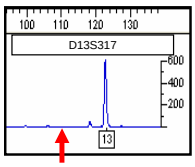
Ohio U miniSTR data



11,13

Reverse primer is inside deletion

AB miniSTR beta-test



"Null" allele

13,13

Reverse primer is on top of deletion

European Labs Have Adopted the NIST-Developed NC (non-CODIS) miniSTRs

FSI (2006) **156(2):** 242-244

Short communication

The evolution of DNA databases—Recommendations for new European STR loci

Peter Gill [a,*], Lyn Fereday [b], Niels Morling [c], Peter M. Schneider [d]

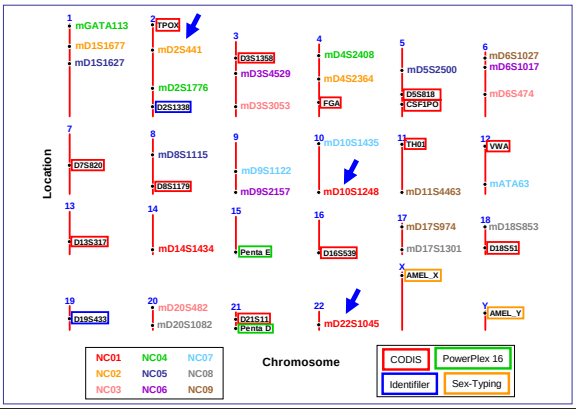
[a] Forensic Science Service, Birmingham, UK
[b] Forensic Science Service, London, UK
[c] Department of Forensic Genetics, Institute of Forensic Medicine, University of Copenhagen, Denmark
[d] Institute of Legal Medicine, University of Cologne, Germany

Received 25 May 2005; accepted 26 May 2005

…recommended that existing multiplexes are re-engineered to enable small amplicon detection, and that three new mini-STR loci with alleles <130 bp (D10S1248, D14S1434 and D22S1045) are adopted as universal. This will increase the number of European standard Interpol loci from 7 to 10.

(D14 has been replaced with D2S441 from NC02)

Chromosomal Locations of New miniSTR Loci

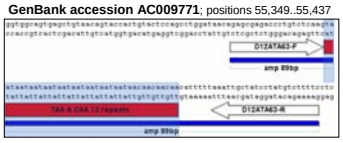


Comparison of heterozygosity values on 26 non-CODIS loci across the U.S. samples examined in this study.

Locus	N	Heterozygosity (Overall)	Rank	African American	Caucasian	Hispanic
D9S2157	661	0.844	1	0.884	0.840	0.779
ATA63 (D12)	659	0.829	2	0.788	0.842	0.879
D10S1248 (NC01)	663	0.792	3	0.825	0.785	0.743
D22S1045 (NC01)	663	0.784	4	0.817	0.785	0.721
D2S441 (NC02)	660	0.774	5	0.798	0.780	0.721
D10S1435	663	0.766	6	0.798	0.770	0.700
D2S1776	654	0.763	7	0.740	0.801	0.734
D3S4529	660	0.761	8	0.752	0.723	0.829
D6S474	648	0.761	9	0.765	0.802	0.679
D5S2500	664	0.747	10	0.757	0.747	0.729
D1S1627	660	0.746	11	0.783	0.737	0.693
D1S1677 (NC02)	660	0.746	12	0.743	0.749	0.743
D6S1017	664	0.740	13	0.807	0.698	0.693
D3S3053	648	0.739	14	0.713	0.724	0.814
D9S1122	659	0.734	15	0.753	0.742	0.686
D17S974	664	0.732	16	0.757	0.702	0.743
D11S4463	664	0.730	17	0.780	0.676	0.743
D4S2408	654	0.722	18	0.752	0.709	0.691
D18S853	664	0.711	19	0.772	0.645	0.721
D20S1082	664	0.696	20	0.792	0.653	0.600
D14S1434 (NC01)	663	0.696	21	0.685	0.721	0.650
D20S482	648	0.691	22	0.673	0.689	0.729
GATA113 (D1)	654	0.668	23	0.673	0.632	0.727
D8S1115	664	0.663	24	0.629	0.660	0.729
D17S1301	664	0.649	25	0.626	0.717	0.564
D4S2364 (NC02)	660	0.511	26	0.385	0.551	0.664

Characterization of miniSTR **D12ATA63**

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



[FAM] – GAGCGAGACCCTGTCTCAAG
GAAAAGACATAGGATAGCAATTT

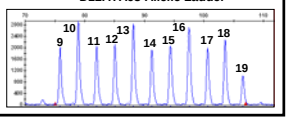
Chr 12 106.825 Mb (12q23.3)

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	0.1500
12	0.2154	0.1004	0.1786
13	0.0173	0.1564	0.0286
14	0.1615	**0.3340**	0.2214
15	0.0577	0.0772	0.0714
16	**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

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

D12ATA63 Allelic Ladder



miniSTR Allele Nomenclature Changes

Due to further sequence analysis conducted in summer and fall of 2006

- **D10S1248 reduced by -1 repeat**
- **D22S1045 increased by +3 repeats**
- D2S441 kept the same
- **D14S1434 reduced by -4 repeats**
- **D1S1677 increased by +1 repeat**
- **D4S2364 reduced by -1 repeat**

Butler, J.M. and Coble, M.D. (2007) Authors' Response to Letter to Editor [regarding nomenclature for new miniSTR locus D10S1248]. *J. Forensic Sci.* 52(2): 494.

See also …/strbase/miniSTR.htm#Nomenclature_Errata

26 New miniSTR Loci Typed (and Sequenced) with Standard Samples

Locus	Standard DNA Template Genotypes 9947A	9948	ABI 007	K562	SRM 2391b Components Genomic 1	Genomic 2	Genomic 3	Genomic 4	Genomic 5	Genomic 6	Genomic 7	Genomic 8
D1GATA113	11,12	7,12	12,12	11,12	11,11	12,13	11,11	13,13	11,12	11,12	10,12	10,12
D1S1627	13,14	11,13	11,14	10,14	10,14	13,14	13,14	11,12	14,15	11,13	11,14	13,14
D1S1677 (NC02)	13,14	13,14	13,13	13,14	12,13	14,16	14,17	14,15	13,14	13,14	12,13	14,16
D2S441 (NC02)	10,14	11,12	14,15	10,14	11,14	11,14	10,14	12,14	11,14	10,11	11,14	11,11 3
D2S1776	10,10	10,12	8,10	11,11	11,12	11,11	8,10	11,12	12,13	11,12	11,12	11,12
D3S3053	9,11	9,12	9,9	12,12	9,12	10,11	9,11	11,11	11,11	9,9	11,11	9,9
D3S4529	13,13	12,12	13,13	14,14	14,15	13,16	14,16	15,16	13,15	15,17	14,16	14,14
D4S2364 (NC02)	9,10	9,10	9,10	9,9	9,9	9,10	9,10	9,9	9,10	8,9	9,9	9,9
D4S2408	9,10	10,10	10,11	10,11	10,10	9,9	8,9	9,10	10,11	9,9	8,11	11,11
D5S2500	14,23	14,17	17,18	14,14	17,18	17,24	17,18	17,18	14,15	14,18	14,20	14,18
D6S474	14,18	17,17	14,14	15,18	15,17	14,17	14,15	14,16	15,18	14,17	15,17	17,17
D6S1017	9,10	8,8	10,10	8,11	10,10	10,12	10,12	7,10	8,9	10,10	7,12	10,12
D8S1115	9,18	15,17	15,17	16,16	16,16	16,16	16,17	9,17	9,15	9,16	9,18	15,16
D9S1122	12,13	12,15	12,12	10,14,15	11,12	12,13	12,12	12,12	11,13	11,12	11,12	13,13
D9S2157	7,13	7,11	13,13	13,13	8,13	9,11	11,13	11,11	7,14	11,13	12,15	11,11
D10S1248 (NC01)	13,16	12,16	12,16	12,12	14,16	13,16	13,16	12,12	14,15	14,15	13,14	11,16
D10S1435	10,11	12,13	11,13	10,12	12,13	11,14	13,14	12,12	11,12	12,12	12,12	11,13
D11S4463	12,13	12,14	14,14	13,14	14,14	13,14	14,15	11,12	14,16	16,17	14,15	14,17
D12ATA63	13,13	13,18	13,17	17,17	14,17	13,17	12,15	16,18	13,15	14,18	16,17	14,15
D14S1434 (NC01)	11,13	13,14	11,14	10,10	13,14	11,13	14,15	10,11	13,14	13,14	10,14	13,13
D17S974	7,10	10,11	9,10	8,8	9,11	9,10	9,9	7,9	11,12	9,9	11,11	8,9
D17S1301	12,12	11,12	12,13	11,12	11,11	11,12	11,12	12,13	11,11	11,11	11,12	12,12
D18S853	11,14	11,11	11,11	12,15	11,14	11,11	11,11	11,13	10,15	11,14	14,14	12,13
D20S482	14,15	13,14	14,15	15,15	14,14	14,16	15,15	14,15	14,15	14,14	14,14	15,16
D20S1082	11,14	11,15	12,14	11,11	11,15	14,15	11,11	14,15	11,14	11,15	14,15	11,15
D22S1045 (NC01)	11,14	16,18	11,16	16,16	14,15	11,16	15,16	17,18	11,14	11,15	15,16	16,17

http://www.cstl.nist.gov/biotech/strbase/miniSTR/miniSTR_NC_loci_types.htm

Standard Reference Materials

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

Traceable standards to ensure accurate measurements in our nation's crime laboratories

SRM 2391b – CODIS STRs
SRM 2392-I – mtDNA
SRM 2395 – Y-STRs
SRM 2372 – DNA quantitation

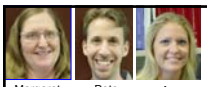
Helps meet DAB Std. 9.5 and ISO 17025

Working to update 2391b with new miniSTRs and 2395 with new Y-STRs

Lab 1 ⟷ Lab 2

Standards Reference Material

Calibration with SRMs enables confidence in comparisons of results between laboratories



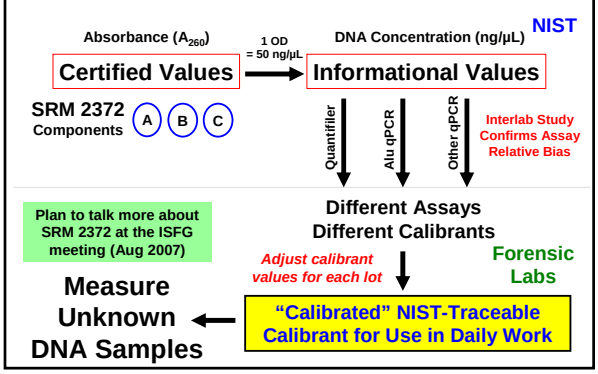
Margaret Kline | Pete Vallone | Amy Decker

DNA Quantitation (qPCR)

- **Production of SRM 2372** (Human DNA Quant Std)
  - Interlab study completed; final characterization underway
- PDI Training: qPCR Course (July 25-26, 2006)
  http://www.cstl.nist.gov/biotech/strbase/qPCRworkshop.htm
- Evaluation of published assays on same samples
  - Promega 2005 and AAFS 2006 presentations
  - Trying to educate ABI on quality control of their materials (Quantifiler lot-to-lot variation)

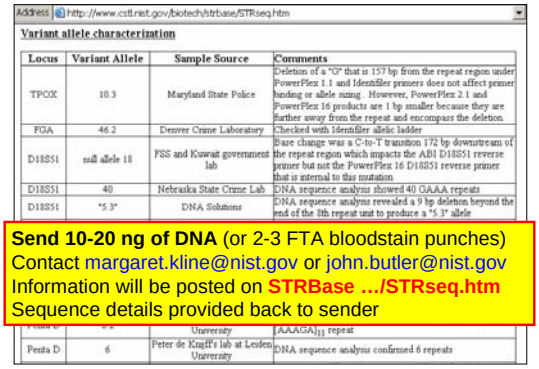
http://www.cstl.nist.gov/biotech/strbase/DNAquant.htm

Overview of SRM 2372 Values and Use



Variant Allele Sequencing Service (Free)

Send us any unusual variant or null alleles and we will sequence them…



Address http://www.cstl.nist.gov/biotech/strbase/STRseq.htm

Variant allele characterization

Locus	Variant Allele	Sample Source	Comments
TPOX	10.3	Maryland State Police	Deletion of a "G" that is 157 bp from the repeat region under PowerPlex 1.1 and Identifiler primers does not affect primer binding or allele sizing. However, PowerPlex 2.1 and PowerPlex 16 products are 1 bp smaller because they are further away from the repeat and encompass the deletion
FGA	46.2	Denver Crime Laboratory	Checked with Identifiler allelic ladder
D18S51	null allele 18	FSS and Kuwait government lab	Base change was a C-to-T transition 172 bp downstream of the repeat region which impacts the ABI D18S51 reverse primer but not the PowerPlex 16 D18S51 reverse primer that is internal to this mutation
D18S51	40	Nebraska State Crime Lab	DNA sequence analysis showed 40 GAAA repeats
D18S51	"5.3"	DNA Solutions	DNA sequence analysis revealed a 9 bp deletion beyond the end of the 8th repeat unit to produce a "5.3" allele
		University	$[AAAGA]_{11}$ repeat
Penta D	6	Peter de Knijff's lab at Leiden University	DNA sequence analysis confirmed 6 repeats

Send 10-20 ng of DNA (or 2-3 FTA bloodstain punches)
Contact margaret.kline@nist.gov or john.butler@nist.gov
Information will be posted on **STRBase …/STRseq.htm**
Sequence details provided back to sender

Pete Vallone | Dave Duewer

Software Tools from NIST

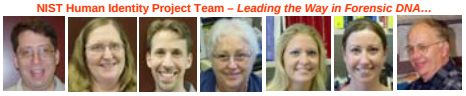
- AutoDimer – multiplex PCR primer screening tool
  http://www.cstl.nist.gov/biotech/strbase/AutoDimerHomepage/AutoDimerProgramHomepage.htm
- mixSTR – mixture component resolution tool
- **Multiplex_QA** – quality assessment tool for monitoring instrument performance over time
- Tools to aid Expert System data review
  - **STR_ConvertFormats.xls** (converts data format)
  - **STR_MatchSamples.xls** (compares samples)

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

Acknowledgments

Funding from interagency agreement 2003-IJ-R-029 between NIJ and the NIST Office of Law Enforcement Standards

NIST Human Identity Project Team – *Leading the Way in Forensic DNA…*



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

Past and Present Collaborators (also funded by NIJ):
Mike Hammer and Alan Redd (U. AZ) for Y-chromosome studies
Tom Parsons, Rebecca Just, Jodi Irwin (AFDIL) for mtDNA coding SNP work
Sandy Calloway (Roche) for mtDNA LINEAR ARRAYs
Bruce McCord and students (FL Int. U.) for miniSTR work
Marilyn Raymond and Victor David (NCI-Frederick) for cat STR work
Artie Eisenberg and John Planz (U. North Texas) for miniSTR testing on bones
Murray Brilliant (U. AZ) for phenotype markers
Ken Kidd (Yale U.) for SNP typing population samples
Sree Kanthaswamy (UC Davis) for dog STR multiplex assay
Tom Reid (DNA Diagnostics Center) for father-son samples

Thank you for your attention…

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

Questions?

See also http://www.dna.gov/research/nist
http://www.cstl.nist.gov/biotech/strbase
john.butler@nist.gov