Supreme Prosecutors' Office
Republic of Korea

International Symposium on Forensic DNA in Law
Seoul, Republic of Korea
November 7-8, 2012

The Future of Forensic DNA

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

NIST

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.

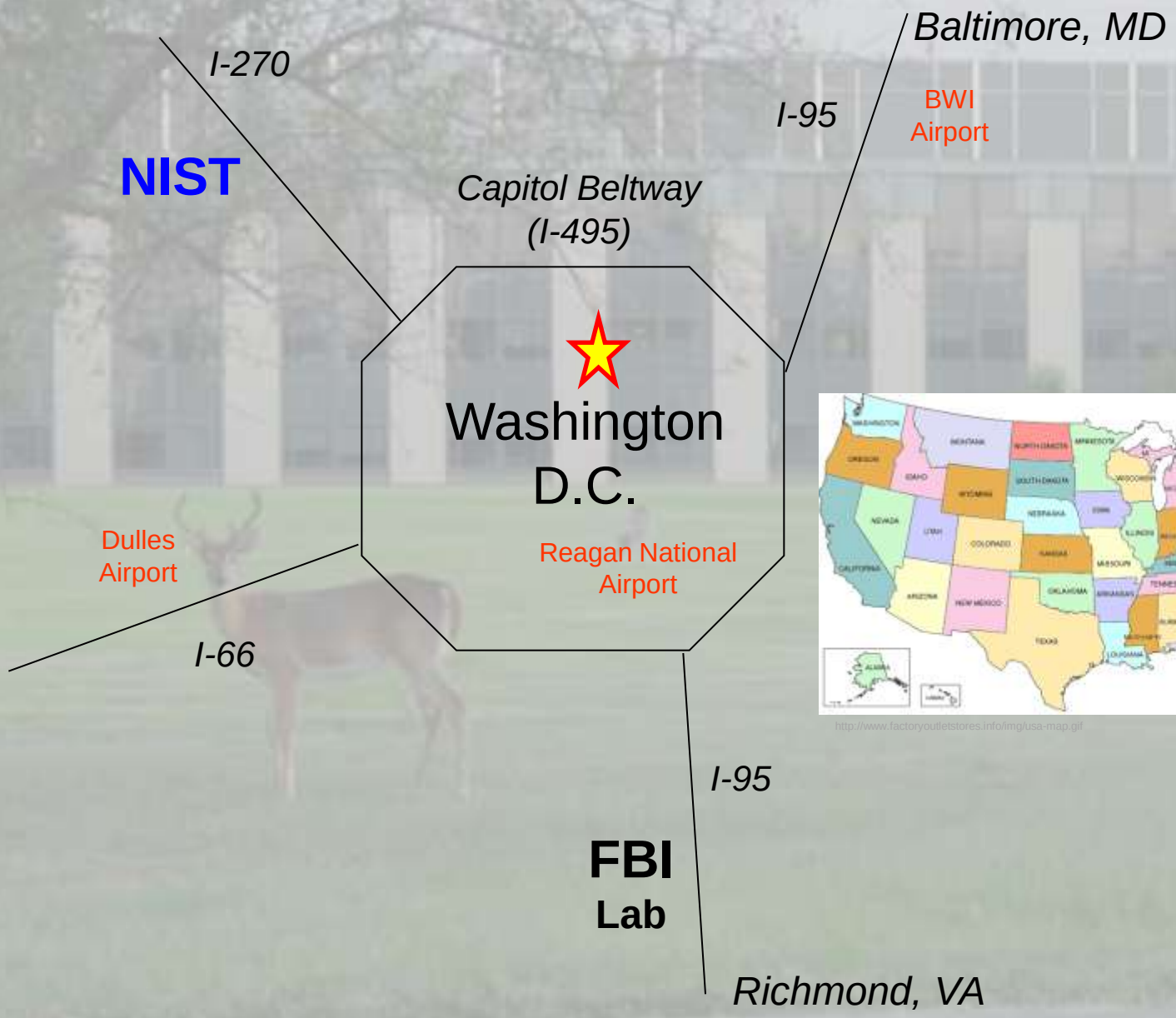
- NIST supplies over 1,300 Standard Reference Materials (SRMs) for industry, academia, and government **use in calibration of measurements**.

- **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

NIST Applied Genetics

NIST Applied Genetics Group

Group Leader

John Butler

Mike Coble

Margaret Kline

Marcia Holden

Pete Vallone

Patti Rohmiller
Office Manager

Becky Hill

Ross Haynes

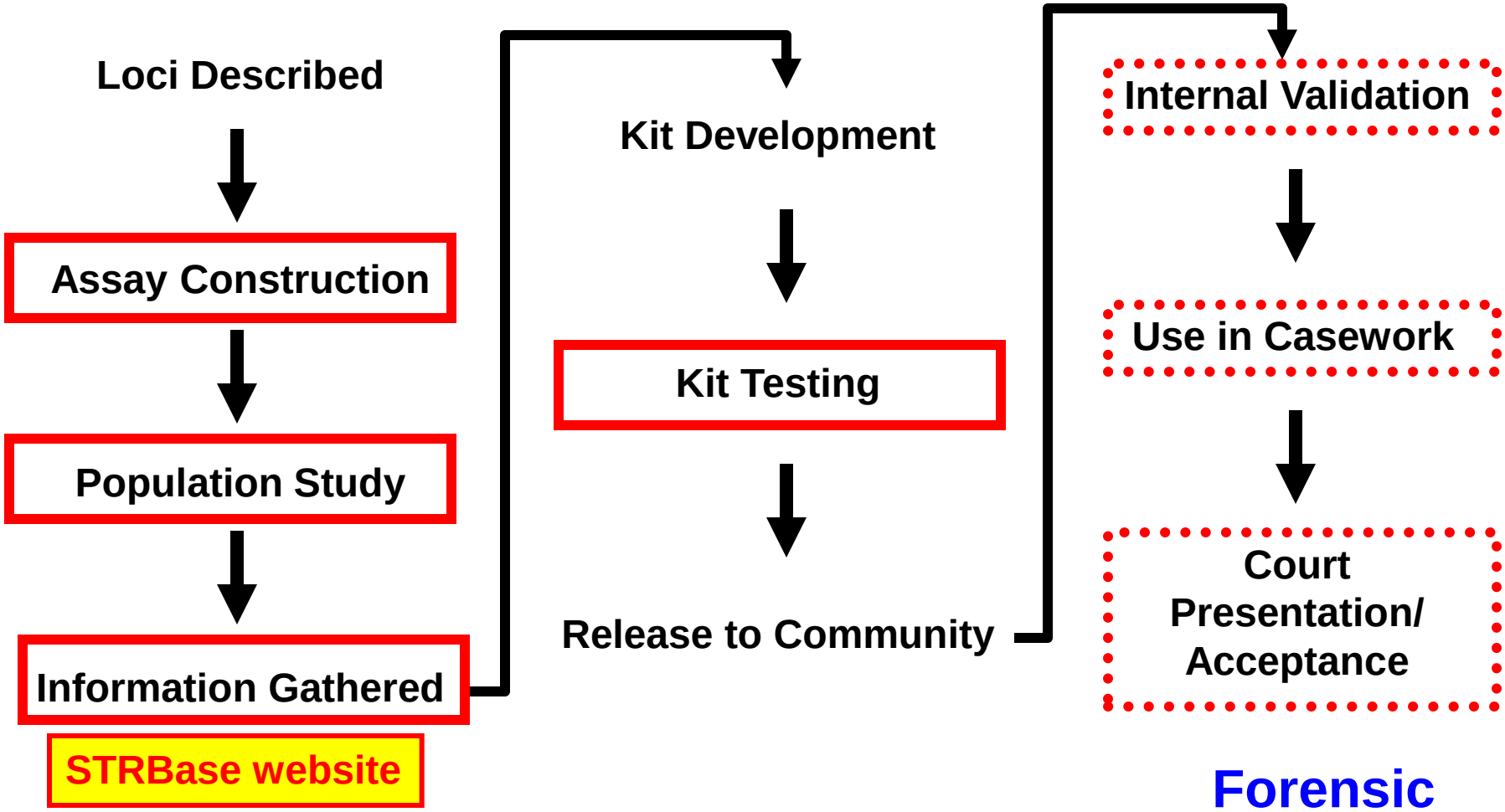
Erica Butts

Kevin Kiesler

Bringing calibration to clinical DNA diagnostics, speed to DNA testing, and technology to the scales of justice

Steps in Adopting Genetic Markers

Role of the NIST Human Identity Project Team



Current Activities at NIST

- **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 (2009, 2011, & 2013)

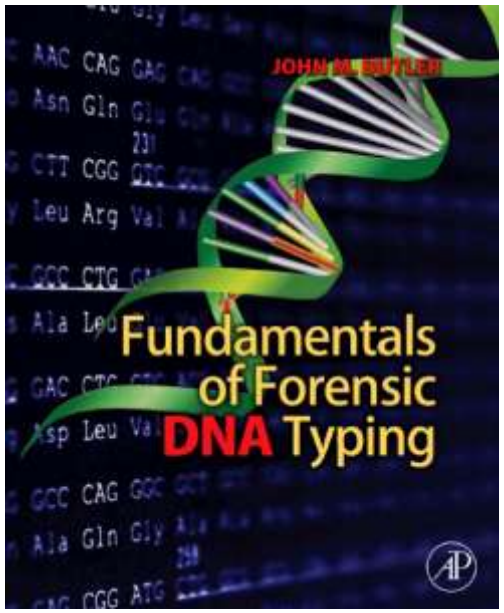
Forensic DNA Typing Textbook

3rd Edition is Three Volumes

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

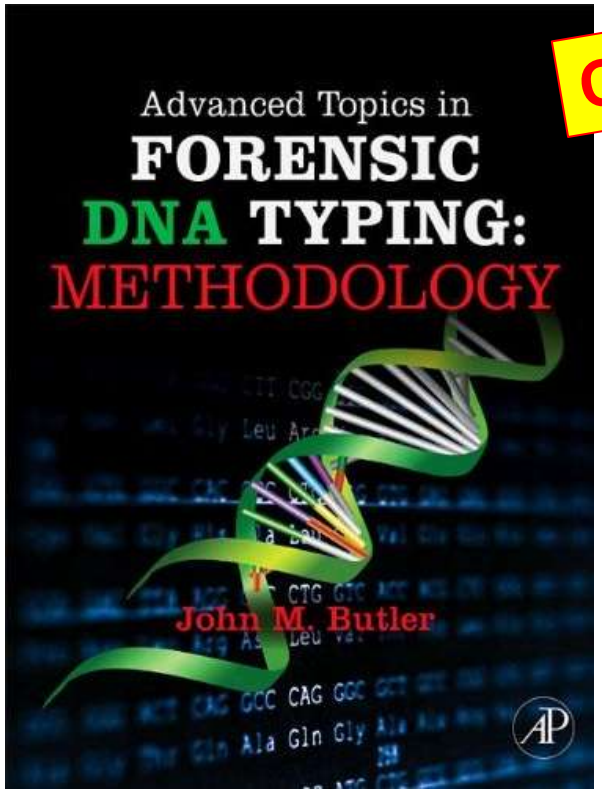
John Butler

For beginning students, general public, & lawyers



Sept 2009

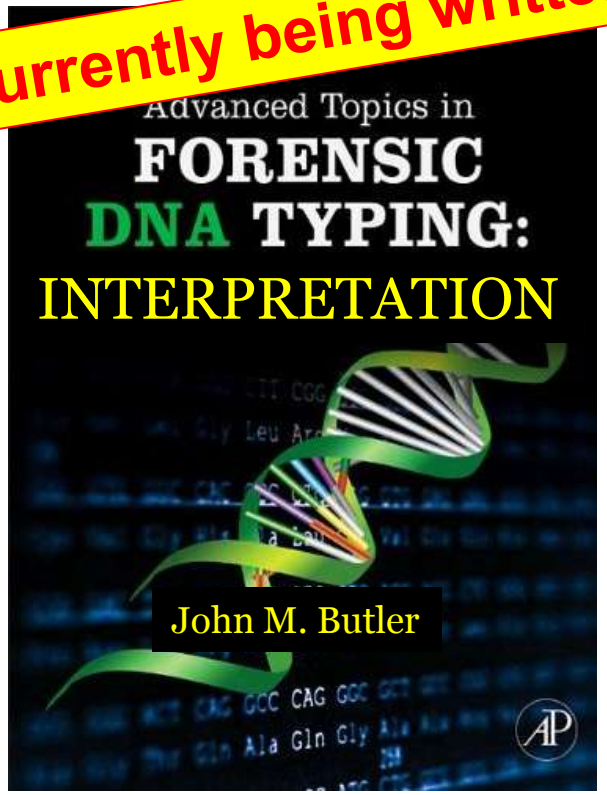
~500 pages



August 2011

~700 pages

Currently being written



2013

~500 pages

Value of a Historical Review

"If you want to understand today, you have to search yesterday."

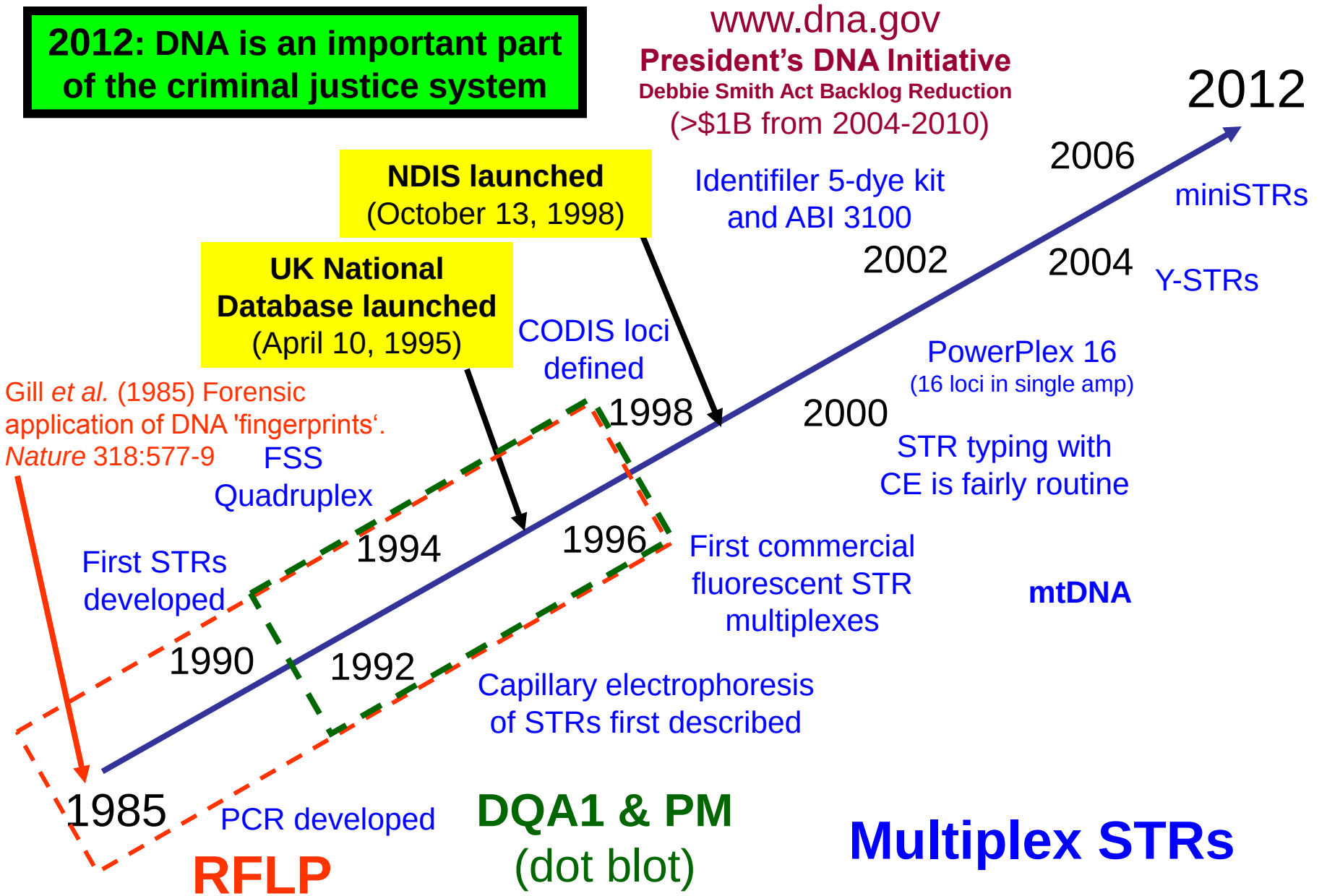
– Attributed to Pearl Buck
(http://www.quotegarden.com/history.html)

Pearl Buck

The Nobel Prize in Literature 1938

http://nobelprize.org/nobel_prizes/literature/laureates/1938/buck.jpg

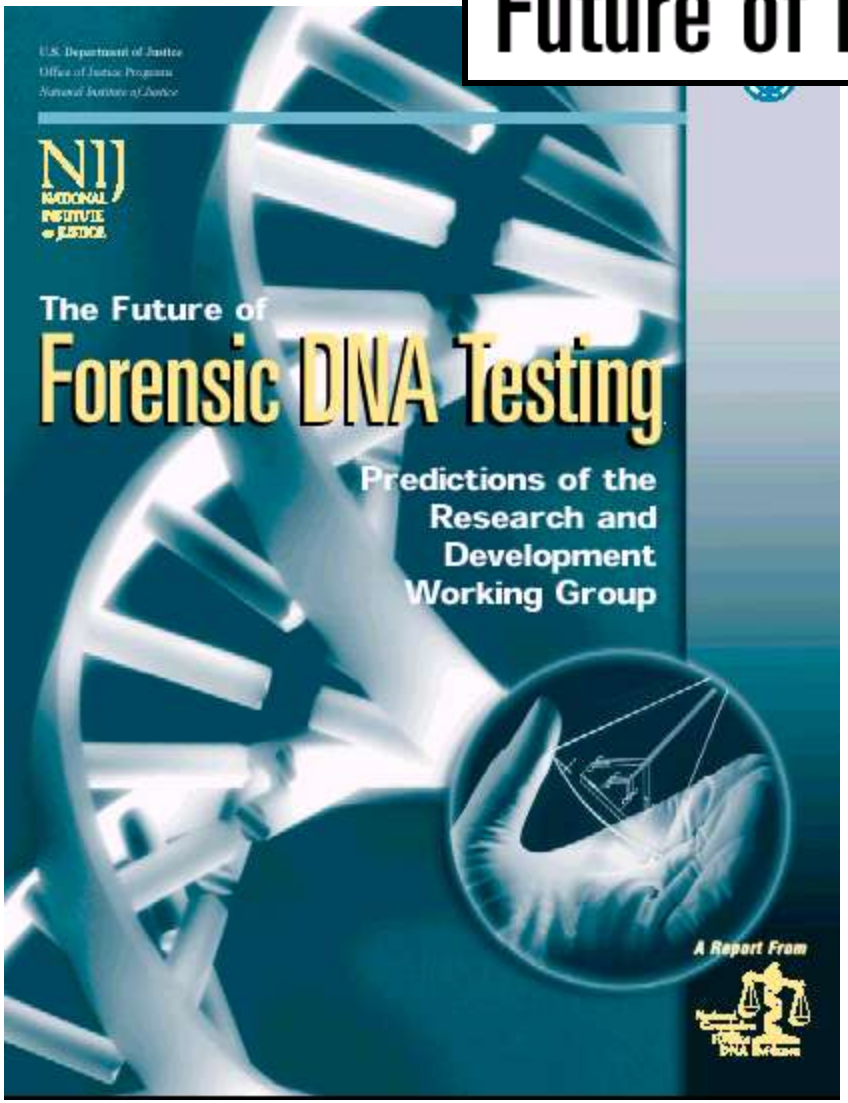
Historical Perspective on DNA Typing



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	2005-2012	Rapid growth of DNA databases, extended applications pursued
Sophistication	*The Future*	*Expanding tools available, confronting privacy concerns*

National Commission on the Future of DNA Evidence



- 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

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

Growth in Numbers of DNA Profiles Present in Various NDIS Indices

(cumulative totals by year)

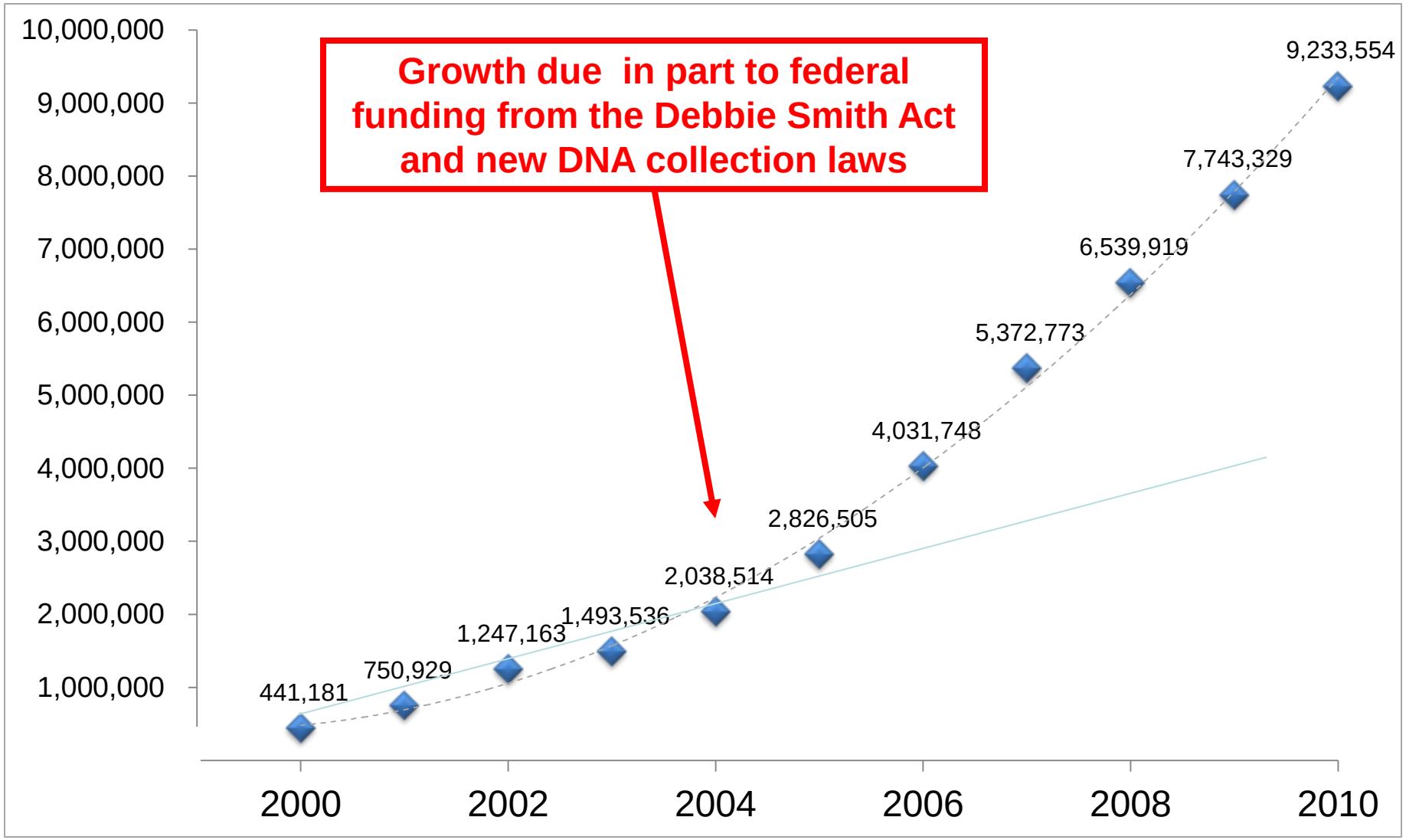
Year ending Dec 31	**Forensic**	**Convicted Offender**	Arrestee	Total Offender*
2000	21,625	441,181	--	441,181
2001	27,897	750,929	--	750,929
2002	46,177	1,247,163	--	1,247,163
2003				
2004				
2005				
2006				
2007	203,401	5,287,505	85,072	5,372,773
2008	248,943	6,398,874	140,719	6,539,919
2009	298,369	7,389,917	351,926	7,743,329
2010	**351,951**	8,559,841	668,849	**9,233,554**

In the last two years of data (2009 & 2010):
103,008 forensic samples added
2,693,635 offender samples added

Source: FBI Laboratory's CODIS Unit

Number of Offender DNA Profiles

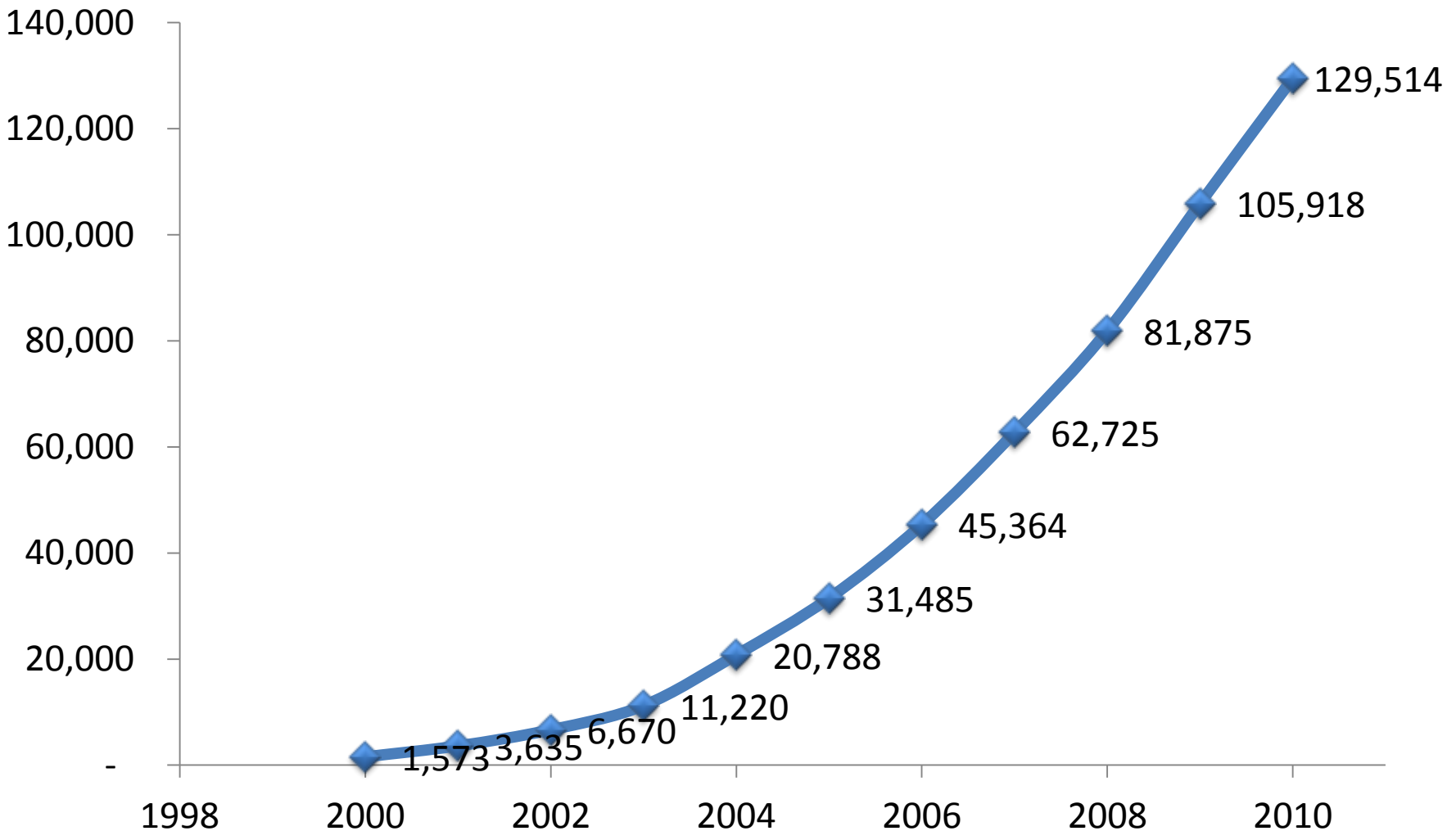
in the U.S. National DNA Database



Source: FBI Laboratory's CODIS Unit

Number of Investigations Aided

in the U.S. National DNA Database



Source: FBI Laboratory's CODIS Unit

Growth of DNA Databases

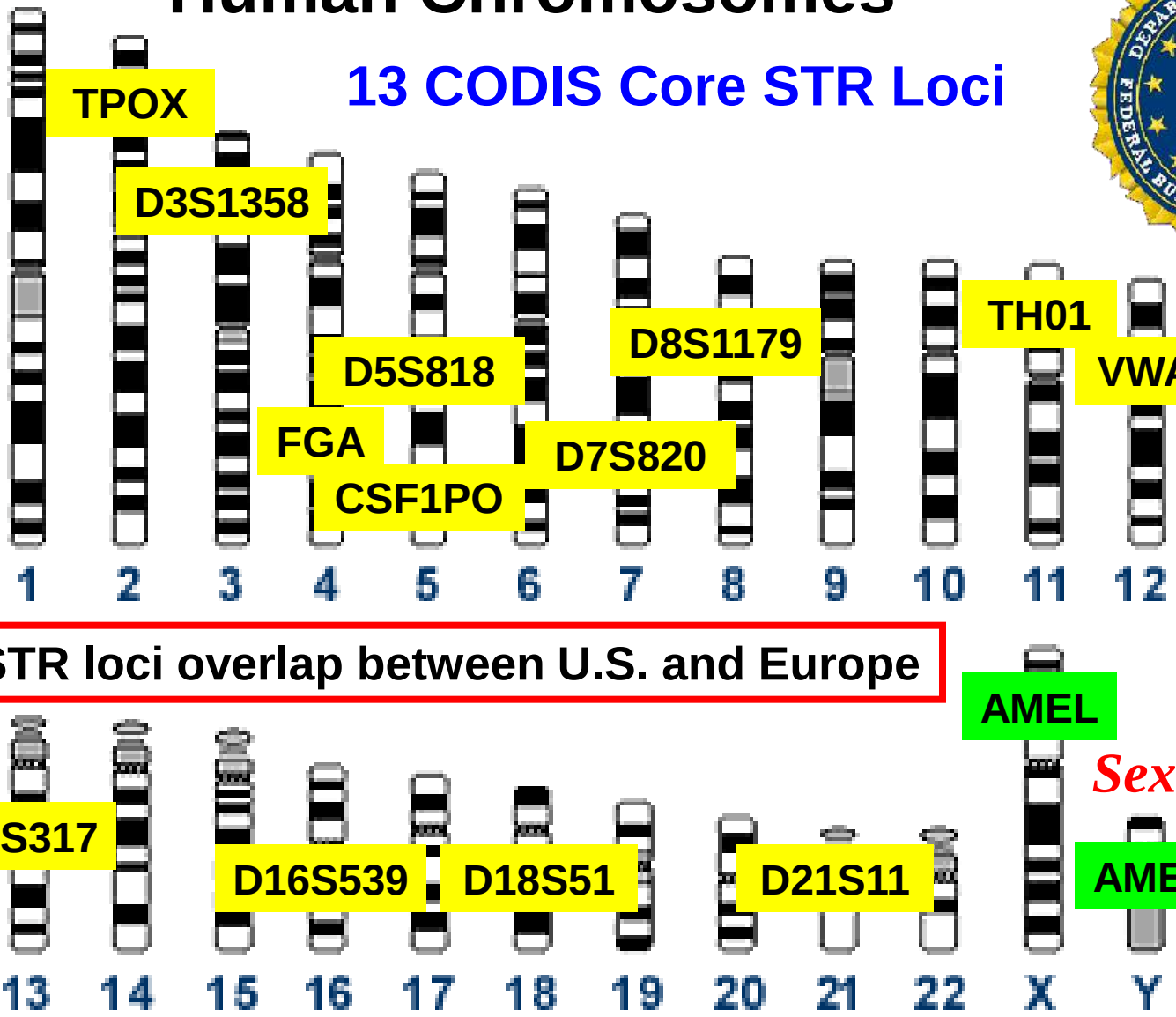
- Within the U.S., we have benefited from significant federal funding over the past decade
- Expanded laws now enable more offenders to be included (currently 26 states and federal government have laws to collect DNA from arrestees)
- Have effectively locked technology with core STR markers used to generate 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



8 STR loci overlap between U.S. and Europe

Sex-typing

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

D12S391
D1S1656
D2S441
D10S1248
D22S1045

5 loci adopted in 2009 to expand to 12 ESS loci

3 miniSTR loci developed at NIST

SE33 → Core locus for Germany

Locus used in China ← **D6S1043**

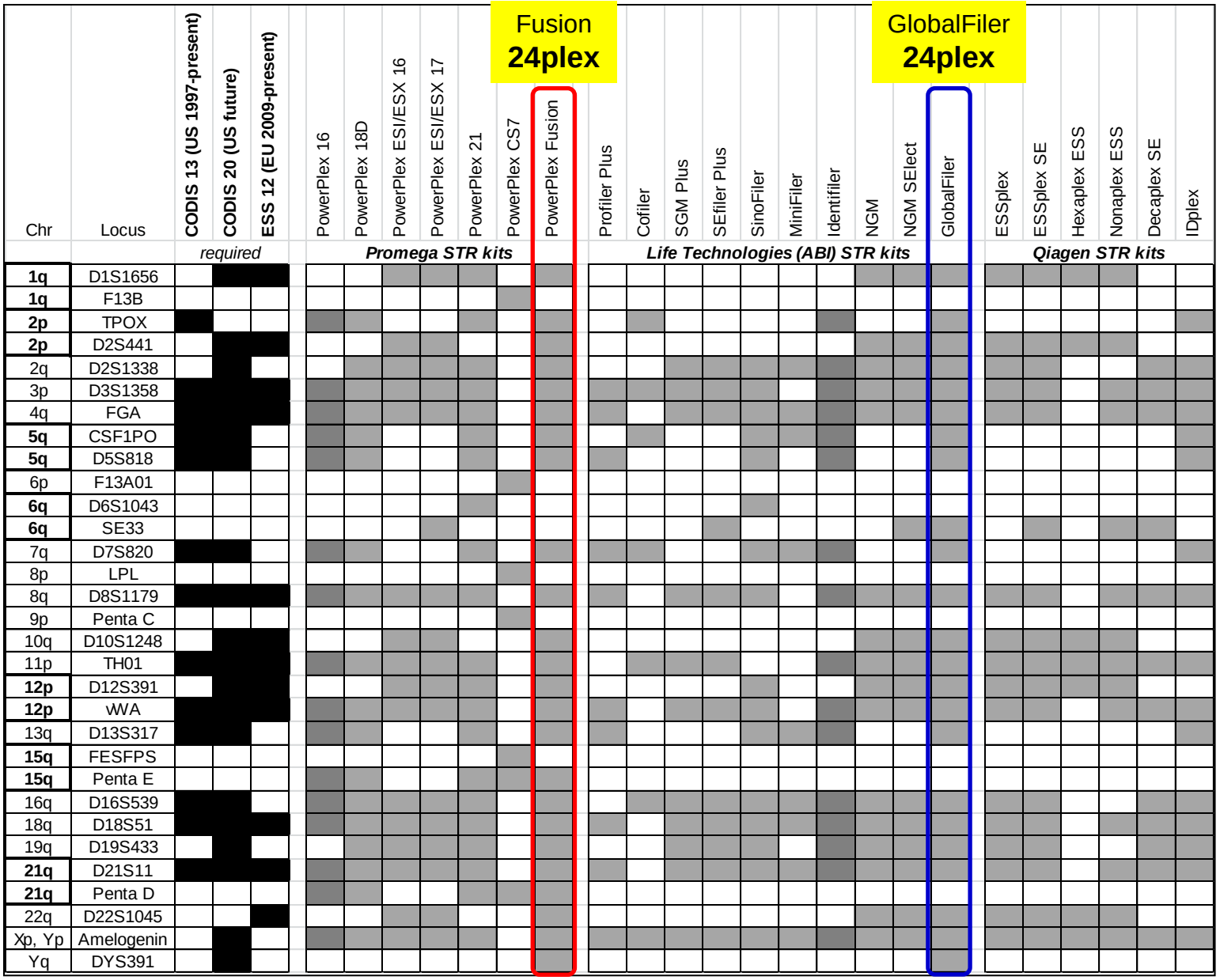
Determination of Additional CODIS Core Loci

D.R. Hares (2012) Expanding the CODIS Core Loci in the United States. *Forensic Sci. Int. Genet.* 6: e52-e54
Addendum to expanding the CODIS core loci in the United States, Forensic Sci. Int. Genet. (2012) doi:10.1016/j.fsigen.2012.01.003

What	Why	Who/How	When
Form a Working Group (WG) to discuss initial selection	Establishes target goals	CODIS Core Loci Working Group with FBI Chair and 5 members; Web meetings	May 2010 - present
Announce proposed additional CODIS core loci	Sets desired target goals and informs manufacturers	WG Chair; Publish proposed listing of CODIS core loci	April 2011 online (published Jan 2012)
Ongoing Progress Reports	Provides updates for DNA community	WG Chair; Present updates on status of CODIS Core Loci project at meetings	2010-2012
Implementation Considerations & Strategy	Identify issues for implementation and timeline	WG	June 2011 - present
Manufacturers develop prototype kits	Creates tools to meet target goals	Manufacturers; Provide status reports to WG for timeline	2011-2012
Test and validate prototype kits	Examines if target goals can be met	Validation Laboratories; Follow QAS compliant validation plan	Beginning in 2012
Review and evaluate data from validation	Evaluates if desired performance is obtained	NIST, SWGDAM and FBI; Provide feedback, if any, to Manufacturers	In conjunction with and at the conclusion of validation
Selection of new CODIS core loci	Allows protocols to be established	FBI; seek input from DNA community and stakeholders; Notify Congress	After evaluation of validation data and kit production factors
Implementation of new CODIS core loci at the National DNA Index System	Enables target goals to be met	All NDIS-participating labs	~ 24 months after selection of new CODIS core loci

http://www.fbi.gov/about-us/lab/codis/planned-process-and-timeline-for-implementation-of-additional-codis-core-loci

STR Loci Covered in Currently Available Commercial Kits

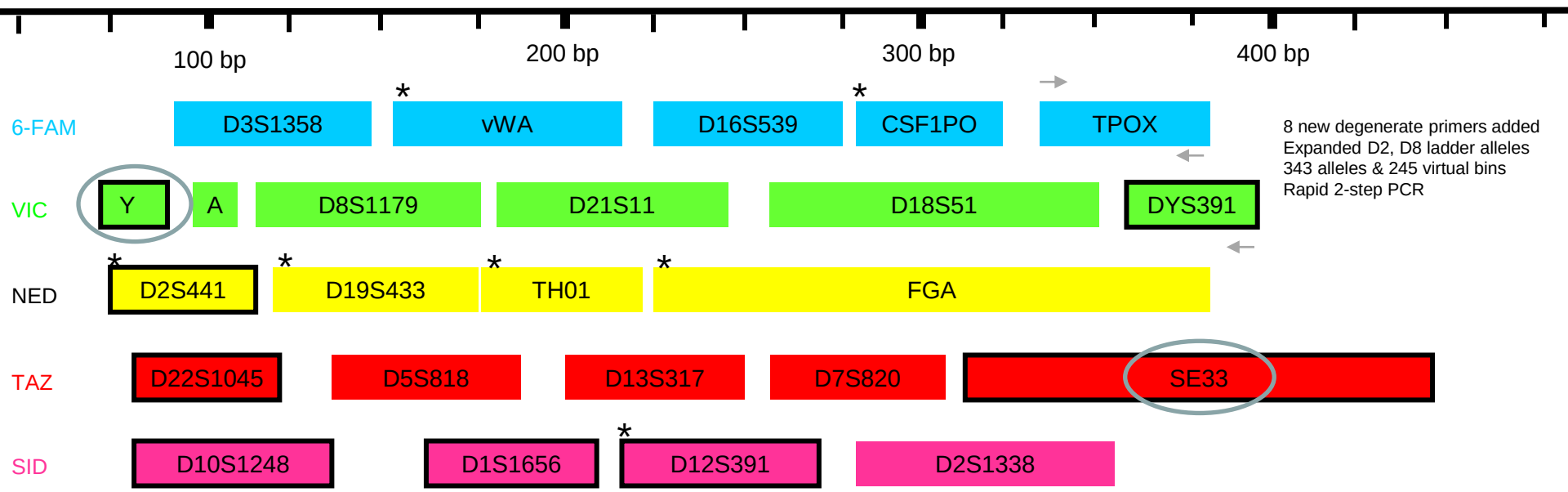


Butler, J.M., & Hill, C.R. (2013) *Topics on Forensic DNA Analysis: Current Practices and Emerging Technologies* (CRC Press).
Chapter 9. Biology and Genetics of New Autosomal STR Loci Useful for Forensic DNA Analysis (in press)

STR Kit Layouts by Dye Label and PCR Product Size

Life Technologies/Applied Biosystems **GlobalFiler** (6-dye – LIZ600 size standard)

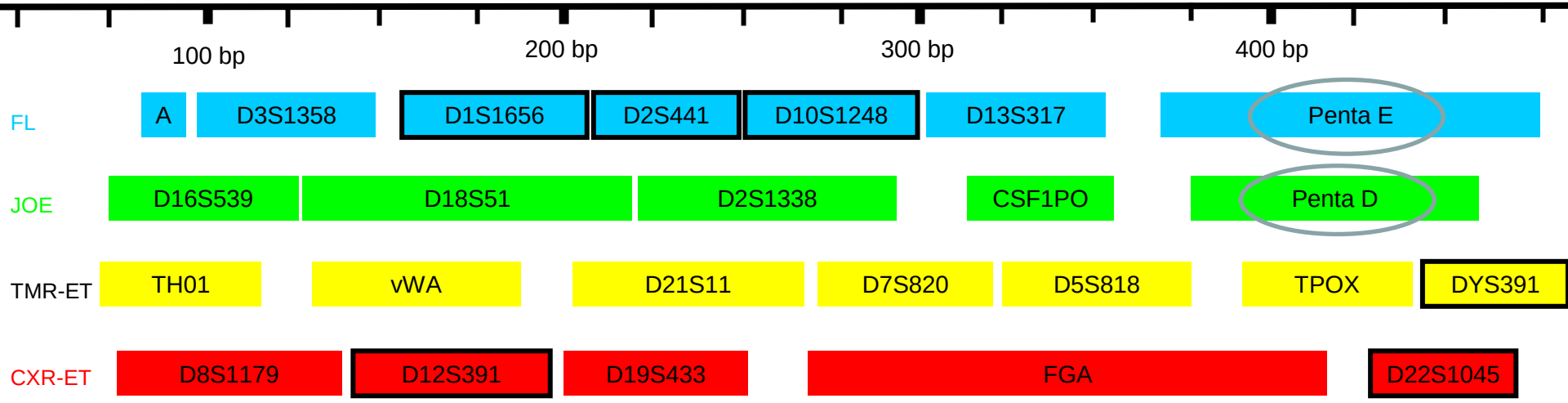
24plex



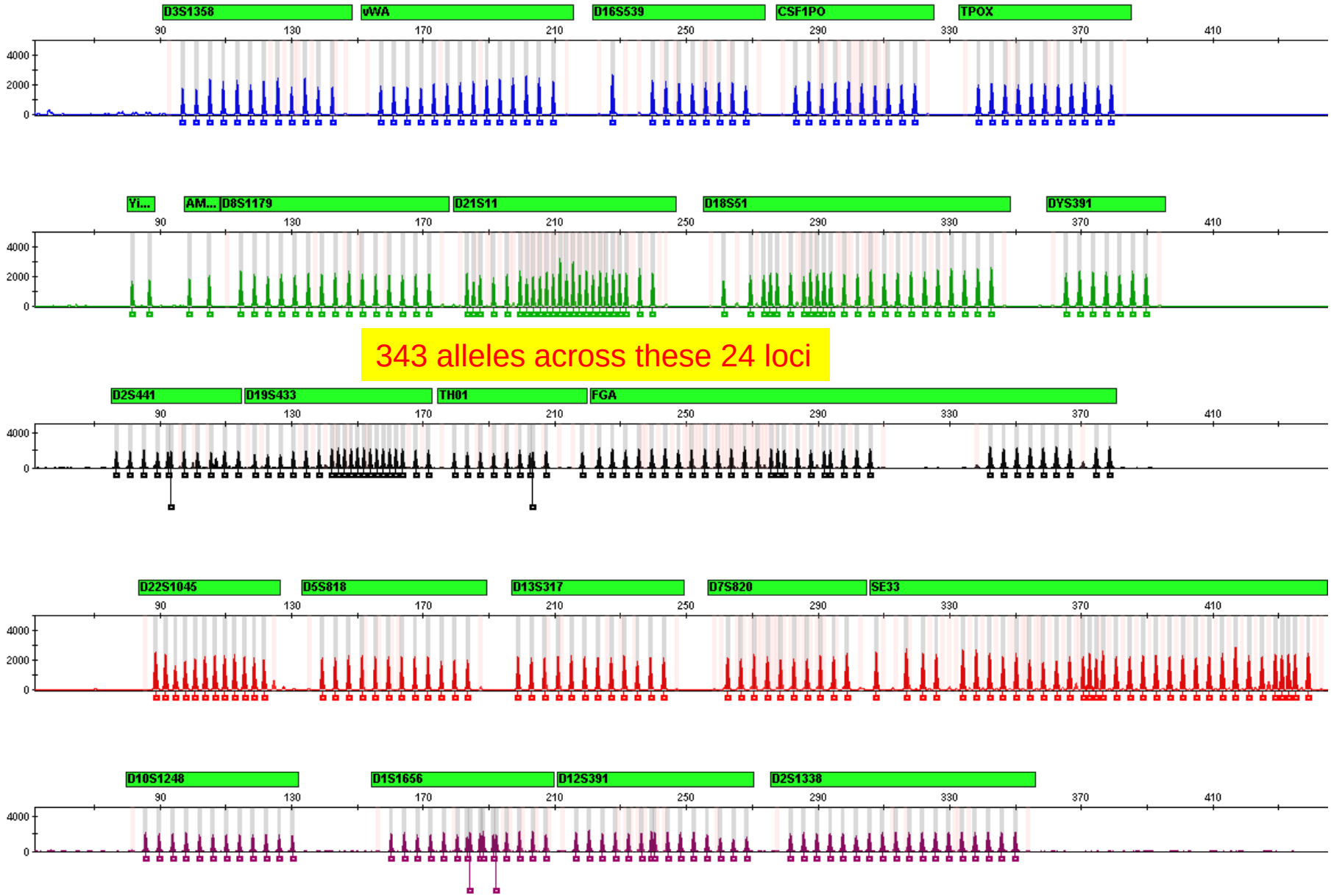
8 new degenerate primers added
Expanded D2, D8 ladder alleles
343 alleles & 245 virtual bins
Rapid 2-step PCR

Promega PowerPlex **FUSION** (5-dye – CC5 internal lane standard 500)

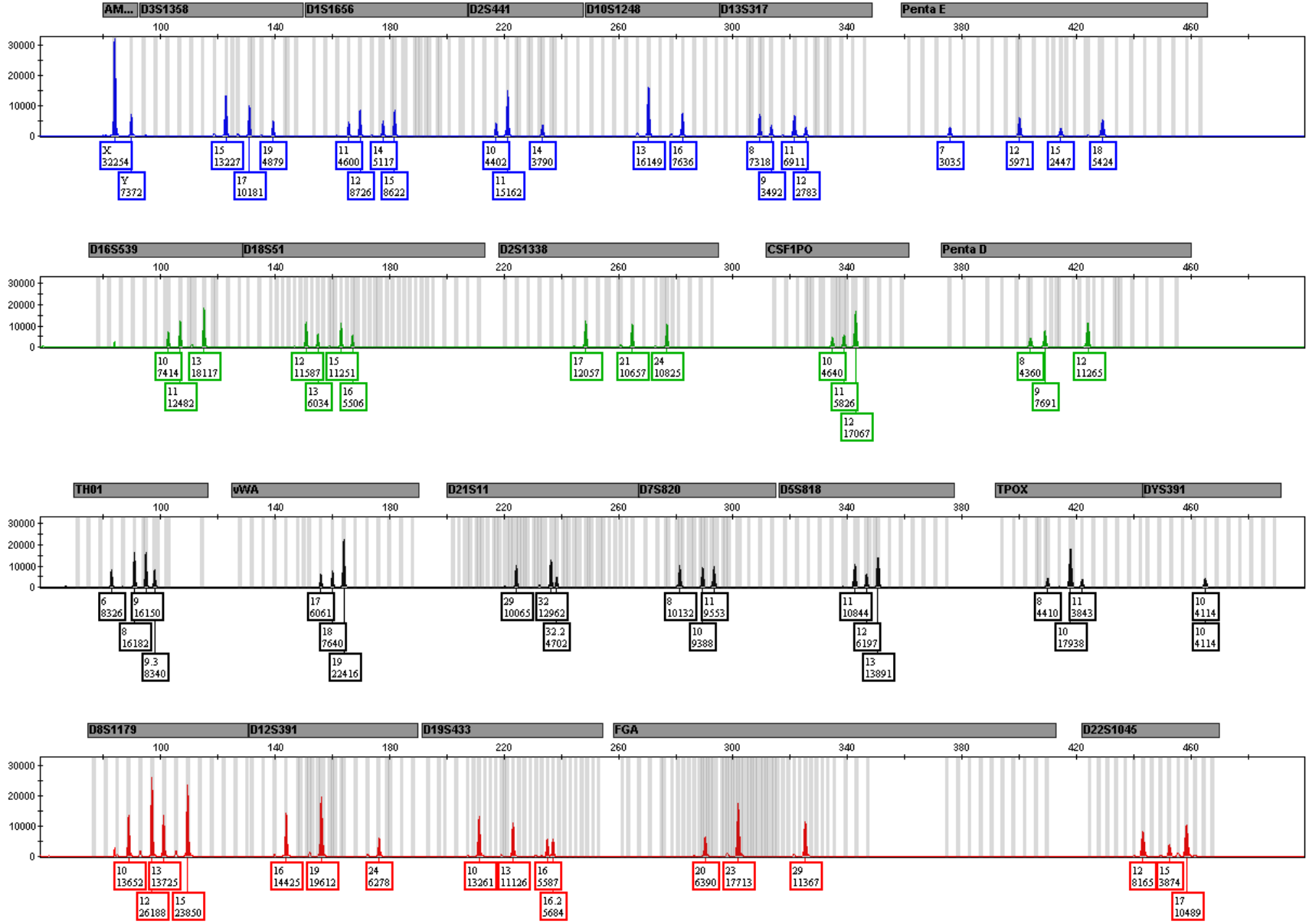
24plex



GlobalFiler Allelic Ladder

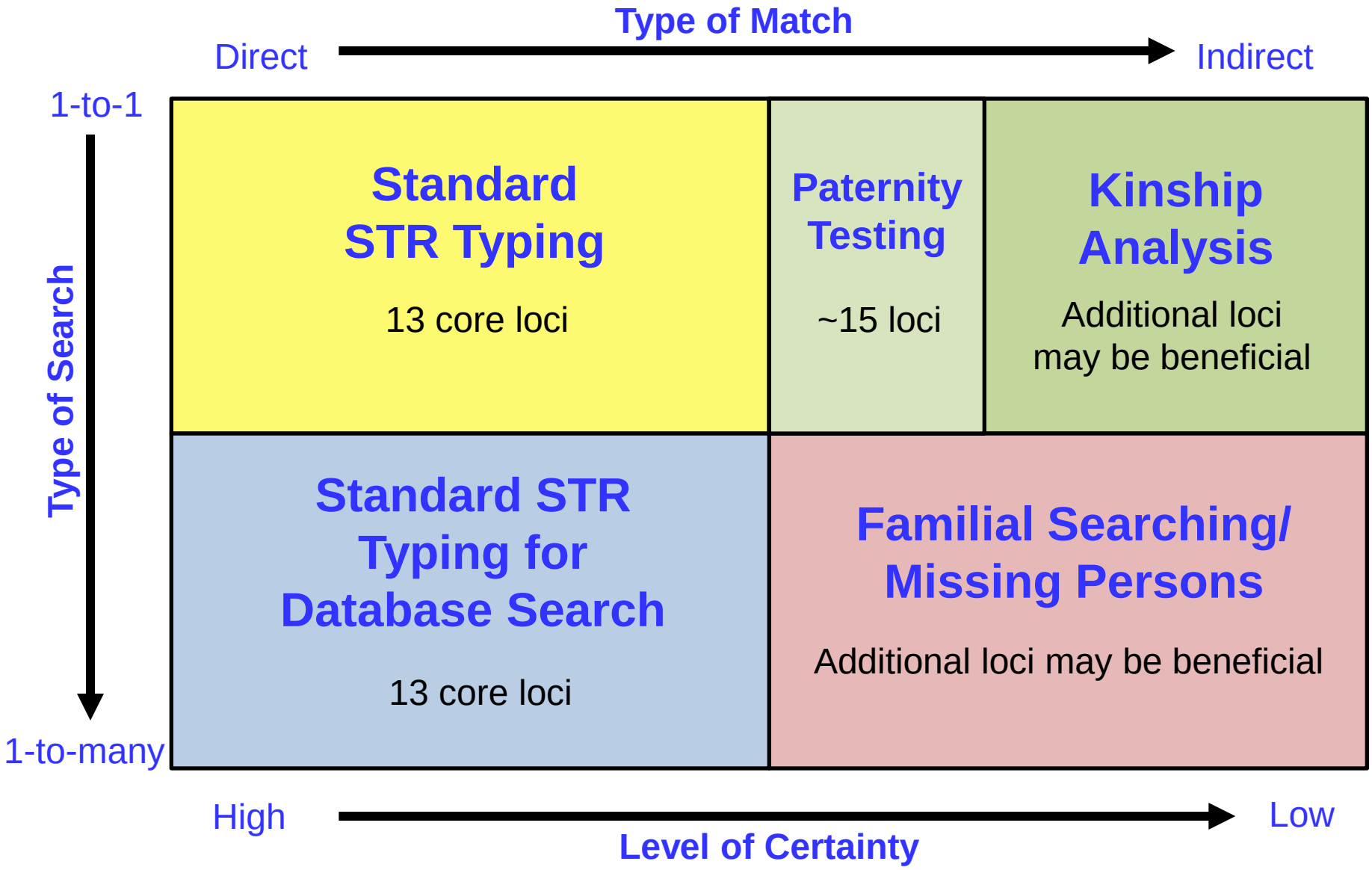


DNA Mixture Detected with PowerPlex Fusion (24plex STR kit)



Size standard not shown

Expanding the Forensic Core Competency



Familial Searching in the U.S.

High-profile success in the Grim Sleeper case has led other states to consider familial searching

Experts say Texas might solve Twilight Serial Rapist cases with family DNA

July 25th, 2010 8:23 am CT

http://www.examiner.com/law-enforcement-in-wichita-falls/experts-say-texas-might-solve-twilight-serial-rapist-cases-with-family-dna

DNA DATABASE

Milwaukee police on hunt for serial killer linked to 7 deaths

May 19, 2009 http://articles.cnn.com/2009-05-19/justice/wisconsin.serial.killer_1_dna-technology-dna-database-prostitutes?_s=PM:CRIME

Familial DNA hunt sought in East Coast rape case

http://www2.insidenova.com/news/2010/aug/04/familial_dna_hunt_sought_in_east_coast_rape_case-ar-428231/

March 21, 2011
Virginia announced familial searching capability

Wednesday December 1, 2010

Virginia could become 3rd state to use familial DNA searches

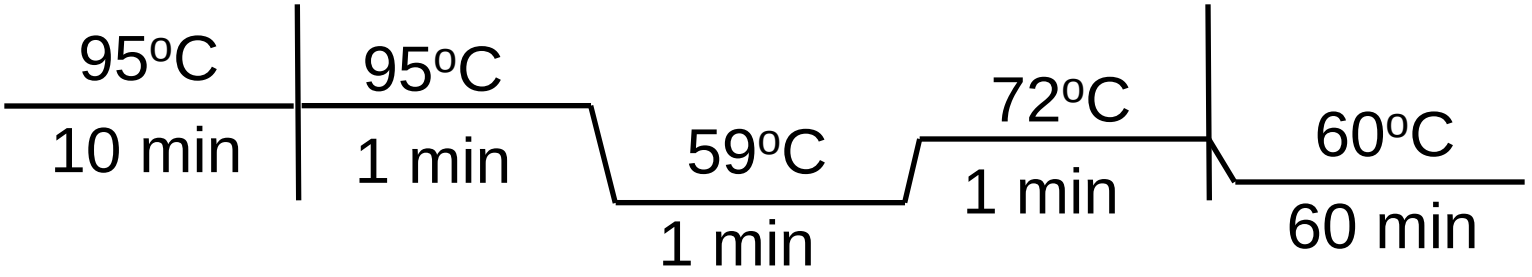
Some concerned practice could stigmatize those related to criminals

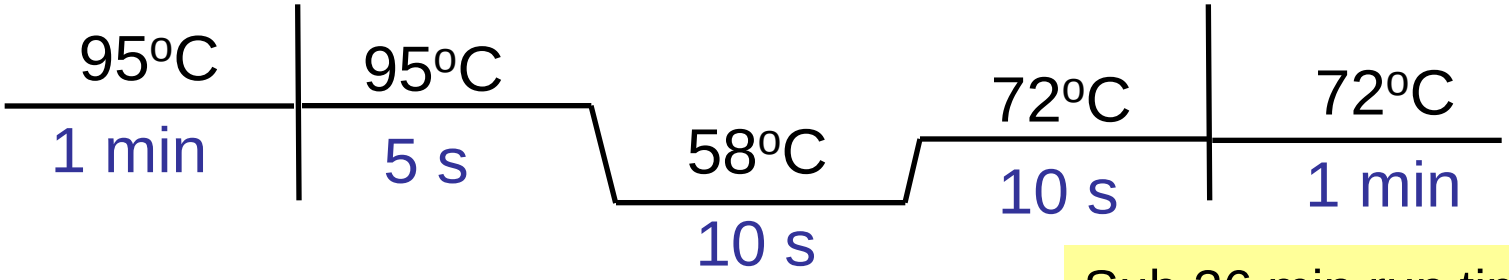
http://www.fairfaxtimes.com/cms/story.php?id=2600

Rapid PCR Thermal Cycling Profile

Identifiler STR kit

28 cycles of PCR



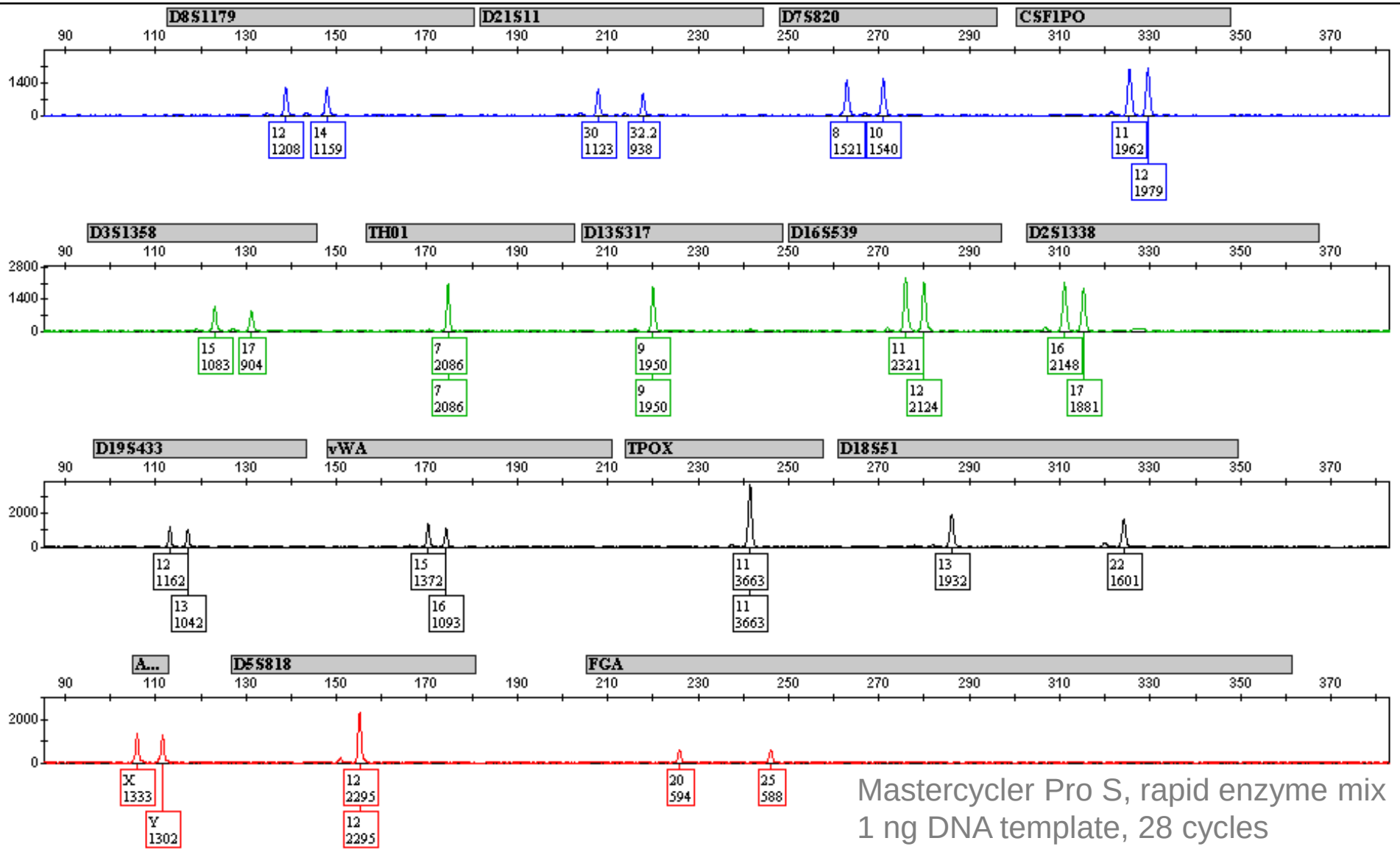


Sub 36 min run time

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

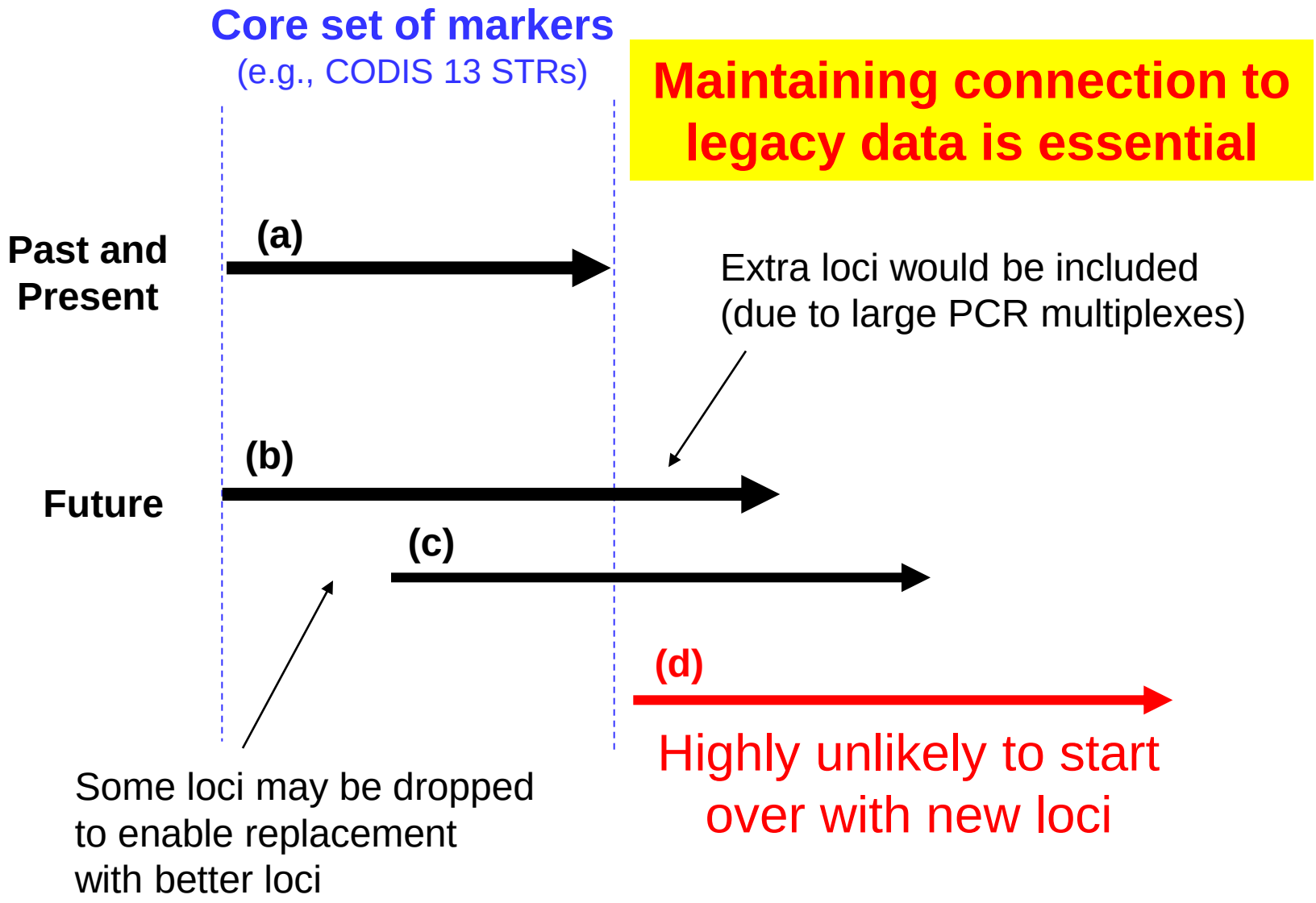
- **Improve overall laboratory throughput**
  - Multiplex PCR amplification is already in many situations the longest part of the DNA analysis process (depending on DNA extraction and DNA quantitation methods)
  - With increased use of robotic sample preparation and expert system data analysis, bottleneck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

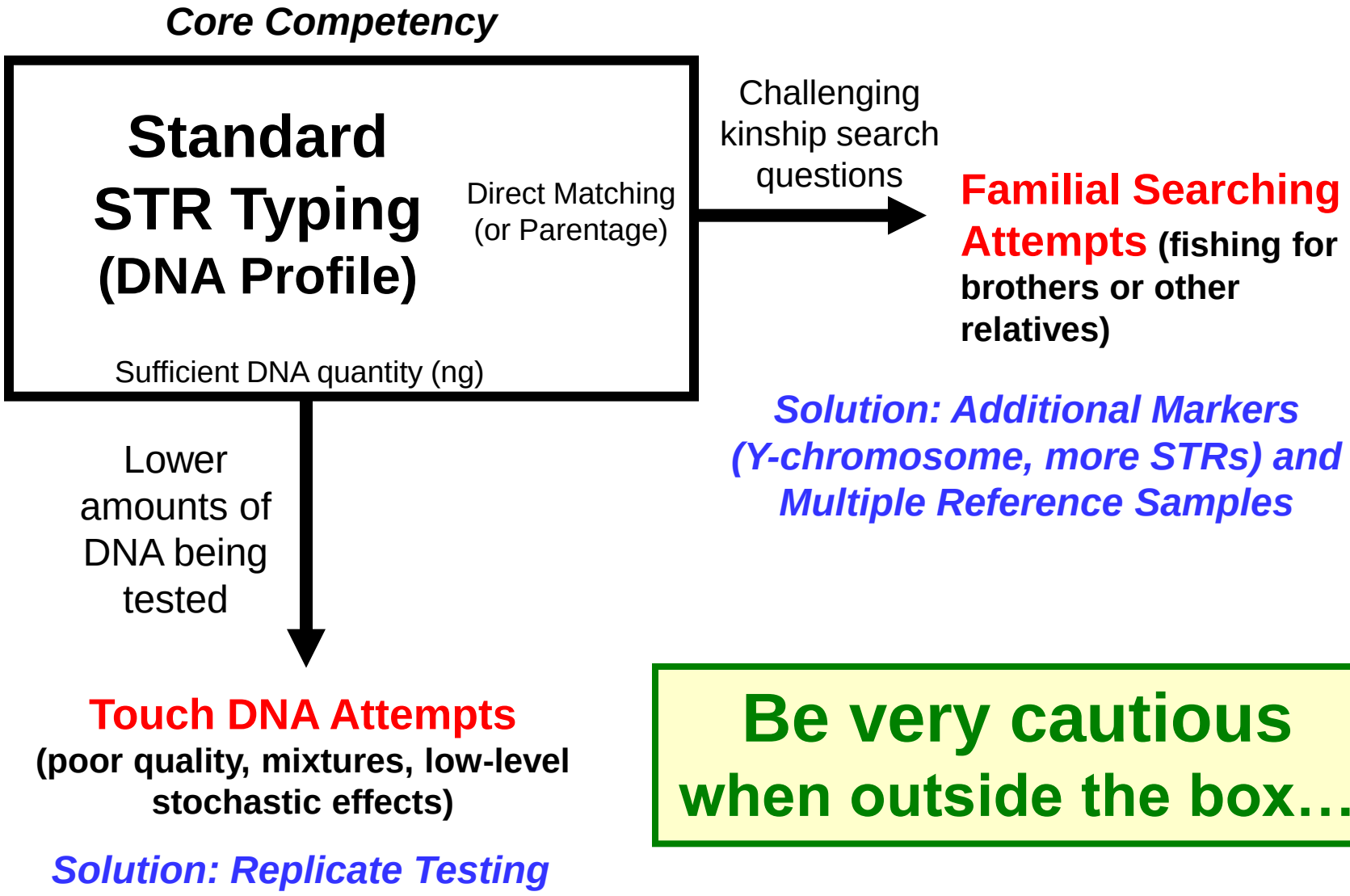


Figure 18.3 in forthcoming Butler (2009) *Fundamentals of Forensic DNA Typing*

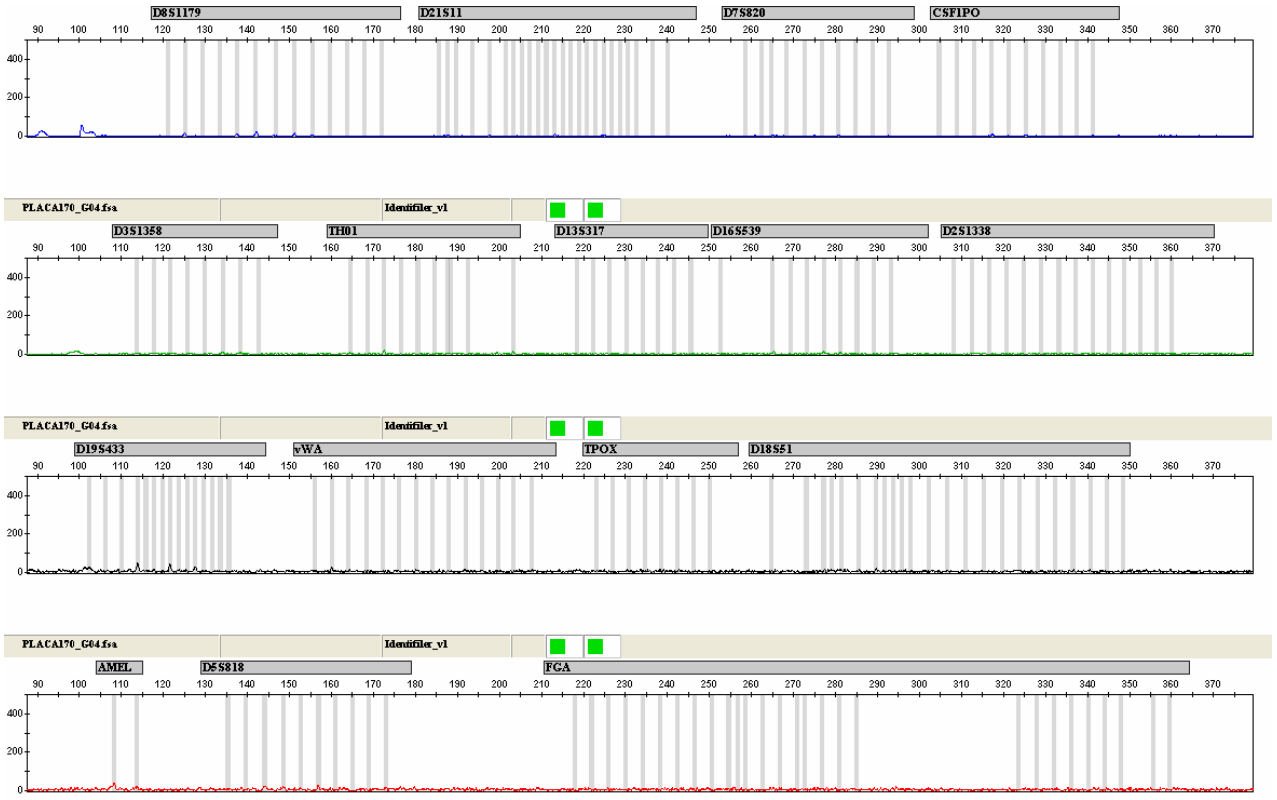
Highly degraded DNA

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)

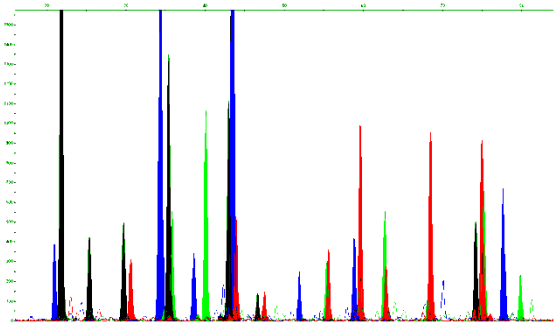
Highly degraded DNA

SNP genotyping in extreme degradation case

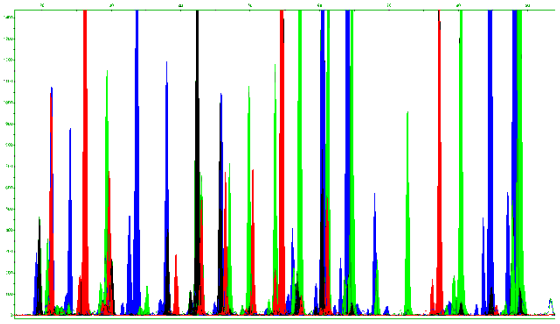
Corpse half buried in a forest for ten years

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

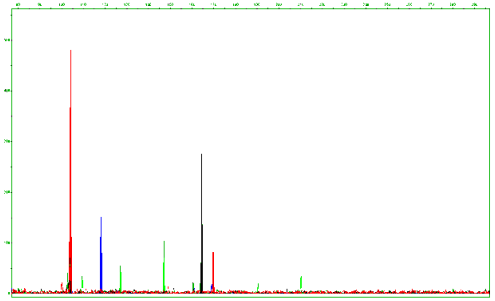
HID 52plex Auto 1: success 100%

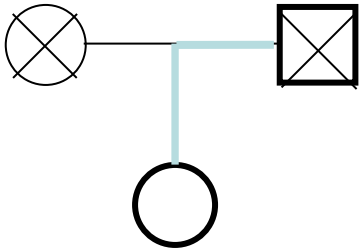


HID 52plex Auto 2 success 100%



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

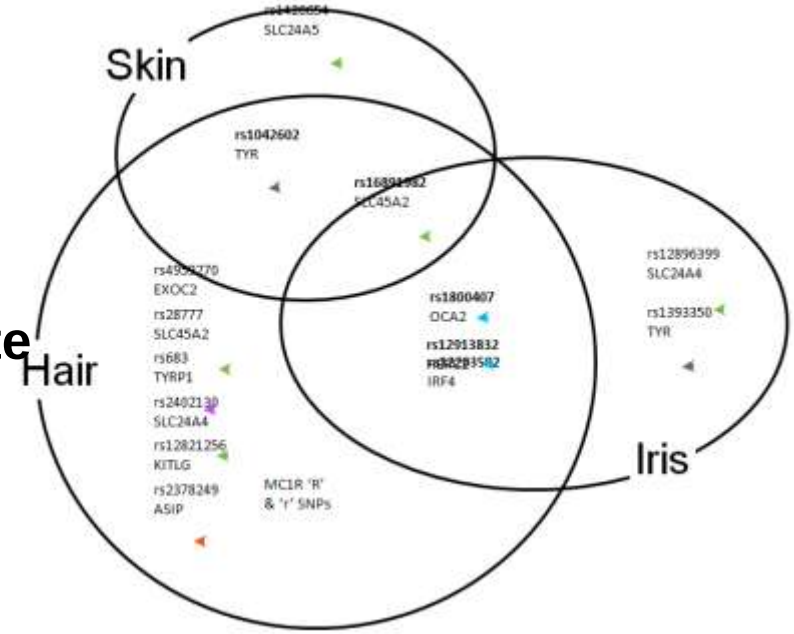
Traits of interest

- **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

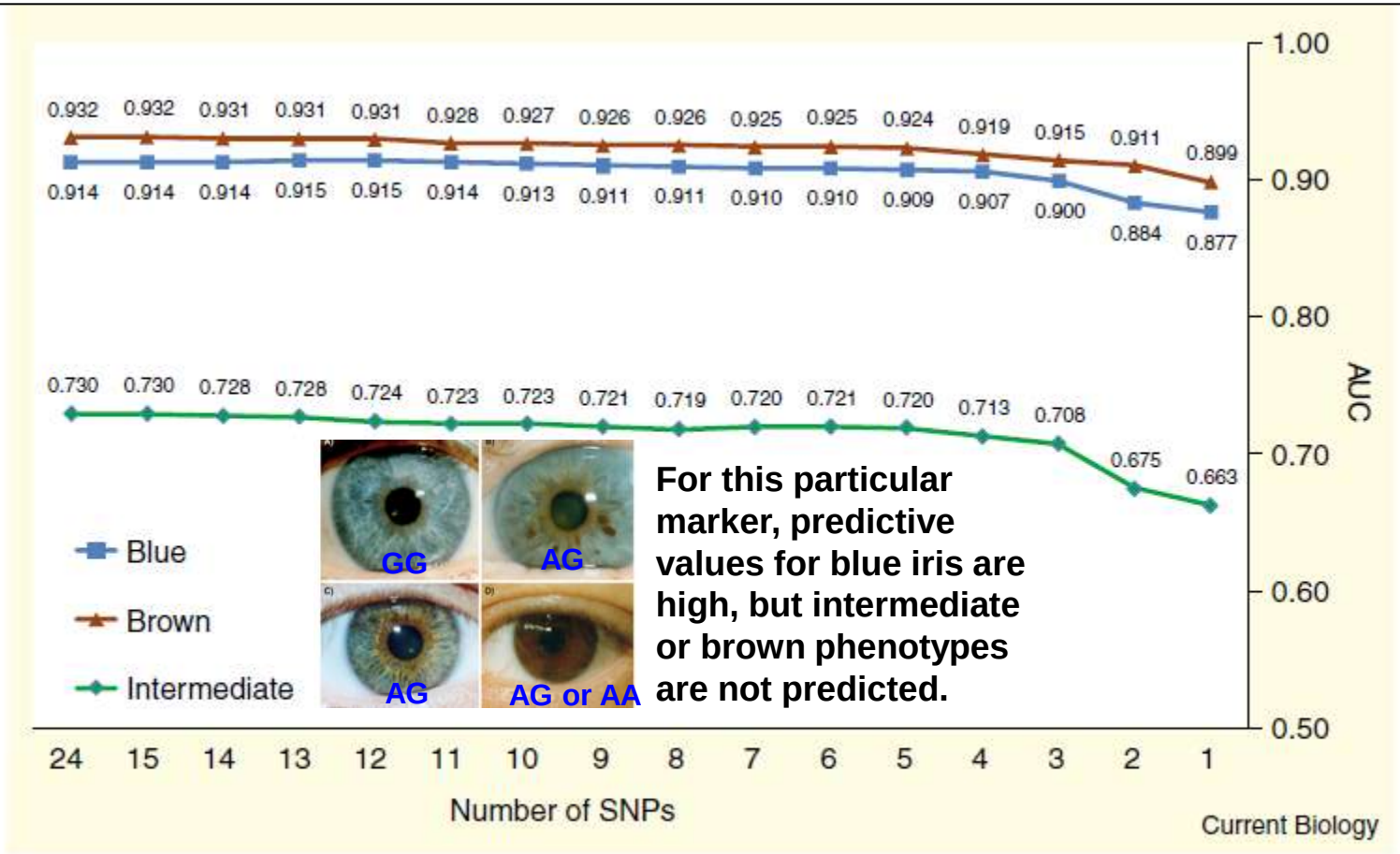


Figure 1. Contribution of 24 SNPs to the prediction accuracy of human eye (iris) color in Dutch Europeans of the Rotterdam Study.

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)

Phenotypic trait prediction

- **Currently several research groups are working on the prediction of phenotypical traits by SNP typing.**
- **Best predictions have been achieved on iris pigmentation.**
- **However the achieved predictive values are still different for each variant. Research is not yet completed.**

- Branicki W, Kayser M et al. (2011). Model-based prediction of human hair color using DNA variants. *Human Genetics;* DOI 10.1007/s00439-010-0939-8.
- Walsh S., et al. (2010) IrisPlex: A sensitive DNA tool for accurate prediction of blue and brown eye colour in the absence of ancestry information. Forensic Sci. Int. Genet. (Epub)
- Kayser M., Schneider P.M. (2009) DNA-based prediction of human externally visible characteristics in forensics: motivations, scientific challenges, and ethical considerations. Forensic Sci. Int. Genet. 3(3):154-61.
- Ruiz Y., C. Phillips et al.(2012) Further development of forensic eye color predictive tests. Forensic Sci. Int. Genet. (accepted for publication).

Slide from Manuel Fondevila (NIST, USC)

NGS Platforms

- Roche
  - 454 FLX
  - **454 GS Junior**
- PacificBio
  - Pacbio RS
- Illumina
  - GAIIx
  - HiSeq
  - HiScanSQ
  - **MiSeq**
- Life Tech
  - 5500 series
  - Ion torrent Proton
  - Ion torrent **PGM** (personal genome machine)

Slide from Peter Vallone (NIST)

Generalized NGS Workflow

≈500 ng of genomic DNA

Hours to days

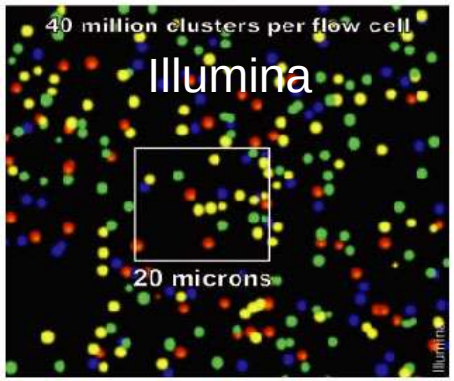
Genomic DNA → Fragment to ≈200 bp → Ligate PCR adapters → PCR → Sequencing

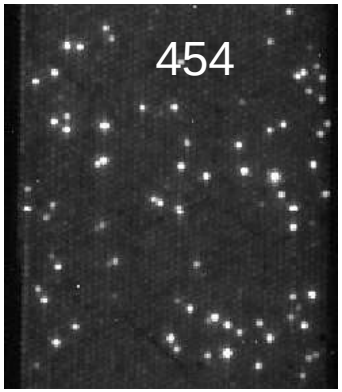
alternative

PCR amplicons → Clean up and quant PCR products

Target specific genes or regions
CODIS STRs, SNPs
≈500 ng of **PCR product**

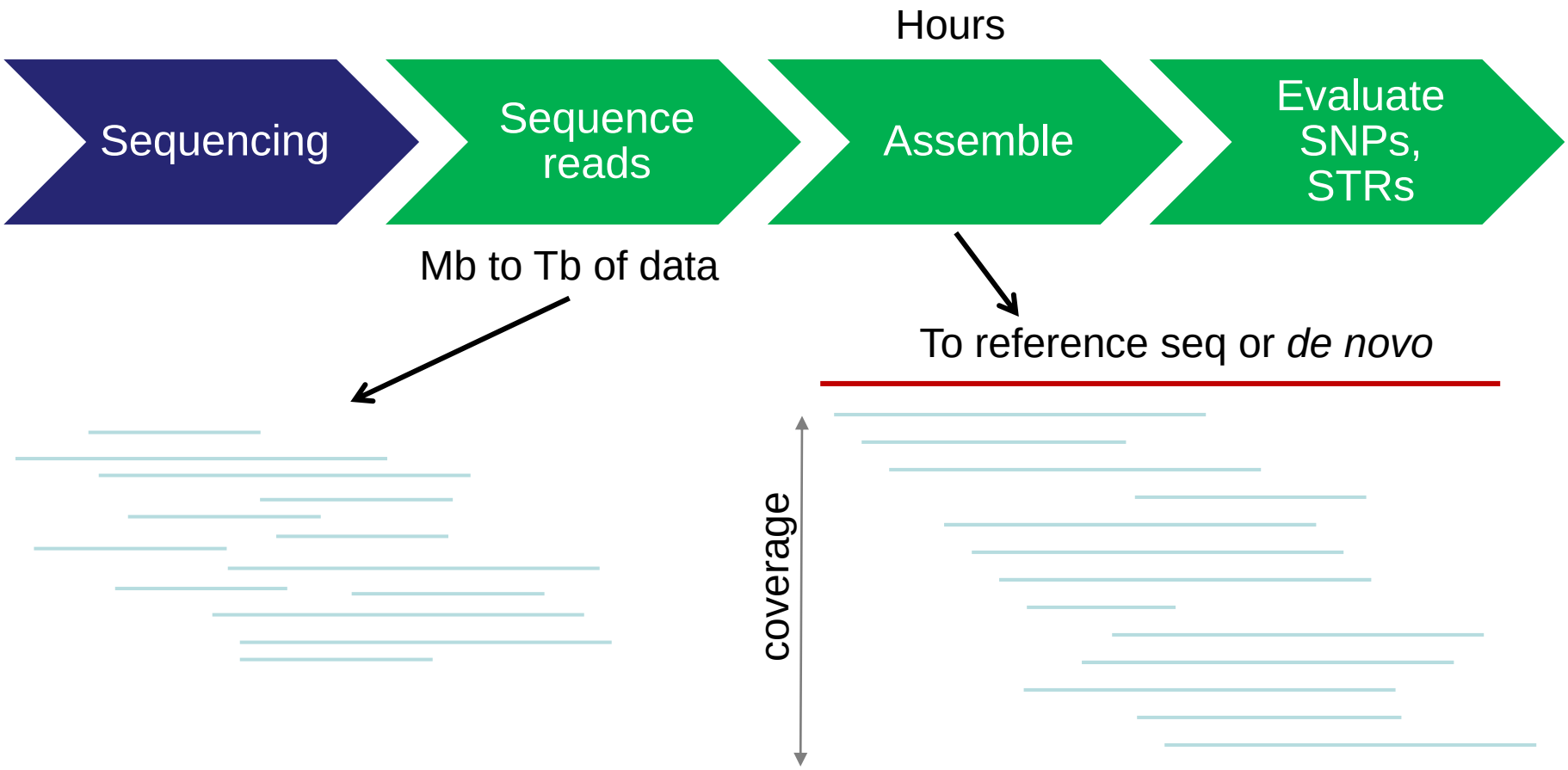
One template per bead/droplet/spot





Slide from Peter Vallone (NIST)

Generalized NGS Workflow



Slide from Peter Vallone (NIST)

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)

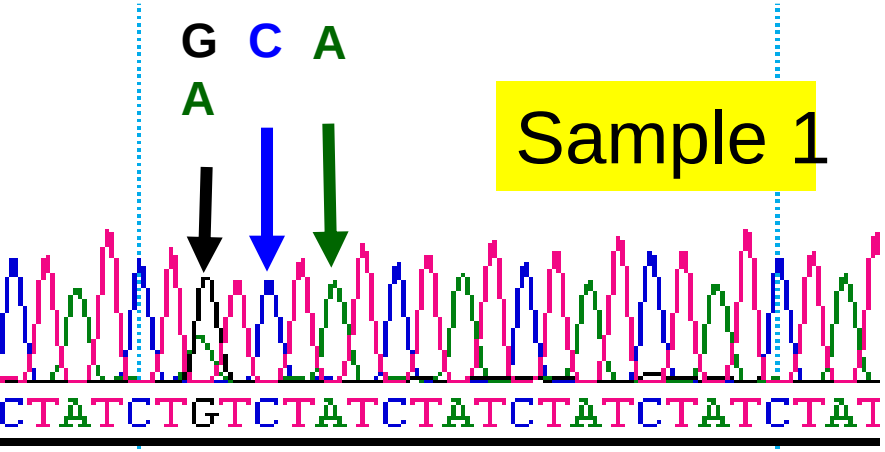
- Opens up new human identity applications: biogeographical ancestry, externally visible traits, complex kinship, degraded samples, mixtures, other applications

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

Slide from Peter Vallone (NIST)

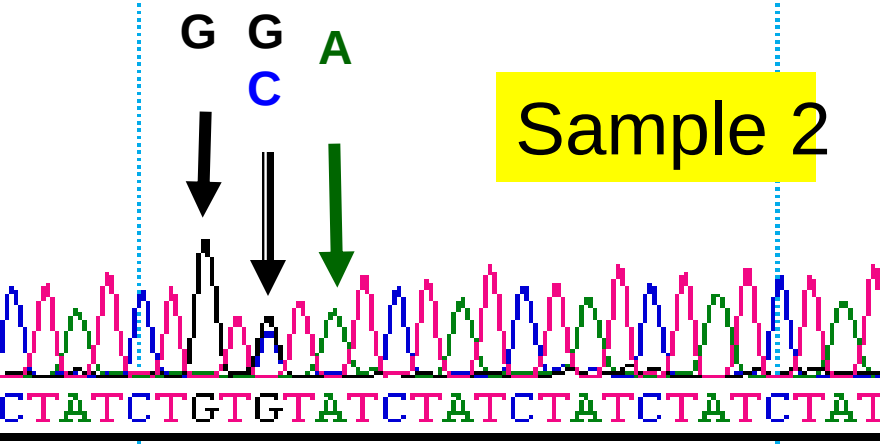
SNPs within the D8S1179 repeat

All 3 samples ‘13,13’ $[TCTA]_{13}$



Allele A - $[TCTA]_{13}$

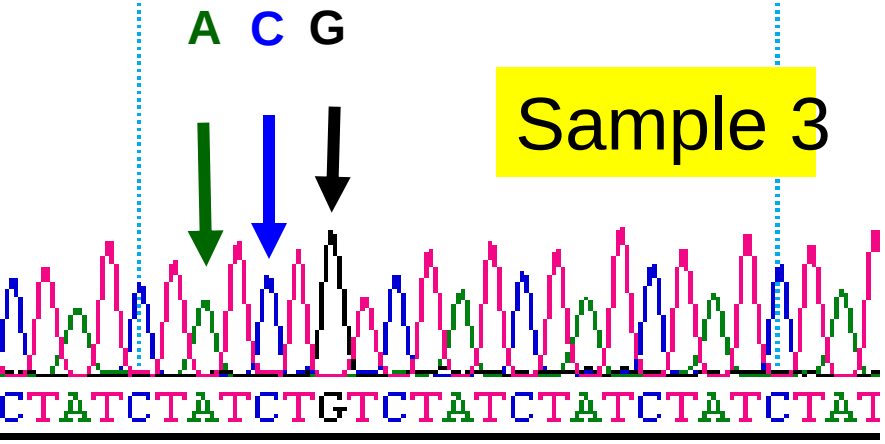
Allele B - TCTA TCT**G** $[TCTA]_{11}$



Allele B - TCTA TCT**G** $[TCTA]_{11}$

Allele C - TCTA TCT**G** T**G**TA $[TCTA]_{10}$

There are **4** different
’13’ alleles in these 3 samples.



Allele D - $[TCTA]_2$ TCT**G** $[TCTA]_{10}$

Allele D - $[TCTA]_2$ TCT**G** $[TCTA]_{10}$

Data provided by Margaret Kline and Becky Hill

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

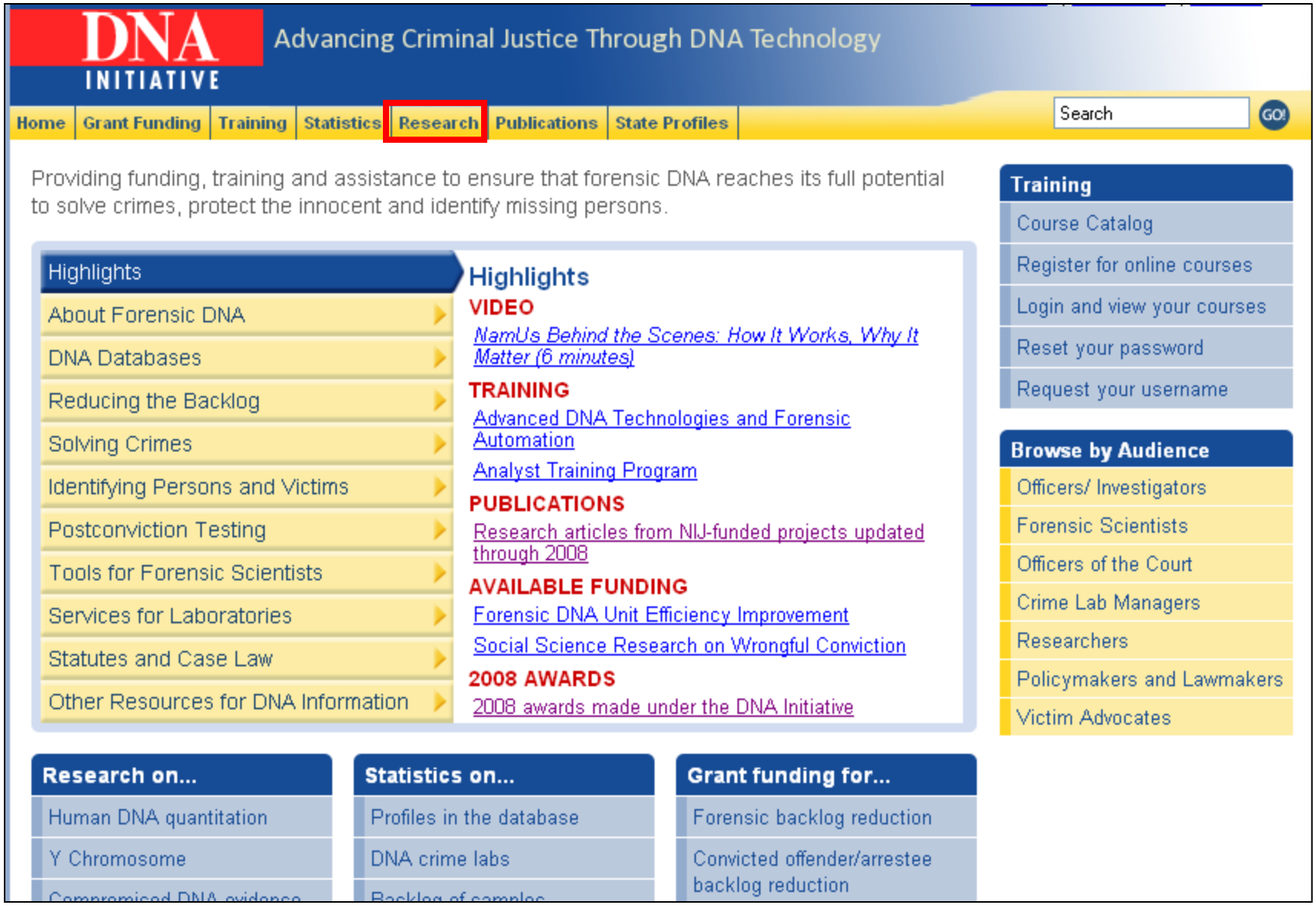
Forensic Science International: Genetics

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]

www.DNA.gov Website



Summary of NIJ-Funded Research

9 areas of funded research

http://www.dna.gov/research/

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

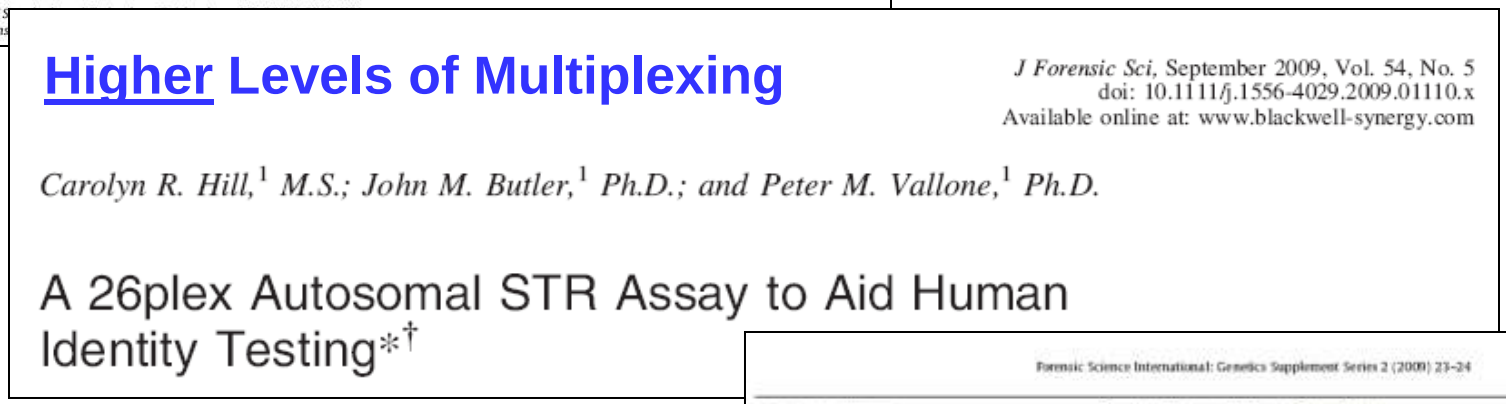
Research article

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

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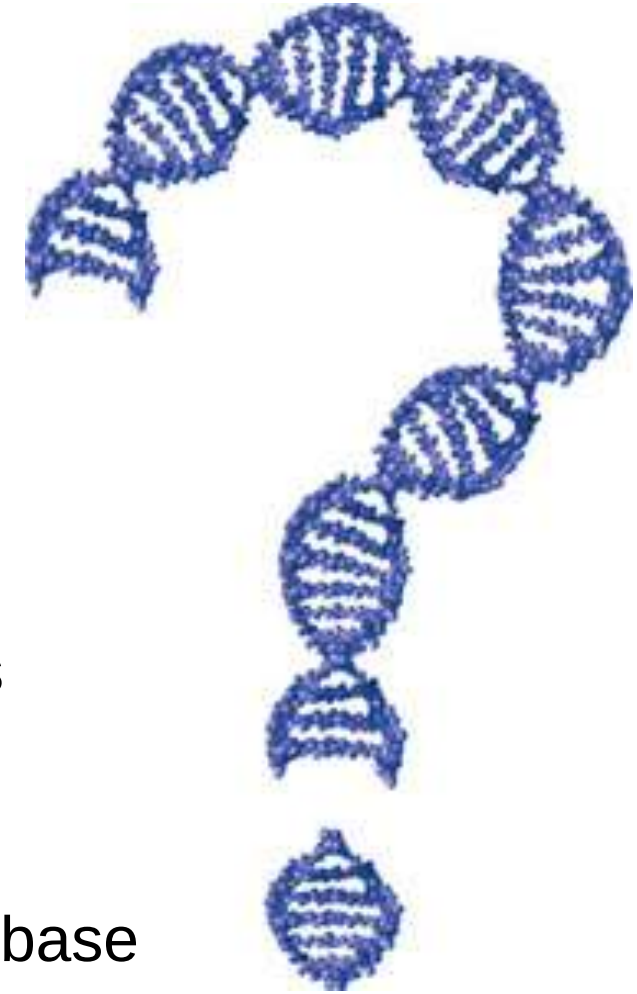
Thank you for your attention

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



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

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