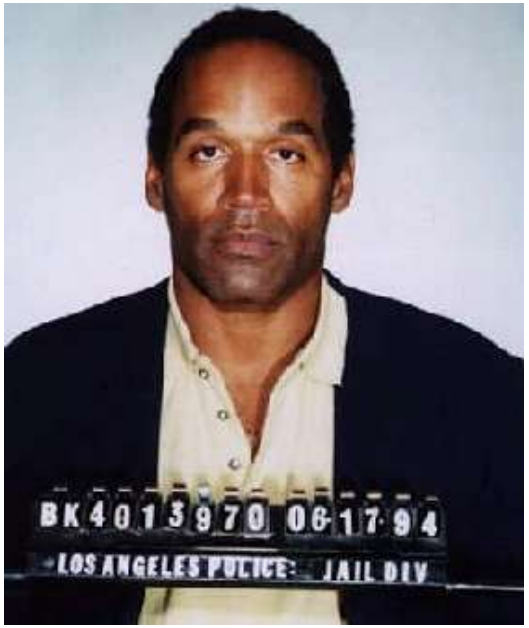
State-of-the-Art Forensic DNA

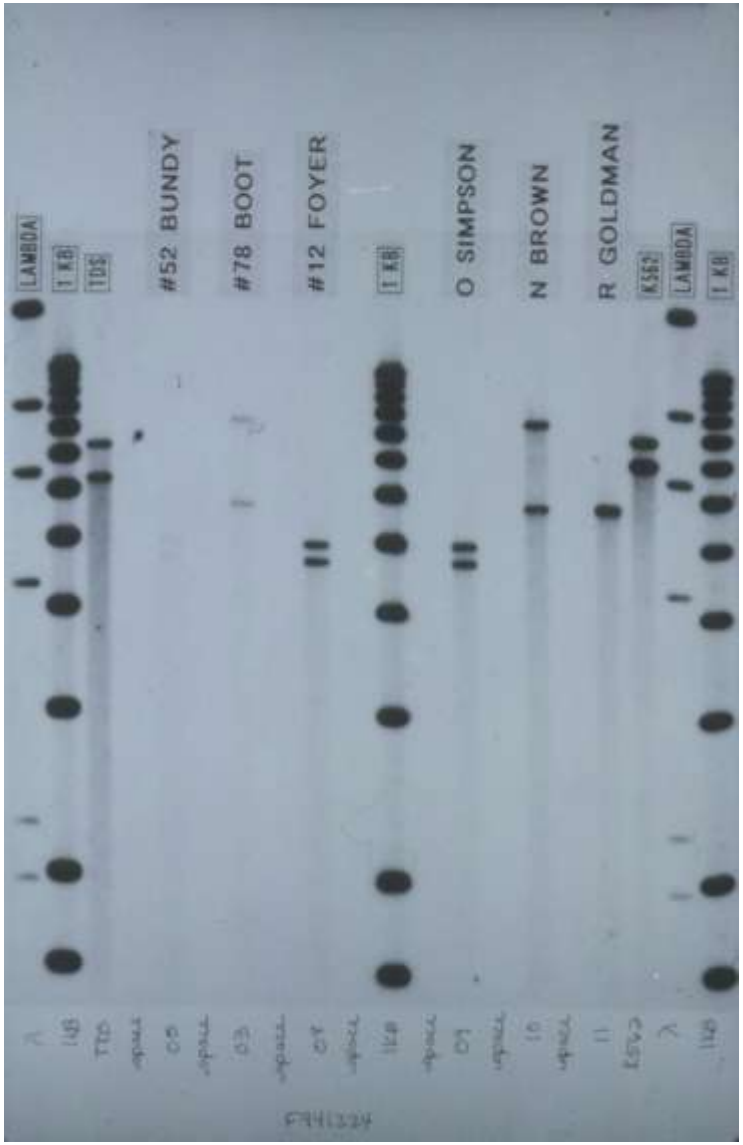
John M. Butler, PhD
National Institute of Standards and Technology
Gaithersburg, Maryland
United States of America

8 May 2013 (São Paulo, Brazil)

NIST

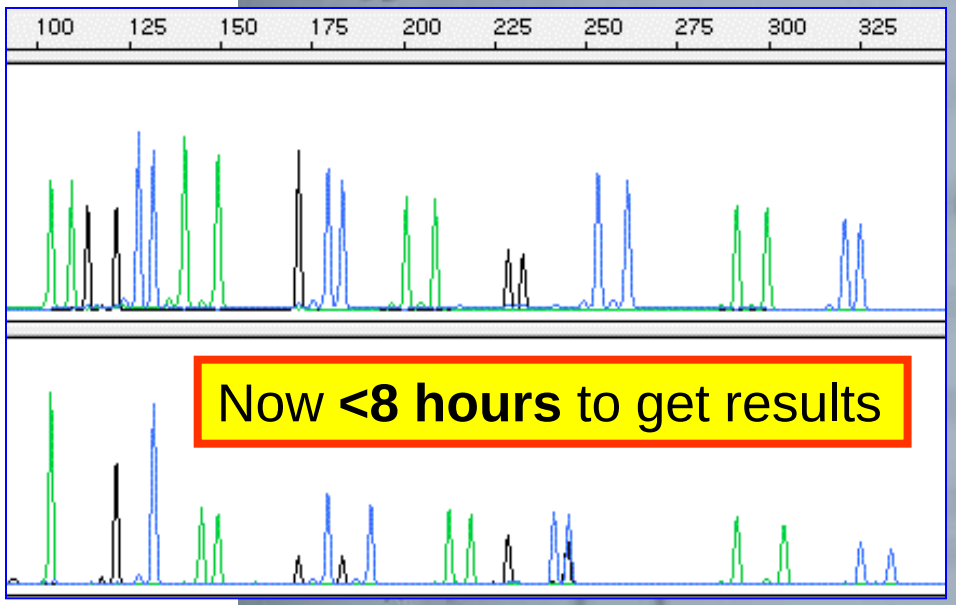
O.J. Simpson: Helped Bring DNA Testing to Knowledge of the General Public





Progress Since 1995…

Almost **8 weeks** needed to get results



Now **<8 hours** to get results

O.J. Simpson DNA testing was performed with RFLP

Steps in Forensic DNA Testing

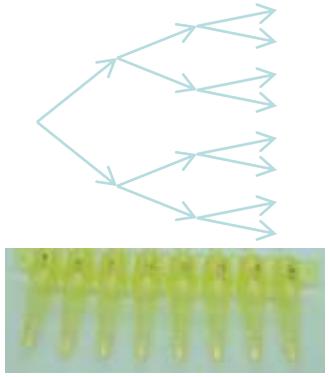
Collection/Storage/ Characterization → **Extraction/ Quantitation** → **Amplification/ Marker Sets** → **Separation/ Detection** → **Interpretation** → **Report**

Mixture interpretation

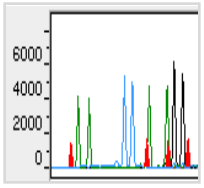
Blood Stain Buccal swab

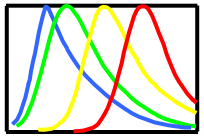
Sample Collection & Storage

DNA Extraction & Quantitation

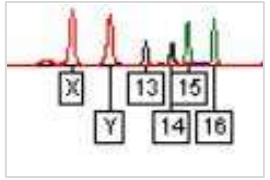


Multiplex PCR Amplification of STR Markers





CE with LIF Detection



Male: 13,14-15,16-…

Data Interpretation , Review & Reporting

GeneAmp 9700 Thermal Cycler

ABI 3500 Genetic Analyzer

GeneMapper*ID-X* software

capillary electrophoresis

Presentation Outline

- **Introduction to NIST**
  - Our role with forensic DNA in the United States
  - Some current projects
- **Near-term future**
  - New autosomal STR loci for expanded core loci
  - Expanded use of databases (e.g., familial searching)
  - Rapid DNA testing
- **More distant future**
  - Loci besides STRs for identity testing?
  - Phenotyping capabilities?
  - Next-generation DNA sequencing?

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.

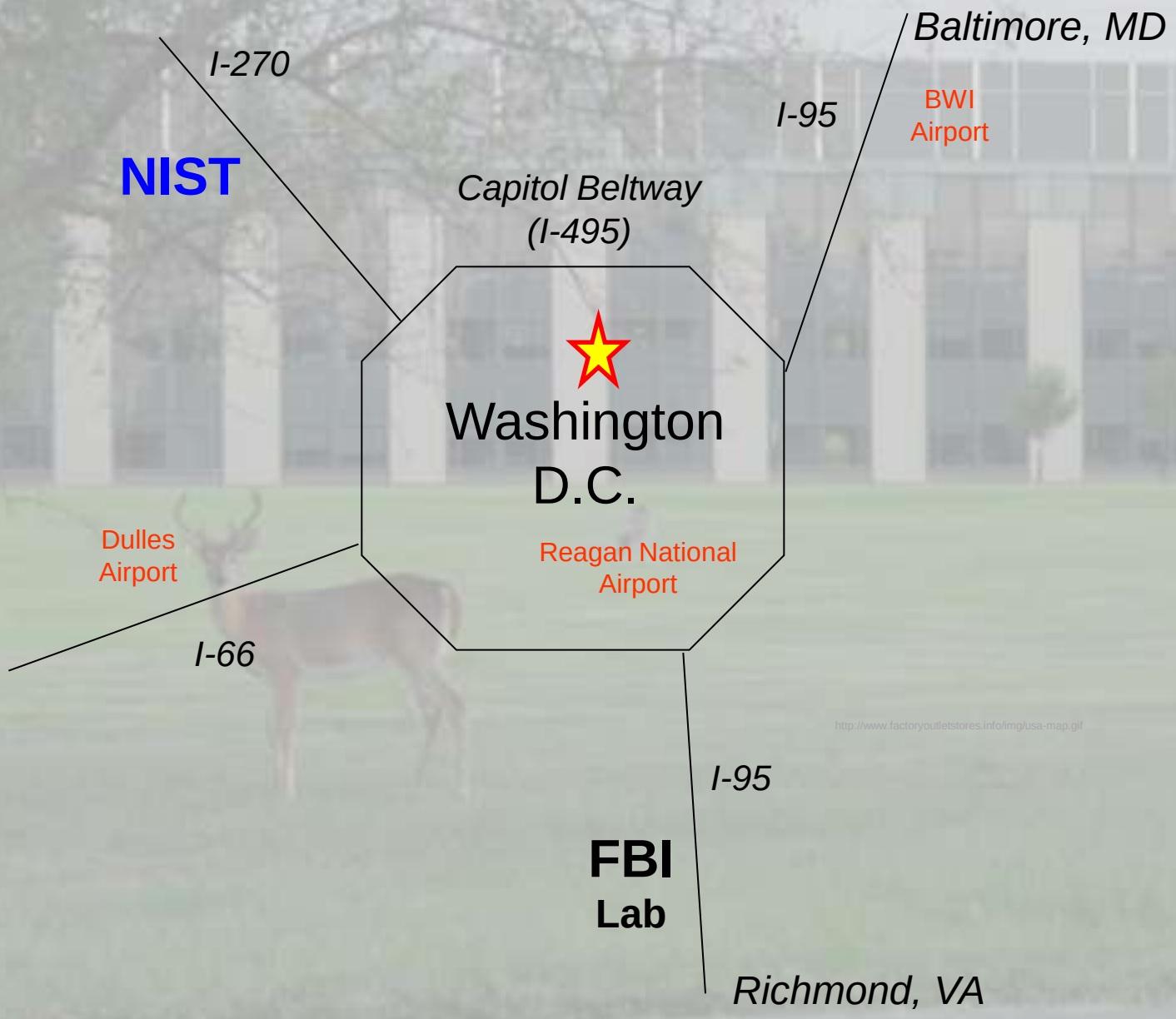
- NIST supplies over 1,300 Standard Reference Materials (SRMs) for industry, academia, and government **use in calibration of measurements**.

- **NIST defines time for the U.S.**

$686 for 3 jars

DNA typing standard

Location of NIST



NIST Today

Major Assets

- ~ 2,900 employees
- ~ 2600 associates and facilities users
- ~ 400 NIST staff on about 1,000 national and international standards committees
- **4 Nobel Prizes in Physics in past 15 years** (including 2012 to David Wineland for quantum physics)

Major Programs

- **NIST Laboratories**
- Baldridge National Quality Program
- Hollings Manufacturing Extension Partnership
- Technology Innovation Program

Joint NIST/University Institutes:

- JILA
- Joint Quantum Institute
- Institute for Bioscience & Biotechnology Research
- Hollings Marine Laboratory

Harry T. Edwards
U.S. Court of Appeals (DC)
Co-Chair, Forensic Science Committee

National Academies Report on Forensic Science

- Released February 18, 2009
- Entitled “Strengthening Forensic Science in the United States: A Path Forward”
- 13 recommendations provided to Congress
- **Recommends establishing a National Institute of Forensic Science (NIFS)**
- NIST and the U.S. Department of Justice announced plans on February 15, 2013 to establish a **National Commission on Forensic Sciences**

THE NATIONAL ACADEMIES
Advisers to the Nation on Science, Engineering, and Medicine

Current Activities at NIST

Applied Genetics Group

Standard Reference Materials

- SRM 2372 (DNA quantitation standard)
- SRM 2391c (STR typing)

Technology Evaluation and Development

- Rapid multiplex PCR protocols (multiplex STR amplification in <35 min)
- Low-level DNA studies
- Mixture interpretation – research and training materials
- Unusual STR allele characterization
- New STR loci and assays (STR 26plex, kit concordance, InDels & SNPs)

• Training Materials

- Workshops on mixture interpretation and CE troubleshooting
- Third edition of *Forensic DNA Typing* textbook (2010, 2012, & 2014)

NIST Reference Materials for Forensic DNA Measurement Assurance

Margaret Kline

DNA quantity measurement calibration

Autosomal and Y-chromosome short tandem repeat (STR) measurement calibration

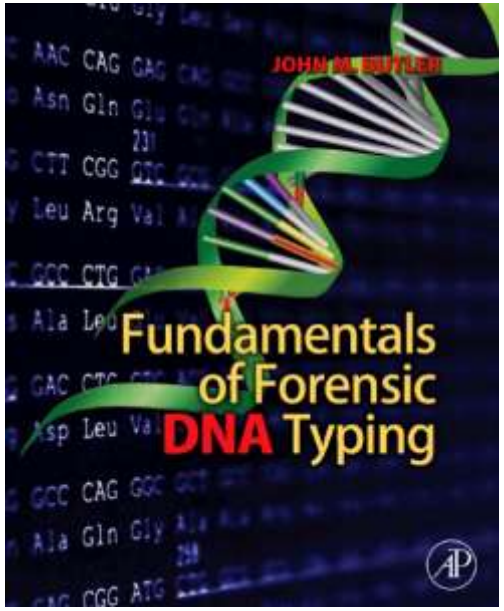
Forensic DNA Typing Textbook

3rd Edition is Three Volumes

Now part of my job at NIST (no royalties are received)

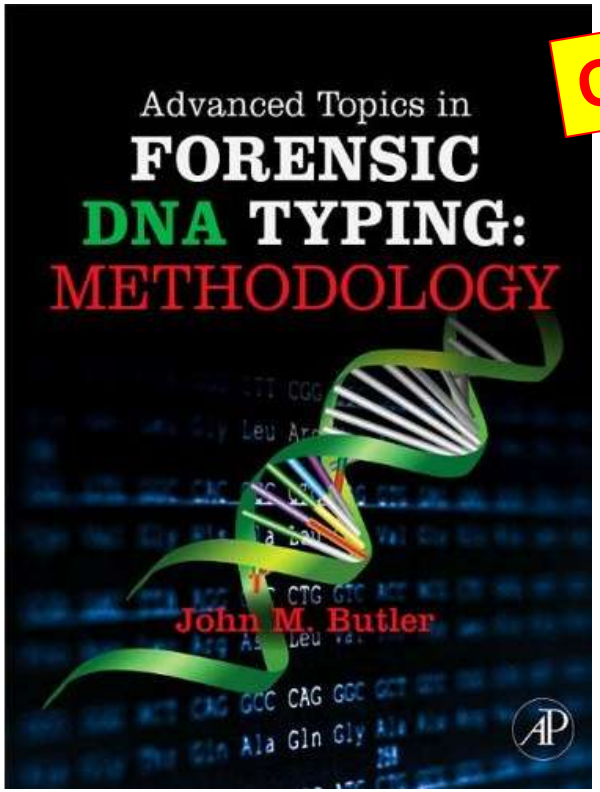
John Butler

For beginning students, general public, & lawyers



Sept 2009

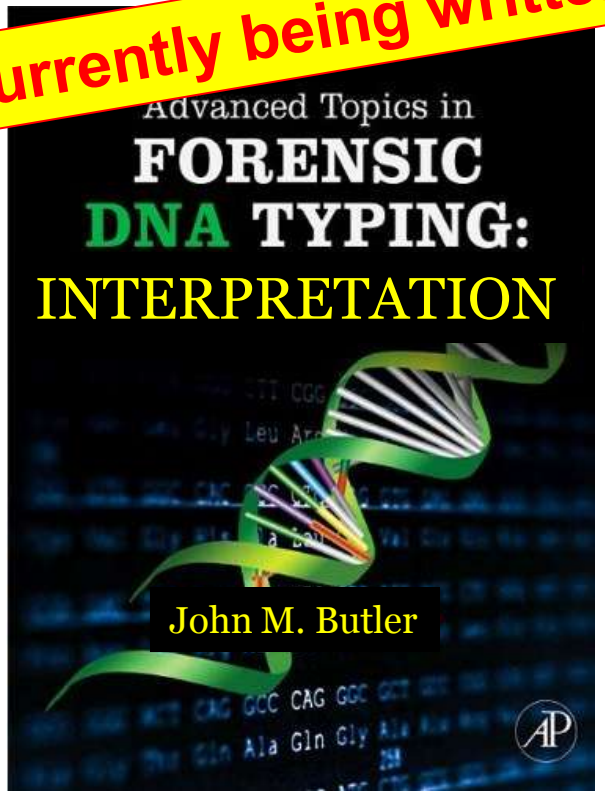
~500 pages



August 2011

~700 pages

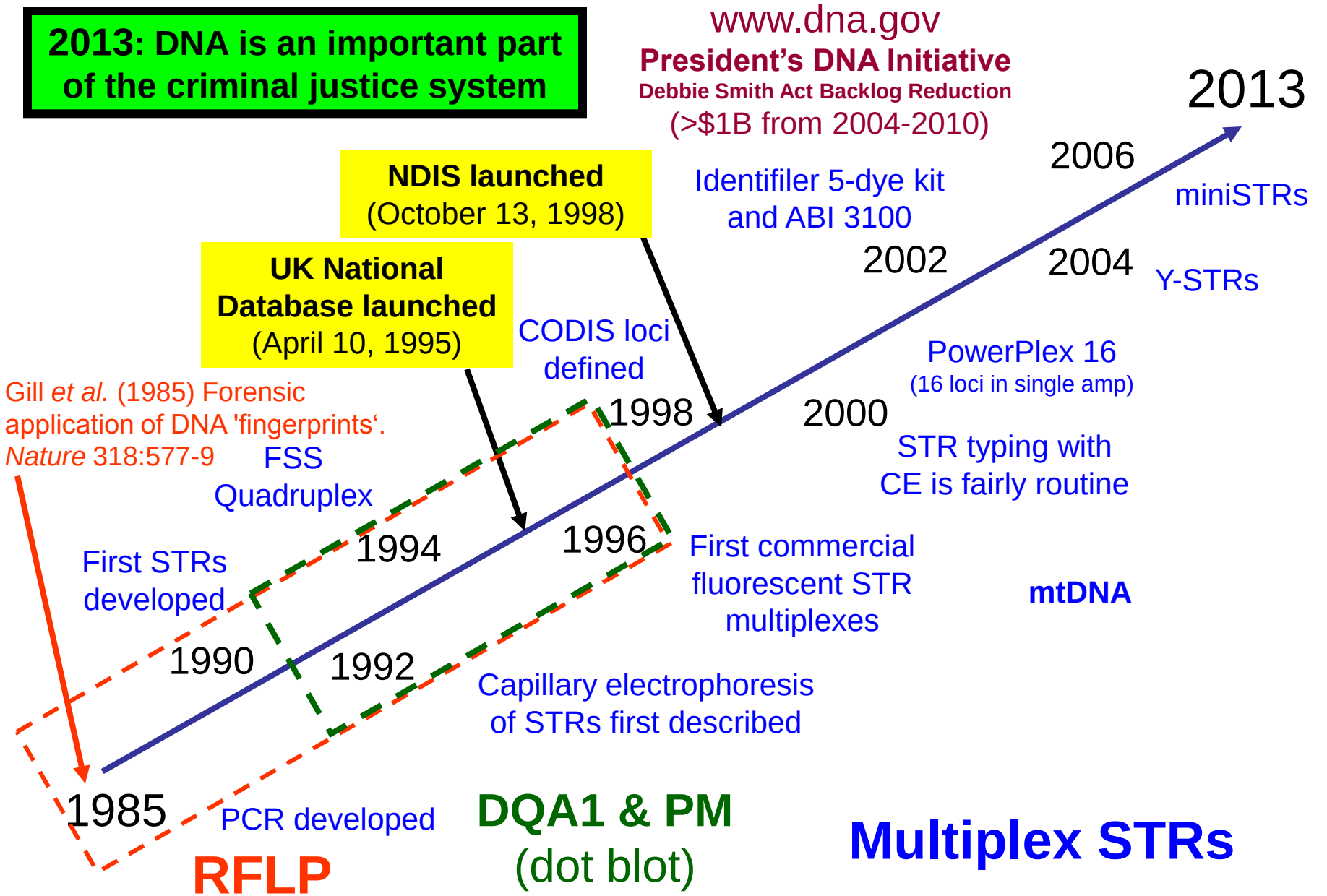
Currently being written



Fall 2014

~500 pages

Historical Perspective on DNA Typing



Stages of Forensic DNA Progression

Stages	Time Frame	Description
Exploration	1985-1995	Beginnings, different methods tried (RFLP and early PCR)
Stabilization	1995-2005	Standardization to STRs, selection of core loci, implementation of Quality Assurance Standards
Growth	2005-2013	Rapid growth of DNA databases, extended applications pursued
Sophistication	*The Future*	*Expanding tools available,* ***confronting privacy concerns***

INNOCENCE PROJECT

http://www.innocenceproject.org

KNOW THE CASES : UNDERSTAND THE CAUSES : FIX THE SYSTEM

ABOUT : DONATE : NEWS &

Rickey Johnson

Served 25 years in Louisiana for a crime he didn't commit.

Kirk Bloodsworth

Incident Year: 1984

Jurisdiction: MD

Charge: Murder, Sexual Assault, Rape

Conviction: First Degree Murder, Sexual Assault, Rape

Sentence: Death

Year of Conviction: 1985

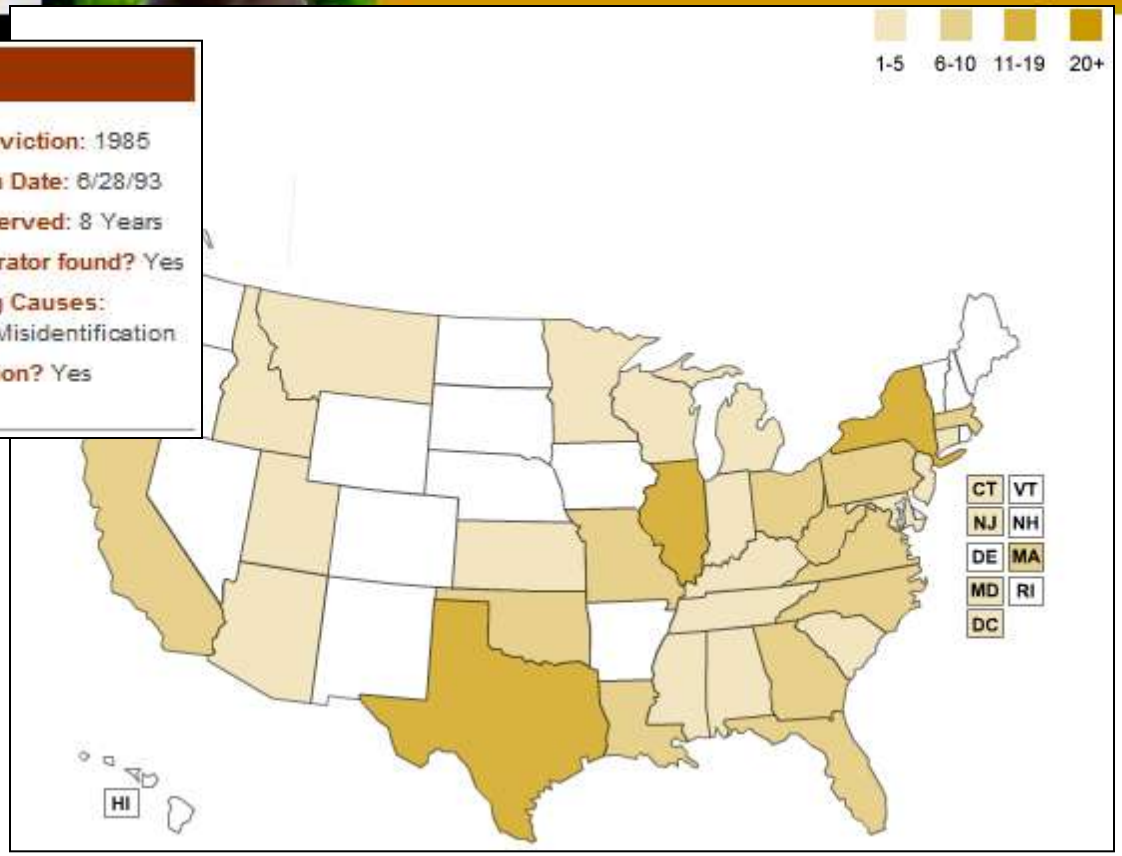
Exoneration Date: 6/28/93

Sentence Served: 8 Years

Real perpetrator found? Yes

Contributing Causes: Eyewitness Misidentification

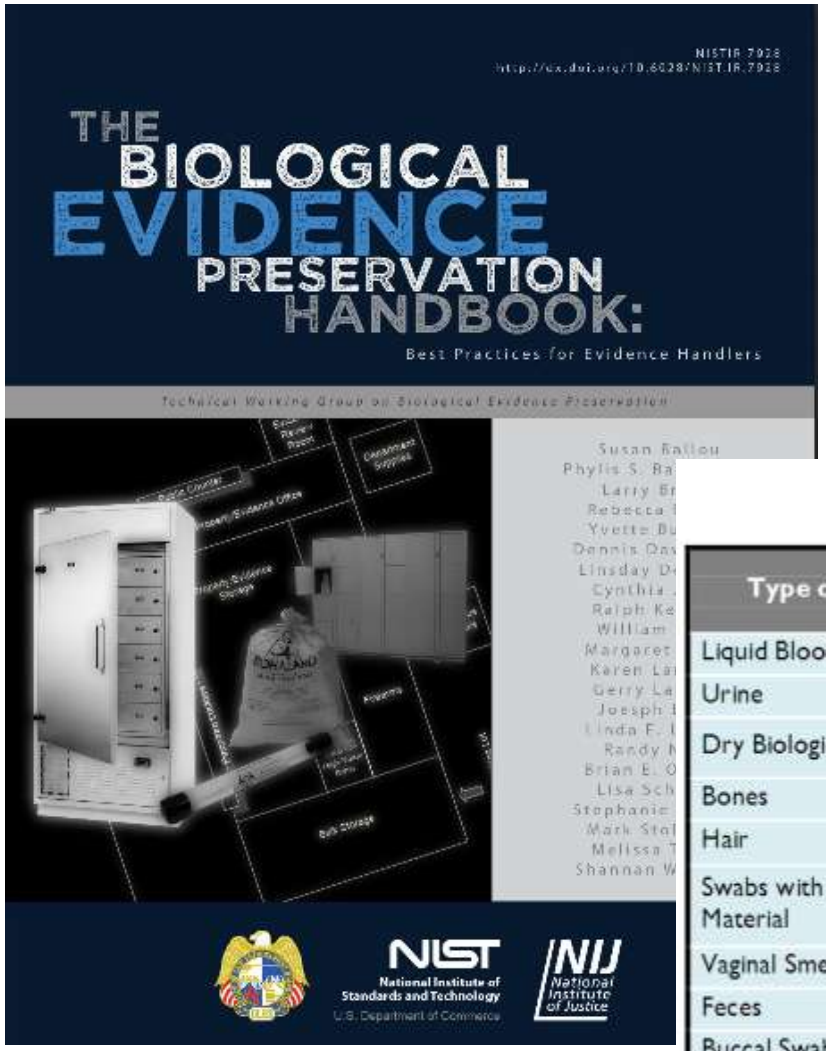
Compensation? Yes



306 exonerated as of May 7, 2013

New Handbook on Biological Evidence Preservation

Available (as free pdf): **http://nvlpubs.nist.gov/nistpubs/ir/2013/NIST.IR.7928.pdf**



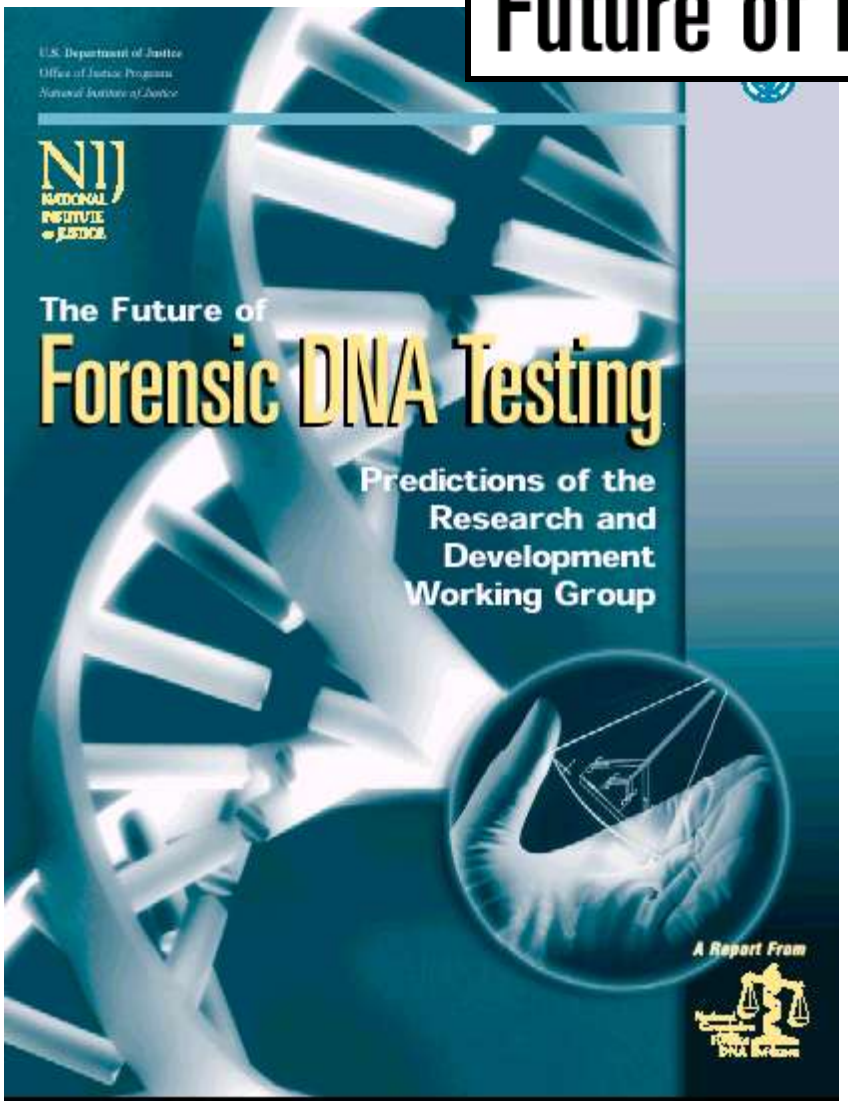
73 page handbook that makes recommendations for evidence retention, safe handling, packaging and storage, chain-of-custody and tracking, and appropriate disposal once evidence retention is no longer required by law

Table III-2: Long-Term Storage Conditions Matrix[1]

Type of Evidence[2]	Frozen	Refrigerated	Temperature Controlled	Room Temperature
Liquid Blood	Never	Best		
Urine	Best			
Dry Biological Stained Items			Best	
Bones			Best	
Hair			Best	Acceptable
Swabs with Biological Material			Best (dried)	
Vaginal Smears			Best	
Feces	Best			
Buccal Swabs			Best	
DNA Extracts	Best (liquid)	Acceptable (liquid)	Acceptable (dried)	

Released April 2013

National Commission on the Future of DNA Evidence



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

- Report published in Nov 2000

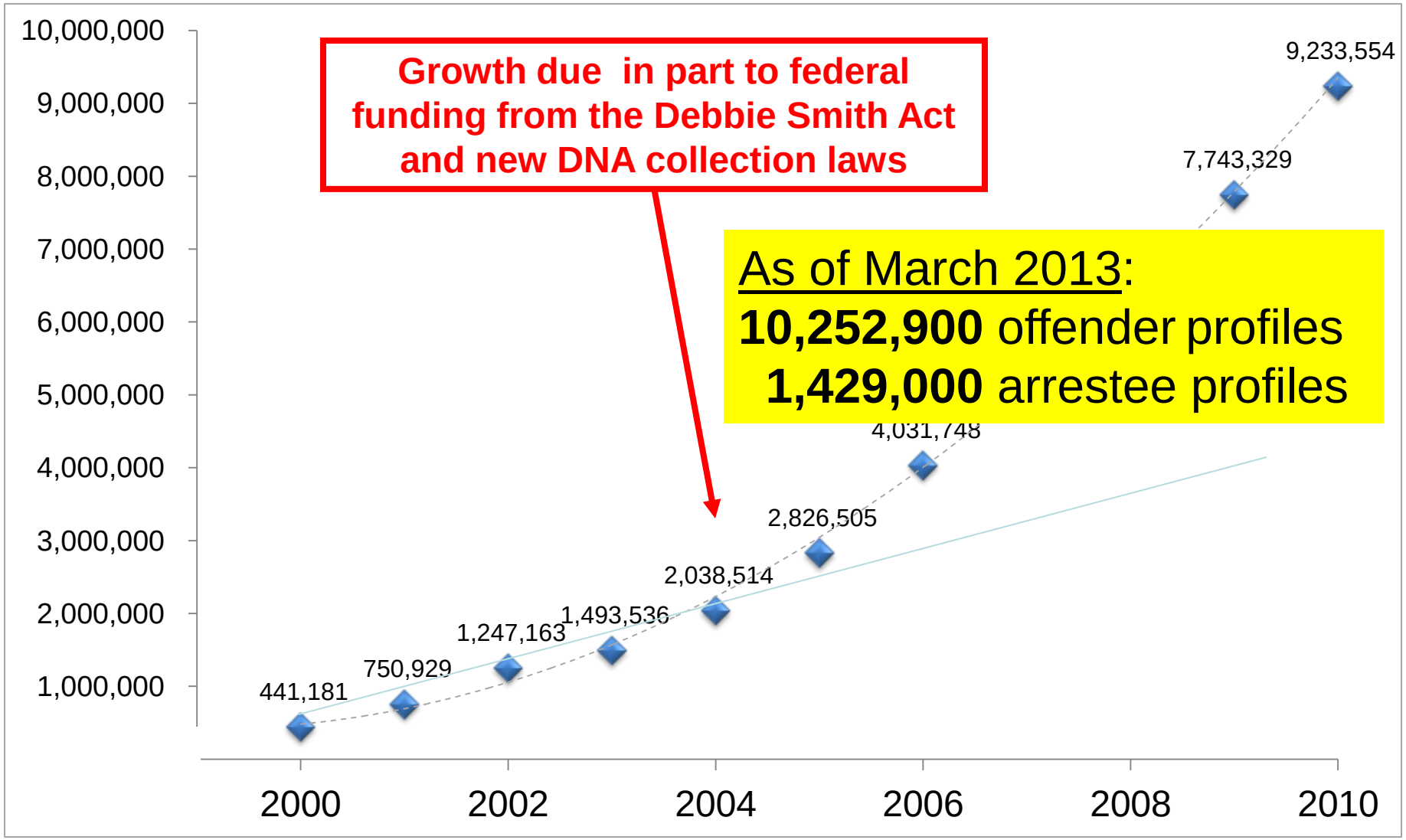
- Asked to estimate where DNA testing would be 2, 5, and 10 years into the future

Conclusions

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

Number of Offender DNA Profiles

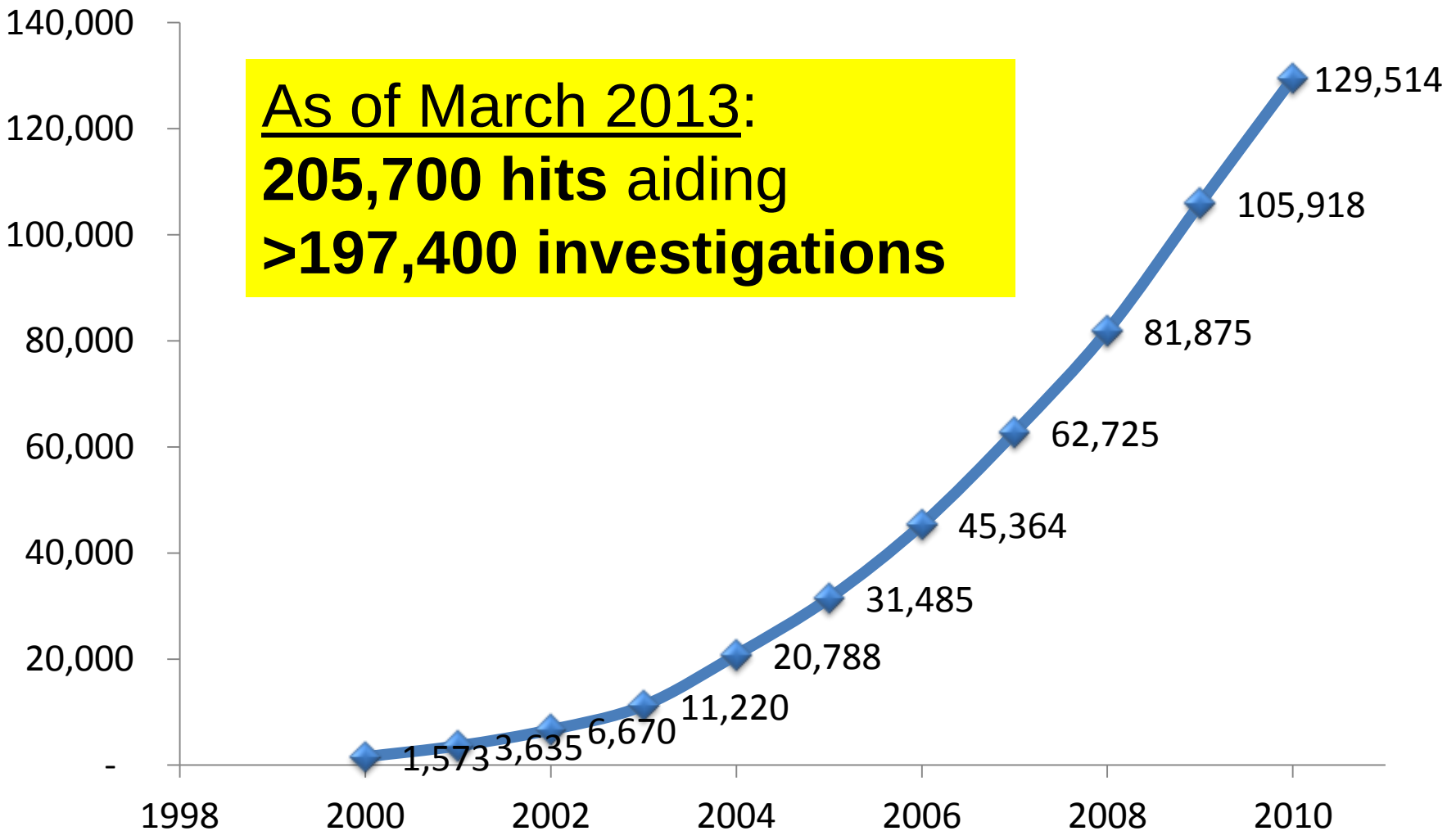
in the U.S. National DNA Database



Source: FBI Laboratory's CODIS Unit

Number of Investigations Aided

in the U.S. National DNA Database



As of March 2013:
205,700 hits aiding
>197,400 investigations

Source: FBI Laboratory's CODIS Unit

Growth of DNA Databases

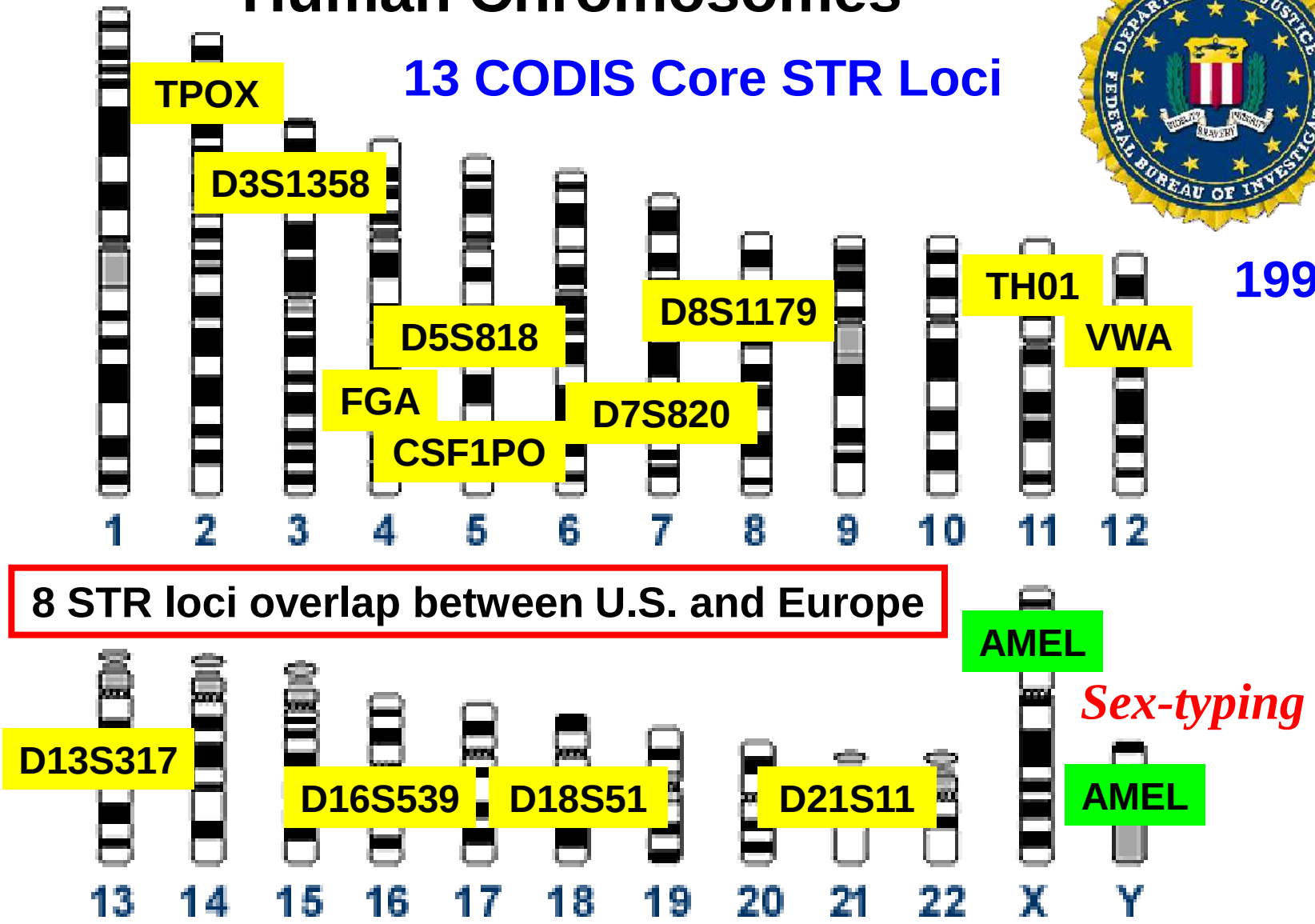
- Within the U.S., we have benefited from significant federal funding over the past decade
- Expanded laws now enable more offenders to be included (currently 28 states and federal government have laws to collect DNA from arrestees)
- Have effectively locked technology with core STR markers used to generate DNA profiles that now number greater than 10 million profiles

Position of Forensic STR Markers on Human Chromosomes

Core STR Loci for the United States

13 CODIS Core STR Loci

1997



Expanding the U.S. CODIS Core Loci

D.R. Hares (2012) Expanding the CODIS Core Loci in the United States. *Forensic Sci. Int. Genet.* 6(1): e52-e54
Addendum to expanding the CODIS core loci in the United States, Forensic Sci. Int. Genet. (2012) 6(5): e135

Contents lists available at ScienceDirect

Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsig

Letter to the Editor

Expanding the CODIS core loci in the United States

CODIS Core Loci Working Group
Formed in May 2010 to make recommendations to FBI CODIS Unit

Douglas Hares (Chair) – FBI
John Butler – NIST
Cecelia Crouse – FL PBSO
Brad Jenkins – VA DFS
Ken Konzak – CA DOJ
Taylor Scott – IL SP

major reasons for expanding the CODIS core loci in the United States:

(1) To reduce the likelihood of adventitious matches [7] as the number of profiles stored at NDIS continues to increase each year (expected to total over 10 million profiles by the time of this publication). There are no signs that this trend will slow down as States expand the coverage of their DNA database programs and increase laboratory efficiency and capacity.
(2) To increase international compatibility to assist law enforcement data sharing efforts.
(3) To increase discrimination power to aid missing persons cases.

Three major reasons for expanding the CODIS core loci in the United States

D.R. Hares (2012) *Forensic Sci. Int. Genet.* 6(1):e52-e54

- **To reduce the likelihood of adventitious matches** as the number of profiles stored at NDIS continues to increase each year

- **To increase international compatibility** to assist law enforcement data sharing efforts

- **To increase discrimination power to aid missing persons cases**

International Comparability

Currently there are 24 autosomal STR markers present in commercial kits

ESS = European Standard Set

13 CODIS loci

U.S.	Europe
TPOX	
CSF1PO	
D5S818	
D7S820	
D13S317	
FGA	FGA
vWA	vWA
D3S1358	D3S1358
D8S1179	D8S1179
D18S51	D18S51
D21S11	D21S11
TH01	TH01
D16S539	D16S539
D2S1338	D2S1338
D19S433	D19S433
Penta D	
Penta E	

7 ESS loci

3 miniSTR loci developed at NIST

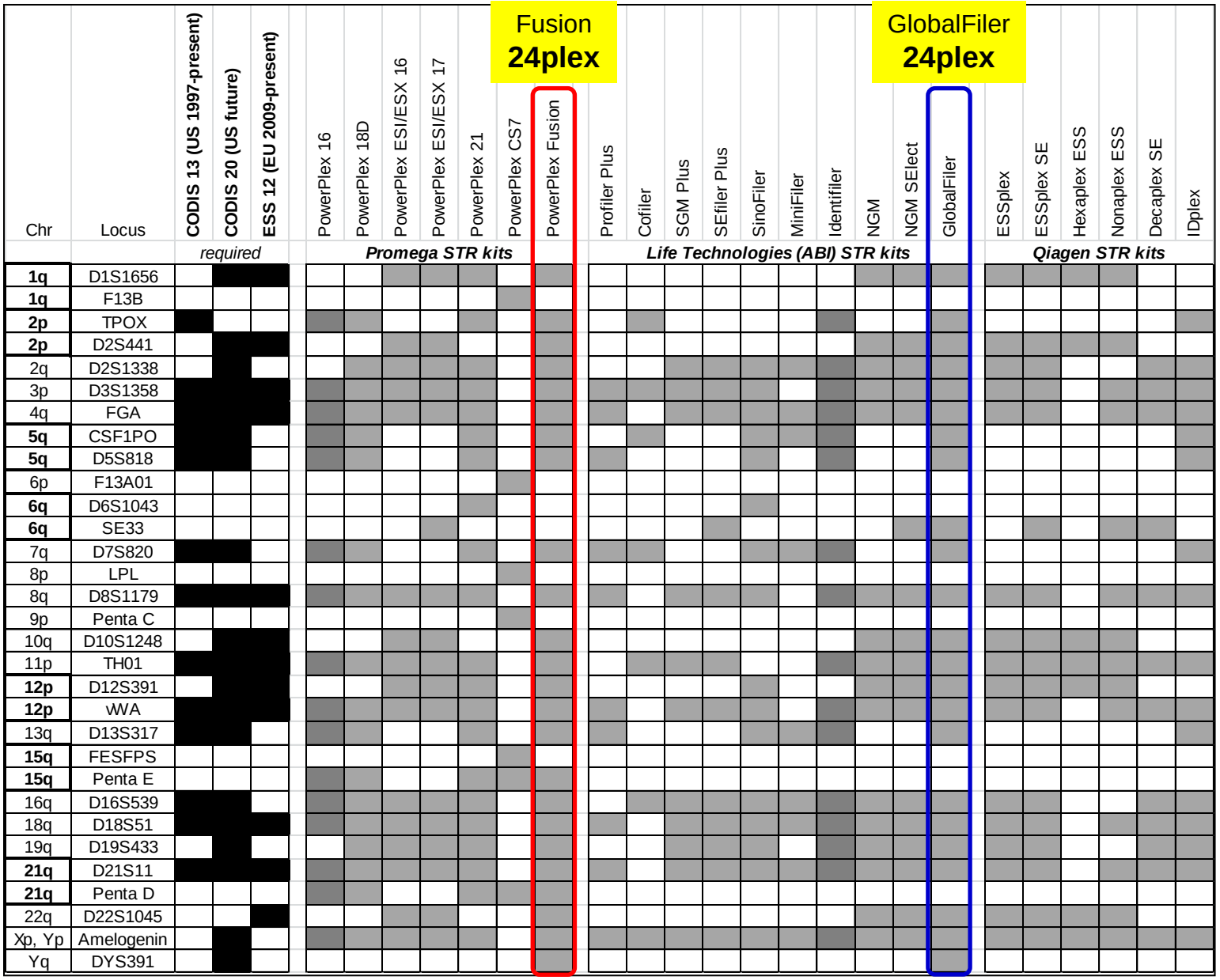
D12S391
D1S1656
D2S441
D10S1248
D22S1045

5 loci adopted in 2009 to expand to 12 ESS loci

Locus used in China ← **D6S1043**

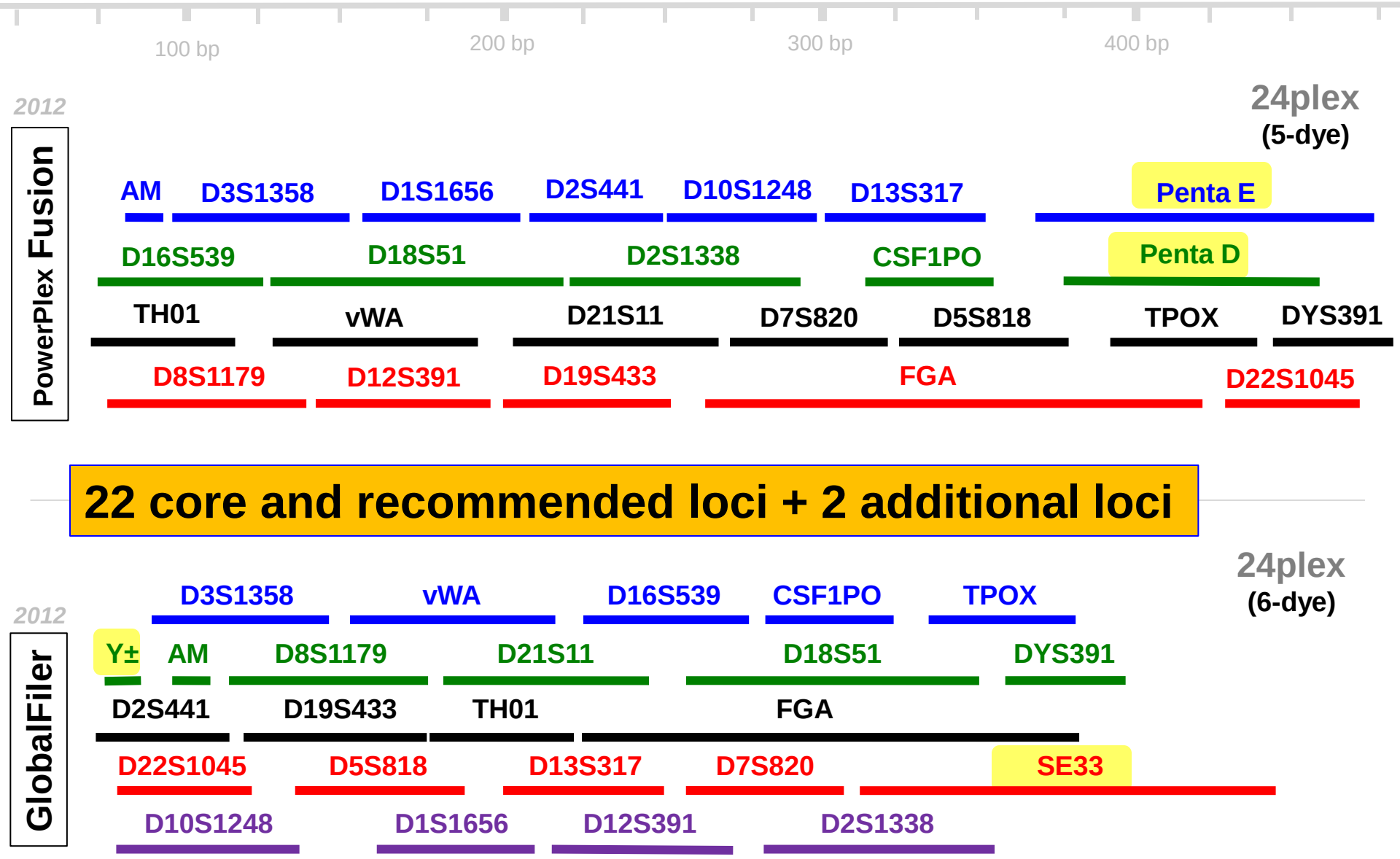
SE33 → Core locus for Germany

STR Loci Covered in Currently Available Commercial Kits

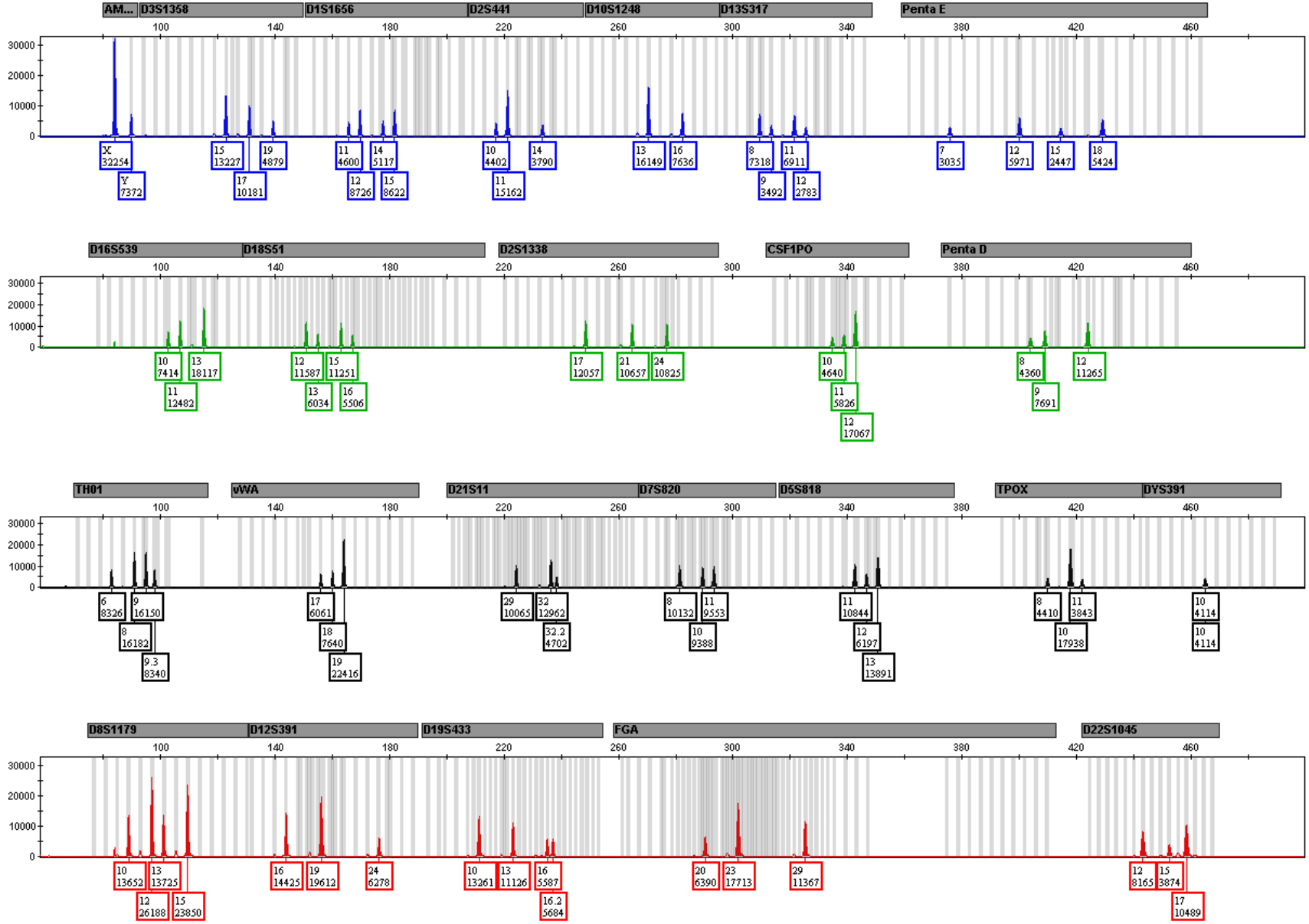


Butler, J.M., & Hill, C.R. (2013) *Topics on Forensic DNA Analysis: Current Practices and Emerging Technologies* (CRC Press).
Chapter 9. Biology and Genetics of New Autosomal STR Loci Useful for Forensic DNA Analysis (in press)

STR Marker Layouts for New U.S. Kits

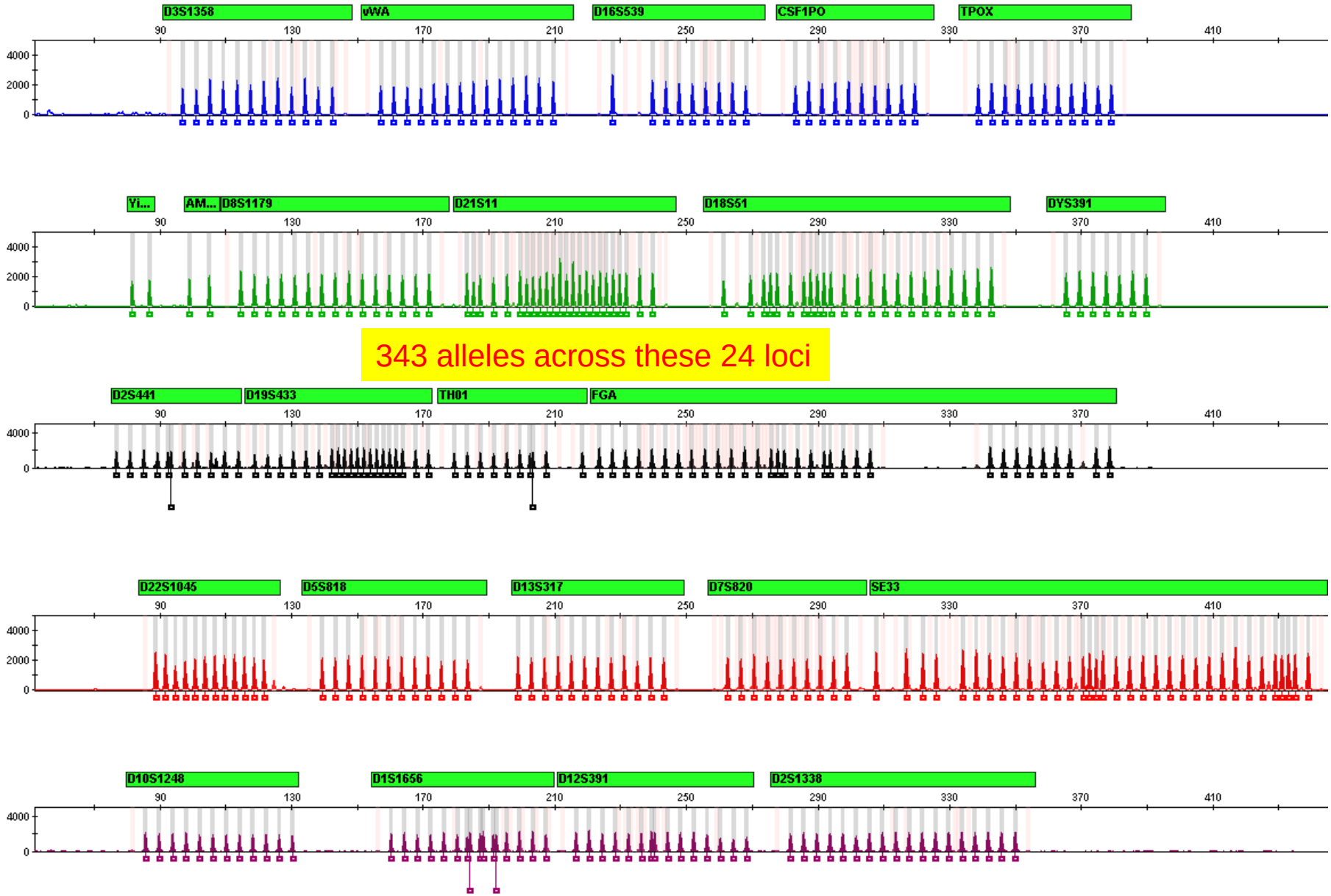


DNA Mixture Detected with PowerPlex Fusion (24plex STR kit)

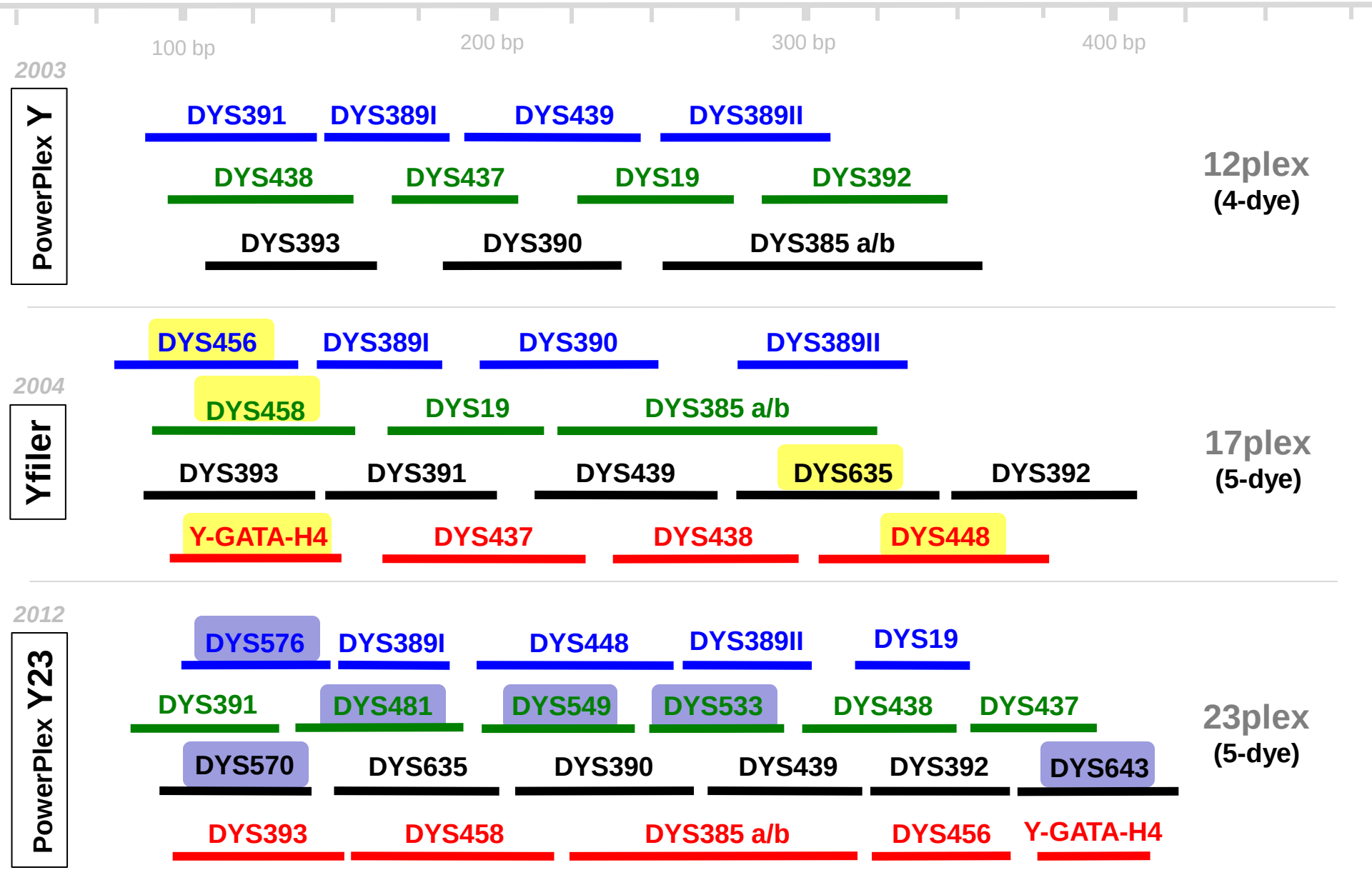


Size standard not shown

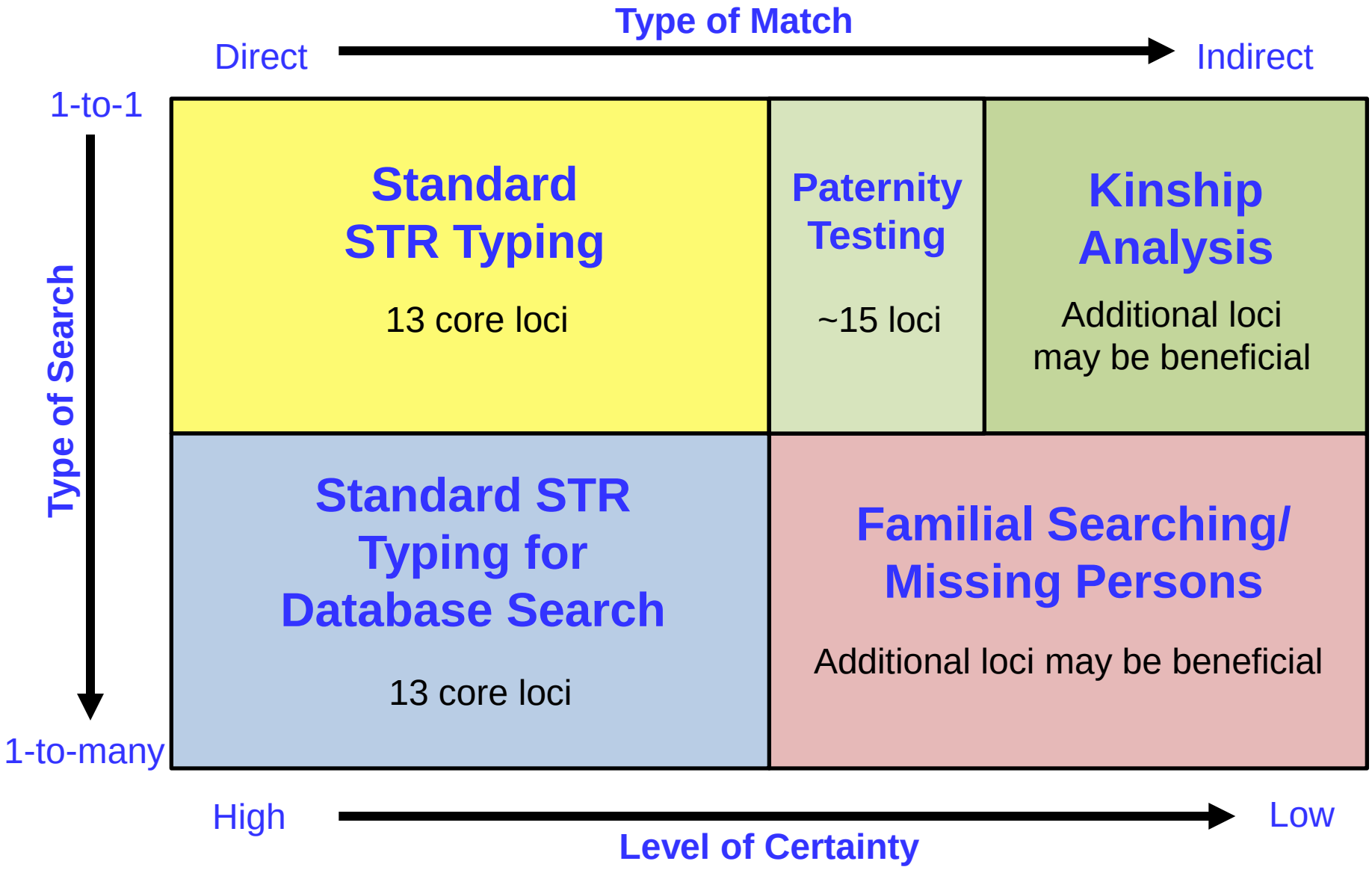
GlobalFiler Allelic Ladder



STR Marker Layouts for Y-STR Kits



Expanding the Forensic Core Competency



CRIME & COURTS

July 7, 2010

Arrest Made in L.A. 'Grim Sleeper' Killings

Published July 07, 2010 | Associated Press

LOS ANGELES -- A one-time police mechanic was arrested and charged Wednesday in the serial killing of 10 people over 25 years after a DNA sample from his son was found to bear a close resemblance to DNA found on the victims.

Lonnie Franklin Jr., 57, was charged with 10 counts of murder, one count of attempted murder and special circumstance allegations of multiple murders that could make him eligible for the death penalty if convicted, District Attorney Steve Cooley said.

Lonnie David Franklin Jr.

He is charged with 10 counts of murder and one count of attempted murder for a series of killings that date back to 1985.

Putative Relative Is Found

- June 30, 2010: Second familial search of the California database yielded one likely relative
- Database profile belonged to Christopher Franklin (31 years old)
  - Profile added to the database in 2009 after a felony weapons possession charge
- Grim Sleeper profile matched C. Franklin's profile with one allele at all 15 loci
- Both individuals shared the same Y-STR profile, indicating a possible paternal relationship

Identifying the Grim Sleeper

- Given that the murders spanned at least 25 years, the paternal relationship was likely father-son

- Undercover police shadowed C. Franklin's father, Lonnie David Franklin, Jr., who lived in the vicinity of the murders

- Police collected a DNA sample from Lonnie Franklin
  - **Direct match between L. Franklin and the Grim Sleeper**

Rapid DNA Efforts


Pete Vallone **Erica Butts**

Accelerated Nuclear DNA Equipment (ANDE) developed by **NetBIo**

http://ishinews.com/wp-content/uploads/2012/10/Rapid-DNA-Miles-1.58MB.pdf

RapidHIT 200 developed by **IntegenX**

http://integenx.com/wp-content/uploads/2010/06/RapidHIT-200.png

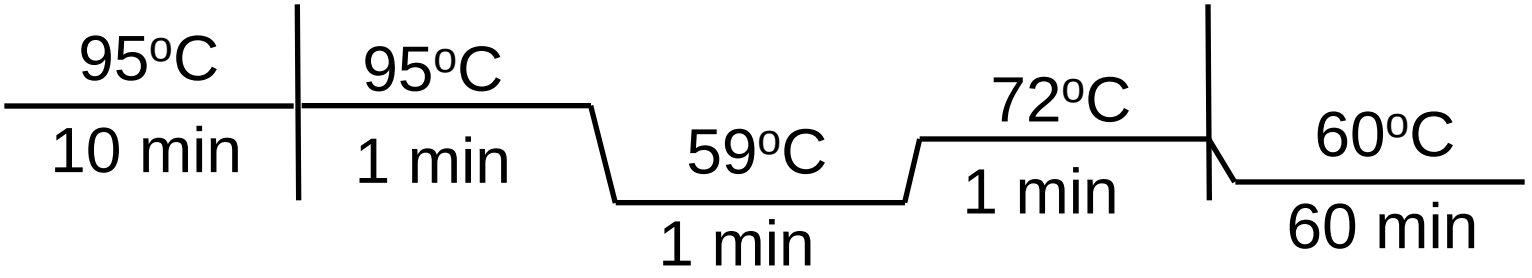
- Evaluating ANDE (NetBio) and IntegenX rapid DNA instruments
  - both instruments are capable of swab in → STR profile out in less than 90 minutes without user intervention
- Exploring rapid DNA techniques including direct PCR and rapid PCR
  - STR profiles generated in <2 hours with standard lab equipment and rapid protocols
  - See ISHI 2012 poster available on STRBase “Rapid DNA Testing Approaches for Reference Samples”

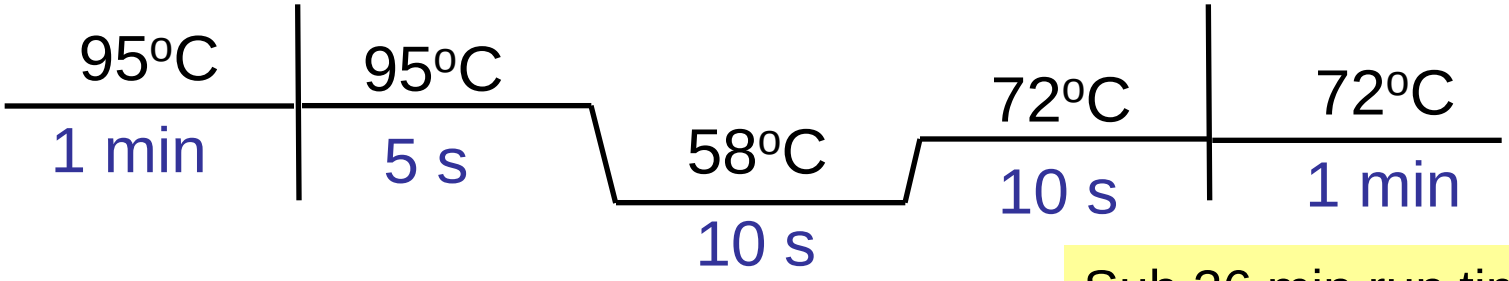
Fastest results swab-to-profile (Identifiler): 57 minutes

Rapid PCR Thermal Cycling Profile

Identifiler STR kit

28 cycles of PCR



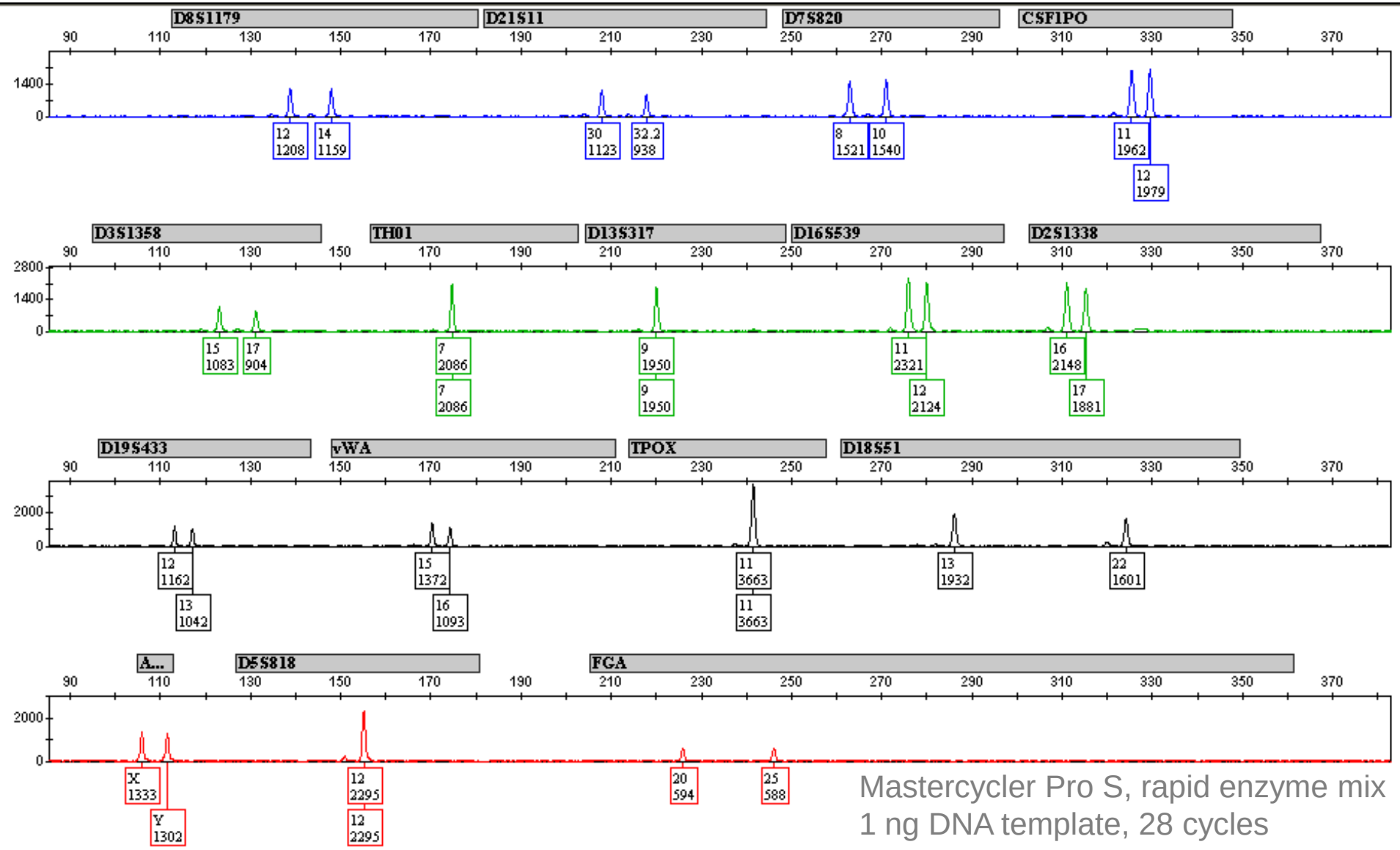


Sub 36 min run time

Maximum heating/cooling rate of ~2 to 6°C/s (cycler dependent)

Slide from Peter Vallone (NIST)

Full Identifiler STR Profile with **19 min PCR**



Mastercycler Pro S, rapid enzyme mix
1 ng DNA template, 28 cycles

Slide from Peter Vallone (NIST)

Potential Applications with Rapid PCR Capabilities

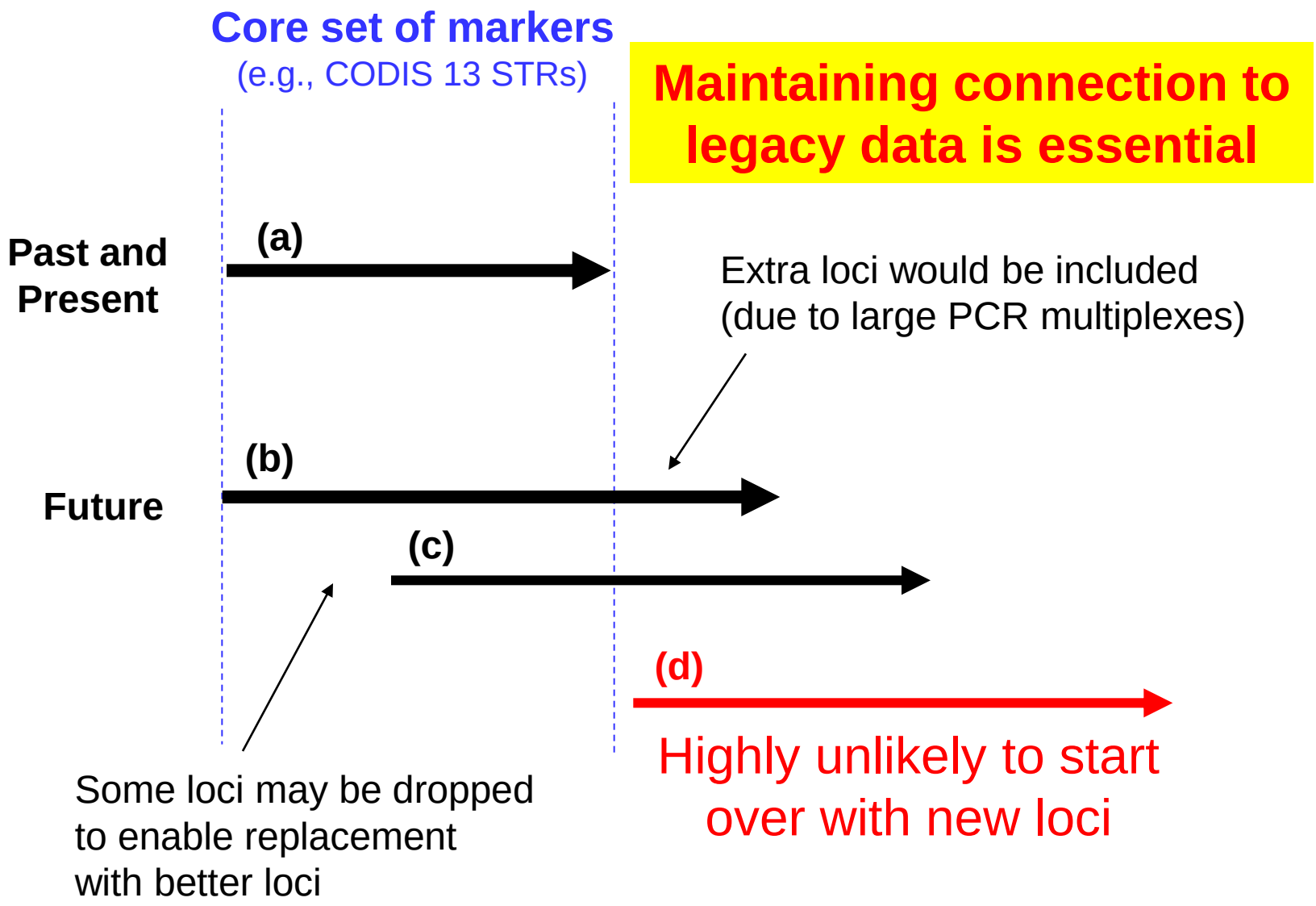
- **Improve overall laboratory throughput**
  - Multiplex PCR amplification is already in many situations the longest part of the DNA analysis process (depending on DNA extraction and DNA quantitation methods)
  - With increased use of robotic sample preparation and expert system data analysis, bottleneck for sample processing will shift to time for PCR amplification…

- **Enable new potential DNA biometric applications** (because the overall DNA analysis process is faster)
  - Permit analysis of individuals at a point of interest such as an embassy, an airport, or a country border

A “Crystal Ball” to the Future?

http://medicalcenter.osu.edu/images/healthconnections/winter2003/dnaCrystalBallIllustration.jpg

Possible scenarios for extending sets of genetic markers to be used in national DNA databases



STRs vs SNPs Article

Butler *et al.* (2007) STRs vs SNPs: thoughts on the future of forensic DNA testing. *Forensic Science, Medicine and Pathology* 3:200-205.

Forensic Sci Med Pathol (2007) 3:200–205
DOI 10.1007/s12024-007-0018-1

ORIGINAL PAPER

STRs vs. SNPs: thoughts on the future of forensic DNA testing

John M. Butler · Michael D. Coble · Peter M. Vallone

- **SNPs are unlikely to replace STRs** for routine forensic DNA testing due to challenges with high-level multiplexing and mixture detection/interpretation

- Most likely use of SNPs will be as ancestry-informative markers (AIMs) **for sample ethnicity estimation**

Compromised Sample Improvements

- Better DNA extraction/recovery
- Continued use of miniSTRs
  - to improve success rates for recovery of information from compromised DNA evidence
- Replicate results for reproducibility
  - to improve reliability with low-template DNA testing

Going Beyond the Core Competencies of Forensic DNA Testing

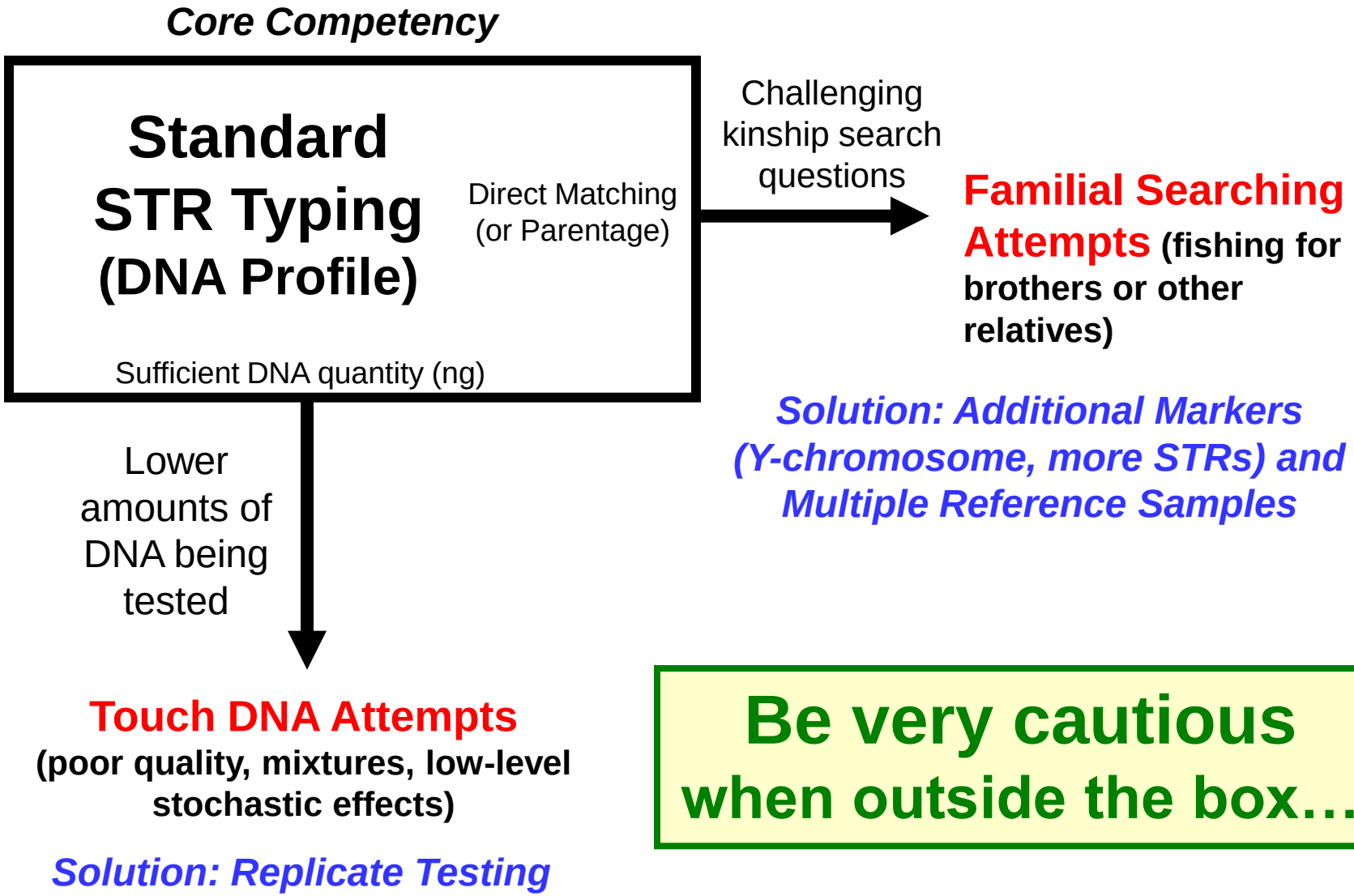


Figure 18.3 in forthcoming Butler (2009) *Fundamentals of Forensic DNA Typing*

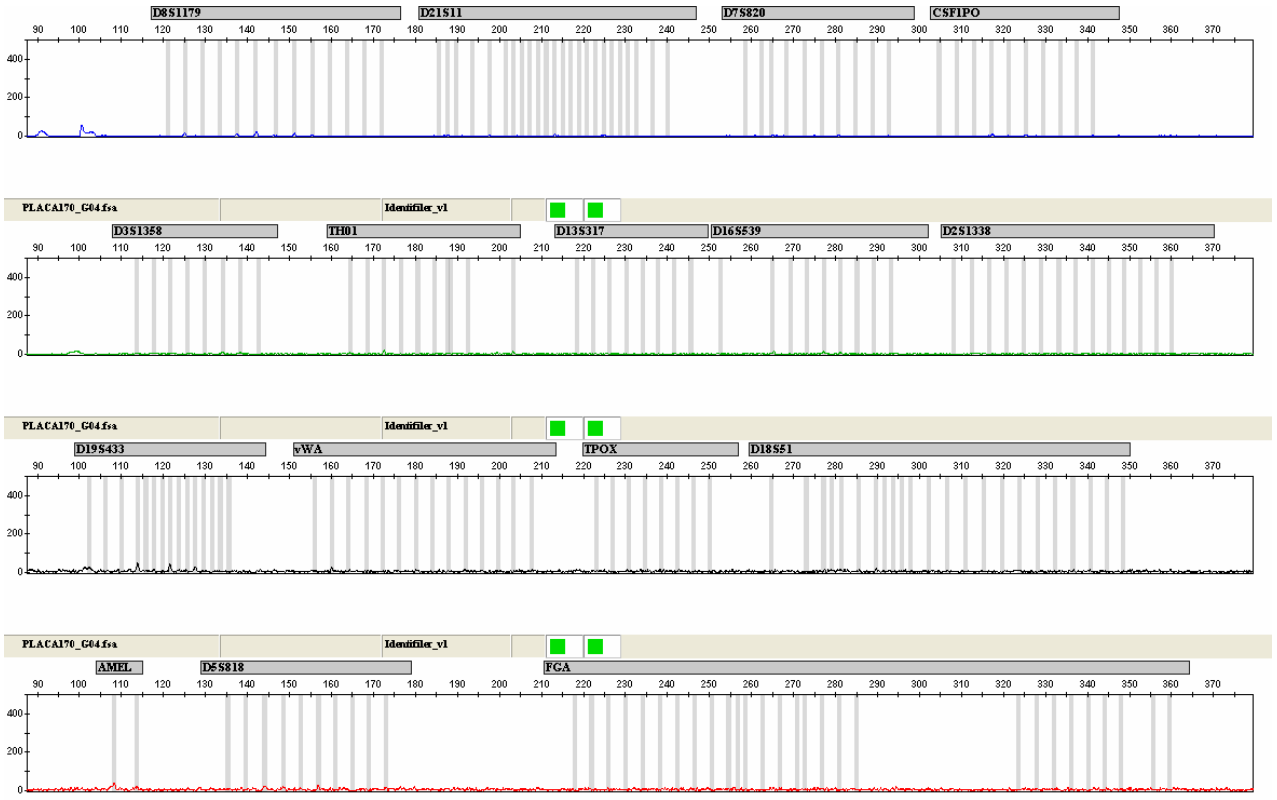
Highly degraded DNA

SNP genotyping in an extreme degradation case

Corpse half buried in a forest for ten years

- **Uncovered by a forest fire**
- **Calcinated remains**

Identifiler success 0%



Slide from Manuel Fondevila (NIST, USC)

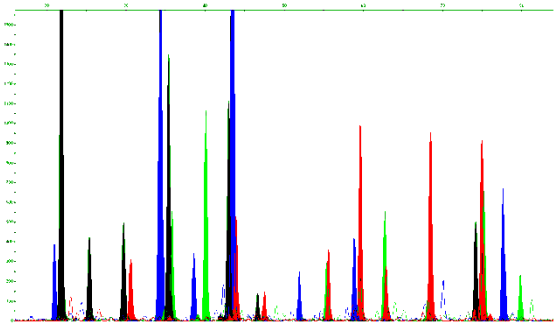
Highly degraded DNA

SNP genotyping in extreme degradation case

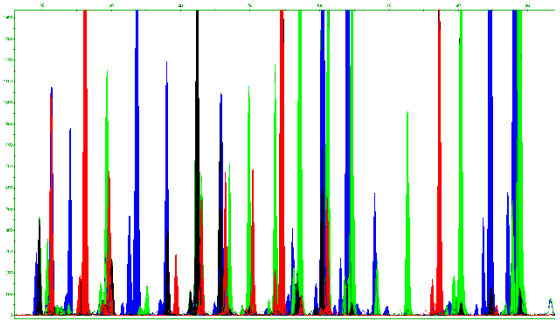
Corpse half buried in a forest for ten years

- **Uncovered by a forest fire**
- **Calcinated remains**

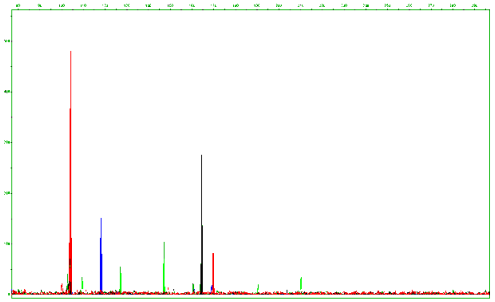
HID 52plex Auto 1: success 100%

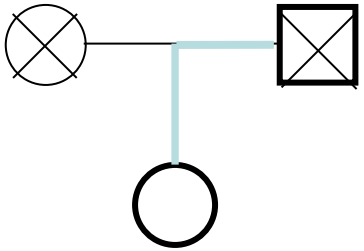


HID 52plex Auto 2 success 100%



MiniFiler success 30%





	STRs	+SNPs
P:	-	99.993

Slide from Manuel Fondevila (NIST, USC)

Geographical Origin Prediction

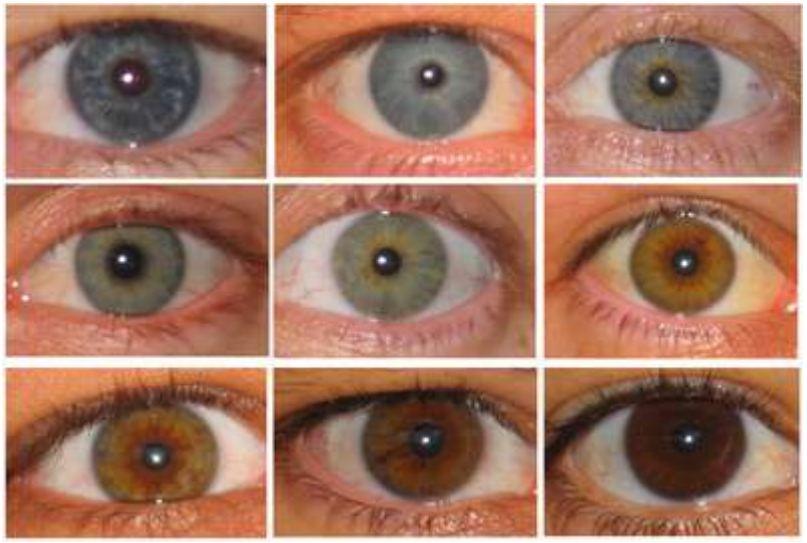
- Lao O, van Duijn K, et al. (2006) Proportioning whole-genome single-nucleotide-polymorphism diversity for the identification of geographic population structure and genetic ancestry. Am J Hum Genet 78: 680-90.
- Phillips, C., Salas, A., et al. (2007) Inferring ancestral origin using a single multiplex assay of ancestry-informative marker SNPs. FSI: Genetics 1: 273-280.
- Halder, I., Shriver, M., et al. (2008) A Panel of Ancestry Informative Markers for Estimating Individual Biogeographical Ancestry and Admixture From Four Continents: Utility and Applications. Hum Mut 29: 648-658.
- Pereira R., Phillips C., et al. (2012) Straightforward inference of ancestry and admixture proportions through ancestry-informative insertion deletion multiplexing. PLoS One;7(1):e29684.

Slide from Manuel Fondevila (NIST, USC)

Phenotypic Trait Prediction

Traits of interest

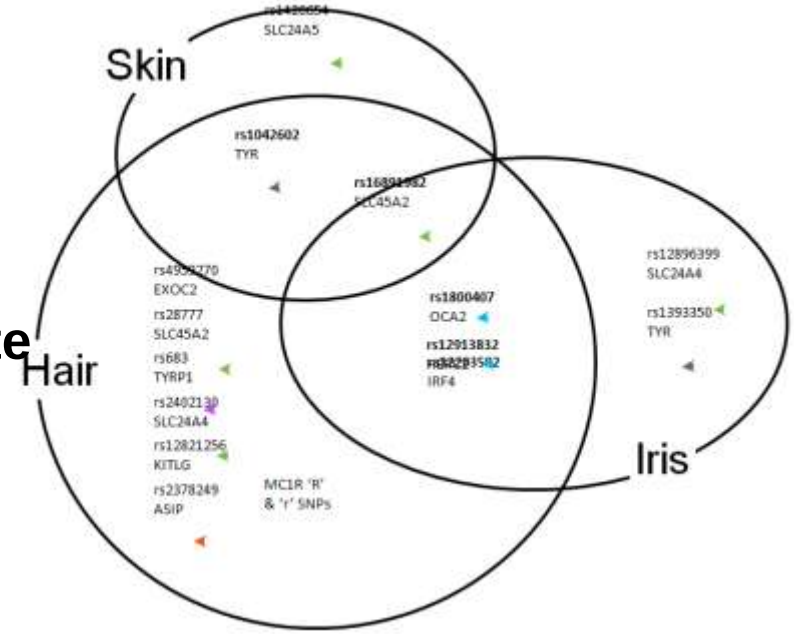
- **Traits whose variation may be classified on discreet categories.**
- **Regulated by a relatively low number of genes.**
- **Fine example: Iris and hair pigmentation.**



Blue

Intermediate

Brown



Slide from Manuel Fondevila (NIST, USC)

Phenotypic trait prediction

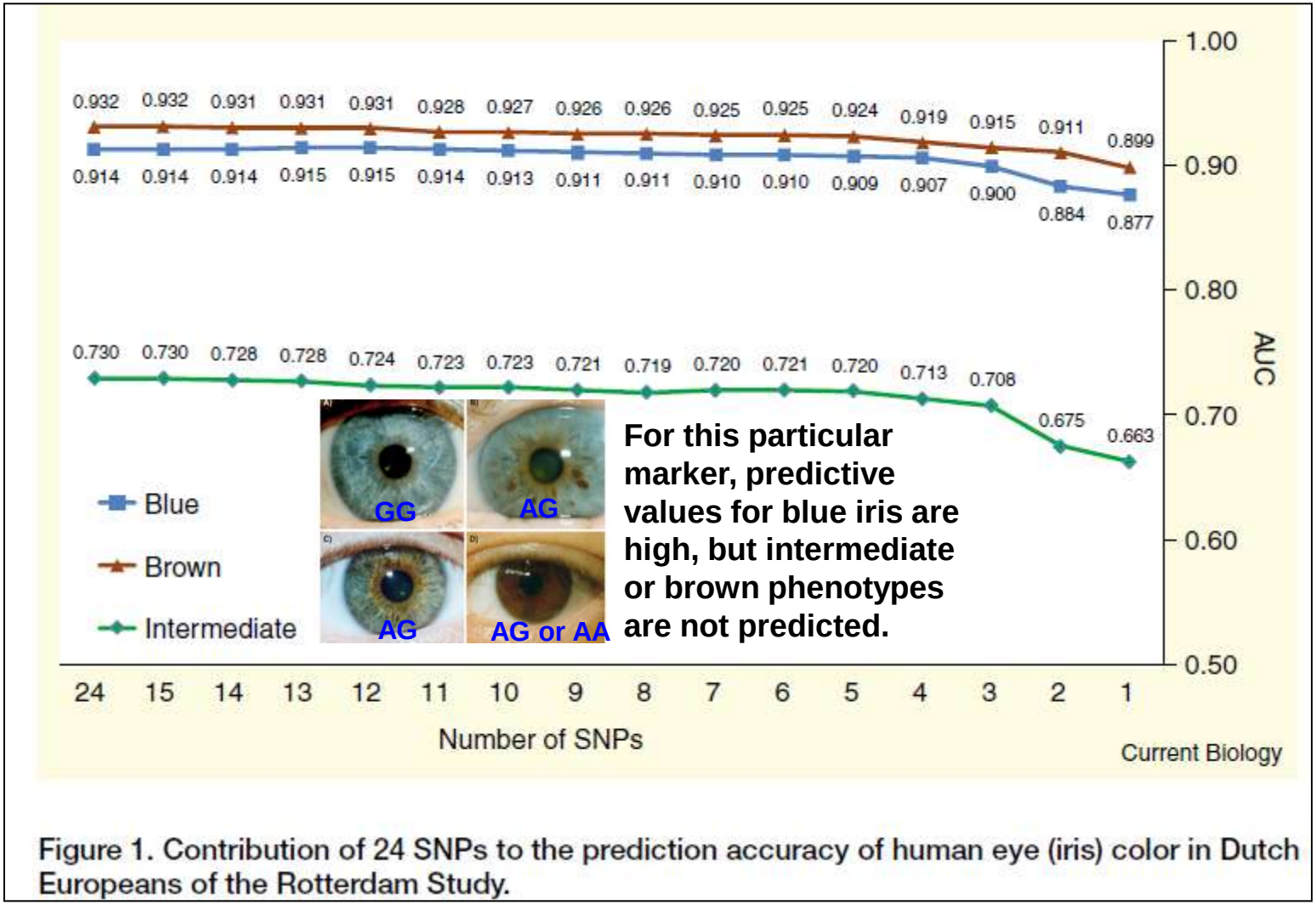


Figure 1. Contribution of 24 SNPs to the prediction accuracy of human eye (iris) color in Dutch Europeans of the Rotterdam Study.

Liu F., et al. (2009). Eye color and the prediction of complex phenotypes from genotypes, Curr. Biol. 19:R192–R193

Slide from Manuel Fondevila (NIST, USC)

Next Generation Sequencing

Forensic Applications

- Going in depth into STR loci and beyond
  - STRs are useful for legacy (databases)
  - SNPs within STRs identify ‘sub-alleles’
  - Millions of bases of sequence variants (SNPs)

- Opens up new human identity applications: biogeographical ancestry, externally visible traits, complex kinship, degraded samples, mixtures, other applications

Applications are currently being addressed
by the forensic genetics community (K*ayser and deKnijff 2011)*

Slide from Peter Vallone (NIST)

Specific issues with STRs

- Typically comprised of tetra nucleotide repeats
- Range 70 - 450+ bp regions
- Longer STRs can be difficult to assemble based on read length
- Illumina GAIIx (read length 150 bp)
  - Generated 1000-2500 bp amplicons (13 core loci)
  - Problems detecting D21S11 **32.2** and **34.2** alleles
  - Issues detecting D18S51
  - Custom informatics tools for assembling STRs

Bornman et al., 2012 Biotechniques Rapid Dispatch: 1-6

Slide from Peter Vallone (NIST)

Next Generation Sequencing

- Challenges
  - Repeating sequences (STRs) and read lengths
  - Sample amount requirements (10 ng to 5 µg)
  - **Cost** and **time** per unit of information
  - Data analysis (storage, assembly, interpretation)
  - Policy, privacy, disease related markers
  - Validation
  - Standards/reference materials
    - Nomenclature
    - Accuracy of sequence information
    - Errors, platform and bioinformatics-based bias

Slide from Peter Vallone (NIST)

Next Generation Sequencing Workshop

- Interagency Workshop on the use of Next-Generation DNA Sequencing for Human Identification and Characterization (Jan 31 2012)
- Discussion of forensic applications of NGS (NIST, DoD, FBI, DHS) – materials can be found at:
  - http://www.nist.gov/mml/bmd/genetics/ngs_hid_workshop.cfm

- We are in the process of looking at platforms to characterize forensic markers (mitochondrial, STRs, SNPs)
- Evaluate accuracy, reproducibility, identify initial requirements for a NGS forensic reference material

Slide from Peter Vallone (NIST)

Some Thoughts on the Future…

- **PCR amplification**
  - Faster enzymes to enable rapid PCR
  - More robust enzymes and master mixes to overcome inhibition
- **Instrumentation**
  - More dye colors to aid higher levels of multiplexing
  - Rapid, integrated devices
  - Alternatives to capillary electrophoresis: PLEX-ID and NGS
- **Quantitative information**
  - qPCR and digital PCR
- **Marker systems**
  - Expanding sets of STR loci for growing DNA databases
  - Other marker systems: SNPs, InDels, X-STRs, RM Y-STRs
  - Body fluid identification with mRNA, miRNA, and DNA methylation
  - Phenotyping for external visible characteristics
  - Challenges with potential whole genome information
- **Data interpretation**
  - Probabilistic genotyping for low-level DNA and mixture interpretation
  - Probability of dropout

We Need Continued Efforts to Improve DNA Interpretation (especially low-level DNA and mixtures)

Forensic Science International: Genetics 6 (2012) 677–678

Contents lists available at SciVerse ScienceDirect

Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsig

Editorial

Focus issue—Analysis and biostatistical interpretation of complex and low template DNA samples

December 2012 – Forensic Science International: Genetics, volume 6, issue 6

Forensic Science International: Genetics 6 (2012) 679–688

Contents lists available at SciVerse ScienceDirect

Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsig

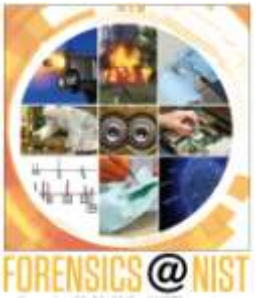
DNA commission of the International Society of Forensic Genetics: Recommendations on the evaluation of STR typing results that may include drop-out and/or drop-in using probabilistic methods

P. Gill [a,b,*], L. Gusmão [c], H. Haned [d], W.R. Mayr [e], N. Morling [f], W. Parson [g], L. Prieto [h], M. Prinz [i], H. Schneider [j], P.M. Schneider [k], B.S. Weir [l]

April 12, 2013 Webcast

http://www.nist.gov/oles/forensics/dna-analyst-training-on-mixture-interpretation.cfm

- **8-hours of DNA mixture interpretation training**
- **11 presentations** from **five different presenters**
  - John Butler, Mike Coble, Robin Cotton, Bruce Heidebrecht, Charlotte Word
- **20 poll questions** asked via SurveyMonkey (>600 participated)
  - Addressed additional questions sent via email or Twitter
- **>1000 participants** (almost entire U.S. represented and >10 countries)
- **Available for viewing or download** for at least six months (storage costs may limit longer-term storage)



NIST FORENSIC SCIENCES

The Future of Forensic DNA

is Similar to the Olympic Motto of

"Swifter, Higher, Stronger"

Resources **Training** **Action**

Recent NIST Publications Demonstrating "Swifter, Higher, Stronger" DNA Analysis

Swifter PCR Amplification

Forensic Science International: Genetics Supplement Series 2 (2009) 111–112

Contents lists available at ScienceDirect

Forensic Science International: Genetics Supplement Series

journal homepage: www.elsevier.com/locate/FSIGSS

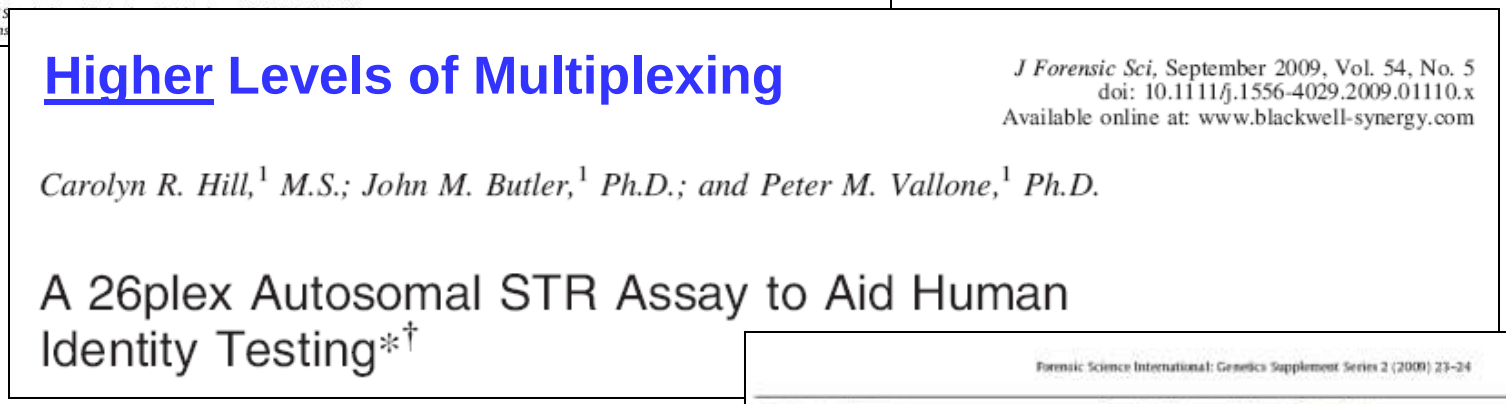
Research article

Rapid amplification of commercial STR typing kits

Peter M. Vallone[a,*], Carolyn R. Hill[a], Daniele Podini[b], John M. Butler[a]

[a] National Institute of S
[b] Department of Forens

Higher Levels of Multiplexing



J Forensic Sci, September 2009, Vol. 54, No. 5
doi: 10.1111/j.1556-4029.2009.01110.x
Available online at: www.blackwell-synergy.com

Carolyn R. Hill,[1] M.S.; John M. Butler,[1] Ph.D.; and Peter M. Vallone,[1] Ph.D.

A 26plex Autosomal STR Assay to Aid Human Identity Testing*†

Stronger Powers of Discrimination

Forensic Science International: Genetics Supplement Series 2 (2009) 23–24

Contents lists available at ScienceDirect

Forensic Science International: Genetics Supplement Series

journal homepage: www.elsevier.com/locate/FSIGSS

Research article

The single most polymorphic STR Locus: SE33 performance in U.S. populations

John M. Butler[a,*], Carolyn R. Hill[a], Margaret C. Kline[a], David L. Duewer[a], Cynthia J. Sprecher[b], Robert S. McLaren[b], Dawn R. Rabbach[b], Benjamin E. Krenke[b], Douglas R. Storts[b]

[a] National Institute of Standards and Technology, Gaithersburg, MD 20899-8312, USA
[b] Promega Corporation, Madison, WI 53711, USA

Acknowledgments

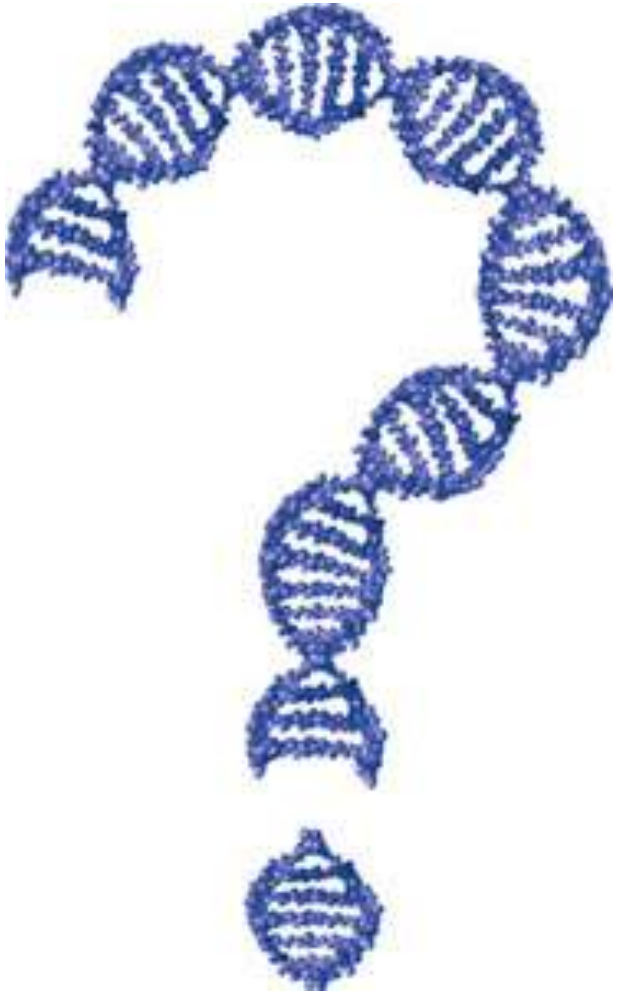
- A great team of scientists at NIST and many wonderful collaborators

- Some slides from Pete Vallone (NIST) and Manuel Fondevila (NIST, USC)

- Funding from National Institute of Justice and FBI Biometrics Center of Excellence for work performed within the NIST Applied Genetics Group

Thank you for your attention

Acknowledgments: A great team of scientists within our NIST Applied Genetics Group and funding from the National Institute of Justice and the FBI



Contact Information

John Butler
NIST Fellow
john.butler@nist.gov
301-975-4049

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

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