


DNA Profiling and Quantitation of Human DNA

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CCQM BAWG (Sevres, France)
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 **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)

Steps in DNA Analysis

Usually 1-2 day process (a minimum of ~5 hours)

Collection

Specimen Storage

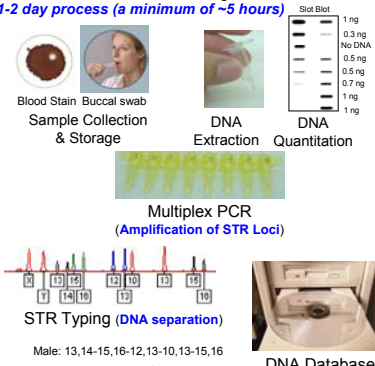
Extraction

Quantitation

Genotyping

Interpretation of Results

Database Storage & Searching



Blood Stain Buccal swab
Sample Collection & Storage

DNA Extraction

DNA Quantitation

Multiplex PCR
(Amplification of STR Loci)

STR Typing (DNA separation)

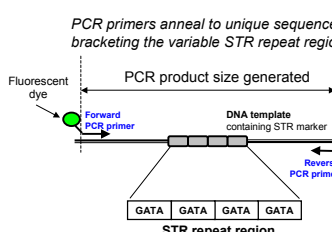
Male: 13,14-15,16-12,13-10,13-15,16

Interpretation of Results

DNA Database

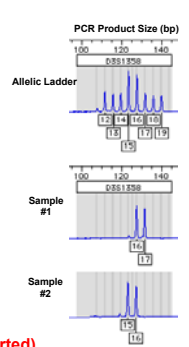
Short Tandem Repeat (STR) Markers

PCR primers anneal to unique sequences bracketing the variable STR repeat region



PCR product size generated

STR repeat region



Allelic Ladder

Sample #1

Sample #2

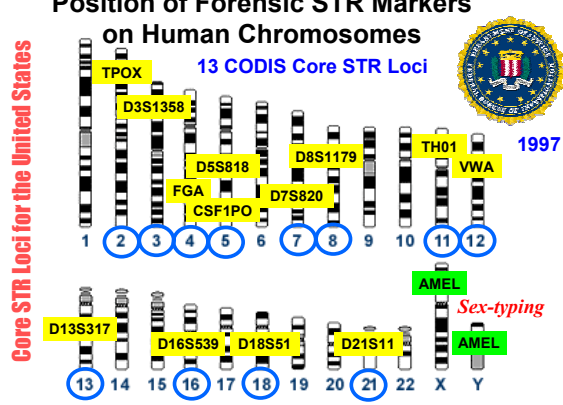
= 11 GATA repeats ("11" is all that is reported)

TCCCAAGCTCTTCCTCTCCCTAGATCAATACAGACAGA
 AGACAGGTGGATAGATAGATAGATAGATAGATAGATA
 GATAGATAGATAGATATCATTGAAAGACAAACAGAGA
 TGGATGATAGATACATGCTTACAGATGCACAC

Position of Forensic STR Markers on Human Chromosomes

13 CODIS Core STR Loci

1997



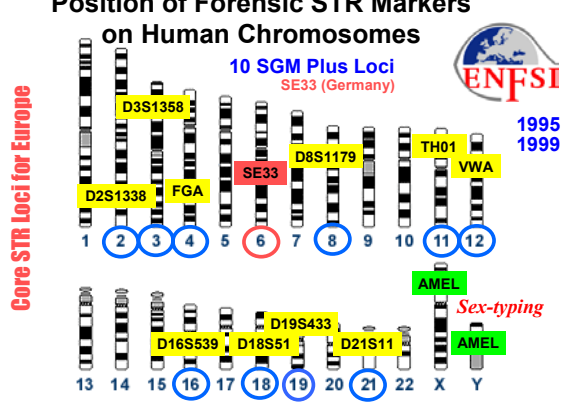
Core STR Loci for the United States

Position of Forensic STR Markers on Human Chromosomes

10 SGM Plus Loci

SE33 (Germany)

1995
1999



Core STR Loci for Europe

Congress Passed **the DNA Identification Act of 1994** (Public Law 103 322)

↓
Formalized the FBI's authority to establish a national DNA index for law enforcement purposes.

FBI's DNA Advisory Board
Quality Assurance Standards
for Forensic DNA Testing Laboratories
(October 1, 1998)



STANDARD 9.5

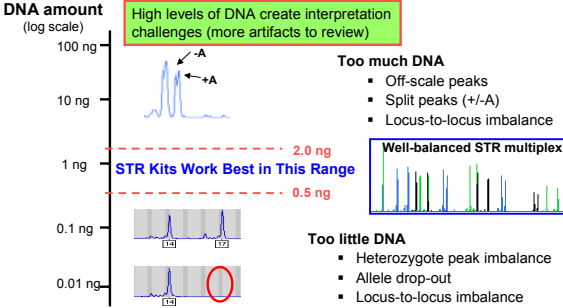
The laboratory shall check its DNA procedures annually or whenever substantial changes are made to the protocol(s) against an appropriate and available NIST standard reference material or standard traceable to a NIST standard.

Human DNA Quantitation

- **FBI STANDARD 9.3** The laboratory shall have and follow a procedure for evaluating the quantity of the human DNA in the sample where possible.
- **No requirement on how accurate DNA quantitation needs to be...**
- Quantitation is important in order to determine how much DNA template to put into the PCR reaction

Importance of DNA Quantitation (prior to multiplex PCR)

DNA amount (log scale)



High levels of DNA create interpretation challenges (more artifacts to review)

Too much DNA

- Off-scale peaks
- Split peaks (+/-A)
- Locus-to-locus imbalance

STR Kits Work Best in This Range

2.0 ng
0.5 ng

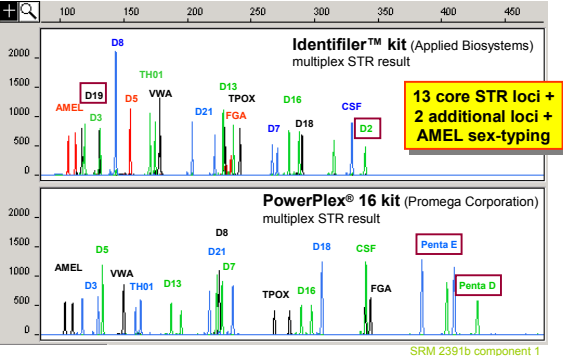
Well-balanced STR multiplex

Too little DNA

- Heterozygote peak imbalance
- Allele drop-out
- Locus-to-locus imbalance

Stochastic effect when amplifying low levels of DNA produces allele dropout.

Commercial STR 16plex Kits





Identifiler™ kit (Applied Biosystems) multiplex STR result

13 core STR loci + 2 additional loci + AMEL sex-typing

PowerPlex® 16 kit (Promega Corporation) multiplex STR result

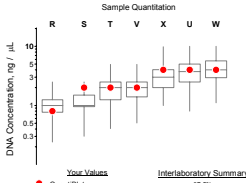
SRM 2391b component 1

The National Institute of Standards and Technology
Gratefully Acknowledges the Participation of the

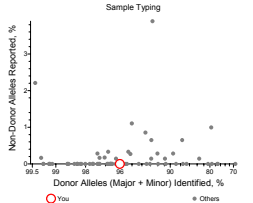



This feedback can be helpful to a laboratory to know where they stand relative to other labs to illustrate opportunities for improvement.

Sample Quantitation



Sample Typing



97.5%
75%
Median
25%
2.5%

Margaret C. Kline, Study Coordinator

Results of NIST Quantitation Study 04

Consisted of:

8 DNA extracts labeled A – H Shipped Dec 2003 –Jan 2004
Shipped to 84 laboratories for quantification.
Labs asked to use multiple methods / multiple analysts
Last day for submission extended from 15 March to 5 April 2004

We received data from 80 Labs (95%)
Total of 287 sets of data
Participants used 19 different quantification methods (primarily variations on Quantiblot and Real-time PCR)

Article will be published next month

To be published in the *Journal of Forensic Sciences* (May 2005)

TECHNICAL NOTE

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Results from the NIST 2004 DNA Quantitation Study*

8 DNA Samples in NIST QS04 Study



Laboratories are only being asked to provide their quant values (no typing results expected)

Mixed source DNA

Single source DNA

Teflon tube

Volume of each DNA sample provided = 100 µL

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

Target [DNA] ng/µL	Method	N _{test}	% Quantitative Results ^a								
			1.5	0.5	0.5	0.16	0.05	0.05	0.05	0.05	
	Quantifiler	37	100	100	100	100	100	100	100	100	100
	Other RT-PCR	23	100	100	100	100	100	100	100	100	100
	"ACES"	14	100	100	100	100	100	100	100	100	100
	AluQuant	13	100	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									

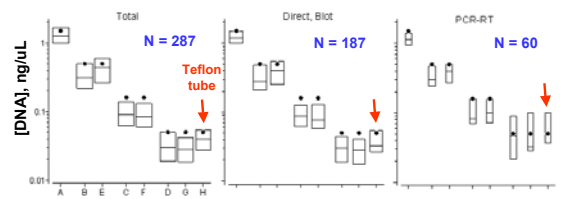
Real-time PCR

Quantiflot

^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)

NIST QS 04 Results-Box plots



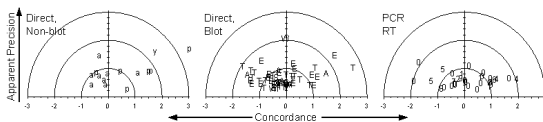
Sample Width of the box is proportional to the number data points.

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)

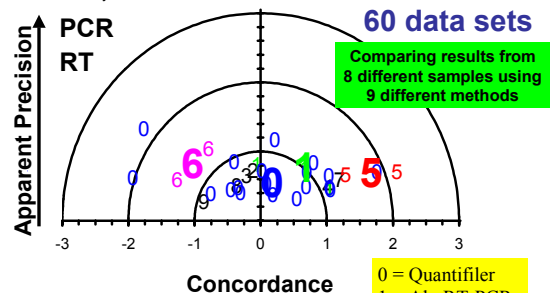
NIST QS 04 Results-Target Plots



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

Interlaboratory Comparisons

Laboratory Performances with Real-Time PCR Methods



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

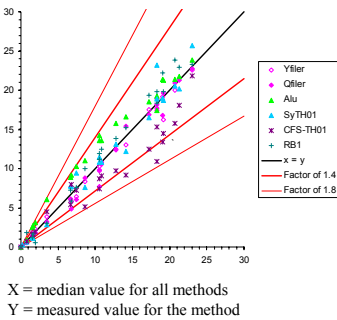
Comparison of real-time qPCR assays

Following Published Protocols

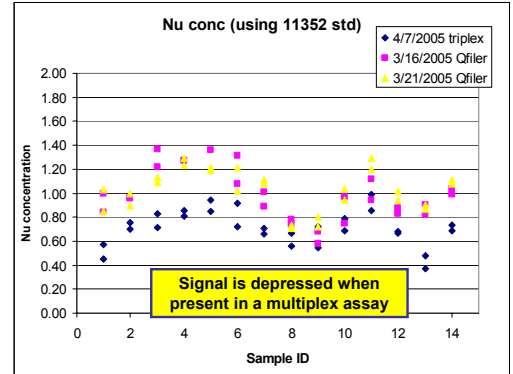
Series of NIST population samples with a range of [DNA] from 40 pg to 23 ng

The same "Standard" was used for all methods (8 dilutions).

Time for the assay:
Alu-RT-PCR ~ 1.25 h (fewer cycles required)
The rest ~ 1.75 h



Recent Examination of Intra-Lab Reproducibility



On-going Studies

- DNA stability in various types of tubes
- Examination of impact of DNA stability at different DNA concentrations
- SRM 2372 Human DNA Quantitation standard is under development (genomic DNA)

Additional Resources

- *Forensic DNA Typing: Biology, Technology, and Genetics of STR Markers (2nd Edition)* by John M. Butler, Elsevier Academic Press, 2005
- Butler, J.M., *et al.* (2004) Forensic DNA typing by capillary electrophoresis using the ABI Prism 310 and 3100 genetic analyzers for STR analysis. *Electrophoresis* 25: 1397-1412.
- NIST website: <http://www.cstl.nist.gov/biotech/strbase>

