National Institute of Standards and Technology

. . .working with industry to develop and apply technology, measurements and standards

NIST Update

John M. Butler

CODIS Meeting
Crystal City, VA
November 15, 2004

NIST Human Identity Project Team


John Butler
(Project Leader)


Pete Vallone


Margaret Kline


Jan Redman

Former Team Member


Rich Schoske


Amy Decker


Mike Coble


Dave Duewer

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

- Resources for "**Challenging Samples**" (degraded DNA and mixtures)
- **Information on New Loci** (Y-Chromosome, new STRs)
- **DNA Quantitation** (Interlab studies, Real-time PCR assay comparisons, SRM 2372)
- **Tools to Aid State and Local Laboratories** (STRBase information, training materials/review articles, validation standardization, QAC tool, calibration datasets)

Tools to Aid State and Local Laboratories

- **STRBase** – standard information source on STR loci
  - **Training Materials –** review articles, workshop slides
  - **Variant allele** cataloging and characterization
- **NIST U.S. Population Samples (typed at many loci)**
- **Validation Standardization** Information
- Calibration Data Sets for Expert Systems
- **Quality Assurance Tool** – to track analytical performance over time
- **Interlaboratory Studies**

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STRBase

Short Tandem Repeat DNA Internet Database

Recent Additions

•**Validation** (summary sheets) …/validation.htm

•**NIST publications** and presentations as pdf files …/NISTpub.htm

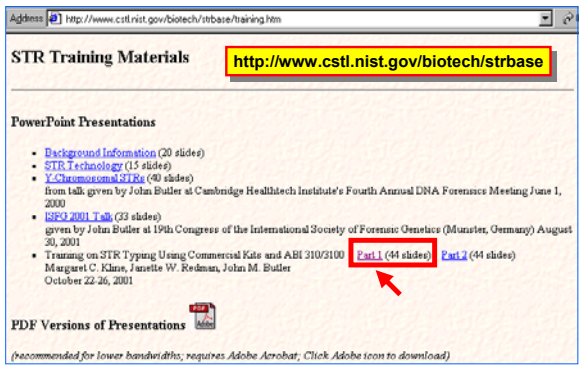
We Regularly Update

•Reference List
•Variant Alleles
•Addresses for Scientists
•Links to Other Web Sites
•Y-STR Information

We will continue to add downloadable PowerPoint files that can be used for training purposes

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

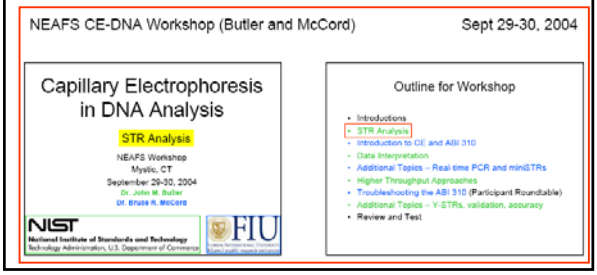
Training Materials on STRBase



NEAFS Workshop Slide Handouts

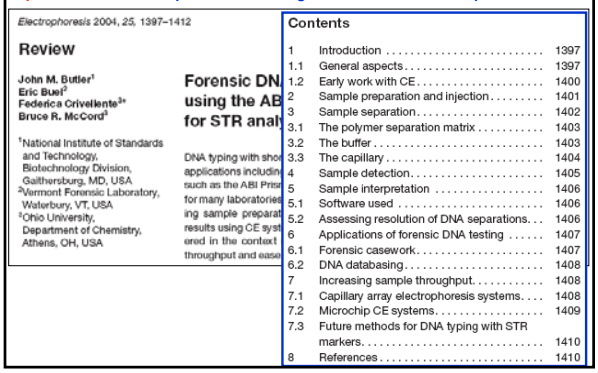
Handouts available as downloadable pdf files from
http://www.cstl.nist.gov/biotech/strbase/NISTpub.htm#NEAFSworkshop

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



Review Article on STRs and CE

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



Position of Each CODIS STR Locus in Human Genome

Locus Name	Chromosomal Location	Physical Position [a]
CSF1PO	5q33.1 c-fms proto-oncogene, 6th Intron	Chr 5 149.484 Mb
FGA	4q31.3 alpha fibrinogen, 3rd Intron	Chr 4 156.086 Mb
TH01	11p15.5 tyrosine hydroxylase, 1st Intron	Chr 11 2.156 Mb
TPOX	2p25.3 thyroid peroxidase, 10th Intron	Chr 2 1.436 Mb
VWA	12p13.31 von Willebrand Factor, 40th Intron	Chr 12 19.826 Mb
D3S1358	3p21.31	Chr 3 45.543 Mb
D5S818	5q23.2	Chr 5 123.187 Mb
D7S820	7q21.11	Chr 7 83.401 Mb
D8S1179	8q24.13	Chr 8 125.863 Mb
D13S317	13q31.1	Chr 13 80.52 Mb
D16S539	16q24.1	Chr 16 86.168 Mb
D18S51	18q21.33	Chr 18 59.098 Mb
D21S11	21q21.1	Chr 21 19.476 Mb

From Table 5.2, *Forensic DNA Typing*, 2nd Edition, p. 96 (J.M. Butler, 2005)

Apparent Null Alleles Observed During Concordance Studies

10/13 CODIS loci affected so far

Locus	STR Kits/Assays Compared	Results	Reference
VWA	PP1.1 vs ProPlus	Loss of allele 19 with **ProPlus**; fine with PP1.1	Kline et al. (1998)
D5S818	PP16 vs ProPlus	Loss of alleles 10 and 11 with **PP16**; fine with ProPlus	Alves et al. (2003)
D13S317	Identifiler vs miniplexes	Shift of alleles 10 and 11 due to deletion outside of **miniplex assay**	Butler et al. (2003), Drabek et al. (2004)
D16S539	PP1.1 vs PP16 vs COfiler	Loss of alleles with **PP1.1**; fine with PP16 and COfiler	Nelson et al. (2002)
D8S1179	PP16 vs ProPlus	Loss of alleles 15, 16, 17, and 18 with **ProPlus**; fine with PP16	Budowle et al. (2001)
FGA	PP16 vs ProPlus	Loss of allele 22 with **ProPlus**; fine with PP16	Budowle and Sprecher (2001)
D18S51	SGM vs SGM Plus	Loss of alleles 17, 18, 19, and 20 with **SGM Plus**; fine with SGM	Clayton et al. (2004)
CSF1PO	PP16 vs COfiler	Loss of allele 14 with **COfiler**; fine with PP16	Budowle et al. (2001)
TH01	PP16 vs COfiler	Loss of allele 9 with **COfiler**; fine with PP16	Budowle et al. (2001)
D21S11	PP16 vs ProPlus	Loss of allele 32.2 with **PP16**; fine with ProPlus	Budowle et al. (2001)

STR Measured Mutation Rates

… /strbase/mutation.htm

STR Locus	Maternal Meioses (%)	Paternal Meioses (%)	Either Parent	Total Mutations	Rate
CSF1PO	70/179,353 (0.04)	727/504,342 (0.14)	303	1,100/683,695	**0.16%**
FGA	134/238,378 (0.06)	1,481/473,924 (0.31)	495	2,110/712,302	**0.30%**
TH01	23/189,478 (0.01)	29/346,518 (0.008)	23	75/535,996	**0.01%**
TPOX	16/299,186 (0.005)	43/328,067 (0.01)	24	83/627,253	**0.01%**
VWA	133/400,560 (0.03)	907/646,851 (0.14)	628	1,668/1,047,411	**0.16%**
D3S1358	37/244,484 (0.02)	429/336,208 (0.13)	266	732/580,692	**0.13%**
D5S818	84/316,102 (0.03)	537/468,366 (0.11)	303	924/784,468	**0.12%**
D7S820	43/334,886 (0.01)	550/461,457 (0.12)	218	811/796,343	**0.10%**
D8S1179	54/237,235 (0.02)	396/264,350 (0.15)	225	675/501,585	**0.13%**
D13S317	142/348,395 (0.04)	608/435,530 (0.14)	402	1,152/783,925	**0.15%**
D16S539	77/300,742 (0.03)	350/317,146 (0.11)	256	683/617,888	**0.11%**
D18S51	83/130,206 (0.06)	623/278,098 (0.22)	330	1,036/408,304	**0.25%**
D21S11	284/258,795 (0.11)	454/306,198 (0.15)	423	1,161/564,993	**0.21%**
Penta D	12/18,701 (0.06)	10/15,088 (0.07)	21	43/33,789	**0.13%**
Penta E	22/39,121 (0.06)	58/44,152 (0.13)	55	135/83,273	**0.16%**
D2S1338	2/25,271 (0.008)	61/81,960 (0.07)	31	94/107,231	**0.09%**
D19S433	22/28,027 (0.08)	16/38,983 (0.04)	37	75/67,010	**0.11%**
F13A01	1/10,474 (0.01)	37/65,347 (0.06)	3	41/75,821	**0.05%**
FES/FPS	3/18,918 (0.02)	79/149,028 (0.05)	None reported	82/167,946	**0.05%**
F13B	2/13,157 (0.02)	8/27,183 (0.03)	1	11/40,340	**0.03%**
LPL	0/8,821 (<0.01)	9/16,943 (0.05)	4	13/25,764	**0.05%**
SE33 (ACTBP2)	0/330 (<0.30)	330/51,610 (0.64)	None reported	330/51,940	**0.64%**

13 CODIS core loci

*Data used with permission from American Association of Blood Banks (AABB) 2002 Annual Report.

Variant Alleles Cataloged in STRBase

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

Off-Ladder Alleles

224 total variants reported as of 04/21/04

- CSF1PO (10)
- D2S1338 (3)
- D3S1358 (16)
- D5S818 (5)
- D7S820 (20)
- D8S1179 (4)
- D13S317 (8)
- D16S539 (10)
- D18S51 (28)
- D19S433 (8)
- D21S11 (21)
- FESFPS (1)
- FGA (62)
- HUMTH01 (4)
- Penta D (8)
- Penta E (6)
- TPOX (7)
- VWA (5)

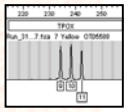
Currently **255** at 13/13 CODIS loci

Tri-Allelic Patterns

56 total patterns reported as of 04/09/04

- CSF1PO (2)
- D3S1358 (4)
- D5S818 (1)
- D7S820 (3)
- D8S1179 (5)
- D13S317 (3)
- D16S539 (1)
- D18S51 (4)
- D21S11 (4)
- FGA (9)
- HUMTH01 (1)
- TPOX (12)
- VWA (7)

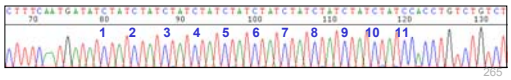
Currently **58** at 13/13 CODIS loci



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)



DYS392 Flanking Region Polymorphism

Normal sequence

G G A C C A A T T T T

C->G

180 bp upstream of the STR repeat

C-to-G Mutation

G G A G C A A T T T T

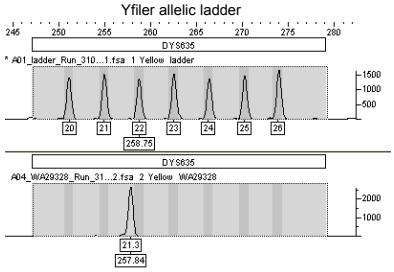
AFDIL sample

PowerPlex Y and Yfiler kits are external to this polymorphism while Y-PLEX 5, which creates a smaller amplicon for DYS392, is internal and therefore not impacted…

DYS635 Variant Allele 21.3

(Y-GATA-C4)

Yfiler allelic ladder



Missing T

T C T A T C A T C T A

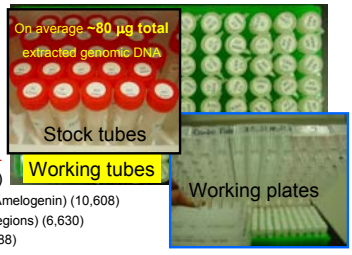
$[TCTA]_4(TGTA)_2[TCTA]_2(TGTA)_2[TCTA]_2(TGTA)_2\,[TCTA]_5\,TC\text{-}A\,[TCTA]_2$

NIST U.S. Population Samples

As of 06/2003 663 males (anonymous; self-identified ethnicities)

260 Caucasians
260 African Americans
140 Hispanics
3 Asians

Whole blood received from Interstate Blood Bank (Memphis, TN)



Working tubes/plates 1 ng/uL

To date: (~85,000 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)
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)
mtDNA full control region sequences by AFDIL

Samples supplied to **OhioU** for miniSTR typing and **AFDIL** for whole mtGenome sequencing

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	**D2S1338 and D19S433 information has been provided to the FBI for inclusion in PopStats to aid statistical calculations**	Butler et al. (2003) JFS
miniSTRs		Drabek et al. (2004) JFS
New autosomal STRs		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)	Schoske et al. (2004) FSI
	Yfiler concordance study	*Data in ABI Yfiler database*
New Y-STRs	**27 additional loci**	**Butler et al., submitted**
Y-SNPs	50 loci spanning haplogroups A-R	Vallone et al. (2004) JFS
mtDNA	LINEAR ARRAY and coding mtSNPs	Kline et al. (2005) JFS
	Full control regions by **AFDIL**	*inclusion in EMPOP*

Validation Standardization Efforts

Presentation at Promega meeting
(October 2004)

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

Validation Standardization Questionnaire (conducted June-August 2004)

Can Validation be Standardized?

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**

Revised SWGDAM Validation Guidelines (July 2004)

http://www.fbi.gov/hq/lab/fsc/backissu/july2004/standards/2004_03_standards02.htm

Forensic Science Communications July 2004 – Volume 6 – Number 3

Standards and Guidelines

Revised Validation Guidelines

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Scientific Working Group on DNA Analysis Methods (SWGDAM)

3. Internal Validation
…a total of **at least 50 samples**
(some studies may not be necessary…)

Program for DNA Analysis by the Technical Working Group on DNA Analysis Methods (*Crime Laboratory Digest* 1995;22(2):21-43) has been revised due to increased laboratory experience, the advent of new technologies, and the issuance of the Quality Assurance Standards for Forensic DNA Testing Laboratories by the Director of the FBI (*Forensic Science Communications* available: www.fbi.gov/hq/lab/fsc/backissu/july2000/codis2a.htm).

The document provides validation guidelines and definitions approved by SWGDAM July 10, 2003.

Common Perceptions of Validation

The goal is not to experience every possible scenario during validation…

"You cannot mimic casework because every case is different."

Effort

Lots of experiments are required

Many labs are examining far too many samples in validation and thus delaying application of casework and contributing to backlogs…

Significant time is required to perform studies

Time

A Thoughtful Comment from One Interviewee

Before a set of validation experiments is performed…

- The question should be asked "Do we already know the answer to this question from the literature or a previous study performed in-house?"
- If the answer is "yes" and we document how we know this answer, **then there is no need to perform that set of validation experiments**.

A good example of this scenario is non-human DNA studies.

Resources to Aid Future Validation Studies

- STRBase Validation Website
  - **http://www.cstl.nist.gov/biotech/strbase/validation.htm**
  - Validation summary sheets
  - *Helpful information on aspects of validation studies*
- NIST Calibration Data Set
  - **set of ~200 sample data files** that can be used to evaluate common STR typing "artifacts" such as stutter, non-template addition, spikes, peak imbalance, tri-allelic patterns, variant alleles, single base resolution
  - *will help meet NDIS Appendix B requirements for Expert Systems evaluation*
- Quality Control Program (Dave Duewer, NIST)
  - Software to monitor STR electropherogram performance (resolution, sensitivity) over time – **can aid performance checks**

New Validation Homepage on STRBase

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

Validation Information to Aid Forensic DNA Laboratories

Validation Summary Sheets

What validated?

Where published?

How?

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 (1:0,1:1,1:10,1:100,1:300,1:1000,0.5:300, 0.25:300,0.125:300, 0.0625:300, 0.03:300 ng M:F)	132
Mixture Ratio (male:male)	6 labs x 2 M/M 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 (480/2400/9600/9700) 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 (1.38/2.06/2.75/3.44/4.13 U) x 4 quantities (1/0.5/0.25/0.13 ng DNA)	20
Primer pair titration	5 amounts (0.5x/0.75x/1x/1.5x/2x) x 4 quantities (1/0.5/0.25/0.13 ng DNA)	20
Magnesium titration	5 amounts (1/1.25/1.5/1.75/2 mM Mg) x 4 quantities (1/0.5/0.25/0.13 ng DNA)	20
Krenke *et al.* (2004) *Forensic Sci. Int., in press*	TOTAL SAMPLES EXAMINED	1269

Laboratory Internal Validation Summaries

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

Soliciting Information on Studies Performed by the Community

Expert System Calibration Data Set

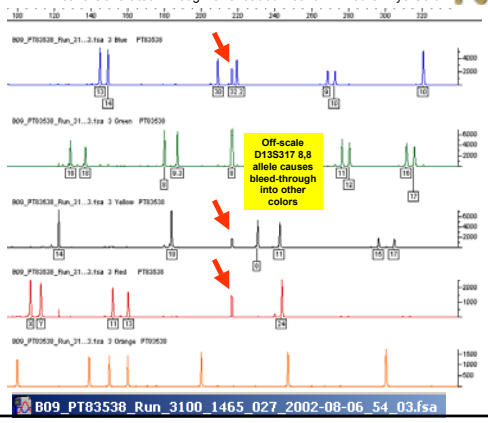
"Electronic SRM" to help meet NDIS Appendix B requirements

These data will be able to used to check software upgrades to ensure reliable performance of the Expert System software

To Help Meet NDIS Appendix B Requirements for Evaluating Expert Systems…

- **200 calibration samples needed**
- Types of challenges (at least 5 of each type)
  - Off-ladder alleles
  - Tri-allelic patterns
  - Non-template addition
  - Spikes and signal overload (bleed-through into another dye channel)
  - Mixtures
  - Degraded DNA
- We welcome suggestions as to other types of challenges to include in the data set
- **Samples are currently being gathered** with plans to generate data using Profiler Plus/COfiler, Identifiler, PowerPlex 16, and SGM Plus (kits have already been purchased)

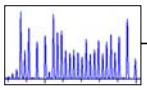
Peaks Generated Through Overloaded Peaks in Another Dye Color



NIST QA/QC Software

Tool being developed by Dave Duewer for STR Process Control

Tracks allelic ladders and positive controls and internal size standards



NCBI Program

Peak Height, Area, Size

X | Y
103 | 436
104 | 569

NIST ControlCharter

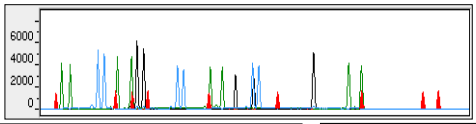
Date vs Sensitivity, Resolution, Precision

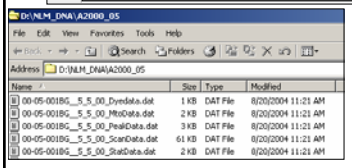
NIST ControlCharter

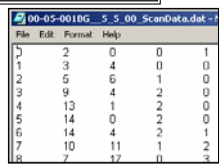
Date vs Signal/Noise

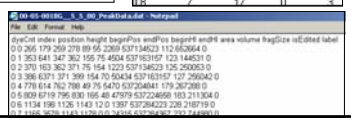
This software does not perform genotyping.
It merely permits a view of analytical parameters over time.

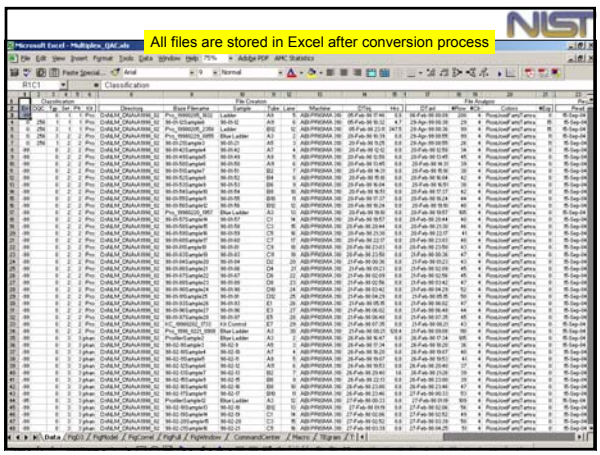
GeneScan Data Converted with NCBI OSIRIS Program





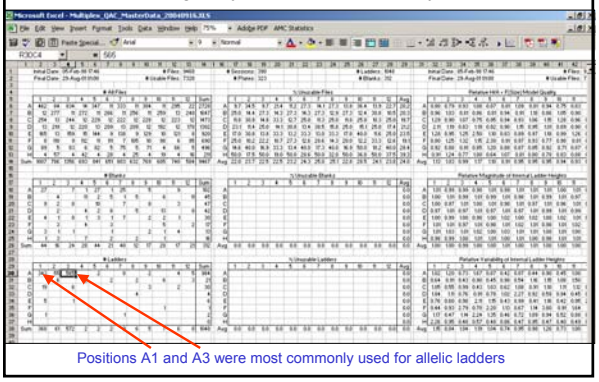




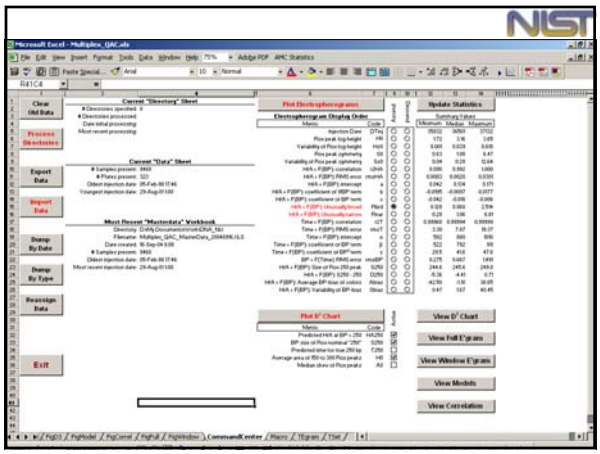


All files are stored in Excel after conversion process

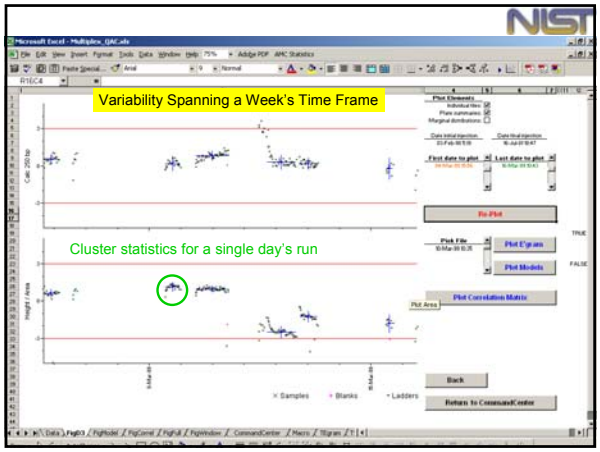
View "plate" statistics for ABI 310 runs across 7328 samples spanning 2.5 years (Feb 1998 to July 2001)

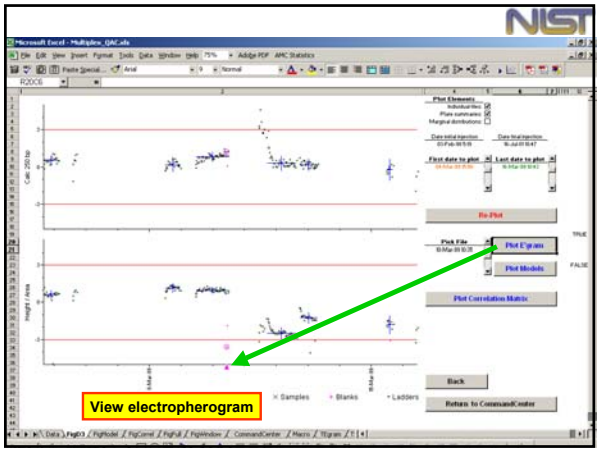


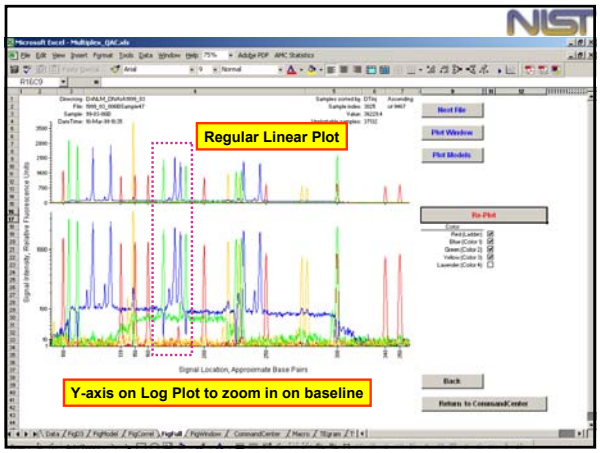
Positions A1 and A3 were most commonly used for allelic ladders

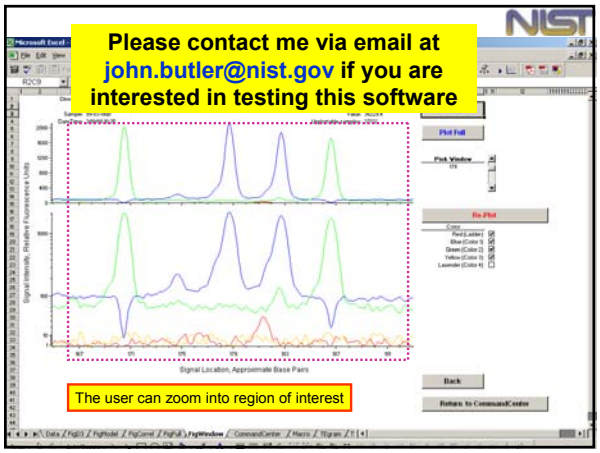


Variability Spanning a 2.5 Year Time Frame with 7,328 Samples



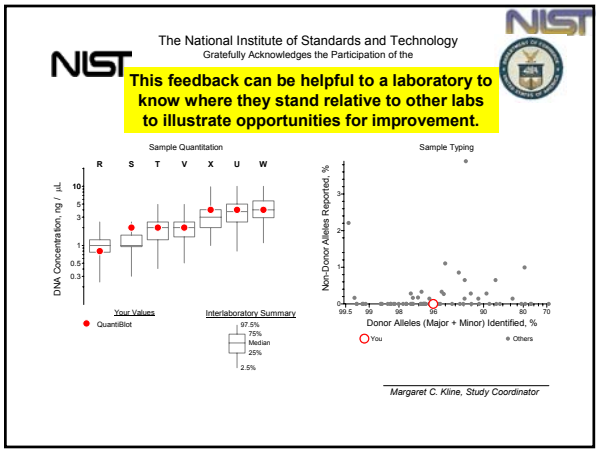






Interlaboratory Studies Conducted by NIST

Goal to help individual labs within forensic community understand their performance relative to other labs



NIST Interlaboratory Studies Involving Forensic DNA Typing

Kline MC, et al. (2005) NIST DNA Quantitation Study, in press

Duewer et al. (2004) MSS#3 Anal Chem, in press

Kline MC, Duewer DL, Redman JW, Butler JM. NIST Mixed Stain Study 3: DNA quantitation accuracy and its influence on short tandem repeat multiplex signal intensity. Anal. Chem. 2003;75:2463-2469.

Duewer DL, Kline MC, Redman JW, Newall PJ, Reeder DJ. NIST Mixed Stain Studies #1 and #2: Interlabo… …ison of DNA Quantification Practice and Short Tandem Repeat Multiplex Performance with Multiple-Source Sa… …Sci. 2001;46(5):1199-1210.

Duewer DL, Gary KT, Reeder DJ. RFLP band size standards: Cell line K562 values from … J Forensic Sci 2000;45(5):1106-1118.

Duewer DL, Richie KL, Reeder DJ. RFLP band size standards: NIST Standa… …ensic Sci 2000;45(5):1093-1105.

Duewer DL, Liu H-K, Reeder DJ. Graphical tools for RFLP DNA … …rensic Sci 1999;44(5):969-77.

Gary KT, Duewer DL, Reeder DJ. Graphical tools … …erformance Charts. J Forensic Sci 1999;44(5):978-82.

Duewer DL, Lalonde SA, Aubin RA, … …ory comparison of autoradiographic DNA profiling measurements: precision and … …(3):465-71.

Kline MC, Duewer DL, … …Richard M. Interlaboratory evaluation of STR triplex CTT. J Forensic Sci 199…

Duewer DL, … …liben JJ, Liu H-K, Mudd JL. Interlaboratory comparison of autoradiographic DNA profili… … Anal Chem 1997:69(10); 1882-92.

Stoloro… … DJ, Buel E, Herrin G Jr. Interlaboratory comparison of autoradiographic DNA profiling measur… …ility and reproducibility of RFLP band sizing, particularly bands of molecular size > 10k base pairs. Anal Che… …; 1941-7.

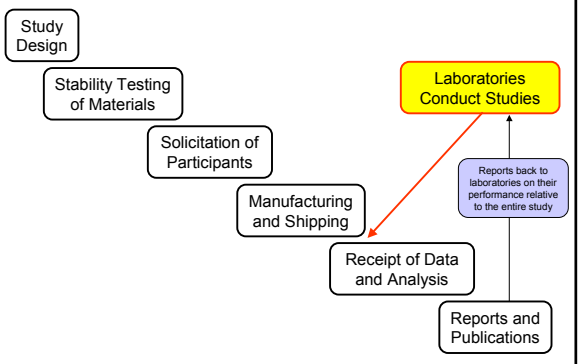
Kline MC, … …nan JW, Reeder DJ, Duewer DL. Intercomparison of DNA sizing ladders in electrophoretic separation matrices and their potential for accurate typing of the D1S80 locus. Applied and Theoretical Electrophoresis 1996:6(1);33-41.

Duewer DL, Currie LA, Reeder DJ, Leigh SD, Liu H-K, Mudd JL. Interlaboratory comparison of autoradiographic DNA profiling measurements. 2. Measurement uncertainty and its propagation. Anal Chem 1995:67(7);1220-31.

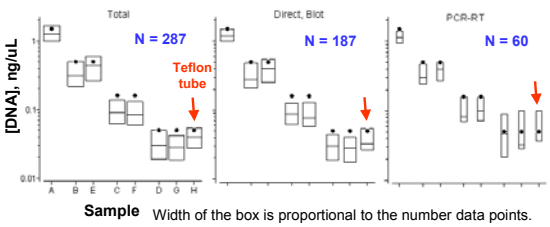
Mudd JL, Baechtel FS, Duewer DL, Currie LA, Reeder DJ, Leigh SD, Liu H-K. Interlaboratory comparison of autoradiographic DNA profiling measurements. 1. Data and summary statistics. Anal Chem 1994:66(20);3303-17.

15 papers in the last 10 years

Process for Interlaboratory Study



NIST QS 04 Results-Box plots



Width of the box is proportional to the number data points.

Line in the box is the median value.
The box represents 50% of the data submitted.

Dot is the target [DNA].

Kline, *et al., J. Forensic Sci., in press (May 2005)*

Table 2. The percent success rate reported for a sample.

		% Quantitative Results[a]							
Target [DNA] ng/μL		1.5	0.5	0.5	0.16	0.16	0.05	0.05	0.05
Method	N_{eval}	A	B	E	C	F	D	G	H
Quantifiler	37	100	100	100	100	100	100	100	100
Other RT-PCR	23	100	100	100	100	100	100	100	100
"ACES"	14	100	100	100	100	100	100	100	100
AluQuant	13	100	100	100	100	100	100	100	100
PicoGreen	12	100	100	92	100	100	92	83	83
ECL	75	100	99	99	93	95	84	77	87
TMB	98	100	100	99	93	94	59	62	63
Yield gel	14	57	0	0	0	0	0	0	0
	286								

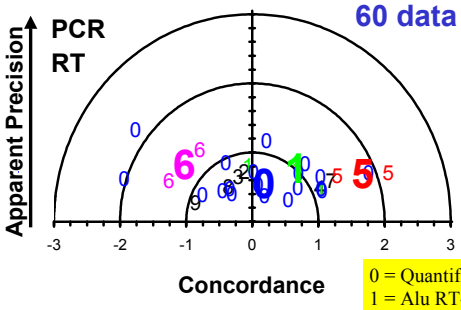
Real-time PCR

Quantiblot

a Quantitative results are those that were reported as values, values reported as the range between contiguous calibration standards, values reported as less-than the lowest calibration standard if smaller than the target [DNA], or values reported as greater-than the highest calibration standard if larger than the target[DNA].

Kline, *et al., J. Forensic Sci., in press (May 2005)*

Laboratory Performances with Real-Time PCR Methods



0 = Quantifiler
1 = Alu RT-PCR
5 = BRCA1
6 = CFS-HUMRT

Kline, *et al., J. Forensic Sci., in press (May 2005)*

New Interlaboratory Study

- Mixture Interpretation Study 2005 (**MIX05**)
- "Paper challenge" (no lab work required)
- Purpose to determine "lay of the land" for current practices in solving STR profile mixtures and reporting the results

- Please pick up a handout pertaining to our SOLICITATION FOR PARTICIPATION…

MIX05 Study

- Mixture results will be supplied to participants
- 3 or 4 case-like mixture scenarios

- Data format options: Mac, NT, GeneMapper
- Kit format options: Profiler Plus/COfiler, PowerPlex 16, Identifiler, SGM Plus

- Data will be shipped early January 2005
- Responses will be due February 28, 2005

Plans for Dissemination of MIX05 Results

- Goal is to understand the "lay of the land" regarding mixture analysis across the DNA typing community

- Results will be discussed at NIJ DNA Grantees Meeting (June 2005), SWGDAM (July 2005), and ISFG (Sept 2005)

- We plan to develop training materials to aid in mixture interpretation with available software tools and to help in standardizing reports involving mixture analysis

Acknowledgements

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Funding:

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

NIST Project Team:

John Butler, Pete Vallone, Margaret Kline, Jan Redman, Amy Decker, Mike Coble, Dave Duewer

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