Seventh Judicial Circuit of Maryland Conference
June 21, 2013
Chesapeake Beach, MD

Everything a Trial Judge Needs to Know about DNA (in a nutshell)

John M. Butler, Ph.D.
National Institute of Standards and Technology
Gaithersburg, Maryland

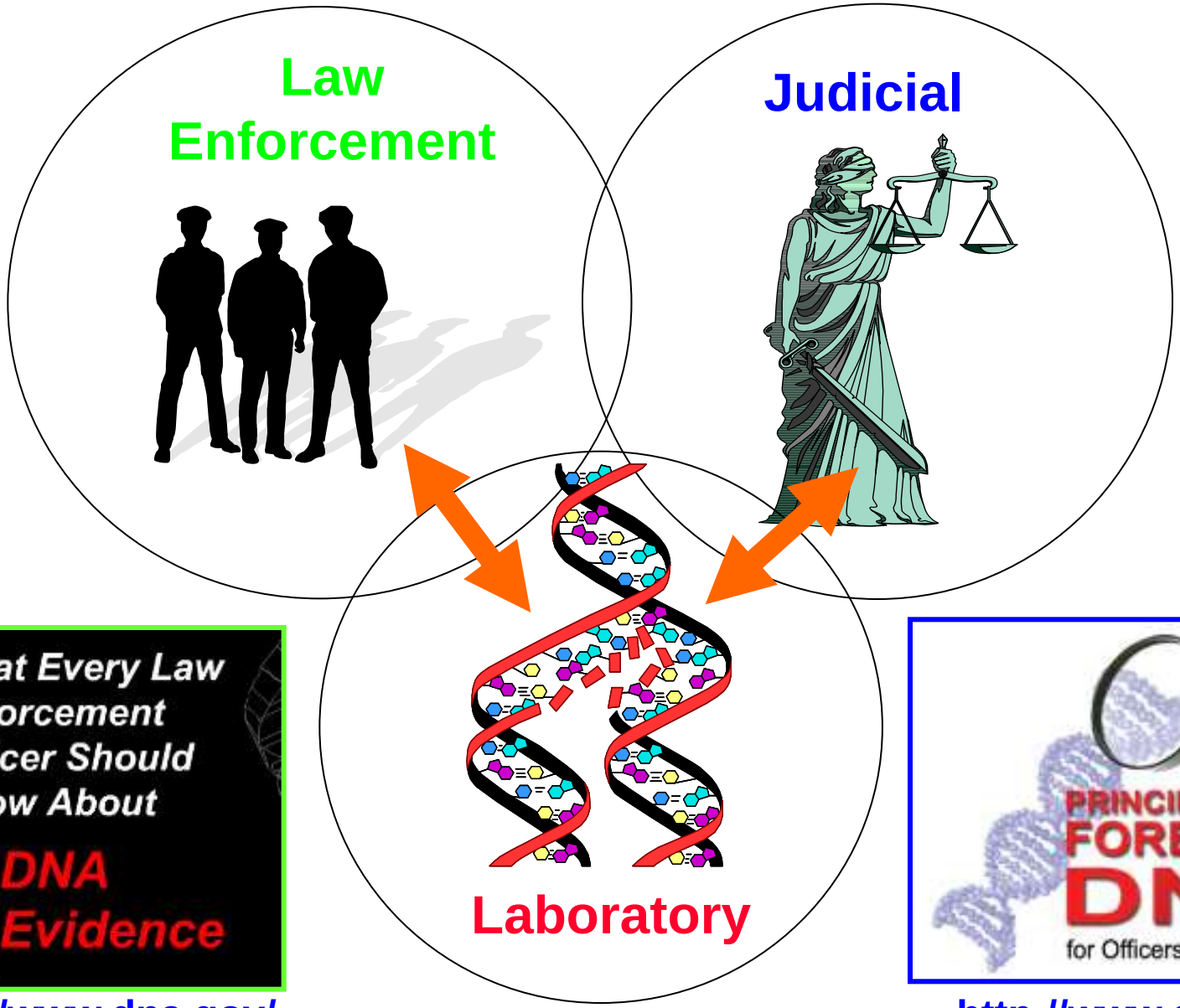
NIST

What Topics Would You Like to Explore?

From 6/21/13 audience

- Key concepts
- How to know if experts are qualified
- Rapid DNA capabilities
- New information in “junk DNA” regions
- How to make DNA understandable to juries
- Should data be accepted without stochastic threshold
- Why racial categories when reporting profile statistics
- Review of DNA basics

Interfaces Between Disciplines Are Crucial

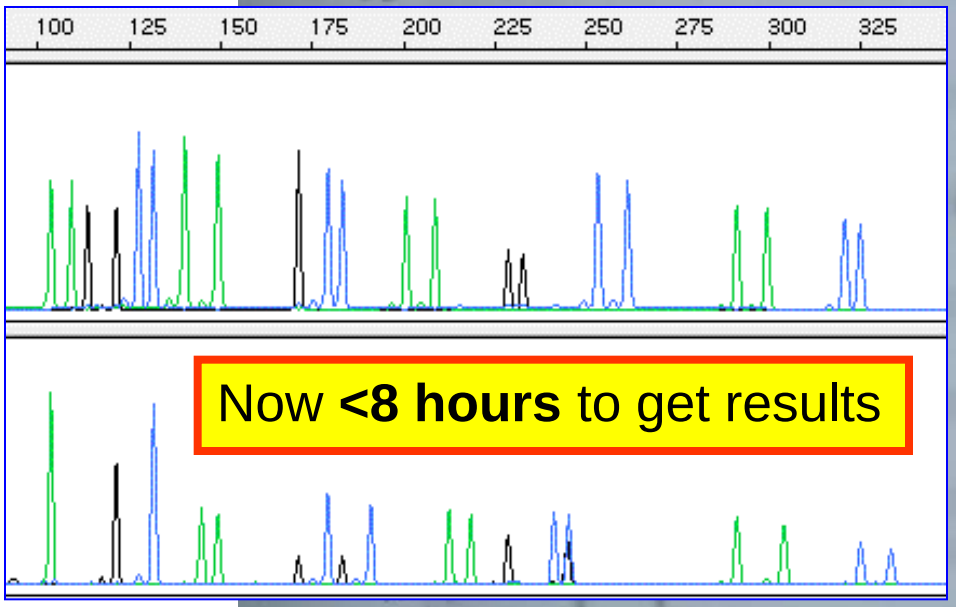


http://www.dna.gov/

http://www.dna.gov/

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

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.**

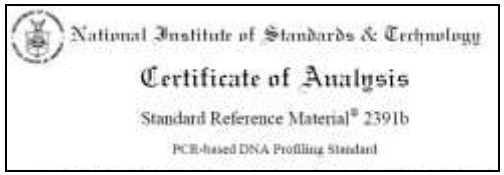
$573 for 3 jars

DNA typing standard

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


National Institute of Standards & Technology

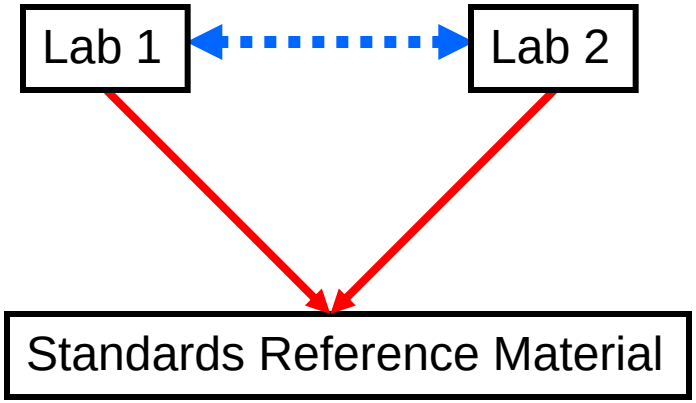
Certificate of Analysis

Standard Reference Material® 2391b

PCR-based DNA Profiling Standard

Helps meet DAB Std. 9.5 and ISO 17025

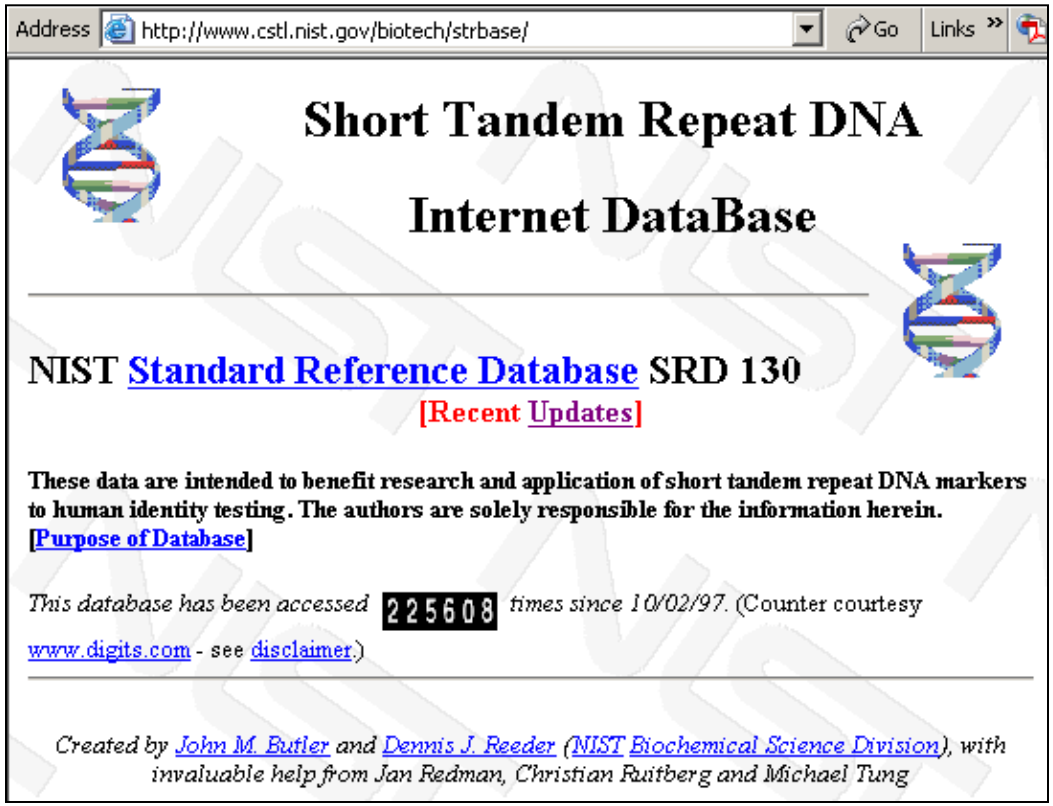
SRM 2391b – CODIS STRs
SRM 2392-I – mtDNA
SRM 2395 – Y-STRs
SRM 2372 – DNA quantitation



Calibration with SRMs enables confidence in comparisons of results between laboratories

Information Resources

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



Includes information on:

- Core STR loci
- Validation
- STR reference list
- NIST publications
- miniSTRs
- Forensic SNPs
- Variant STR alleles
- Population data resources
- Addresses of scientists

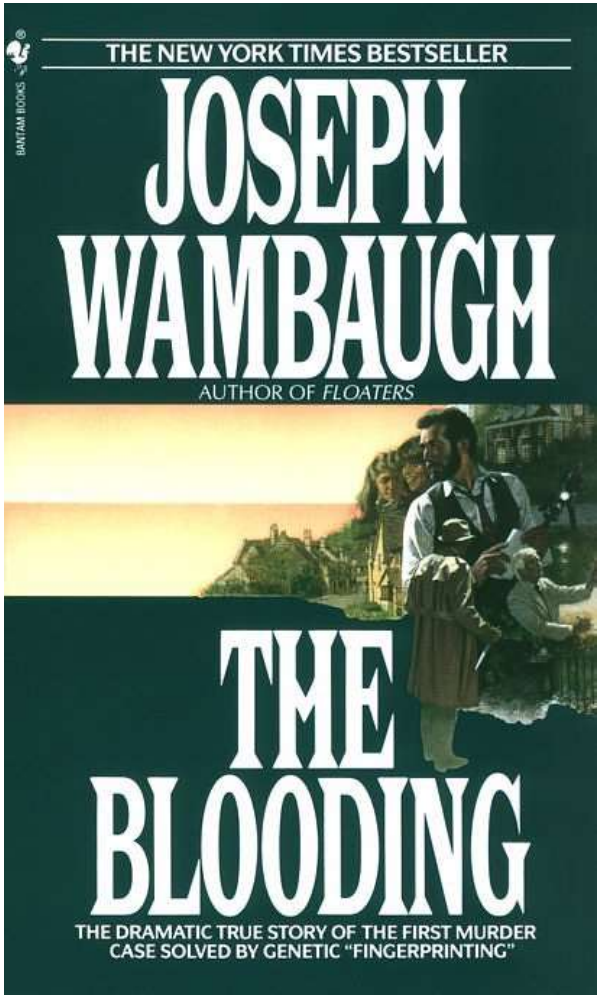
Provides up-to-date information and has been used in court cases to support application of DNA technology

Applications of Forensic DNA Typing

- Forensic cases -- **matching suspect with evidence**
- Paternity testing -- **identifying father**
- Missing persons investigations
- Military DNA “dog tag”
- Convicted felon DNA databases
- Mass disasters -- **putting pieces back together**
- Historical investigations

Involves generation of DNA profiles usually with the same core STR (short tandem repeat) markers and then MATCHING TO REFERENCE SAMPLE

Lessons from the First Case Involving DNA Testing



Describes the first use of DNA (in 1986) to solve a double rape-homicide case in England; about 5,000 men asked to give blood or saliva to compare to crime stains

- Connection of two crimes (1983 and 1986)
- Use of DNA database to screen for perpetrator (DNA only done on 10% with same blood type as perpetrator)
- Exoneration of an innocent suspect
- DNA was an investigative tool – did not solve the case by itself (confession of accomplice)

A local baker, Colin Pitchfork, was arrested and his DNA profile matched with the semen from both murders. In 1988 he was sentenced to life for the two murders.

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

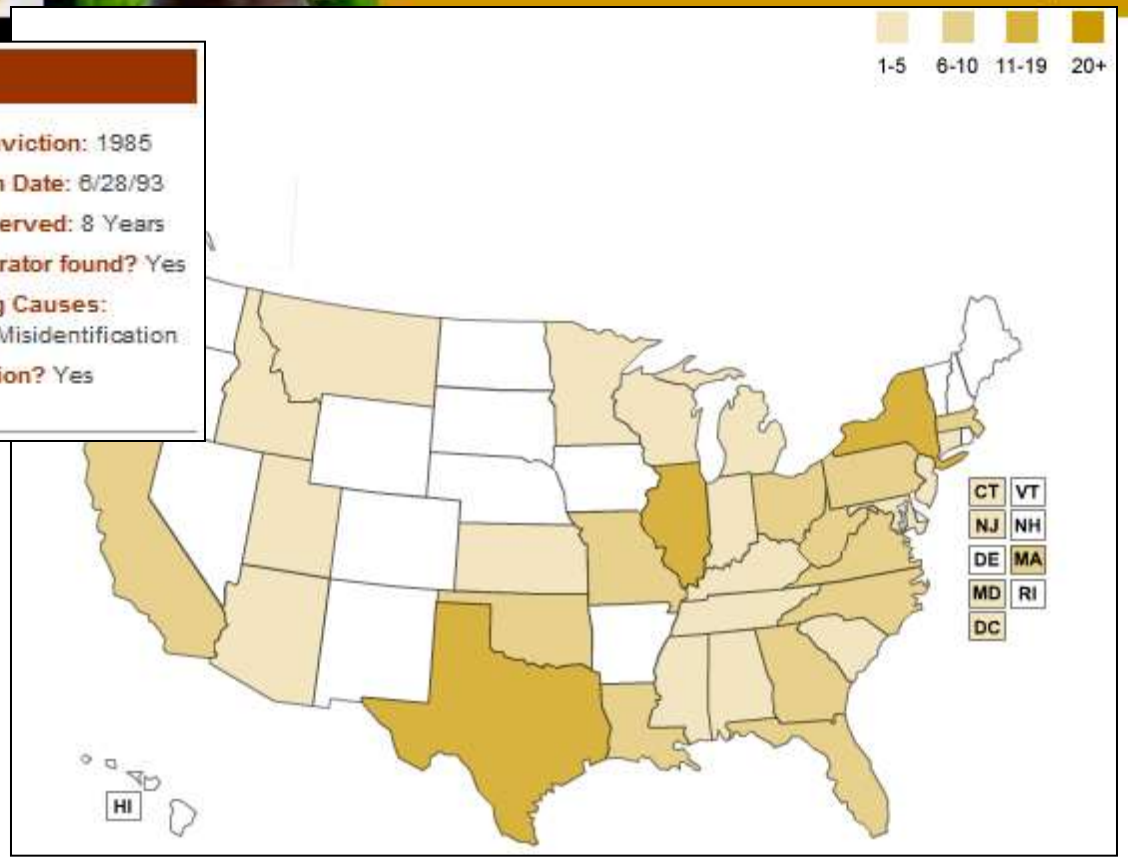
Exoneration Date: 6/28/93

Sentence Served: 8 Years

Real perpetrator found? Yes

Contributing Causes: Eyewitness Misidentification

Compensation? Yes

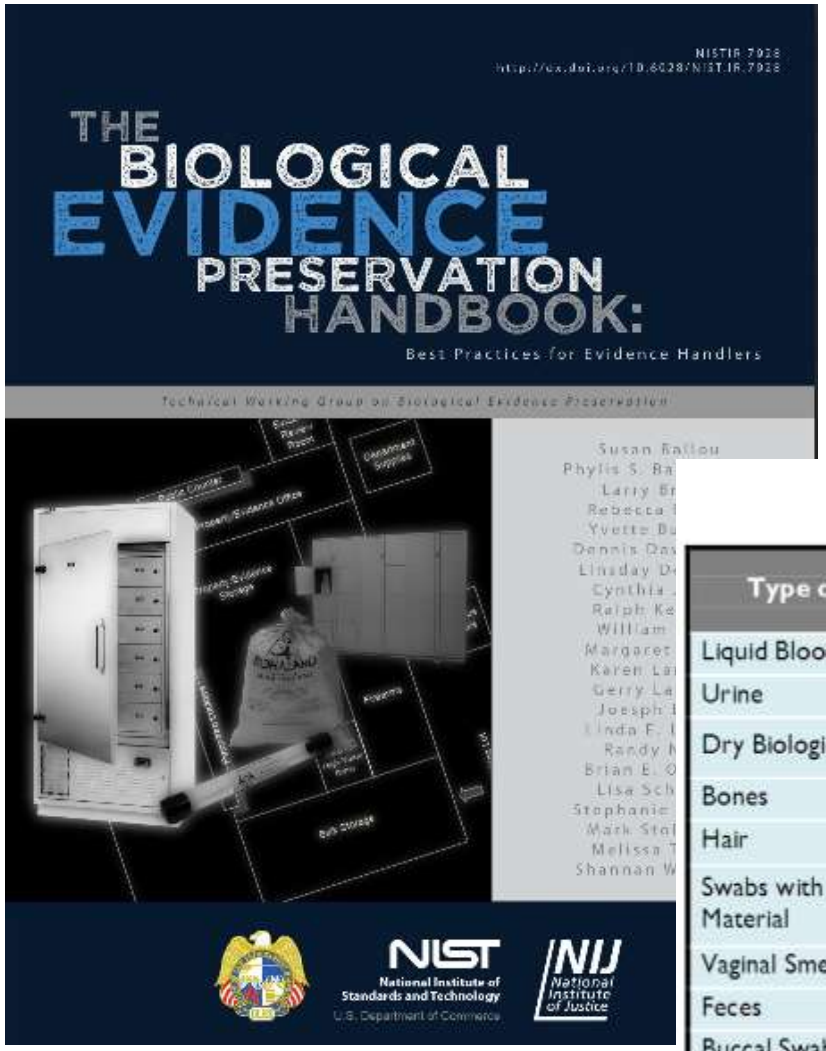


308 exonerated as of June 19, 2013

4 in Maryland

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

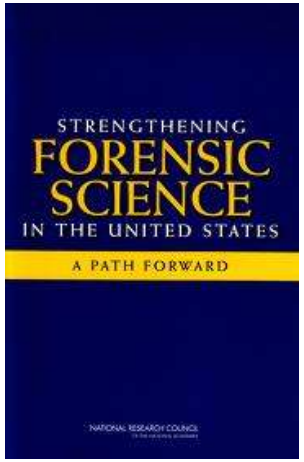
Table III-2: Long-Term Storage Conditions Matrix[1]

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

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

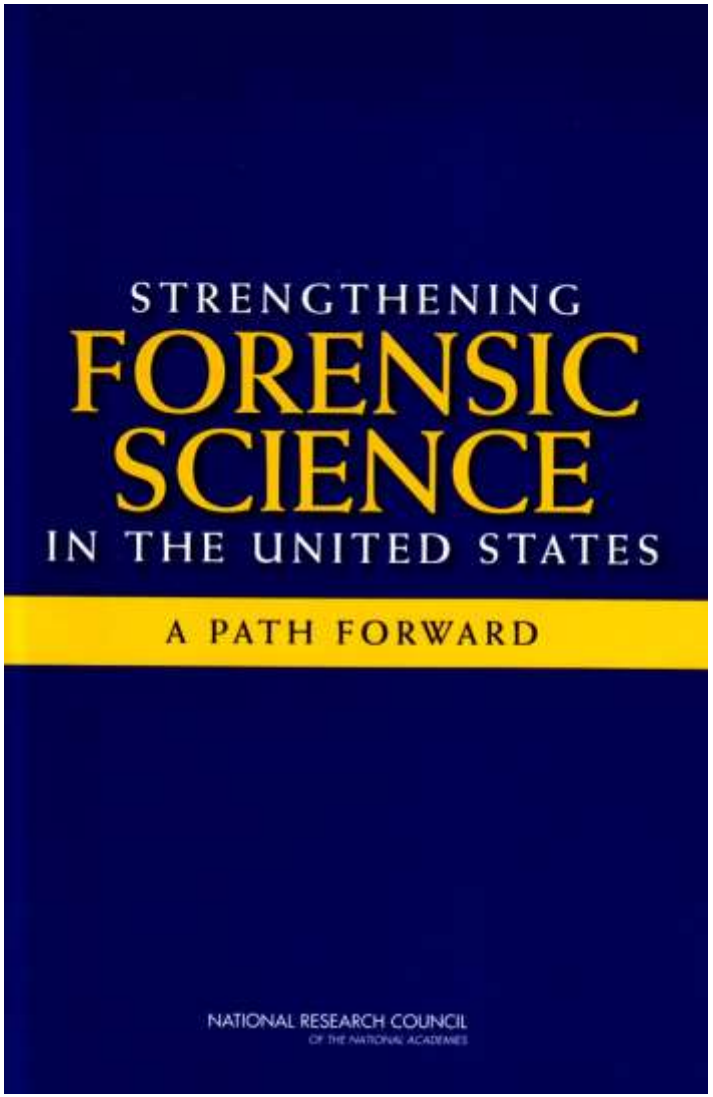
National Academies Report on Forensic Science



- 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 Science**

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

NAS Report (2009)



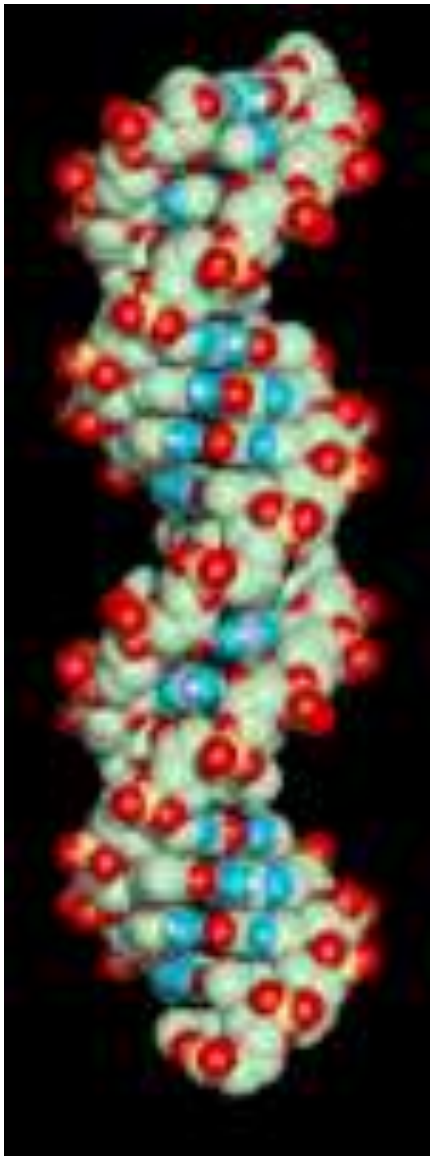
"[DNA analysis] has set the bar higher for other forensic science methodologies, because it has provided a tool with a higher degree of reliability and relevance than any other forensic technique."

p.41

http://www.nap.edu/catalog.php?record_id=12589

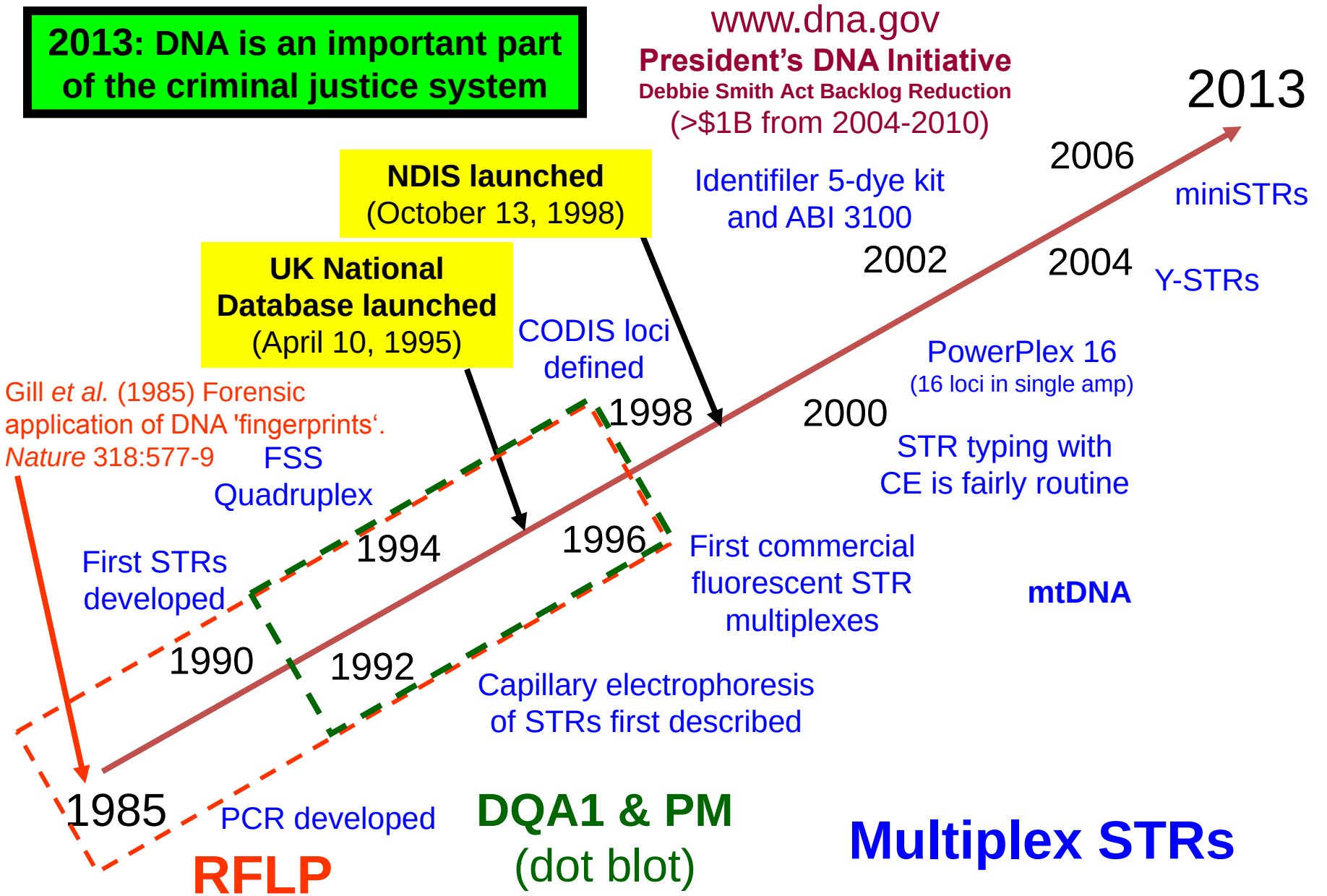
Methods for Human Identification

Fingerprints have been used since 1901



DNA since 1986

Historical Perspective on DNA Typing



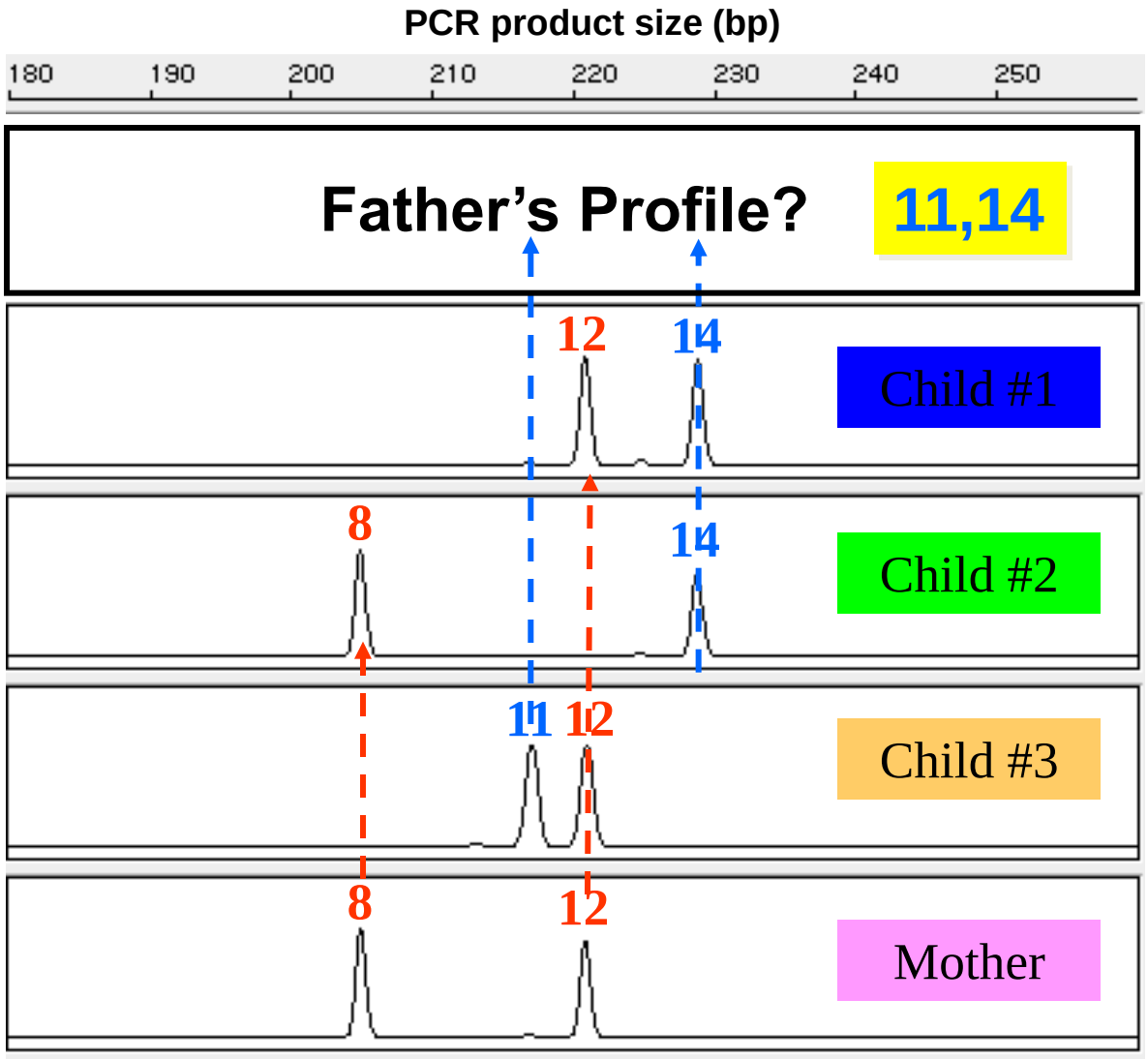
Stages of Forensic DNA Progression

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***

We are finding new ways to use DNA…

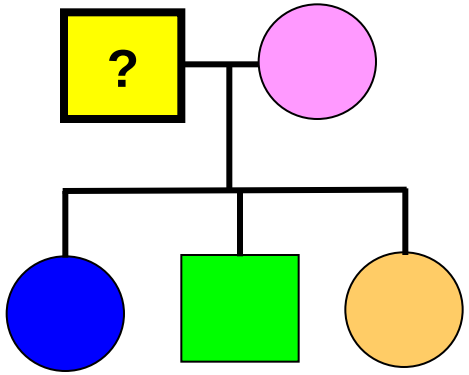
http://www.freewebs.com/desireealbano/bizarro.jpg

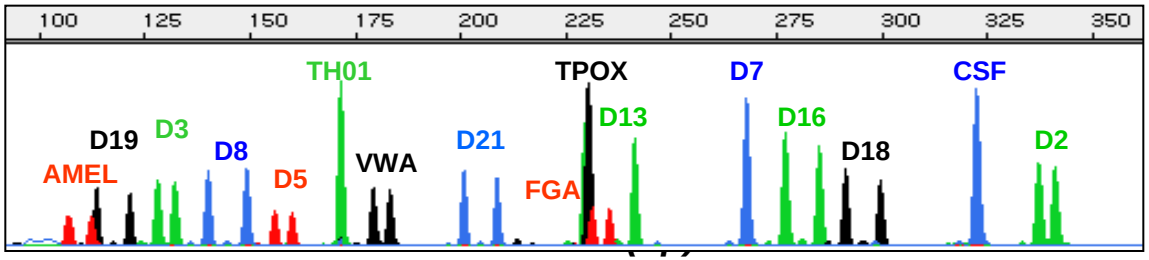
PATERNITY TESTING

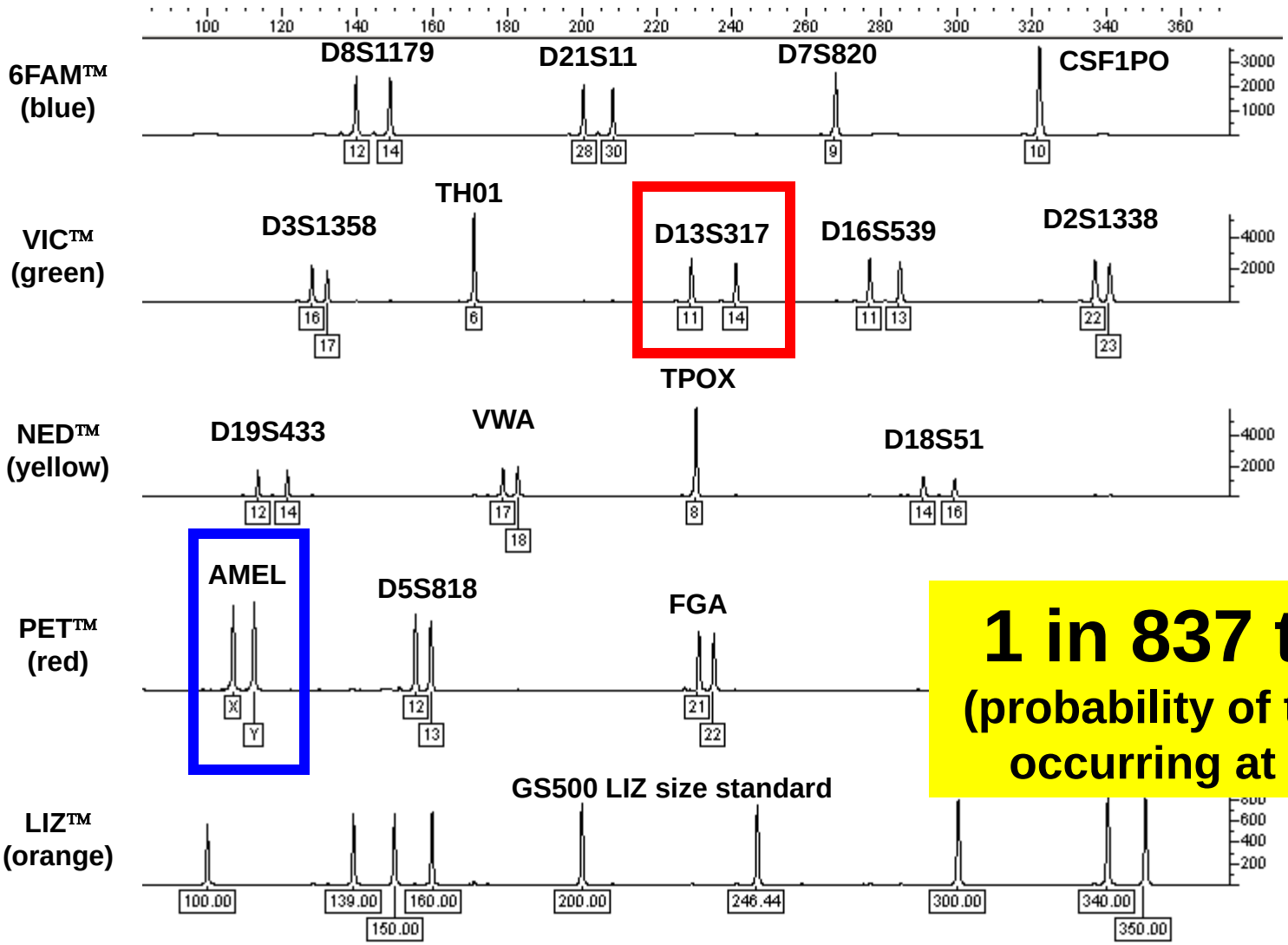


STR Alleles from D13S317

Alleged Father(s) is asked to donate DNA sample







1 in 837 trillion

(probability of this profile occurring at random)

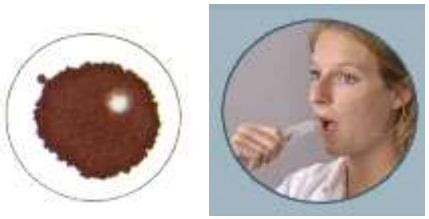
Lab Procedures

Steps in DNA Analysis

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

Steps Involved

- Collection
- Specimen Storage
- Extraction
- Quantitation
- Multiplex PCR
- STR Typing
- Interpretation of Results
- Database
  Storage & Searching
- Calculation of Match Probability

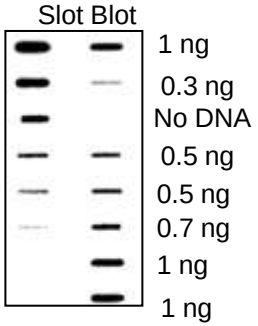


Blood Stain Buccal swab

Sample Collection & Storage

Biology

DNA Extraction



DNA Quantitation

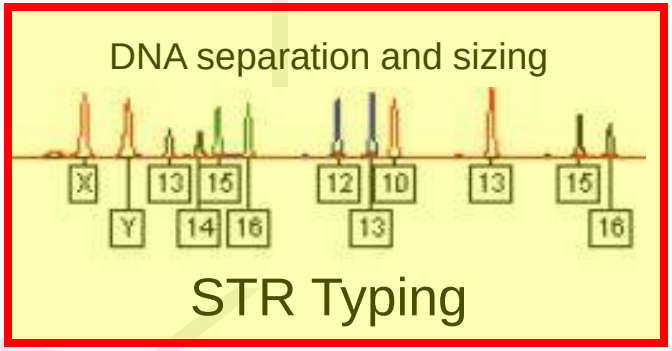
Multiplex PCR Amplification

Genetics

If a match occurs, comparison of DNA profile to population allele frequencies to generate a case report with probability of a random match to an unrelated individual

DNA Database Search

Technology



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

Interpretation of Results

Crime Scene Collection of Evidence

http://projects.nfstc.org/gallery/main.php?g2_itemId=626

- Police officers and crime scene investigators respond to the scene of a crime to collect biological evidence to be used in forensic DNA testing

- Investigators must be careful not to contaminate the evidence with their own DNA

DNA Evidence Received in the Lab

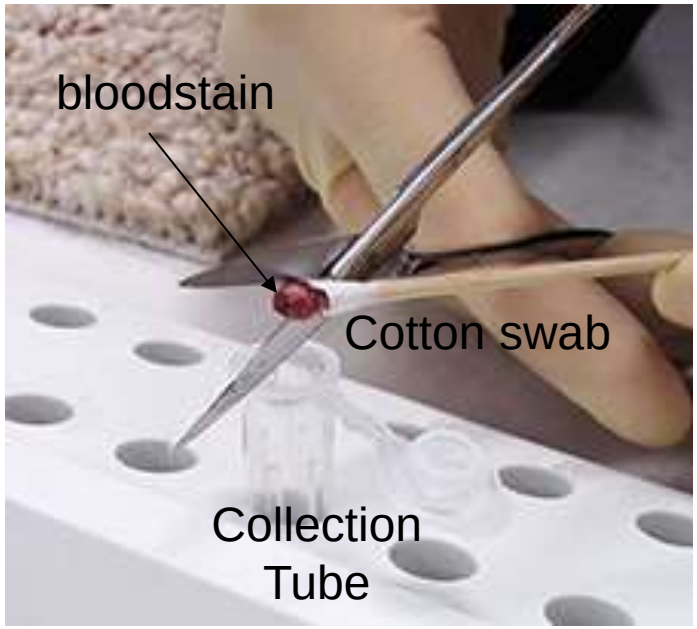
http://projects.nfstc.org/gallery/main.php?g2_itemId=789

http://projects.nfstc.org/gallery/main.php?g2_itemId=749

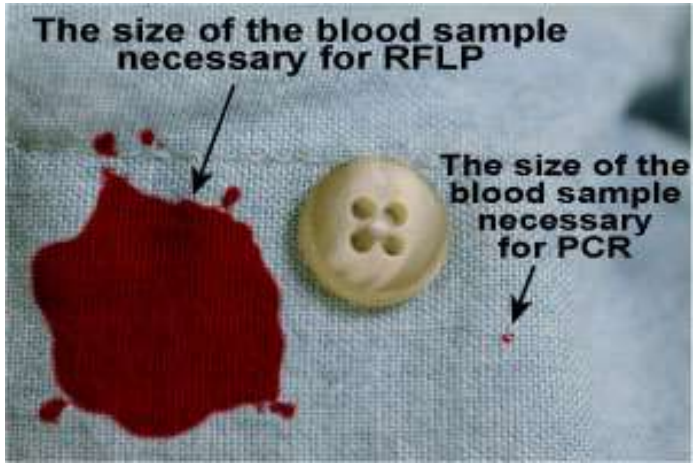
- Evidentiary samples (commonly in the form of cotton swabs) are brought or shipped to the DNA laboratory after collection from the crime scene or victim

- Sexual assault evidence collection kits provide swabs and bags for clothing collections from the victim

DNA Collection



http://projects.nfstc.org/gallery/main.php?g2_itemId=653

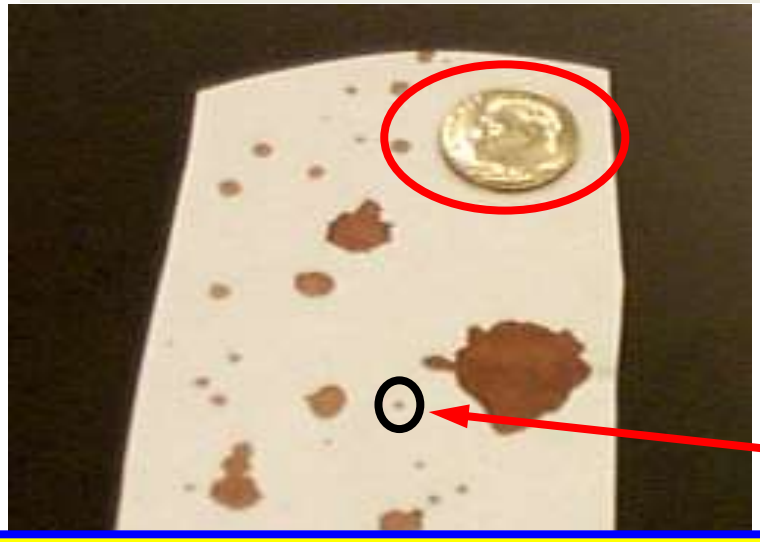


http://projects.nfstc.org/gallery/main.php?g2_itemId=668

- Cotton swabs are commonly used to collect biological material from bloodstains or semen from sexual assault victims
- The amount of DNA needed has decreased dramatically in the past decade due to sensitivity of the PCR process (which makes millions of copies of targeted regions)

Sources of Biological Evidence

- **Blood**
- **Semen**
- **Saliva**
- **Urine**
- **Hair**
- **Teeth**
- **Bone**
- **Tissue**



Blood Sample

Only a very small amount of blood is needed to obtain a DNA profile

best results with >100 cells, but DNA profiles can be recovered from as little as a single cell

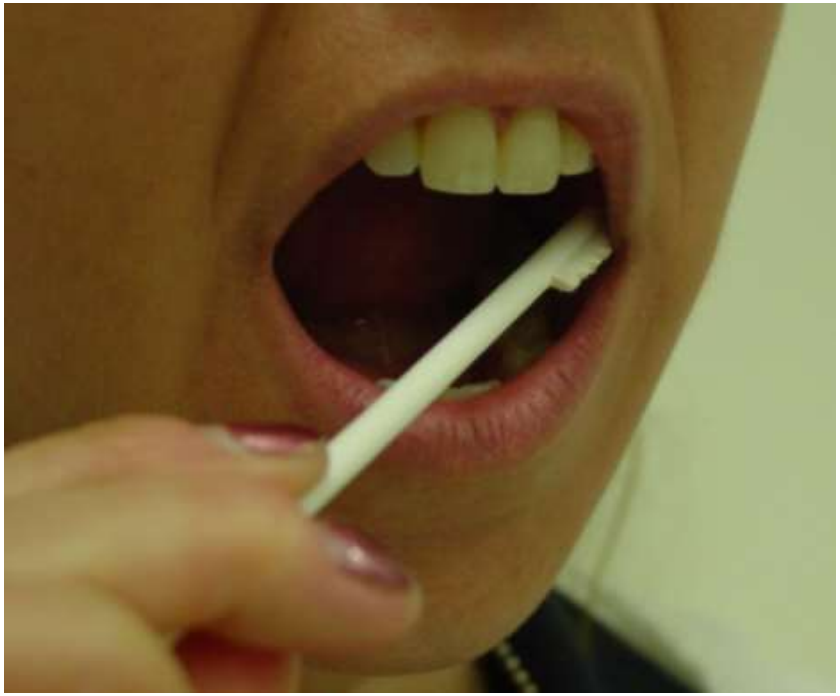
DNA Reference Sample from Suspect

http://projects.nfstc.org/gallery/main.php?g2_itemId=658

http://shop.armorforensics.com/mm5/graphics/00000002/products/4-4980b_sml.jpg

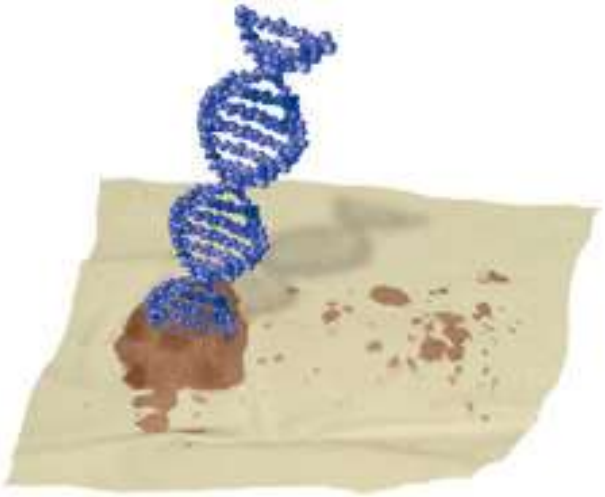
- Blood samples may be collected but require a phlebotomist to draw blood
- Easier to collect a buccal swab from the inside of an individual's mouth, which scrapes off some cheek cells

Buccal Swab DNA Collection



- The inside of the check is scrubbed to collect cells
- Less invasive than drawing blood
- Swab must be dried before storing and shipping to lab to avoid mold and bacterial growth

DNA Extraction



http://projects.nfstc.org/gallery/main.php?g2_itemId=675

- DNA is extracted from proteins that protect it in the nucleus of a cell
- Chemicals are added to digest the protecting proteins and produce “naked” DNA molecules
- The final solution looks like a tube of water

DNA Quantitation

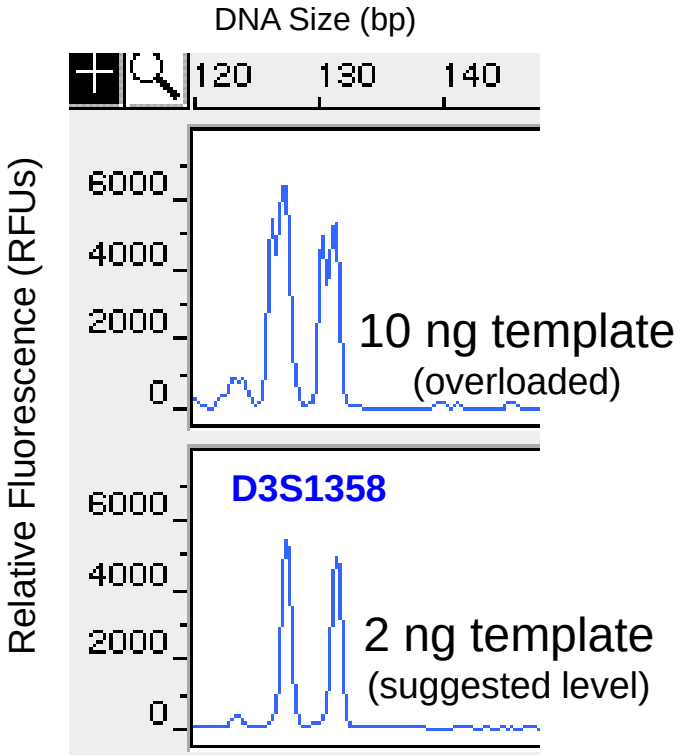
ABI 7500: an instrument used to perform “real-time quantitative PCR”

- DNA quantitation is important to determine how much human DNA (as opposed to bacterial DNA) is present in a sample
- A commonly used DNA quantitation kit is called Quantifiler (sold by Applied Biosystems)

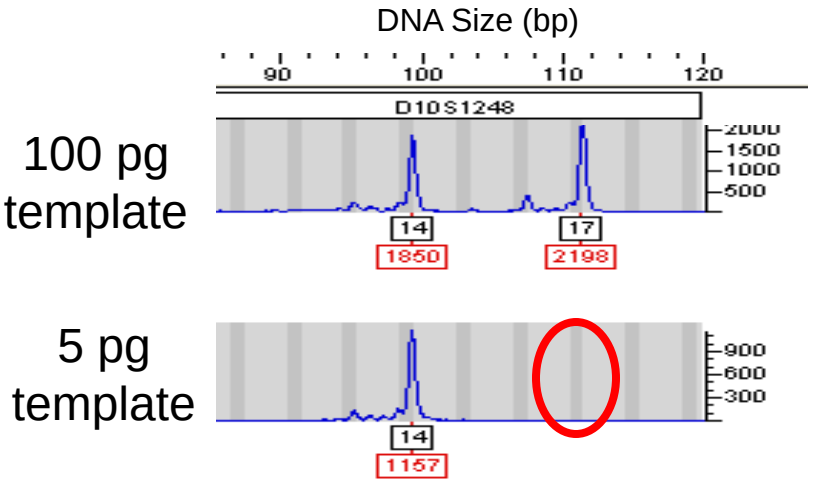
Impact of DNA Amount into PCR

Reason that DNA Quantitation is Important Prior to Multiplex Amplification

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



- Too little DNA
  - Heterozygote peak imbalance
  - Allele drop-out
  - Locus-to-locus imbalance

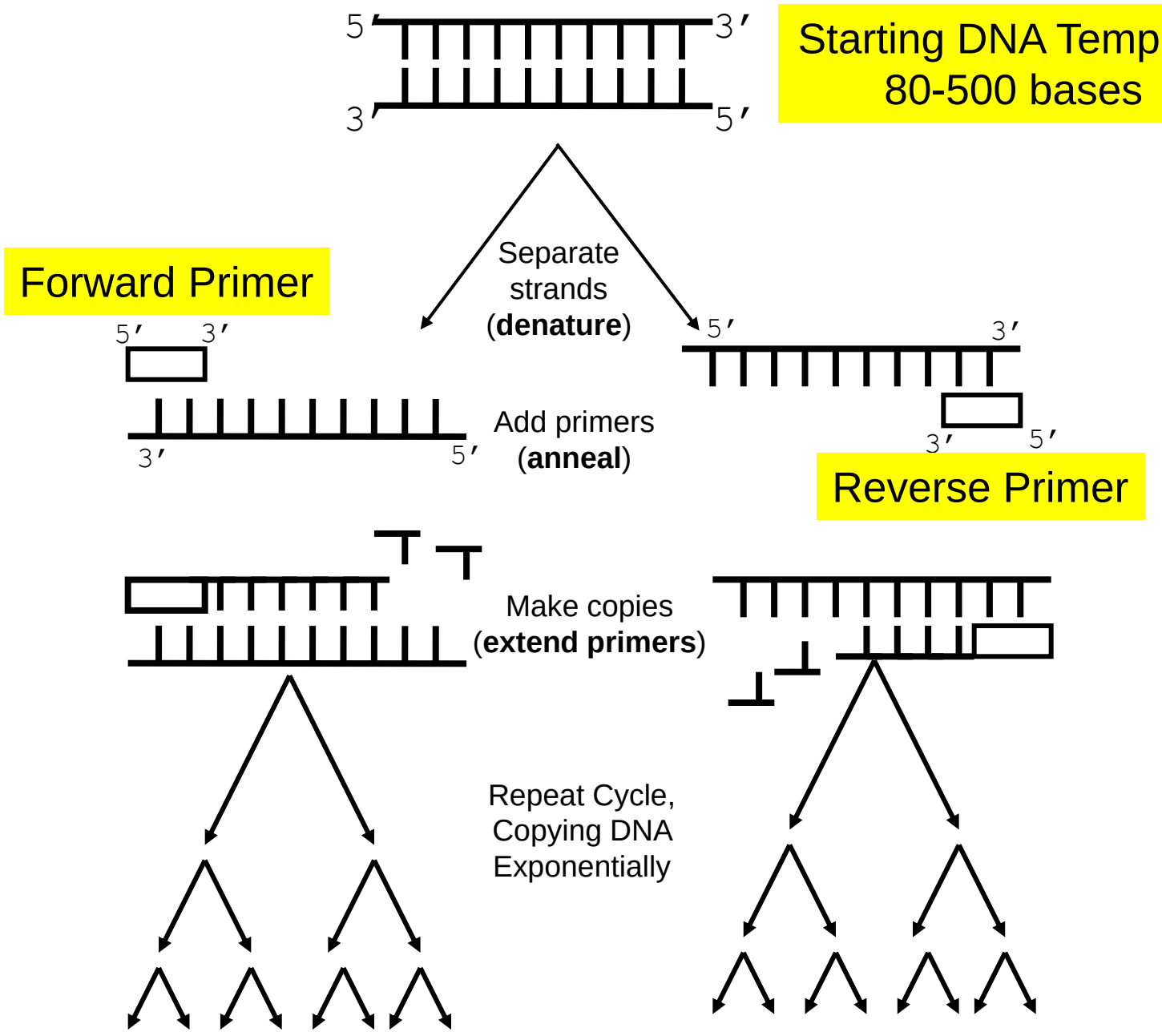


Stochastic effect when amplifying low levels of DNA produces allele dropout

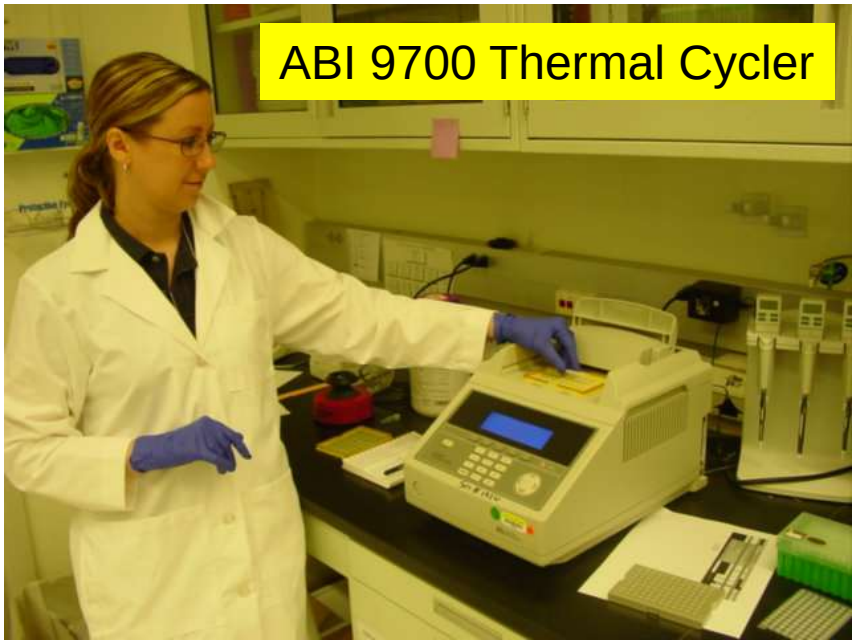
PCR Amplification

- PCR = polymerase chain reaction
- Process that copies a particular region of DNA using two “primers” (short pieces of DNA)
- Each strand of DNA is used as a template to create a replicate that permits a doubling of the number of target molecules with each cycle of heating and cooling

PCR Process


5′
3′
3′
5′
Starting DNA Template
80-500 bases
Separate
strands
(**denature**)
Forward Primer
5′
3′
3′
5′
Add primers
(**anneal**)
5′
3′
3′
5′
Reverse Primer
Make copies
(**extend primers**)
Repeat Cycle,
Copying DNA
Exponentially

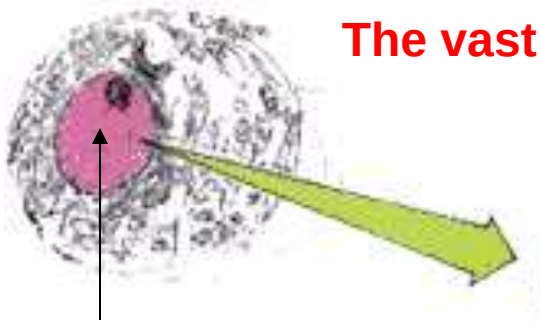
PCR Amplification (Thermal Cycling)



- The polymerase chain reaction (PCR) copies sections of DNA through heating and cooling the sample
- Each DNA strand is copied with each temperature cycle
- A thermal cycler heats and cools DNA samples (usually 28 cycles)

DNA in the Cell

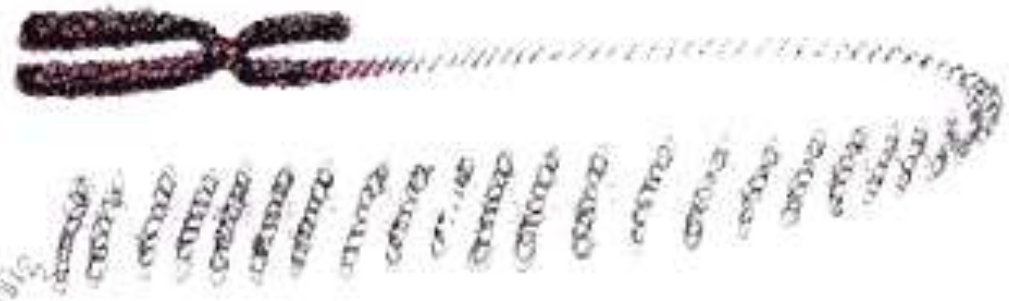
The vast majority of DNA is the same from person to person



cell nucleus

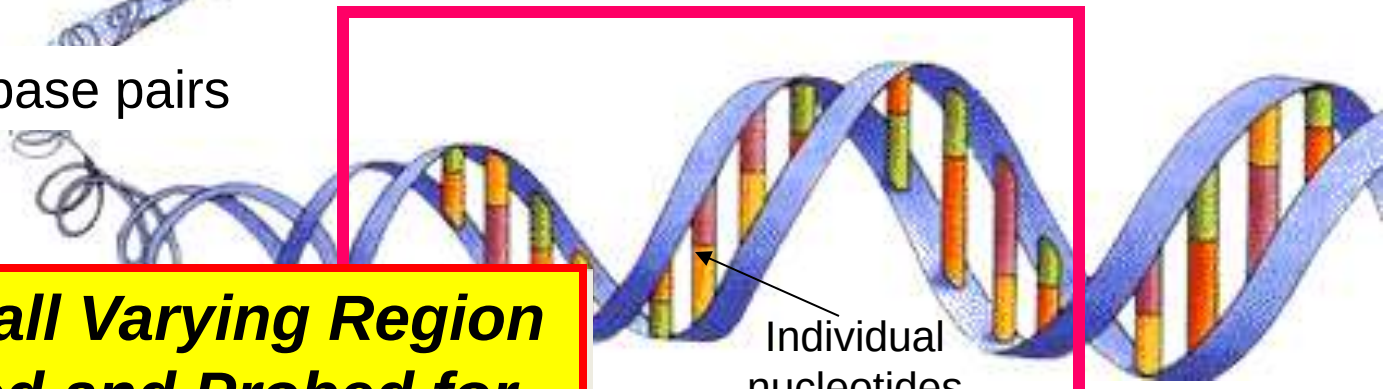
chromosome

22 pairs + XX or XY



Double stranded
DNA molecule

~3 billion total base pairs

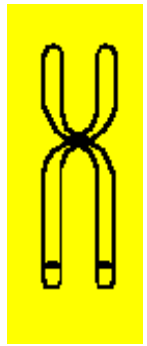


Only a Small Varying Region is Targeted and Probed for Each DNA Marker Examined

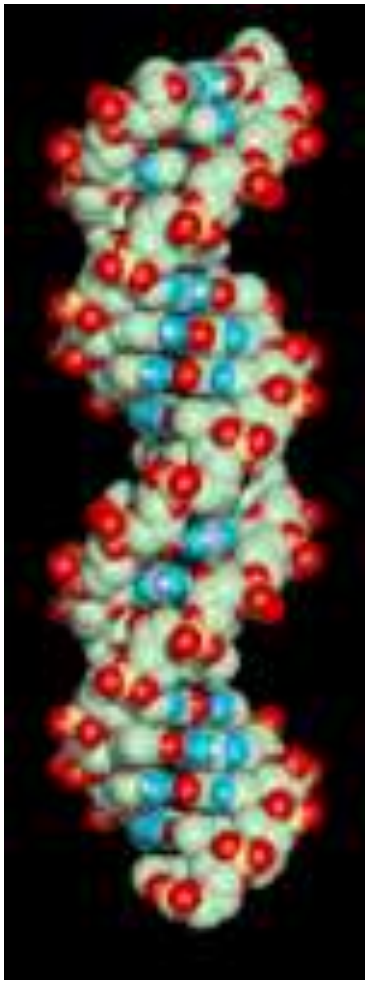
Identification of Information

Printed Information	Genetic Information
Library	**Body**
Book	**Cell**
Chapter	**Nucleus**
Page Number	**Chromosome**
Line on Page	**Locus (part of chromosome)**
Word	**Short DNA sequence**
Letter	**DNA nucleotides**

D13S317

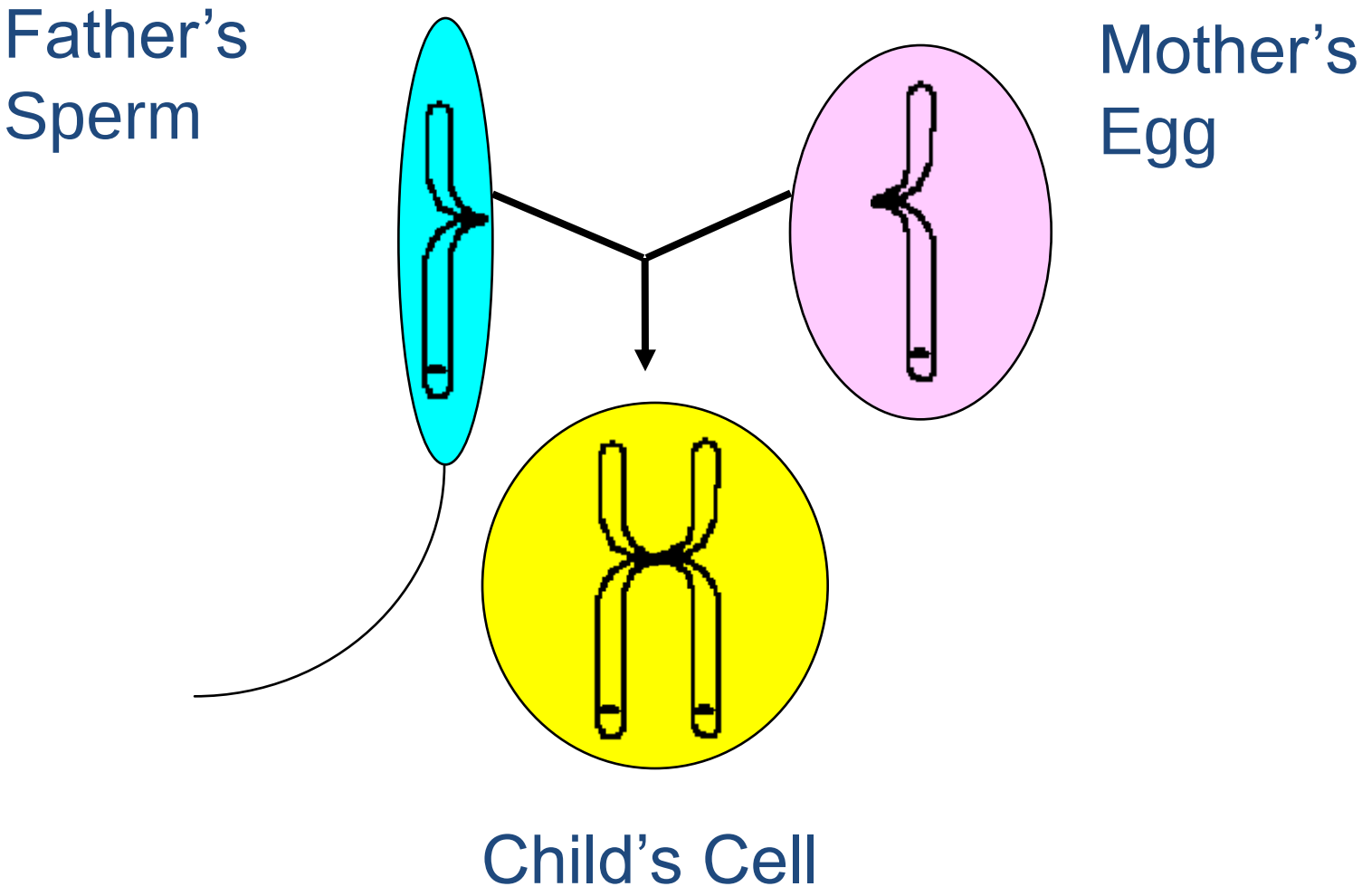


Characteristics of DNA

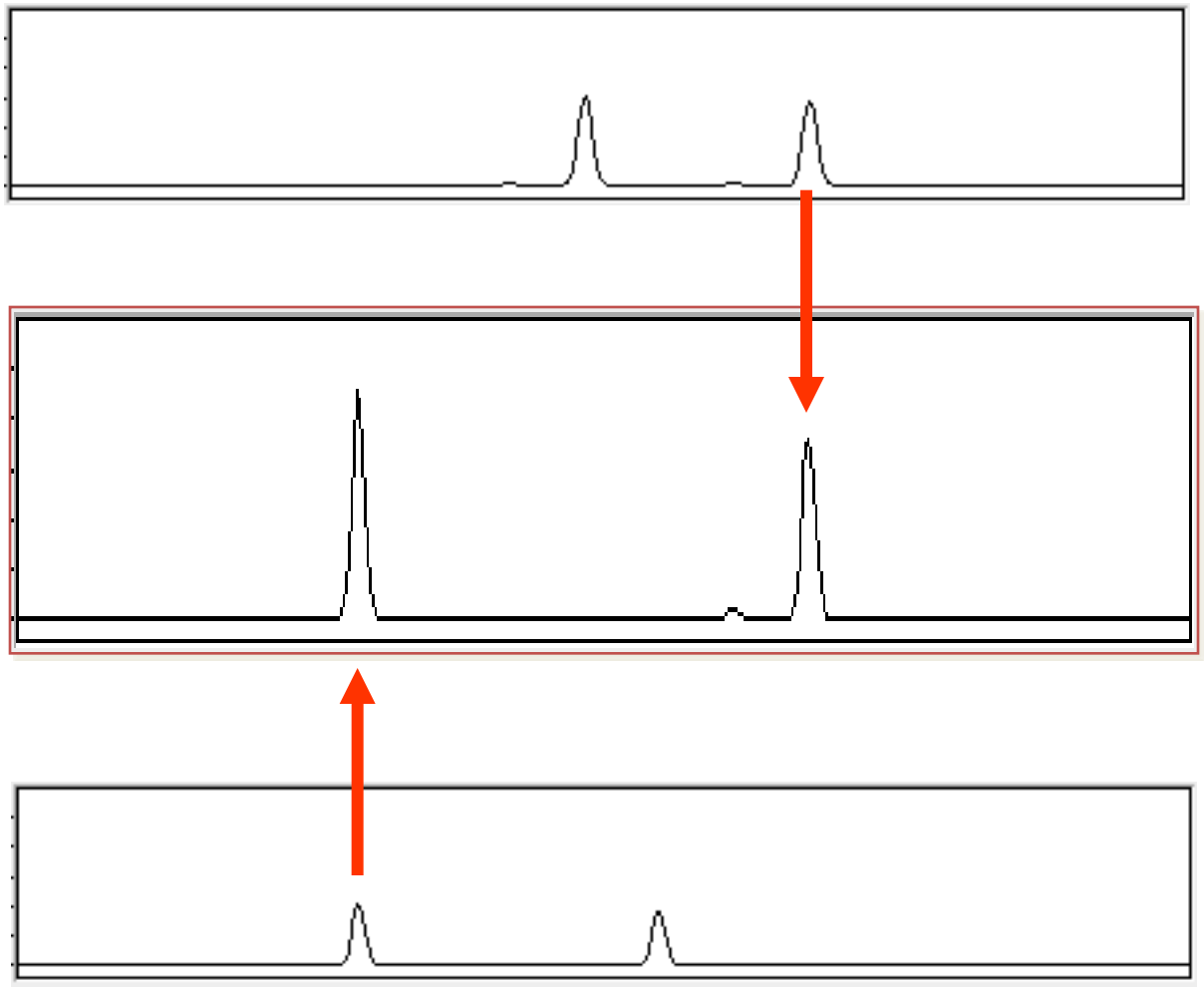


- Each person has a unique DNA profile (except identical twins).
- Each person's DNA is the same in every cell.
- An individual’s DNA profile remains the same throughout life.
- Half of your DNA comes from your mother and half from your father.

Our DNA Comes from our Parents



Inheritance Pattern of DNA Profiles



DAD

CHILD

MOM

Basis of DNA Profiling

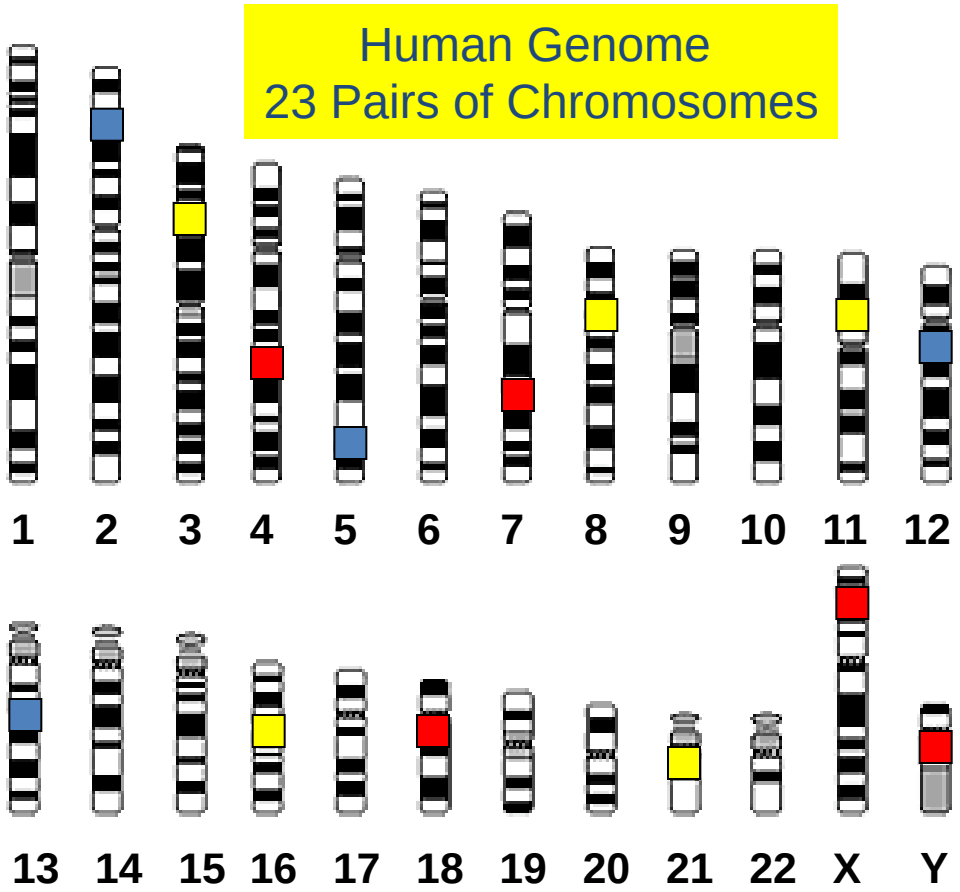
The genome of **each individual is unique** (with the exception of identical twins) and **is inherited from parents**

Probe subsets of genetic variation in order to differentiate between individuals (statistical probabilities of a random match are used)

DNA typing must be **performed efficiently and reproducibly** (information must hold up in court)

Current standard DNA tests **DO NOT look at genes** – little/no information about race, predisposal to disease, or phenotypical information (eye color, height, hair color) is obtained

What is a DNA Profile?



Nuclear DNA

3.2 billion bp

Unique regions of the human genome are targeted

These regions consist of a few hundred base pairs

The regions are copied by the polymerase chain reaction (PCR) – **billions of exact copies**

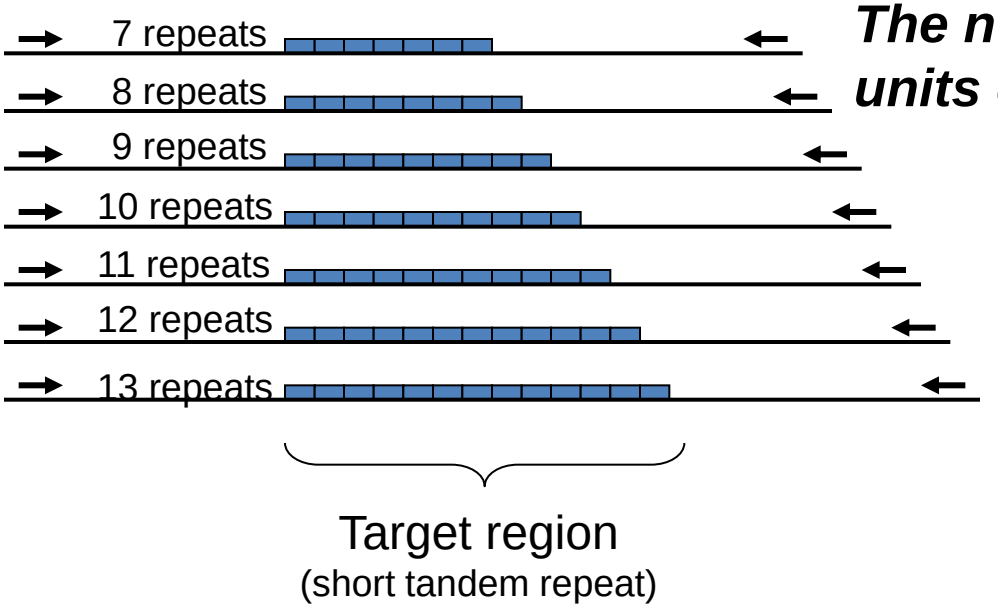
The copied fragments now contain fluorescent dyes for detection

Short Tandem Repeat (STR) Markers

An accordion-like DNA sequence that occurs between genes

TCCCAAGCTCTTCCTCTTCCCTAGATCAATACAGACAGAAGACA
GGTG**GATAGATAGATAGATAGATAGATAGATAGATAGATAGATA**
GATATCATTGAAAGACAAAACAGAGATGGATGATAGATACATGCT
TACAGATGCACAC

= 11 GATA repeats (“11” is all that is reported)

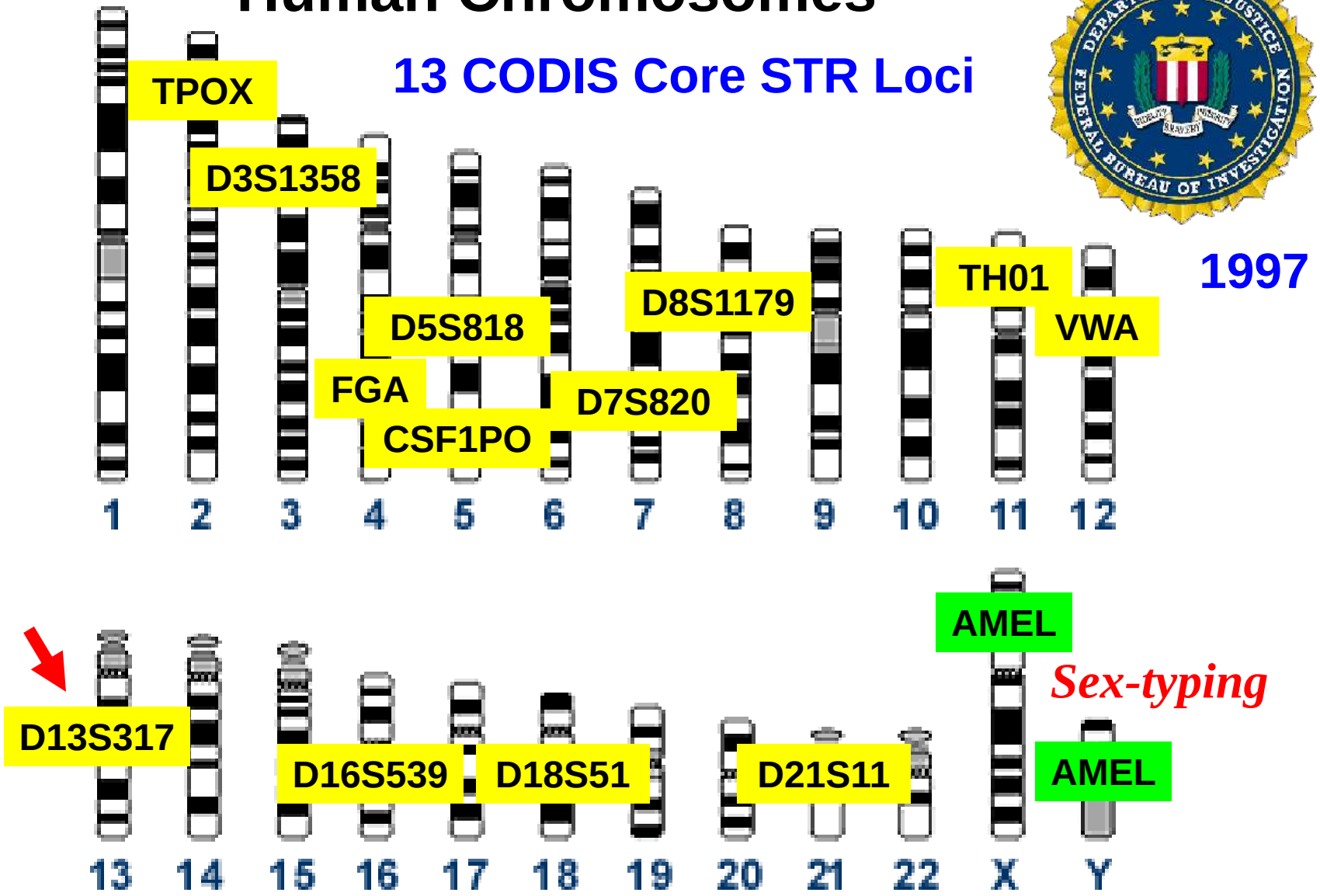


The number of consecutive repeat units can vary between people

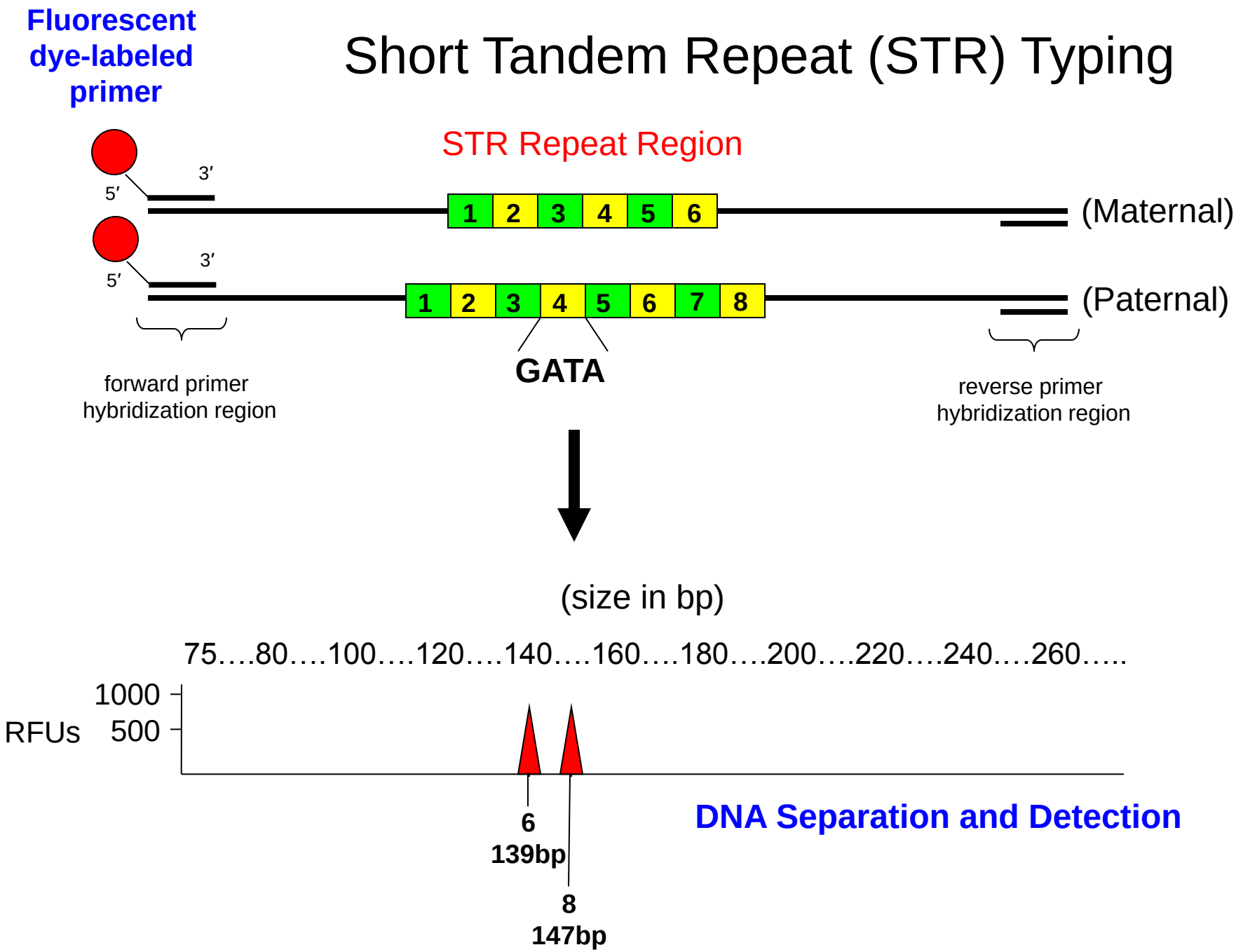
The FBI has selected **13 core STR loci** that must be run in all DNA tests in order to provide a common currency with DNA profiles

Position of Forensic STR Markers on Human Chromosomes

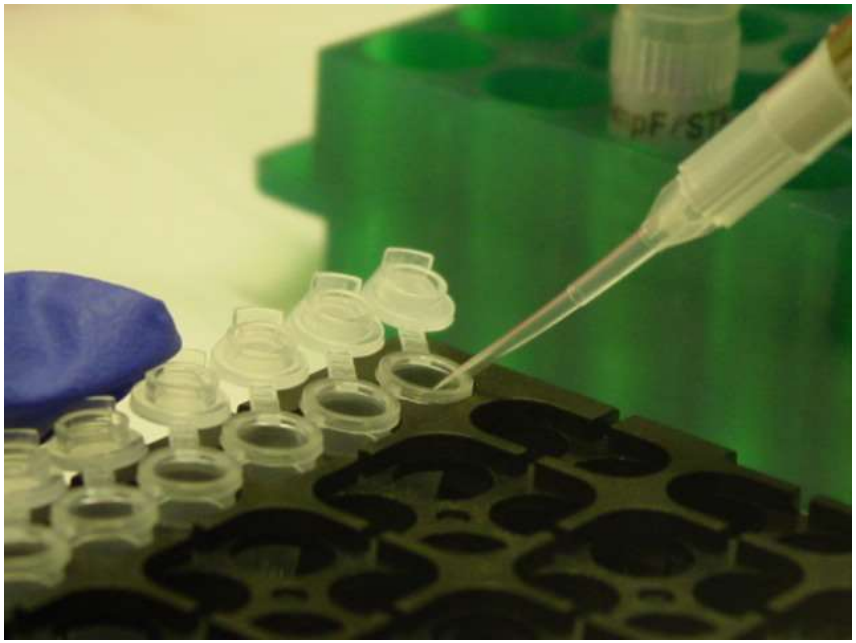
Core STR Loci for the United States



Short Tandem Repeat (STR) Typing



DNA Reaction Setup



Strip of 8 tubes containing **~25 µL** of solution

- DNA sample is added (about 1 ng based on DNA quantitation performed) – **10 µL**
- PCR primers and other reaction chemicals from an STR typing kit are added – **15 µL**

STR Typing Kit

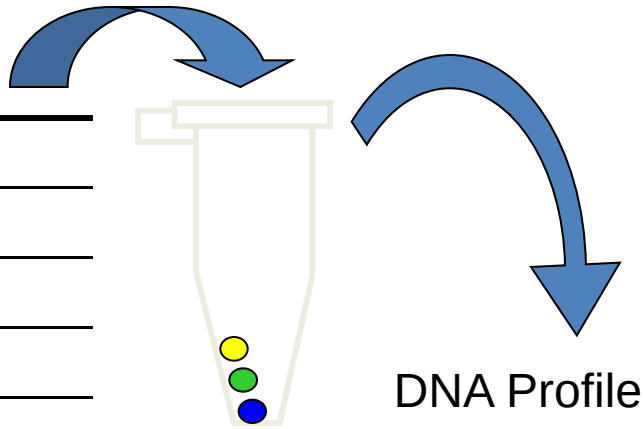
- Kit Components:
  - Primer mix
  - PCR Reaction Buffer and Building Blocks
  - DNA Polymerase (Taq Gold)
- Most expensive reagent
- Common kits used:
  - Identifiler (Applied Biosystems)
  - Profiler Plus/COfiler (Applied Biosystems)
  - PowerPlex 16 (Promega)

What is in an STR Typing Kit?

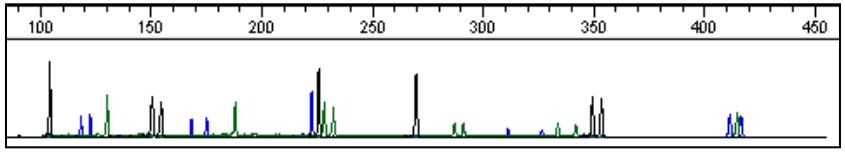
- Primer mix
  - containing fluorescently labeled oligonucleotides used to target specific regions of the human genome
  - Applied Biosystems has not published their primer sequences
  - PowerPlex 16, which amplifies 16 genomic sites, contains 32 PCR primers

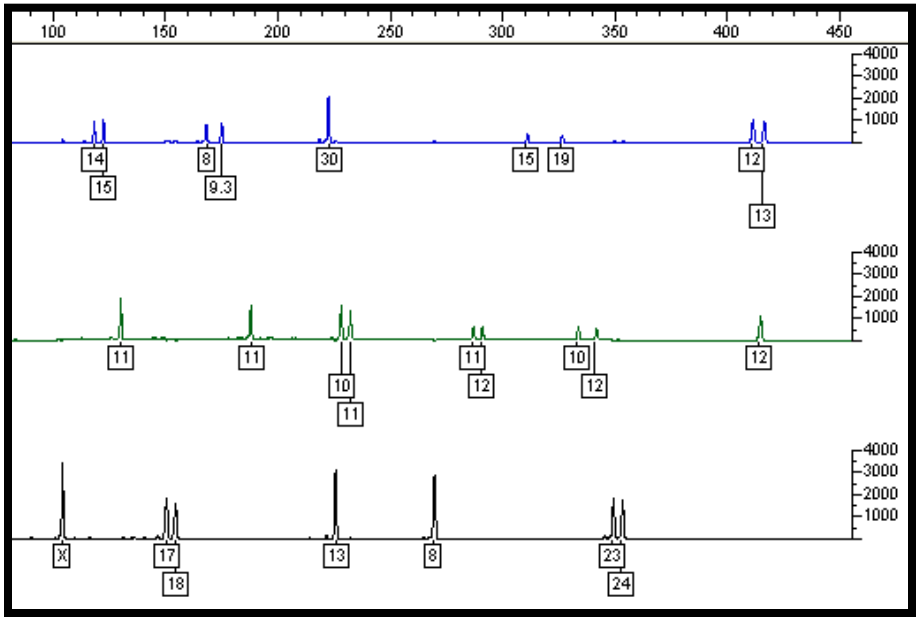
PCR Primers in an STR Kit

Locus	Dye	Promega PP16 Primer Sequences
D3S1358-F		ACTGCAGTCCAATCTGGGT
D3S1358-R	FL	ATGAAATCAACAGAGGCTTGC
TH01-F	FL	GTGATTCCCATTGGCCTGTTC
TH01-R		ATTCCTGTGGGCTGAAAAGCTC
D21S11-F		ATATGTGAGTCAATTCCCCAAG
D21S11-R	FL	TGTATTAGTCAATGTTCTCCAGAGAC
D18S51-F	FL	TTCTTGAGCCCAGAAGGTTA
D18S51-R		ATTCTACCAGCAACAACACAAATAAAC
PentaE-F		ATTACCAACATGAAAGGGTACCAATA
PentaE-R	FL	TGGGTTATTAATTGAGAAAACTCCTTACAATTT
D5S818-F		GGTGATTTTCCTCTTTGGTATCC
D5S818-R	JOE	AGCCACAGTTTACAACATTTGTATCT
D13S317-F		ATTACAGAAGTCTGGGATGTGGAGGA
D13S317-R	JOE	GGCAGCCCAAAAAGACAGA
D7S820-F	JOE	ATGTTGGTCAGGCTGACTATG
D7S820-R		GATTCCACATTTATCCTCATTGAC
D16S539-F		GGGGGTCTAAGAGCTTGTAAAAAG
D16S539-R	JOE	GTTTGTGTGTGCATCTGTAAGCATGTATC
CSF1PO-F	JOE	CCGGAGGTAAAGGTGTCTTAAAGT
CSF1PO-R		ATTTCCTGTGTCAGACCCTGTT
PentaD-F	JOE	GAAGGTCGAAGCTGAAGTG
PentaD-R		ATTAGAATTCTTTAATCTGGACACAAG
AMEL-F	TMR	CCCTGGGCTCTGTAAAGAA
AMEL-R		ATCAGAGCTTAAACTGGGAAGCTG
vWA-F		GCCCTAGTGGATGATAAGAATAATCAGTATGTG
vWA-R	TMR	GGACAGATGATAAATACATAGGATGGATGG
D8S1179-F	TMR	ATTGCAACTTATATGTATTTTTGTATTTCATG
D8S1179-R		ACCAAATTGTGTTCATGAGTATAGTTTC
TPOX-F		GCACAGAACAGGCACTTAGG
TPOX-R	TMR	CGCTCAAACGTGAGGTTG
FGA-F	TMR	GGCTGCAGGGCATAACATTA
FGA-R		ATTCTATGACTTTGCGCTTCAGGA

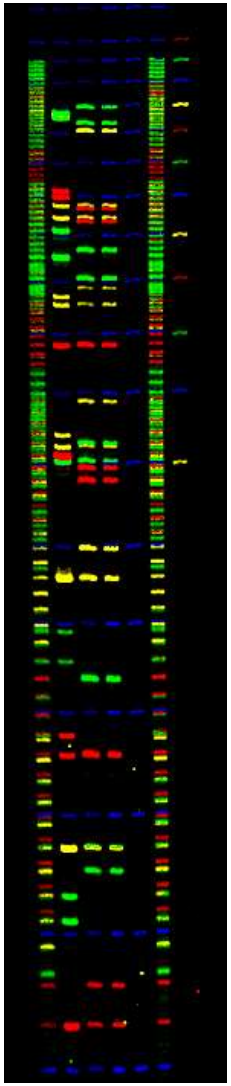


DNA Profile

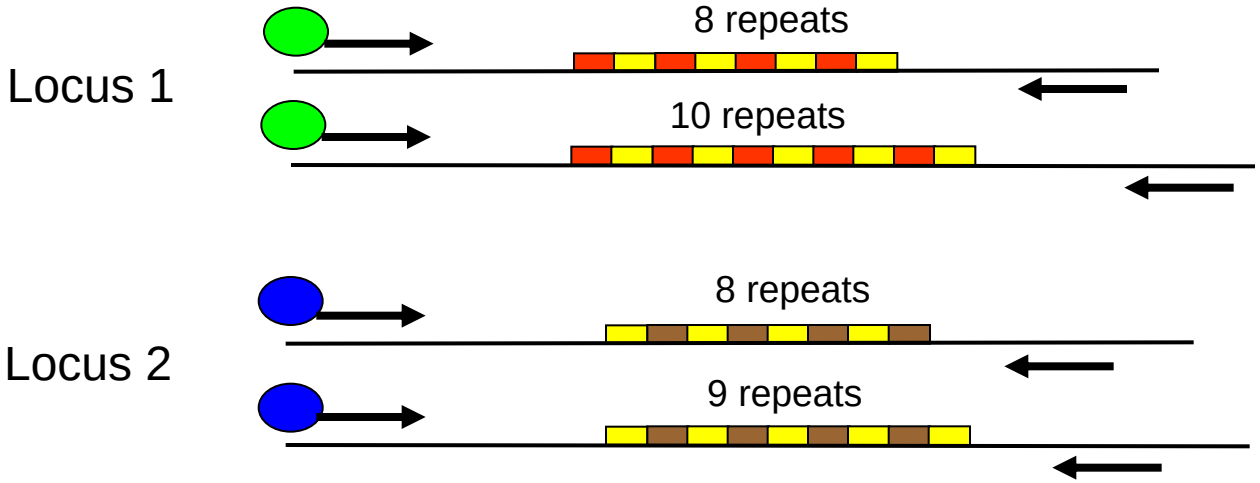


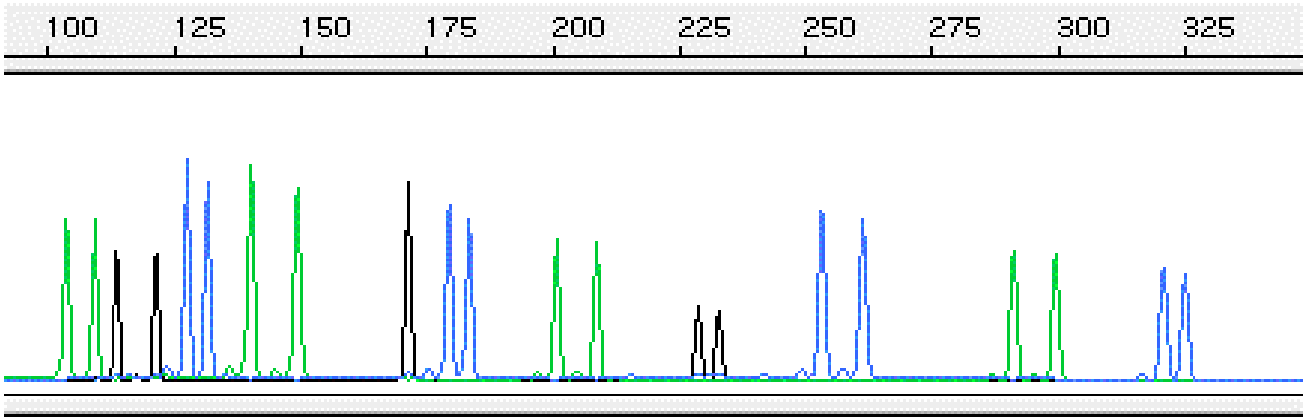


The polymerase chain reaction (PCR) is used to amplify STR regions and label the amplicons with fluorescent dyes using locus-specific primers



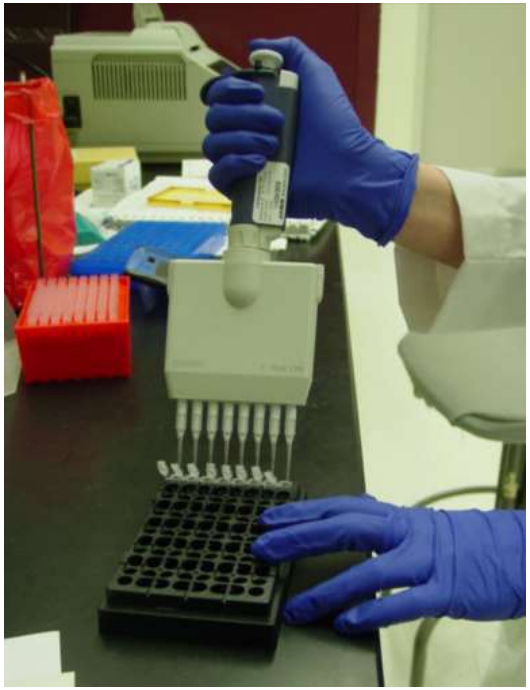
Scanned Gel Image





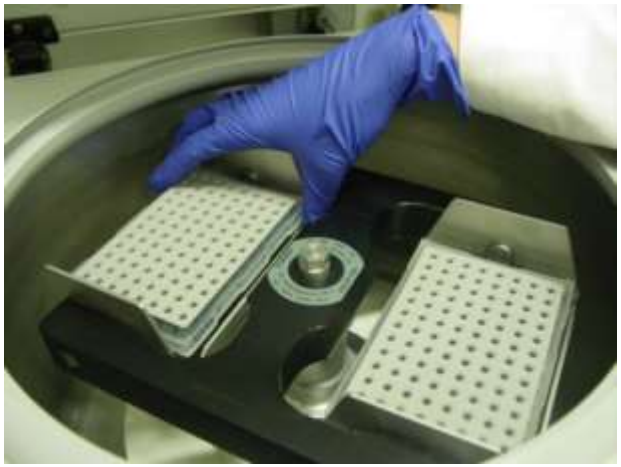
Capillary Electropherogram

Transfer of DNA Samples



- Following PCR, a small portion of the sample is transferred for analysis
- This aliquot of the sample is mixed with a molecular size marker (termed an internal size standard) that permits calibration of sizing measurements

Sample Plates Spun Down via a Centrifuge

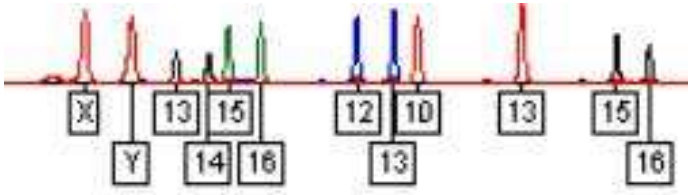


- Sample plates are spun to remove bubbles that would interfere with the injection (loading) process onto the capillary electrophoresis instrument

ABI 3130xl DNA Analysis Instrument

- Import sample names
- Determine run conditions (voltages and times to be used based on laboratory protocols)

Data Collection on ABI 3130xl Instrument

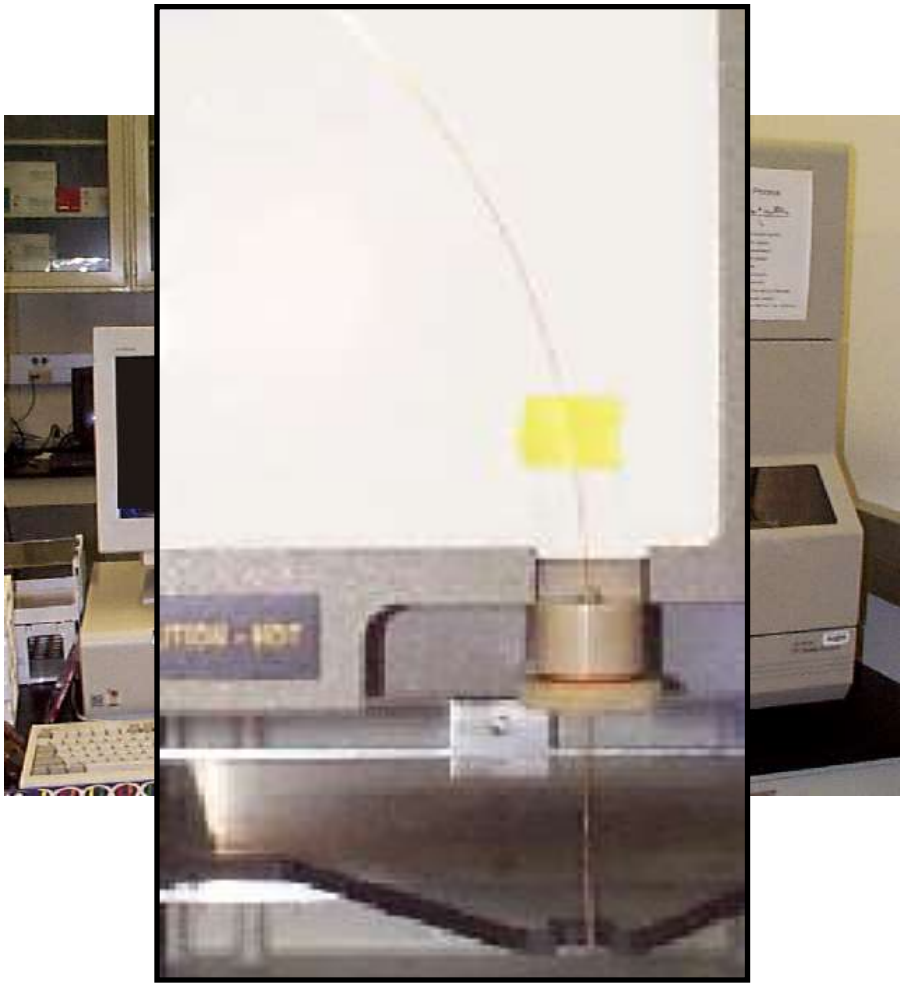


DNA Profile

- Data analysis is performed on an Applied Biosystems (ABI) 3130xl capillary electrophoresis instrument

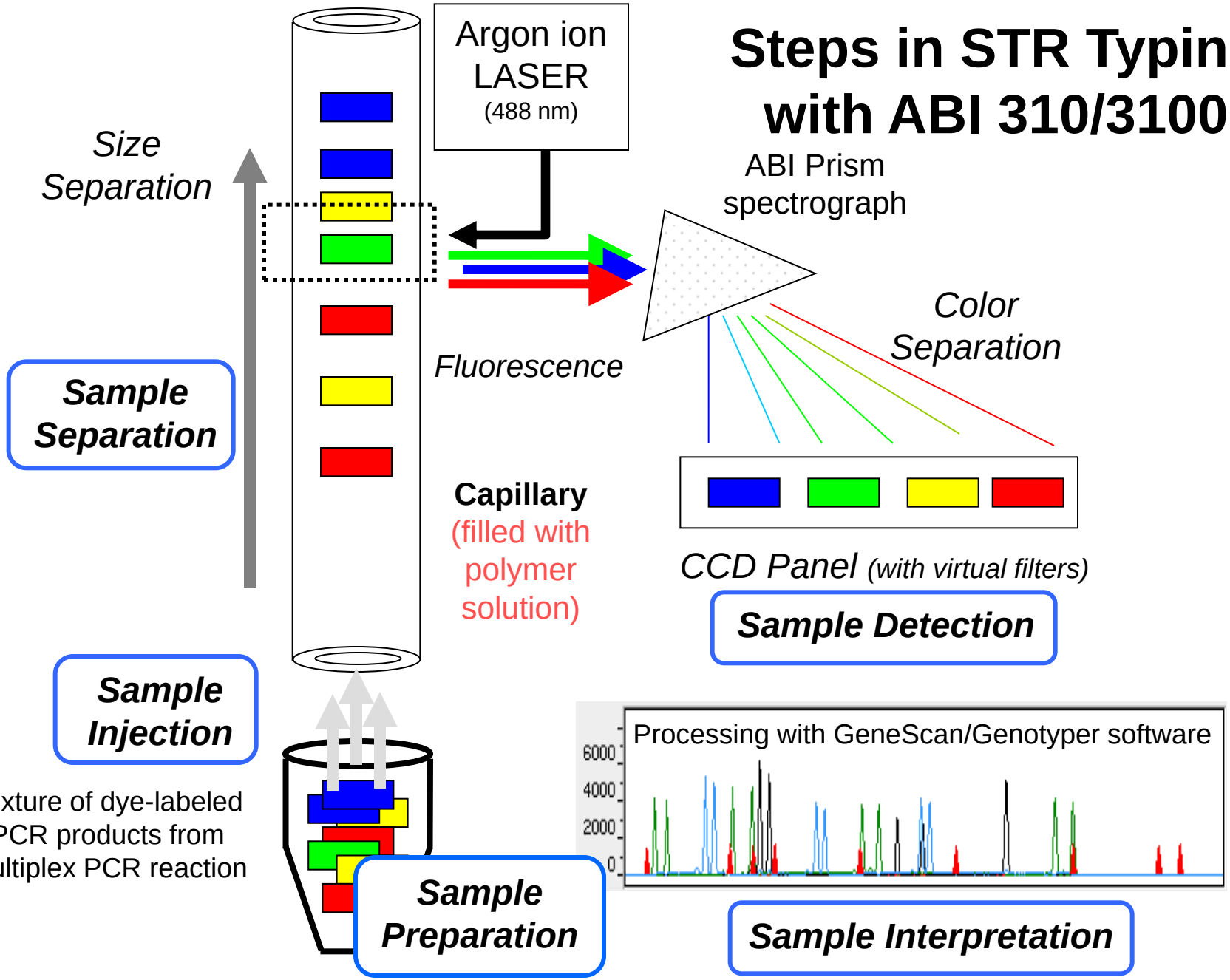
Capillary Electrophoresis Instrumentation

ABI 310
single capillary

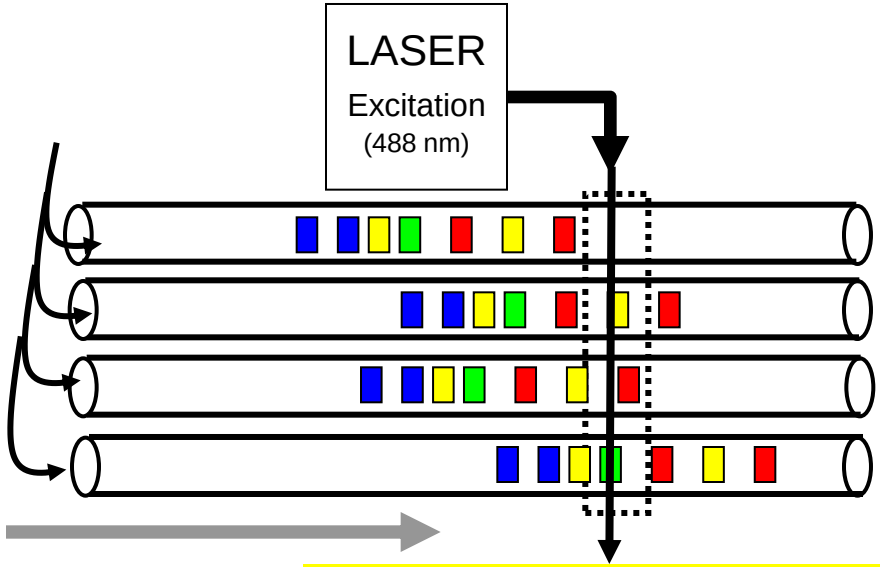


ABI 3100
16-capillary array

Steps in STR Typing with ABI 310/3100



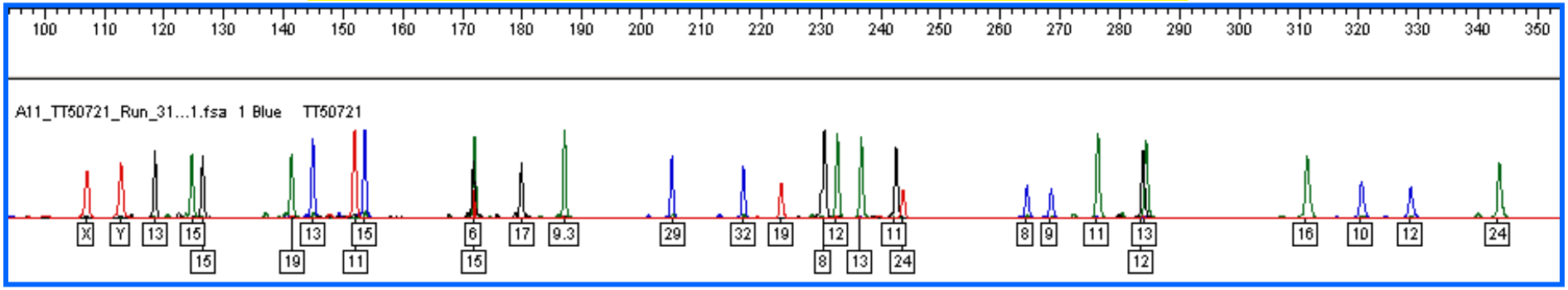
A DNA Profile is Produced by Separating DNA Molecules by Size and Dye Color



The labeled fragments are separated (based on size) and detected on a gel or capillary electrophoresis instrument

~2 hours or less

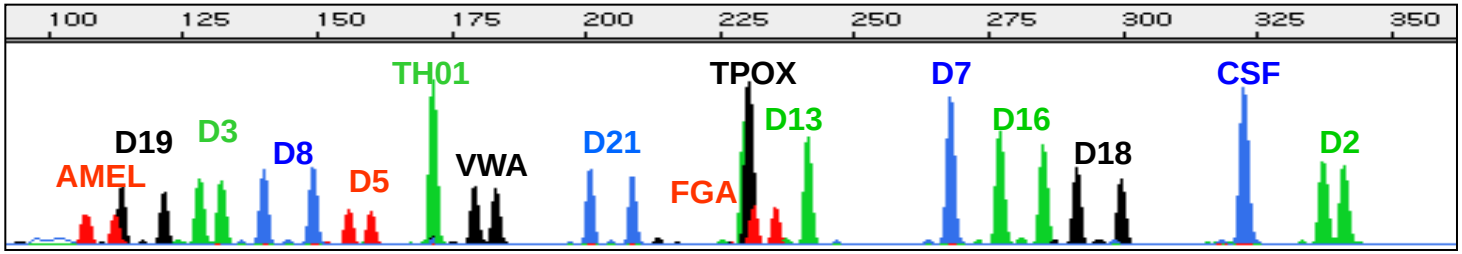
Fragment size ranges from 100 - 350 base pairs



Peaks represent labeled DNA fragments separated by electrophoresis
This ‘profile of peaks’ is unique for an individual – a DNA type

DNA Profile Frequency with all 13 CODIS STR loci

AmpFlSTR® Identifiler™ (Applied Biosystems)



What would be entered into a DNA database for searching:

16,17-
17,18-
21,22-
12,14-
28,30-
14,16-
12,13-
11,14-
9,9-
9,11-
6,6-
8,8-
10,10

Locus	allele	value	allele	value	1 in	Combined
D3S1358	**16**	*0.2533*	**17**	*0.2152*	**9.17**	**9.17**
VWA	**17**	*0.2815*	**18**	*0.2003*	**8.87**	**81**
FGA	**21**	*0.1854*	**22**	*0.2185*	**12.35**	**1005**
D8S1179	**12**	*0.1854*	**14**	*0.1656*	**16.29**	**16,364**
D21S11	**28**	*0.1589*	**30**	*0.2782*	**11.31**	**185,073**
D18S51	**14**	*0.1374*	**16**	*0.1391*	**26.18**	**4,845,217**
D5S818	**12**	*0.3841*	**13**	*0.1407*	**9.25**	**44,818,259**
D13S317	**11**	*0.3394*	**14**	*0.0480*	**30.69**	**1.38 x 10^{9}**
D7S820	**9**	*0.1772*			**31.85**	**4.38 x 10^{10}**
D16S539	**9**	*0.1126*	**11**	*0.3212*	**13.8**	**6.05 x 10^{11}**
THO1	**6**	*0.2318*			**18.62**	**1.13 x 10^{13}**
TPOX	**8**	*0.5348*			**3.50**	**3.94 x 10^{13}**
CSF1PO	**10**	*0.2169*			**21.28**	**8.37 x 10^{14}**

PRODUCT RULE

The Random Match Probability for this profile in the U.S. Caucasian population is **1 in 837 trillion (10^{12})**

The Same 13 Locus STR Profile in Different Populations

1 in 837 trillion

1 in 0.84 quadrillion (10^{15}) in U.S. Caucasian population (NIST)
1 in 2.46 quadrillion (10^{15}) in U.S. Caucasian population (FBI)*
1 in 1.86 quadrillion (10^{15}) in Canadian Caucasian population*

1 in 16.6 quadrillion (10^{15}) in African American population (NIST)
1 in 17.6 quadrillion (10^{15}) in African American population (FBI)*

1 in 18.0 quadrillion (10^{15}) in U.S. Hispanic population (NIST)

These values are **for unrelated individuals**
assuming no population substructure (using only p^2 and 2 pq)

NIST study: Butler, J.M., *et al*. (2003) Allele frequencies for 15 autosomal STR loci on U.S. Caucasian, African American, and Hispanic populations. *J. Forensic Sci*. 48(4):908-911. (http://www.cstl.nist.gov/biotech/strbase/NISTpop.htm)

*http://www.csfs.ca/pplus/profiler.htm

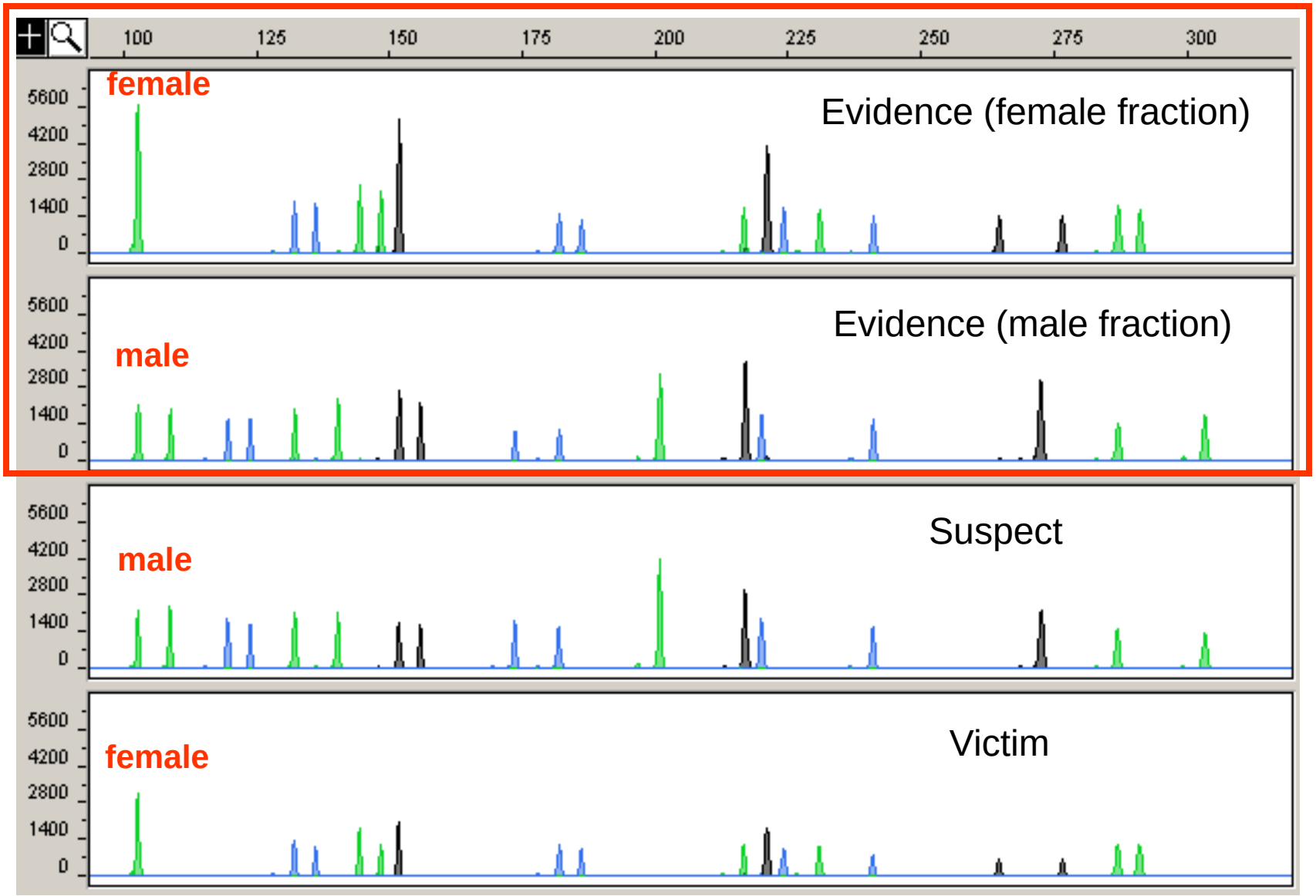
DNA Testing Requires a Reference Sample

A DNA profile by itself is fairly useless because it has no context…

DNA analysis for identity only works by comparison – **you need a reference sample**

Crime Scene Evidence compared to **Suspect(s)** (Forensic Case)
Child compared to **Alleged Father** (Paternity Case)
Victim's Remains compared to **Biological Relative** (Mass Disaster ID)
Soldier's Remains compared to **Direct Reference Sample** (Armed Forces ID)

Differential extraction used to separate sperm (male fraction) from vaginal epithelial cells (female fraction)



USACIL case 01-1738

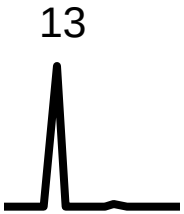
Four samples are typically associated with a sexual assault forensic DNA case…

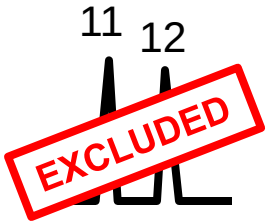
Three Possible Outcomes
of Evidence Examination

"Evidence"
Question (**Q**) Sample

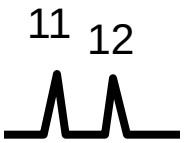
"Suspect"
Known (**K**) Sample

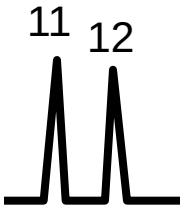
- **Exclusion** (no match)





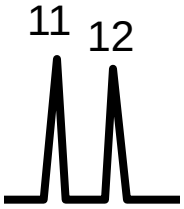
- **Inclusion** (match)





- **Inconclusive result**

No result
(or a complex mixture)



Unable to make Q → K comparison

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

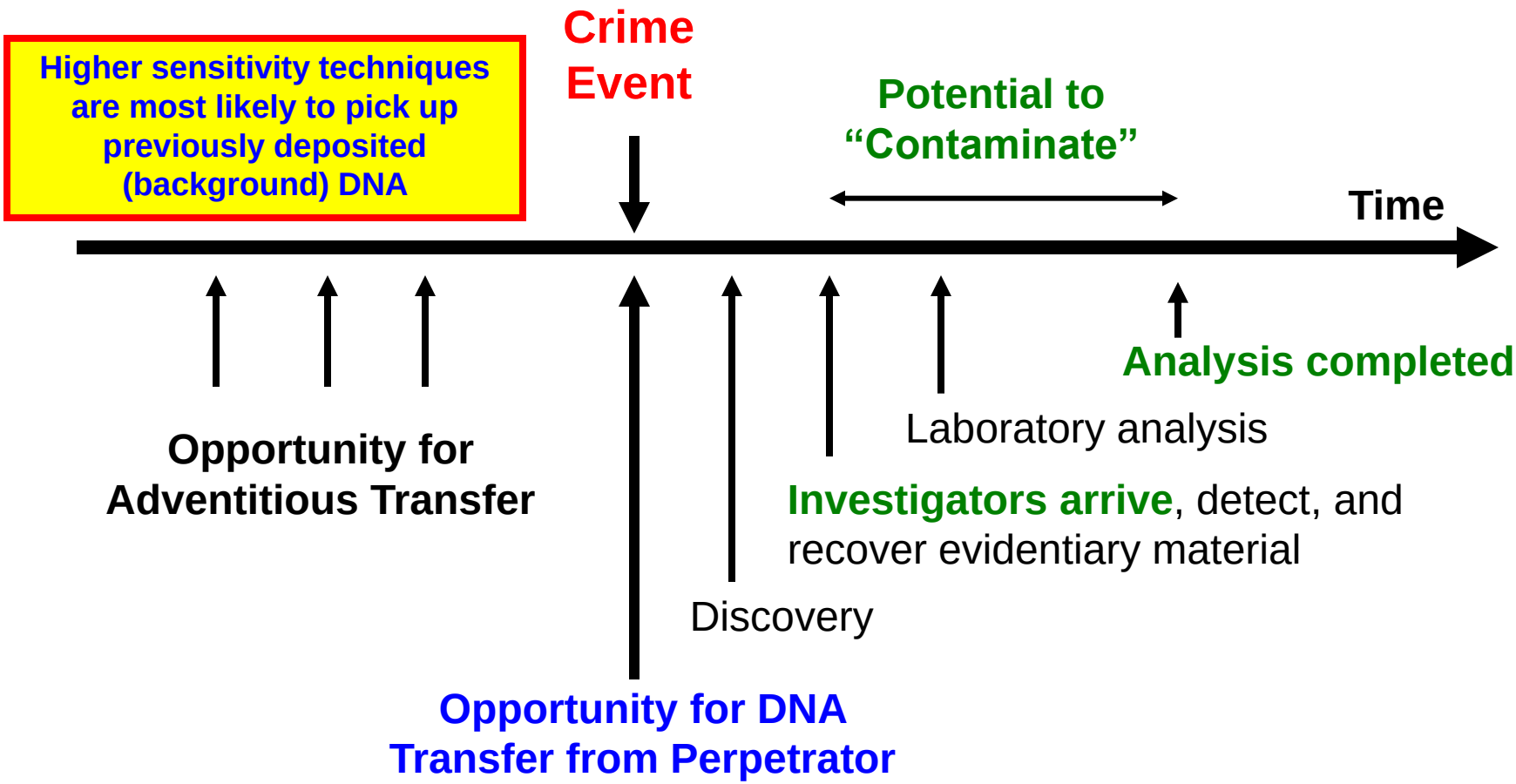
RapidHIT 200 developed by **IntegenX**

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

Time Line Showing the Potential for DNA Deposition/Transfer



Adapted from Gill, P. (2002) *BioTechniques* 32(2): 366-385, Figure 5

DNA Mixture Interpretation
April 12, 2013 Webcast

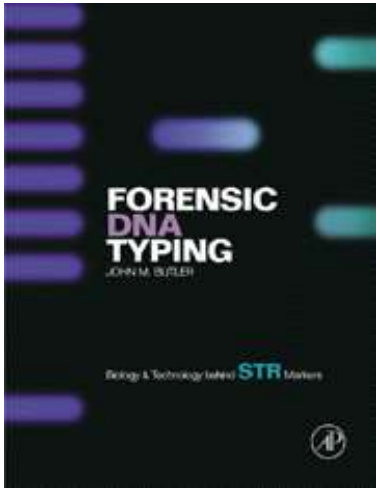
http://www.nist.gov/oles/forensics/dna-analyst-training-on-mixture-interpretation.cfm

- **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)

Left to right:
Gladys Arrisueno (NIST, Twitter feed monitor & poll questions)
John Paul Jones (NIST, webcast organizer)
Mike Coble (NIST, presenter)
John Butler (NIST, presenter & organizer)
Charlotte Word (Consultant, presenter)
Robin Cotton (Boston University, presenter)
Bruce Heidebrecht (Maryland State Police Lab, presenter)

Forensic DNA Typing Textbooks Have Set the Standard for the Field

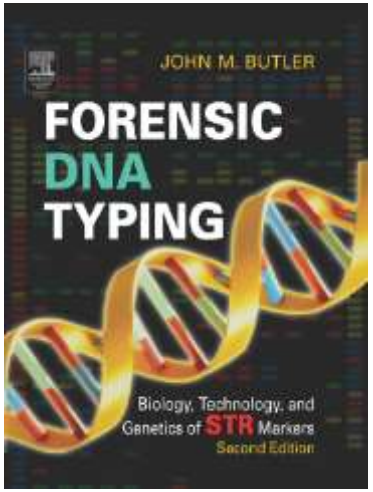
1st Edition



Jan 2001

335 pages

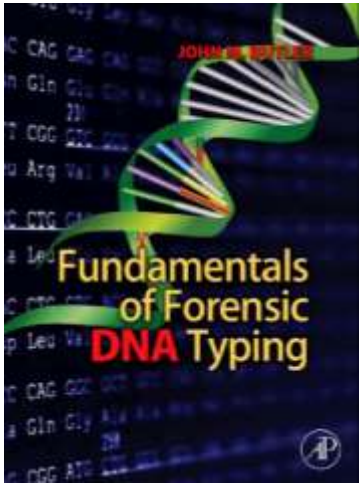
2nd Edition



Feb 2005

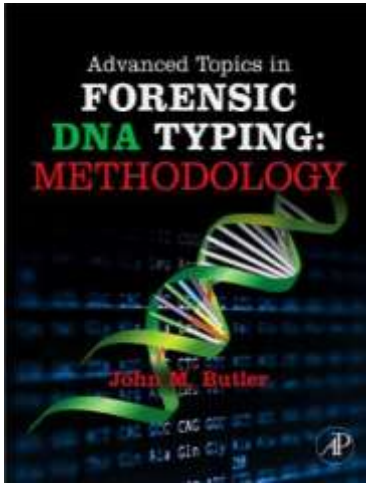
688 pages

3rd Edition (3 volumes)



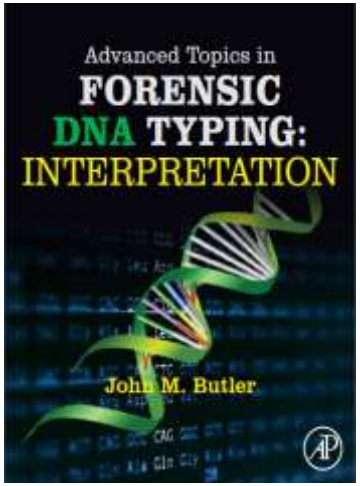
Sept 2009

520 pages



Aug 2011

704 pages



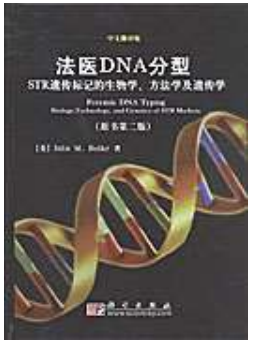
Fall 2014

(being written)

~500 pages

Language Editions

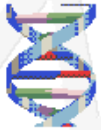
Chinese (2007)



Japanese (2009)

NIST **STRBase** Website

Serving the Forensic DNA Community for >15 Years



Short Tandem Repeat DNA

Internet DataBase

NIST Standard Reference Database SRD 130 [Recent Updates]

Serving the forensic DNA and human identity testing communities for over 10 years... **These data are intended to benefit research and application of short tandem repeat DNA markers to human identity testing. The authors are solely responsible for the information herein.**
Please Rate Our Products and Services: http://tsapps.nist.gov/MSDSurvey/default.aspx?ID=5&DB=130

This database has been accessed 458551 *times since 10/02/97.* (Counter courtesy www.digits.com - see disclaimer)

Created by ***John M. Butler***
and Dennis J. Reeder (NIST Biochemical Science Division),
with invaluable help from Jan Redman, Christian Ruitberg and Michael Tung
Site creators' curriculum vitaes available using links above.

Partial support for the design and maintenance of this website is being provided by The National Institute of Justice through the NIST Office of Law Enforcement Standards.

General Information

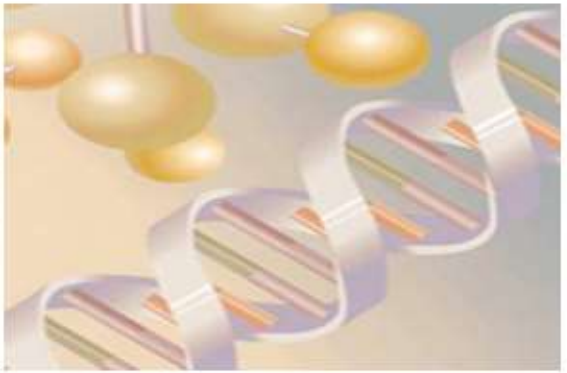
- Purpose of STRBase/NAR 2001 Paper describing STRBase/Overview Presentation
- Publications and Presentations from NIST Human Identity Project Team
- NIJ-Funded Projects
- Training Materials
- Links to other web sites
- Glossary of commonly used terms

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

SWGDAM Website and Resources Available

http://www.swgdam.org/resources.html

- Home
- ByLaws
- Members
- Committees
- Meetings
- Publications



Additional Resources

Beginning with the development or/and revision of its next draft guidance document(s), SWGDAM will make a "Draft for Comment" or other work product available for the purpose of receiving comments from the general public. This "Draft for Comment" solicitation will be open for a minimum of 60 days, usually through SWGDAM.org. SWGDAM will make all reasonable efforts to advise the forensic DNA community of the open comment period for a proposed guidance document or standard, guideline, best practice, study, or other recommendation and/or finding via as many avenues as possible to include posting notices through discipline-specific and related professional organizations. SWGDAM strongly encourages all interested parties to regularly monitor SWGDAM.org for the posting of such draft documents as well. All public comments received by SWGDAM will forwarded to the appropriate SWGDAM Committee for review and consideration as a part of its formal business practice for the development of the guidance documents or other work product.

The following information resources have been produced and reviewed by members of the ***Mixture Committee*** *of SWGDAM and are available at*
www.cstl.nist.gov/biotech/strbase/mixture/SWGDAM-mixture-info.htm

Link to http://www.cstl.nist.gov/biotech/strbase/mixture/SWGDAM-mixture-info.htm

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