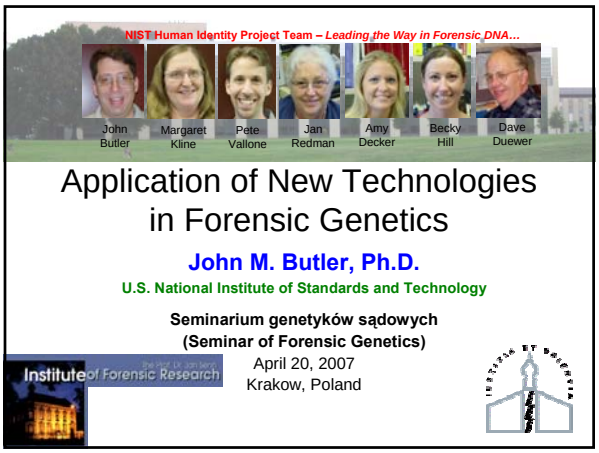


Application of New Technologies in Forensic Genetics

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

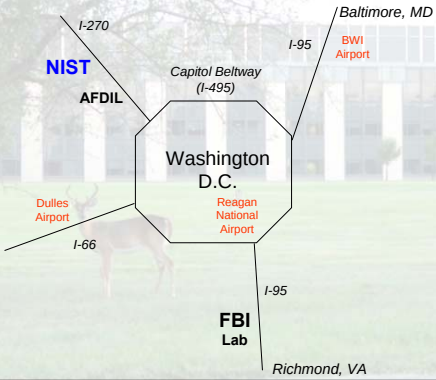
Seminarium genetyków sądowych
(Seminar of Forensic Genetics)
April 20, 2007
Krakow, Poland

NIST History and Mission

- National Institute of Standards and Technology (NIST) was created in 1901 as the National Bureau of Standards (NBS). The name was changed to NIST in 1988.
- NIST is **part of the U.S. Department of Commerce** with a mission to develop and promote measurement, standards, and technology to enhance productivity, facilitate trade, and improve the quality of life.
- NIST supplies over 1,300 Standard Reference Materials (SRMs) for industry, academia, and government **use in calibration of measurements**.
- **NIST defines time for the U.S.**


DNA typing standard

Location of NIST (near Washington, DC)



NIST Gaithersburg Campus


Administration (Building 101)

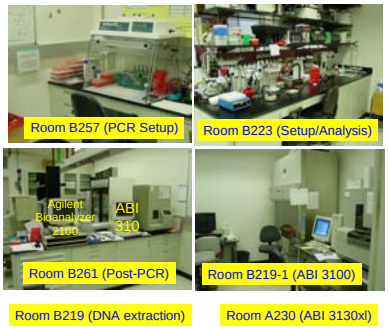
Located in Gaithersburg, Maryland, on approximately 234 hectares (578 acres) just off Interstate 270 about **25 miles northwest of Washington, D.C.**

http://www.nist.gov

~2,500 staff


Advanced Chemical Sciences Laboratory (Building 227)

NIST Human Identity Project Team Laboratory Space
(within Building 227)



Equipment List

GeneAmp 9700 (3)
GeneAmp 9600
ABI 310
ABI 3100 (now 3130xl)
ABI 3130xl
FMBIO III+
ABI 7500 real-time PCR
ABI 7000

Agilent Bioanalyzer 2100
Varian UV spec
Varian HPLC
Bruker TOF-MS
Corbet robot
-80 ºC freezers

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

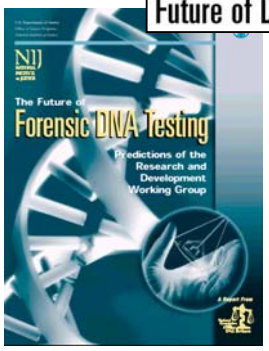
- **Standards** http://www.cstl.nist.gov/biotech/strbase
  - Standard Reference Materials
  - Standard Information Resources (STRBase website)
  - Interlaboratory Studies
- **Technology**
  - Research programs in SNPs, miniSTRs, Y-STRs, mtDNA, qPCR
  - Assay and software development, expert system review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

Where Is the Future Going for DNA Technology That Can Be Applied to Forensic DNA Typing?

Constant state of evolution (like computers)

- Higher levels of multiplexes
- More rapid DNA separations
- Better data analysis software
- New DNA Markers

National Commission on the Future of DNA Evidence



http://www.ojp.usdoj.gov/nij/pubs-sum/183697.htm

- Report published in Nov 2000
- Asked to estimate where DNA testing would be 2, 5, and 10 years into the future

Conclusions

STR typing is here to stay for a few years because of DNA databases that have grown to contain millions of profiles

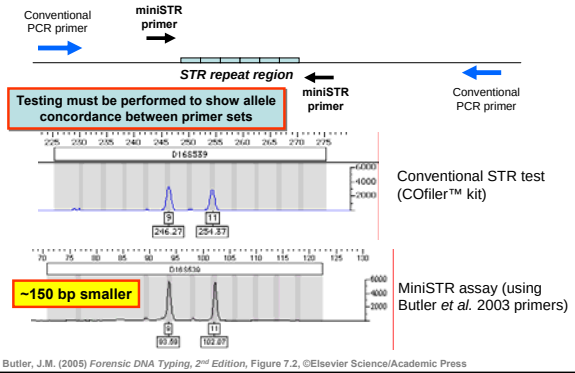
Status of Genetic Marker Systems Used in Forensic DNA Testing

- **STRs** – widely used in national databases today
- **miniSTRs** – used in research and WTC; new MiniFiler kit just being released
- **mtDNA** – used in specialty labs for highly degraded specimens
- **Y-STRs** – growing use due to kits now available
- **SNPs** – research; likely to be limited in use

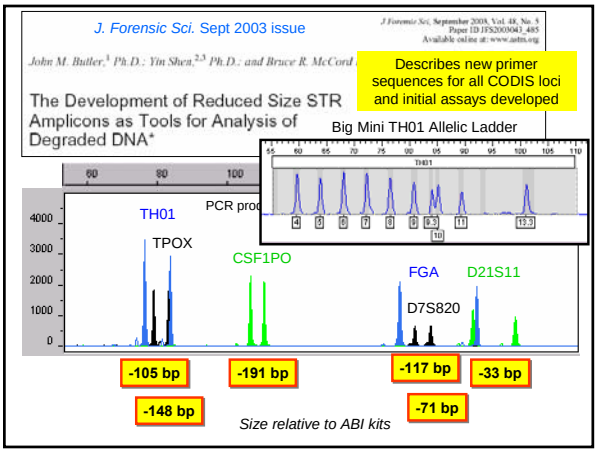
Technology: NIST Research Programs

- 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

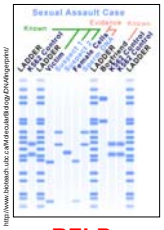
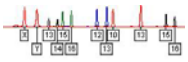
A miniSTR is a reduced size STR amplicon that enables higher recovery of information from degraded DNA samples



Butler, J.M. (2005) *Forensic DNA Typing, 2nd Edition*, Figure 7.2, ©Elsevier Science/Academic Press



The DNA Field Moves Forward…

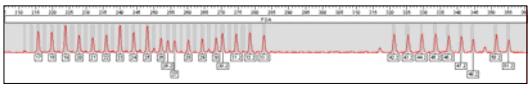
The Past	The Present	The Future
		
RFLP	STRs	miniSTRs
500 – 25,000 bp	100 - 500 bp	50 - 150 bp

How would additional loci be useful?

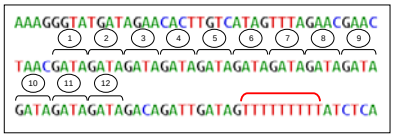
- Obtaining additional information with degraded DNA samples (miniSTRs)
- Resolving common genotypes within populations
- Kinship analysis

Why go beyond core STR Loci?

(1) Large Allele Ranges (e.g. FGA)



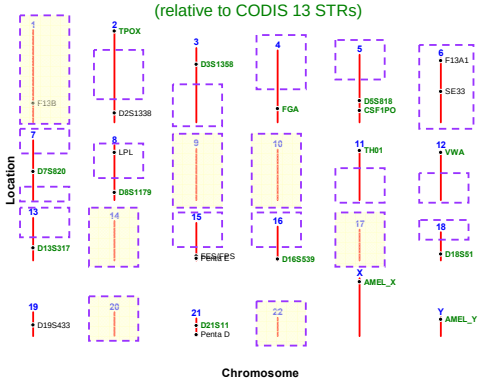
(2) "Unclean" Flanking Sequences (e.g. D7S820)



Butler, JM, Shen, Y., McCord, BR (2003) *JFS* 48(5): 1054-1064

Locations of Focus for Additional Loci

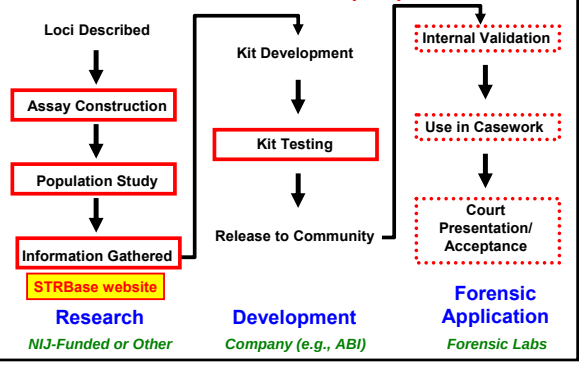
(relative to CODIS 13 STRs)



(3) A large amount of unused chromosomal locations

Steps in Applying Forensic DNA Technology

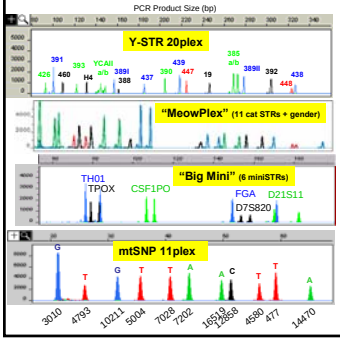
Role of the NIST Human Identity Project Team



Assay Development with Collaborators

Pete Vallone — John Butler

(Usually Other NIJ-Funded Researchers)



- **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…**

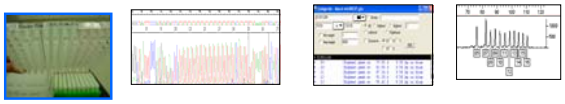
Characterization of New Loci

"Computer Work"

Candidate STR marker selection (e.g. literature searches) → Pull down sequence data from the web (e.g. NCBI) → Identify Chromosome Location (e.g. Human BLAT Search) → Screen for PCR Primers (e.g. Primer3) → Test primers for Multiplex-ability (e.g. AutoDimer - NIST)

"Laboratory Work"

Test Markers on Population samples | Sequence homozygotes to determine allele sizes | Build Macros for Genotyping | Construct Allelic Ladders

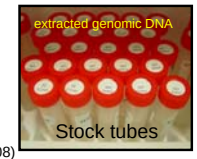


Standard U.S. Population Dataset

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: (>100,000 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)
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)
New miniSTR loci – for 26 loci, 17,238 genotypes
mtDNA full control region sequences by AFDIL

Genotypes with various human identity testing markers

NIST Work with Father-Son Samples

- Samples obtained from paternity testing laboratory as buccal swabs, extracted with DNA-IQ, quantified, diluted to 0.5 ng/uL
- To-date: **100 father-son pairs** of **U.S. Caucasian**, **African American**, **Hispanic**, and **Asian** (**800 samples**)
- **Verified** autosomal STR allele sharing **with Identifiler** (QC for gender and potential sample switches)
- Typed with Yfiler (17 Y-STRs) – **examined mutations**

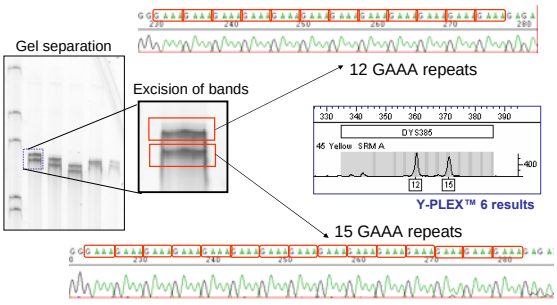
Certify New Loci for NIST Standard Reference Materials (SRMs)

Genotype SRM components with new loci → **Sequence all alleles present for each locus** → **Verify that all genotypes match sequencing data**

↓

Complete Report of Analysis (ROA) → **Update SRM Certificate of Analysis**

Sequencing Individual DYS385 Alleles



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

Y-Chromosome Standard NIST SRM 2395

Human Y-Chromosome DNA Profiling Standard

- **5 male samples** + 1 female sample (neg. control)
- **100 ng of each (50 µL at ~2 ng/µL)**
- **22 Y STR markers sequenced**
- **9 additional Y STR markers typed**
- **42 Y SNPs typed** with Marligen kit

Certified for all loci in commercial Y-STR kits:

Y-PLEX 6
Y-PLEX 5
Y-PLEX 12
PowerPlex Y

SWGDAM recommended loci: DYS19, DYS385 a/b, DYS389I/II, DYS390, DYS391, DYS392, DYS393, DYS438, DYS439

Helps meet FBI Standard 9.5 (and ISO 17025)…traceability to a national standard

New STR Loci Information on STRBase

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


New STR Loci Under Development by the NIST Forensics/Human Identity Project Team

Value of Additional MiniSTR Loci

Becky Hill | Mike Coble | John Butler

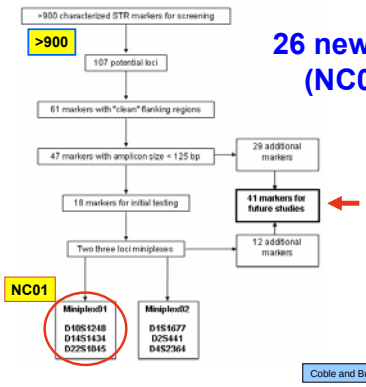
miniSTRs, MiniFiler, and Non-CODIS (NC) Loci

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; a**rticle 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

Initial Testing Results with Potential miniSTR Loci

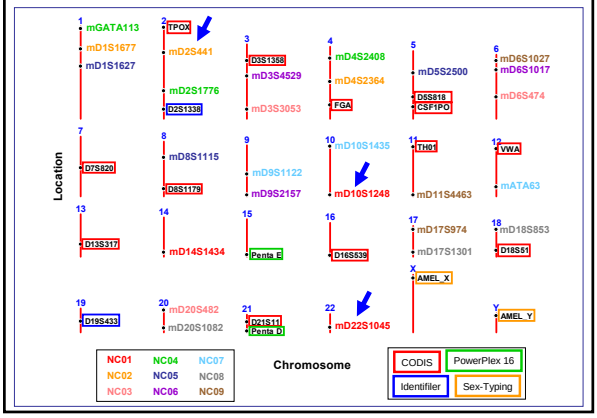


26 new miniSTRs (NC01-NC09)

20 additional loci characterized across U.S. population groups

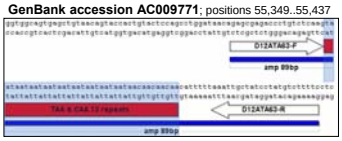
Coble and Butler (2005) *J. Forensic Sci.* 50(1): 43-53

Chromosomal Locations of New miniSTR Loci



Characterization of miniSTR **D12ATA63**

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



[FAM] – GAGCGAGACCCTGTCTCAAG
GAAAAGACATAGGATAGCAATTT

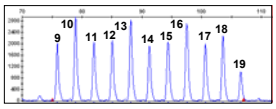
Chr 12 106.825 Mb
(12q23.3)

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



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

European Labs Have Adopted the NIST-Developed NC 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)

Going Beyond Commercial Y-STR Kits

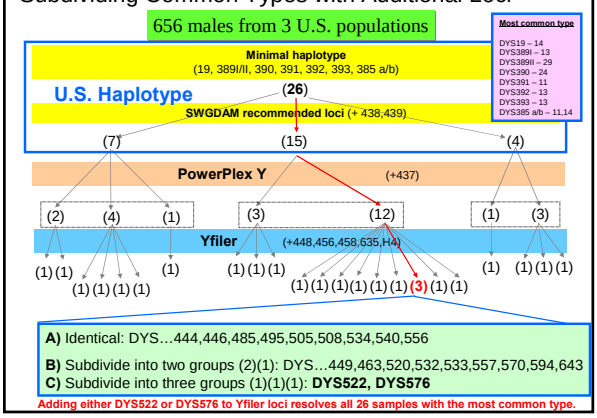
- Most forensic DNA laboratories (certainly in the U.S.) will **only use commercially available kits** due to quality control issues
- Using these kits as a starting point, **are there additional loci that would be beneficial in separating samples with common types**, which could be advocated to companies for possible future adoption in Y-STR kits?
- Is it possible to regularly **resolve individuals from the same paternal lineage** (e.g., fathers and sons) if enough Y-STRs are examined?

Data Set Used to Examine Common Types

- Yfiler kit (**17 Y-STR loci**) run on all NIST male U.S. population samples
  - makes up ~20% of Applied Biosystems database
  - **submitted to the YHRD**
- Additional **20 Y-STR loci** run on full set of NIST population samples *(and several less polymorphic ones only on subset of samples)*
  - Butler, J.M., Decker, A.E., Vallone, P.M., Kline, M.C. (2006) Allele frequencies for 27 Y-STR Loci with U.S. Caucasian, African American, and Hispanic samples. *Forensic Sci. Int.* 156:250-260.

Subdividing Common Types with Additional Loci

656 males from 3 U.S. populations



A) Identical: DYS…444,446,485,495,505,508,534,540,556

B) Subdivide into two groups (2)(1): DYS…449,463,520,532,533,557,570,594,643

C) Subdivide into three groups (1)(1)(1): **DYS522, DYS576**

Adding either DYS522 or DYS576 to Yfiler loci resolves all 26 samples with the most common type.

Subdividing Common Types with Additional Loci

Most common type
DYS19 – 14
DYS389I – 13
DYS389II – 29
DYS390 – 24
DYS391 – 11
DYS392 – 13
DYS393 – 13
DYS385 a/b – 11,14

Percent Unresolved

3.96 %	(minimal haplotype)
3.50 %	(US haplotype)
2.89 %	(PowerPlex Y)
0.46 %	(Yfiler)
All resolved	(18-37 loci)

Provides confidence that Yfiler does a pretty good job of separating unrelated paternal lineages

A) Identical (no improvement over Yfiler):
DYS…444,446,485,495,505,508,534,540,556

B) Subdivide into two groups (2)(1):
DYS…449,463,520,532,533,557,570,594,643

C) Subdivide into three groups (1)(1)(1):
DYS522 or DYS576

The 26 samples with the most common type can be resolved in this sample population with use of the 17 Yfiler loci plus DYS522 or DYS576

# times haplotype observed	9 MHL
1	429
2	34
3	13
4	4
5	3
6	1
7	1
8	1
9	2
10	.
11	1
12	.
13	1
15	.
26	1
HD	0.996644
%DC	0.748476
# HT	491

429 of the 656 had a unique haplotype with the MHL loci, 34 sample haplotypes were observed twice in the sample set, 13 sample haplotypes were observed three times, etc.

With the 9 loci of the minimal haplotype (MHL) run on 656 samples, 26 samples had the most common type

Total = 656 samples

# times haplotype observed	9 MHL	11 SWGDAM
1	429	486
2	34	33
3	13	10
4	4	6
5	3	1
6	1	1
7	1	2
8	1	.
9	2	.
10	.	1
11	1	.
12	.	.
13	1	.
15	.	1
26	1	.
HD	0.996644	0.998529
%DC	0.748476	0.824695
# HT	491	541

With the 11 loci of the SWGDAM haplotype run on 656 samples, 15 samples had the most common type

Total = 656 samples

# times haplotype observed	9 MHL	11 SWGDAM	12 PPY
1	429	486	505
2	34	33	34
3	13	10	14
4	4	6	3
5	3	1	2
6	1	1	.
7	1	2	1
8	1	.	.
9	2	.	.
10	.	1	.
11	1	.	.
12	.	.	1
13	1	.	.
15	.	1	.
26	1	.	.
HD	0.996644	0.998529	0.999064
%DC	0.748476	0.824695	0.853659
# HT	491	541	560

With the 12 loci of the PowerPlex Y haplotype (PPY) run on 656 samples, 12 samples had the most common type

Total = 656 samples

# times haplotype observed	9 MHL	11 SWGDAM	12 PPY	17 Yfiler
1	429	486	505	626
2	34	33	34	12
3	13	10	14	2
4	4	6	3	.
5	3	1	2	.
6	1	1	.	.
7	1	2	1	.
8	1	.	.	.
9	2	.	.	.
10	.	1	.	.
11	1	.	.	.
12	.	.	1	.
13	1	.	.	.
15	.	1	.	.
26	1	.	.	.
HD	0.996644	0.998529	0.999064	0.999916
%DC	0.748476	0.824695	0.853659	0.97561
# HT	491	541	560	640

With the 17 loci in Yfiler across the 656 samples, there are 626 unique haplotypes, 12 haplotypes that were observed twice and 2 haplotypes that were observed three times

Total = 656 samples

# times haplotype observed	9 MHL	11 SWGDAM	12 PPY	17 Yfiler	ALL 37
1	429	486	505	626	652
2	34	33	34	12	2
3	13	10	14	2	.
4	4	6	3	.	.
5	3	1	2	.	.
6	1	1	.	.	.
7	1	2	1	.	.
8	1	.	.	.	.
9	2	.	.	.	.
10	.	1	.	.	.
11	1	.	.	.	.
12	.	.	1	.	.
13	1	.	.	.	.
15	.	1	.	.	.
26	1	.	.	.	.
HD	0.996644	0.998529	0.999064	0.999916	0.999991
%DC	0.748476	0.824695	0.853659	0.97561	0.996951
# HT	491	541	560	640	654

When all 37 loci (Yfiler + 20 new loci) are run on 656 samples, only two haplotypes are observed twice

Total = 656 samples

Challenges of Defining Nomenclature for New Loci

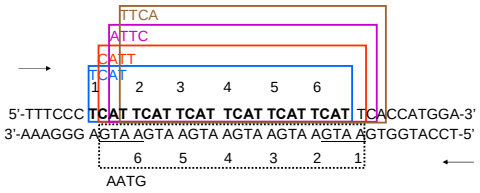
STR Repeat Nomenclature

International Society of Forensic Genetics (ISFG) – *Int. J. Legal Med.* (1997) 110:175-176

- For sequences within genes, use the coding strand
- For other sequences, select the first GenBank database entry or original literature description
- Define the repeat sequence which will provide the largest number of consecutive repeats
- If two sequences are repeated, include both motifs in determining the repeat number
- Microvariants: should be designated by the number of complete repeats and the number of base pairs of the partial repeat separated by a decimal point (Int. J. Legal Med. 1994, 107:159-160) *e.g. TH01 allele 9.3*

Nomenclature Example

(TH01)

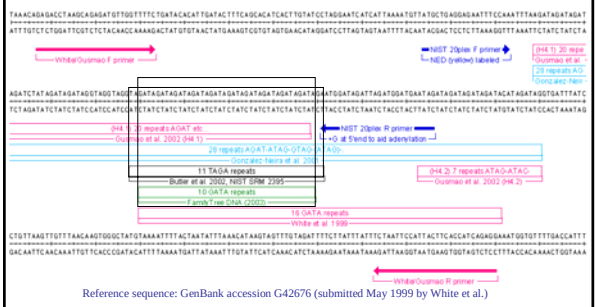


Edwards *et al.* (1991) used **AATG** (adopted early on by Promega)
Kimpton *et al.* (1993) used **TCAT** (Forensic Science Service) – ***most widely used now***

Differences in nomenclature can lead to confusion or even worse problems with database matches—standardization and consistency in use is essential…

Use of "TAGA" vs "GATA" results in a single repeat difference

(Y-GATA-H4)



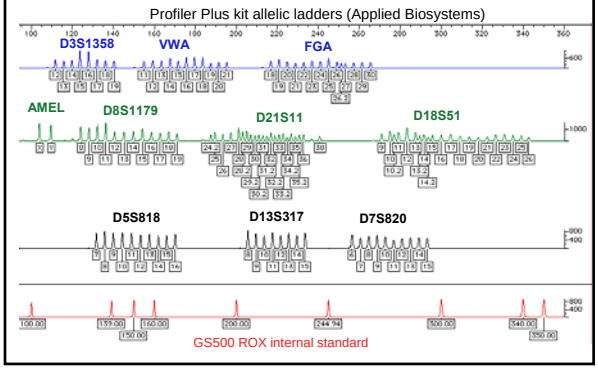
Reference sequence: GenBank accession G42676 (submitted May 1999 by White et al.)

This simple difference has impacted the genetic genealogy community

NIST SRM 2395 follows ISFG guidelines (for our primer pair): first adjacent repeat starting from 5'end is TAGA

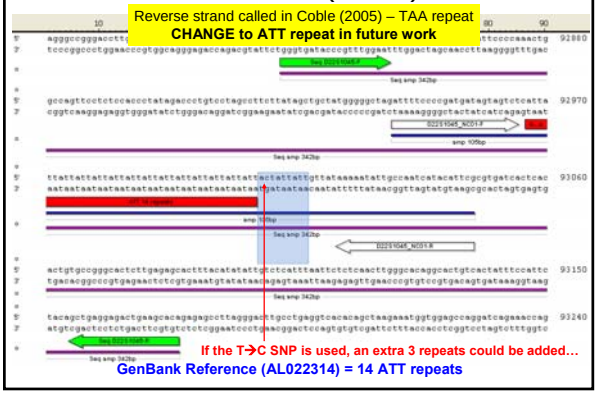
Companies Supply Allelic Ladders in STR Kits to Aid Interlaboratory Consistency

Profiler Plus kit allelic ladders (Applied Biosystems)



D22S1045 (NC01)

Reverse strand called in Coble (2005) – TAA repeat
CHANGE to ATT repeat in future work



If the T→C SNP is used, an extra 3 repeats could be added…

GenBank Reference (AL022314) = 14 ATT repeats

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**

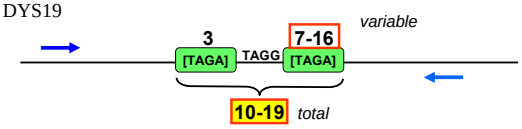
Butler, J.M. and Coble, M.D. (2007) Authors' Response to Letter to Editor [regarding nomenclature for new miniSTR locus D10S1248]. *J. Forensic Sci.* 52(2): 494.

See also …/strbase/miniSTR.htm#Nomenclature_Errata

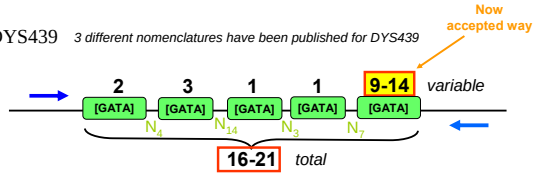
Y STR Allele Nomenclatures

SRM 2395 as an international standard should help resolve issues

DYS19



DYS439 *3 different nomenclatures have been published for DYS439*



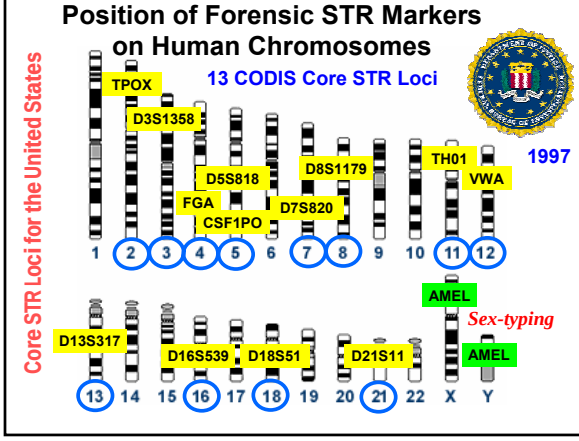
Uses of Additional Loci in the Forensic Community

- All STR loci
  - Missing persons investigations
  - Identification of mass disaster victims
  - Paternity testing
- Y-STR specific
  - Kinship analysis
  - Human migration and evolutionary studies
  - Historical and genealogical research

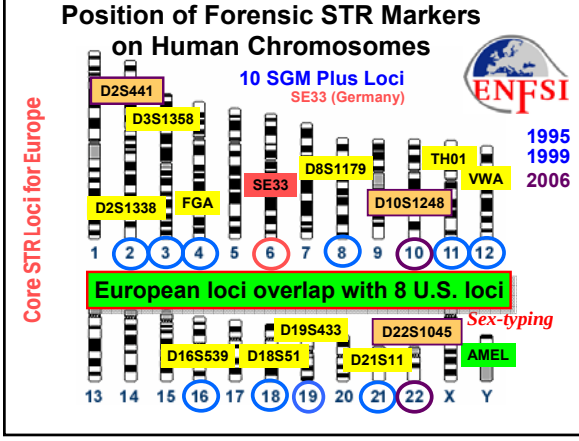
Publications on new loci

- Coble, M.D. and Butler, J.M. (2005) Characterization of new miniSTR loci to aid analysis of degraded DNA. *J. Forensic Sci.* 50: 43-53.
- Butler, J.M., Decker, A.E., Vallone, P.M., Kline, M.C. (2006) Allele frequencies for 27 Y-STR loci with U.S. Caucasian, African American, and Hispanic samples. *Forensic Sci. Int.* 156:250-260.
- Coble, M.D., Hill, C.R., Vallone, P.M., Butler, J.M. (2006) Characterization and performance of new miniSTR loci for typing degraded samples. *Progress in Forensic Genetics 11*, Elsevier Science: Amsterdam, The Netherlands, International Congress Series 1288, 504-506.
- Decker, A.E., Kline, M.C., Vallone, P.M., Butler, J.M. (2007) The impact of additional Y-STR loci on resolving common haplotypes and closely related individuals. *FSI Genetics, in press.*
- Hill, C.R., Coble, M.D., Butler, J.M. (2007) Characterization of 26 miniSTR loci for improved analysis of degraded DNA samples. *submitted*.

Position of Forensic STR Markers on Human Chromosomes



Position of Forensic STR Markers on Human Chromosomes



Review Article on Core STR Loci

J Forensic Sci, March 2006, Vol. 51, No. 2
doi:10.1111/j.1556-4029.2006.00046.x
Available online at: www.blackwell-synergy.com

John M. Butler,[1] Ph.D.

Genetics and Genomics of Core Short Tandem Repeat Loci Used in Human Identity Testing

Journal of Forensic Sciences 2006, 51(2): 253-265

- Reviews STR kits, genomic locations, mutation rates, potential genetic linkage, and known variant alleles for autosomal STR and Y-STR loci
- **Covers characteristics of 18 autosomal loci (13 core CODIS loci, D2, D19, Penta D, Penta E, SE33) and 11 SWGDAM-recommended Y-STR loci**

STRBase

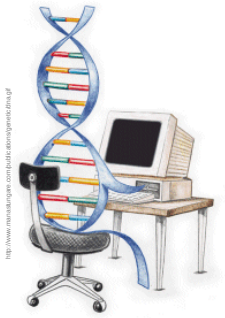
Short Tandem Repeat DNA Internet Database

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

General Information	Forensic Interest Data	Supplemental Info
•Intro to STRs (downloadable PowerPoint)	•FBI CODIS Core Loci	•Reference List **>2500**
•STR Fact Sheets	•DAB Standards	•Technology Review
•Sequence Information	•NIST SRMs 2391	•Addresses for Scientists
•Multiplex STR Kits	•Published PCR Primers	•Links to Other Web Sites
•Variant Allele Reports	•Y-Chromosome STRs	•DNA Quantitation
•Training Slides	•Population Data	•mtDNA
	•Validation Studies	•New STRs
	•miniSTRs	•Forensic SNPs

New information is added regularly…

The Future



More Robotics

Expert Systems

Animal & Plant DNA

Physical Characteristics

Ethnicity Estimation

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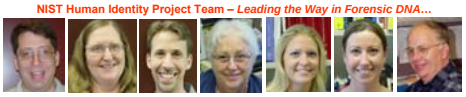
NIST Human Identity Project Team – ***Leading the Way in Forensic DNA…***



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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

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

Questions?

See also http://www.dna.gov/research/nist

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