



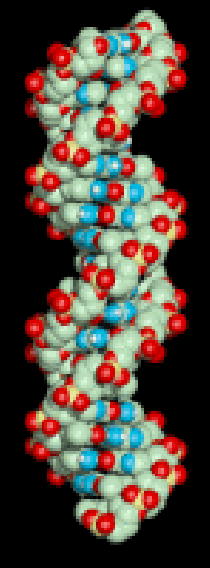
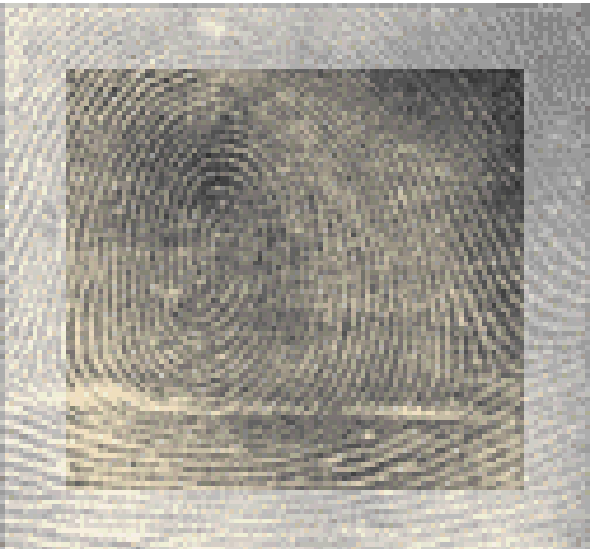
NIST
National
Institute of
Standards
and Technology

... working with industry to develop and apply technology, measurements and standards

Forensic DNA Typing: Application to Mass Disaster Investigations, Paternity Testing and Human Identification

Dr. Peter M. Vallone
NIST Biotechnology Division

Methods for Human Identification



Fingerprints have been used since 1901

DNA since 1986

Forensic DNA Testing

The genome of each individual is unique (with the exception of identical twins)

Probe subsets of genetic variation in order to differentiate between individuals

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

Typically, we are not looking at genes – little/no information about race, predisposal to disease, or phenotypical information (eye color, height, hair color) is obtained

Applications for Human Identity Testing

Forensic cases - **matching suspect with evidence**

Paternity testing - **identifying father**

Historical investigations

Missing persons investigations

Mass disasters - **putting pieces back together**

Military DNA “dog tag”

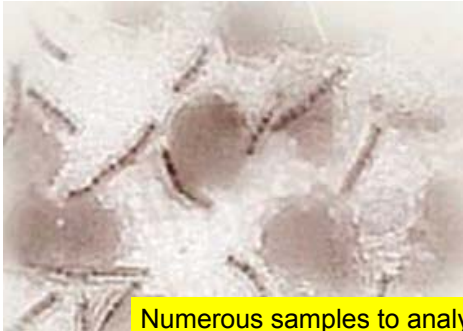
Convicted felon DNA databases

As DNA analysis has shown its usefulness, the number of samples gathered for testing purposes has gone up dramatically...

Anthrax Detection

- Bacterial samples grown in culture
- If turbid after 6 hours, they are plated out and a fluorescent antibody test is done (3 hr)
- DNA detection with TaqMan assay (2-2.5 hr)
 - 5 probes performed in duplicate
 - **RAPID** PCR cycling
- If positive for PCR, then redone at 24 hours

Ruggedized
Advanced
Pathogen
Identification
Device

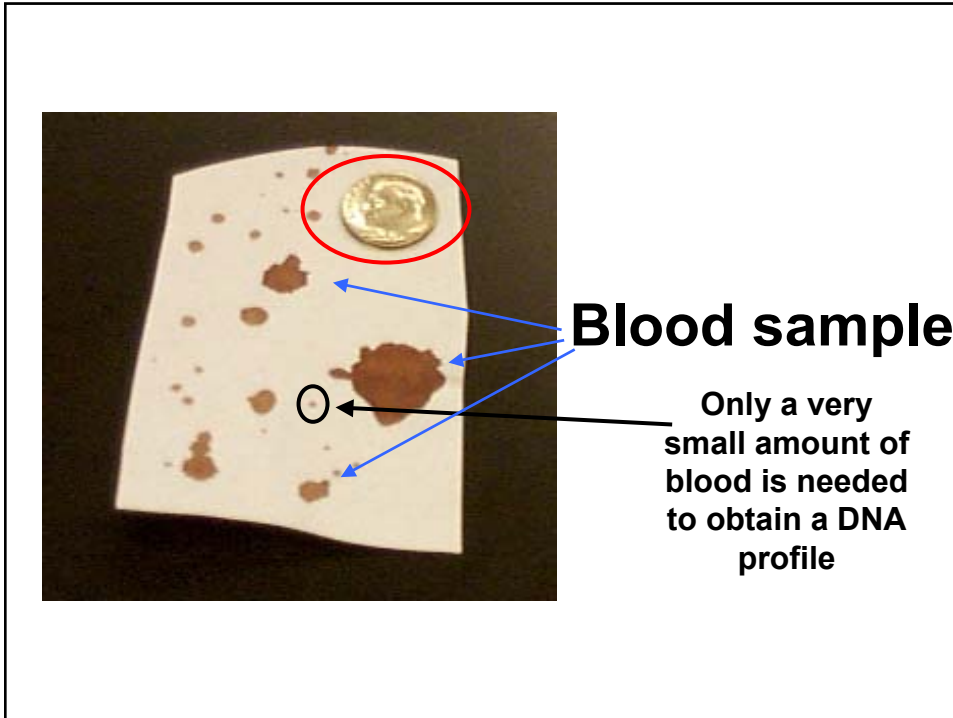


Numerous samples to analyze; public pressure to get results quickly; accuracy better be good...

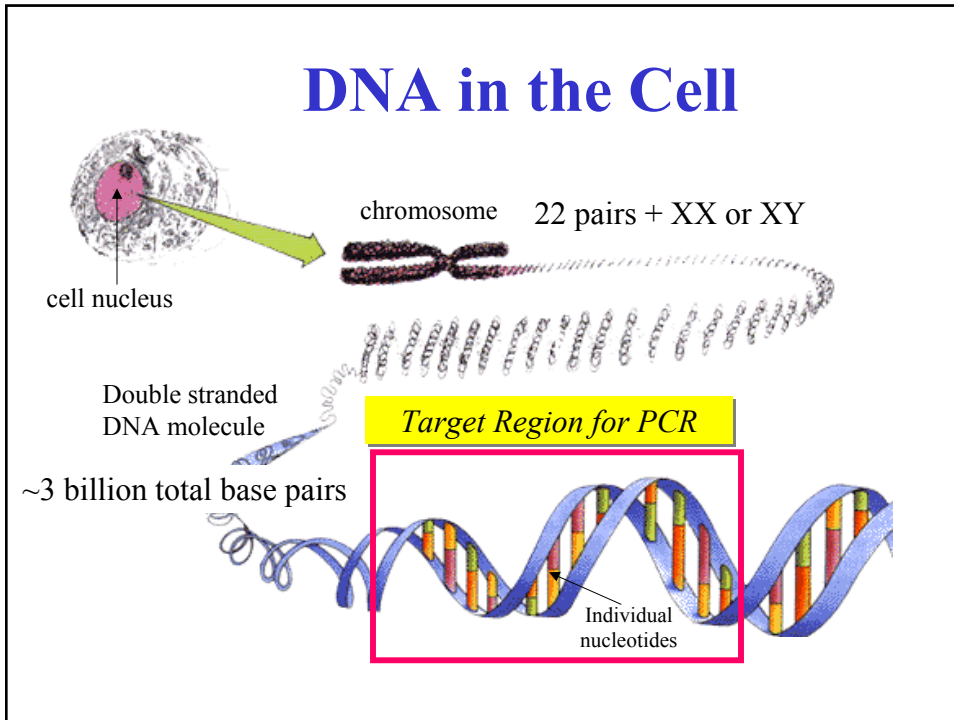
Sources of Biological Evidence

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





Biology



What Type of Genetic Variation?

- Length Variation

short tandem repeats (**STRs**)

CTAGTCGT(**GATA**)(**GATA**)(**GATA**)GCGATCGT

- Sequence Variation

single nucleotide polymorphisms (**SNPs**)

insertions/deletions

GCTAGTCGATGCTC(**G/A**)GCGTATGCTGTAGC

Basic Concepts

PCR polymerase chain reaction – method of amplifying a specific region of the genome – go from 1 to over a billion copies in about 2 hours

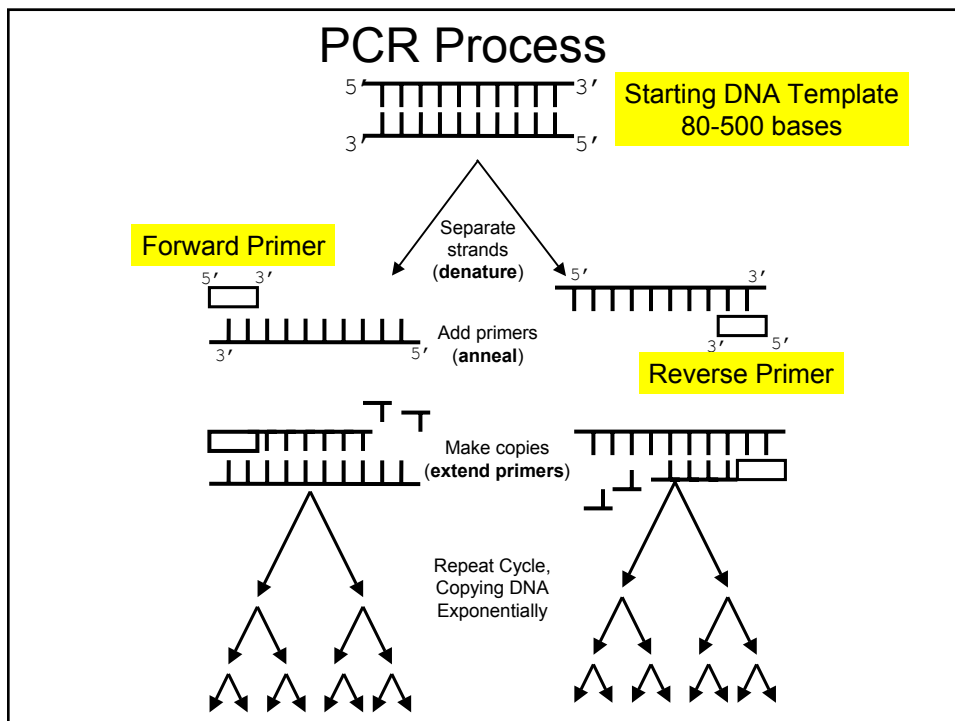
Locus region of the genome being examined

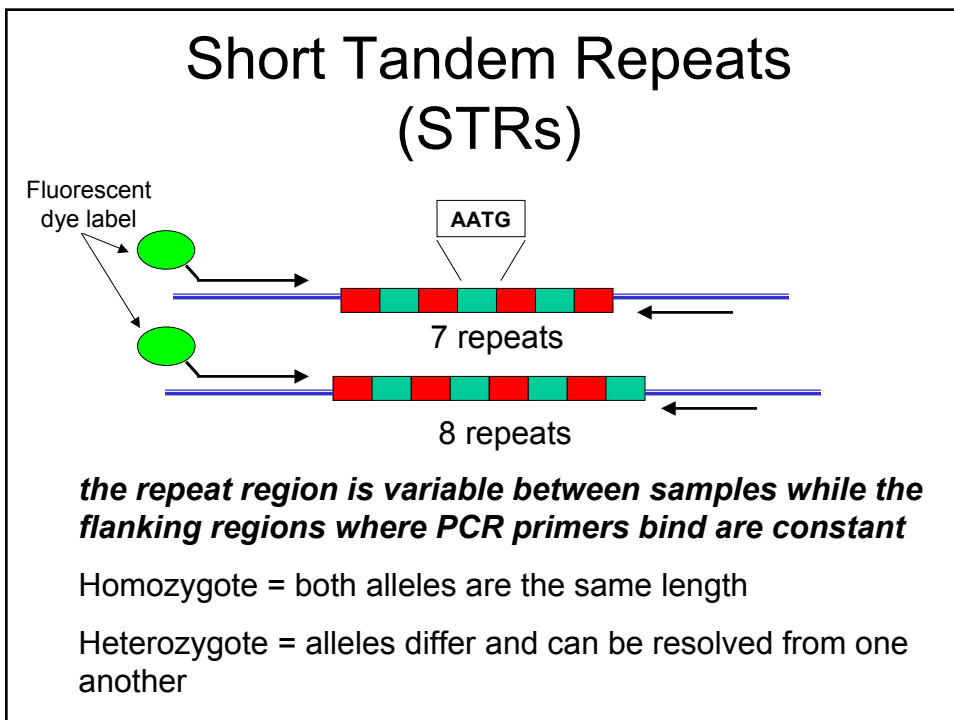
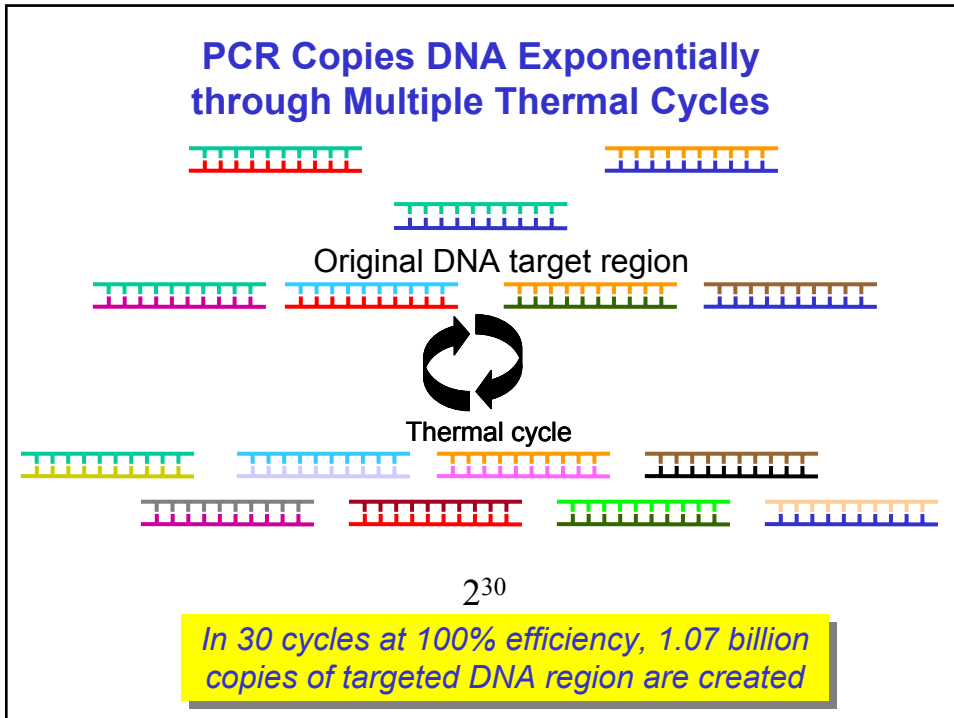
Allele the state of the genetic variation being examined
(**STRs** = number of repeat units)
(**SNPs** = base sequence at the site)

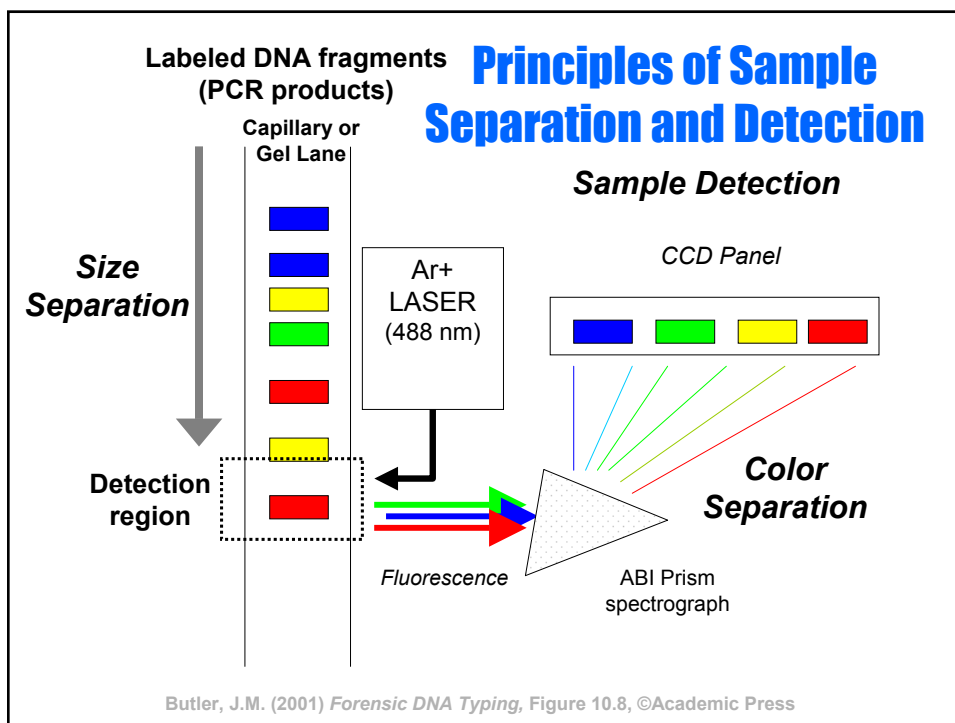
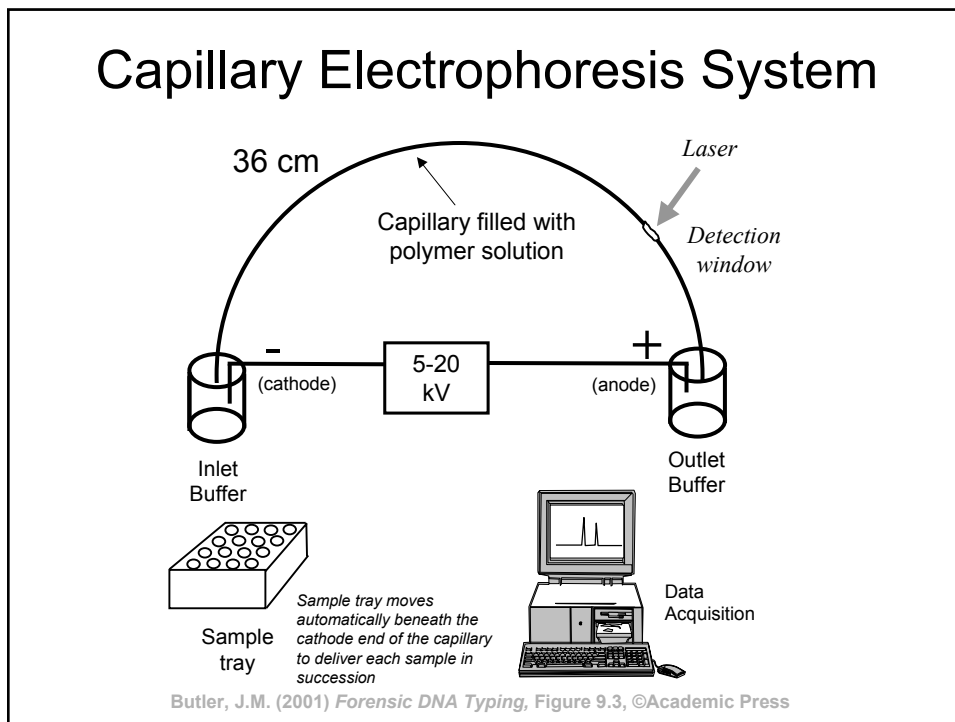
Chromosomes are paired so...

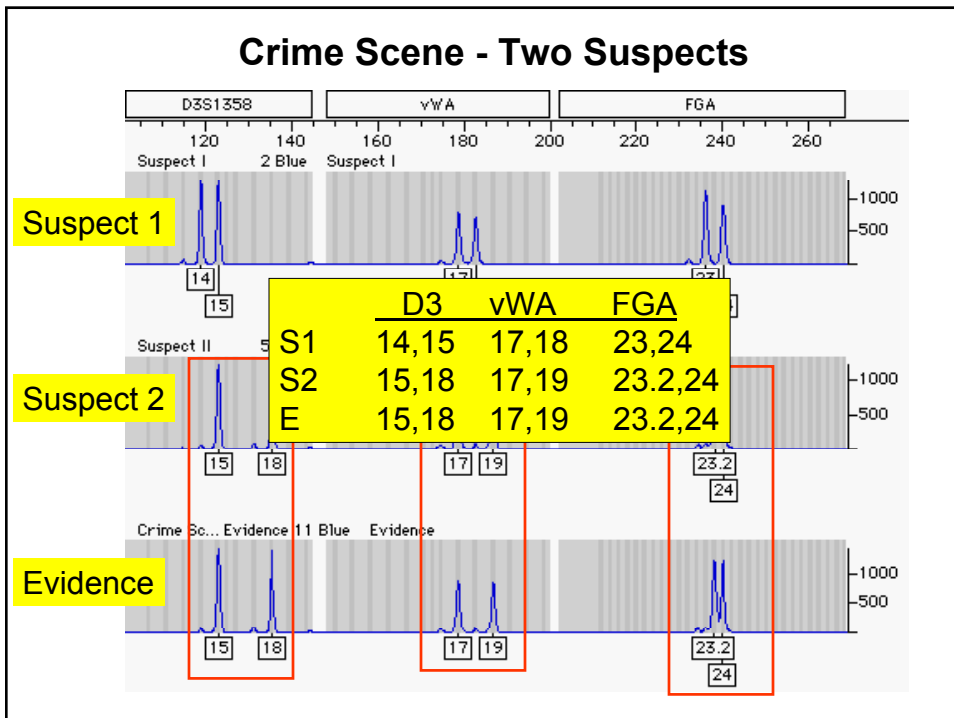
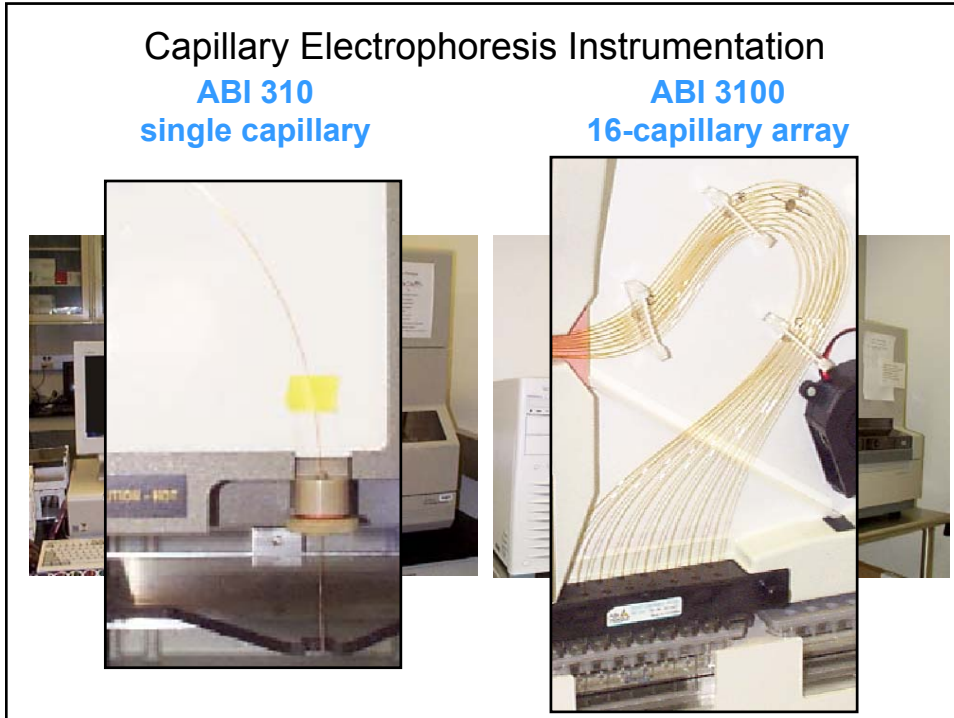
Homozygous – Alleles are identical on each chromosome

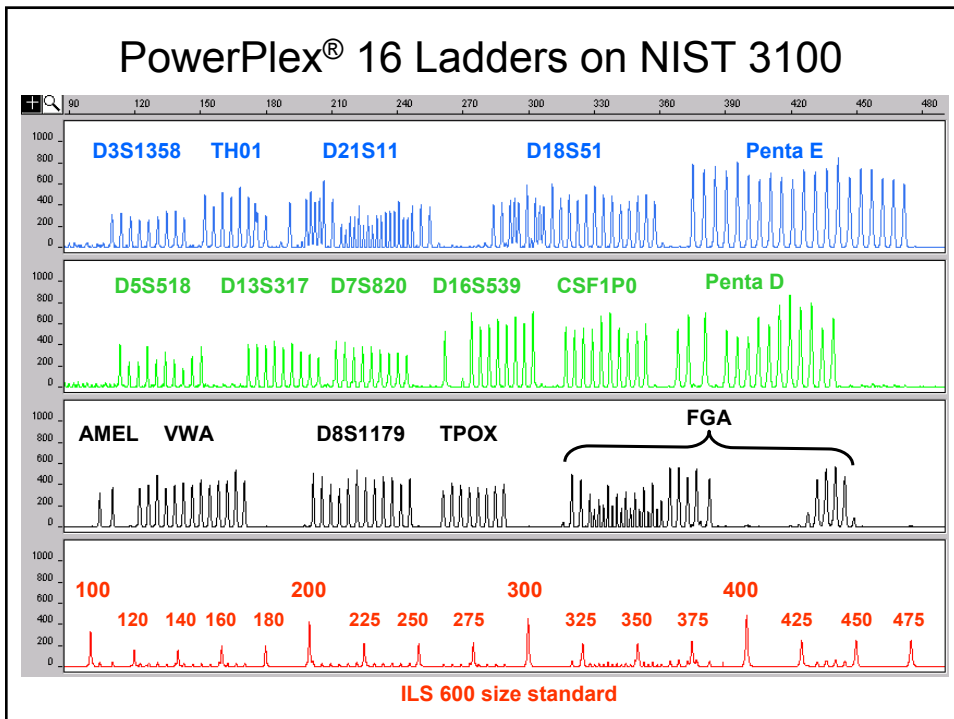
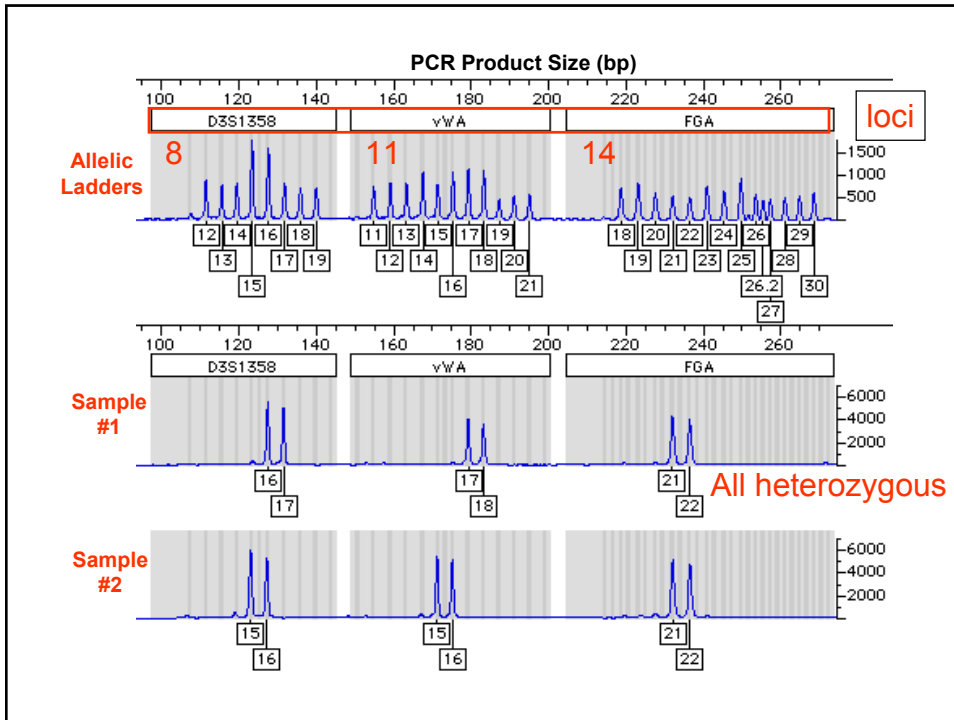
Heterozygous - Alleles differ on each on each chromosome



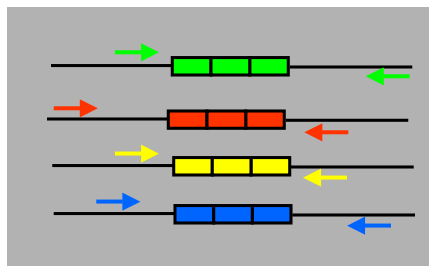








Multiplex PCR (Parallel Sample Processing)



Multiple primers target more than one site on the DNA strand

Commercial kits are available for targeting and simultaneously amplifying 15 STR markers



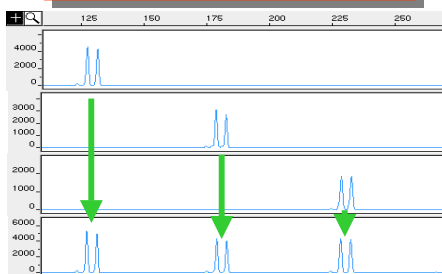
Spectrally distinguishable fluorescent dyes are used as labels

Advantages of Multiplex PCR

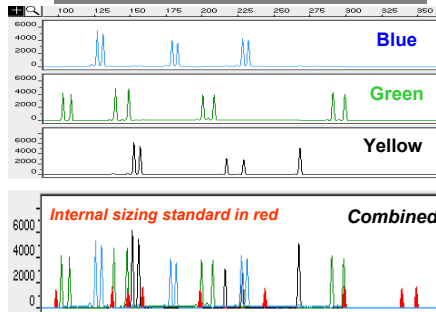
- Increases information obtained per unit time (increases power of discrimination)
- Reduces labor to obtain results
- Reduces template required (smaller sample consumed)

Methods for Parallel Sample Processing

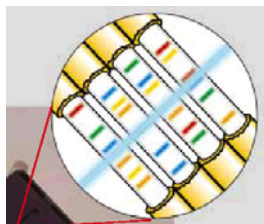
Multiplex by Size

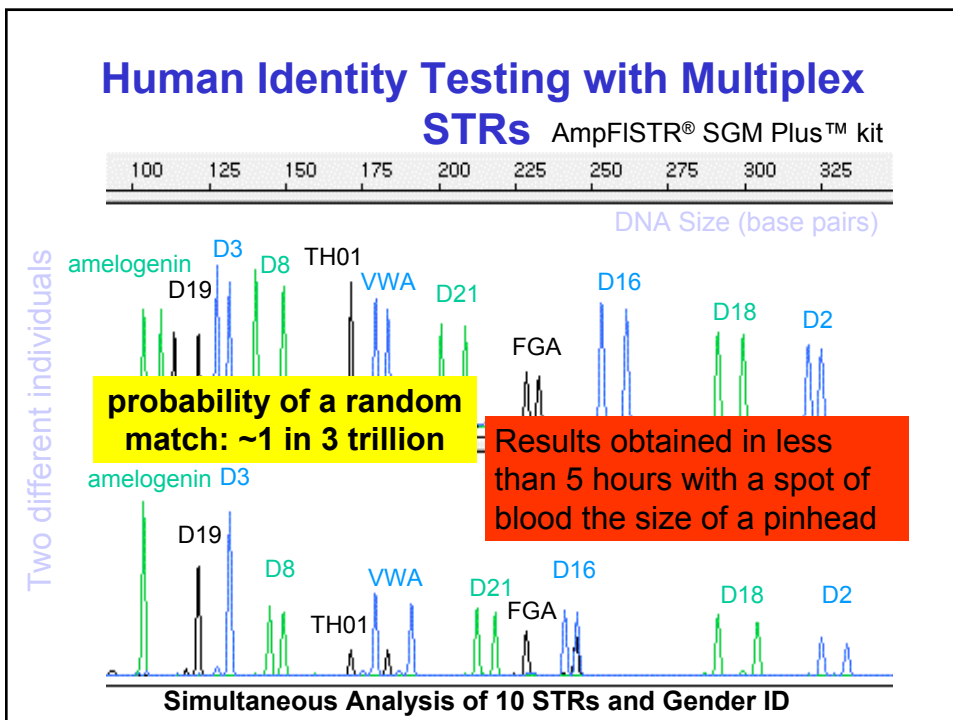
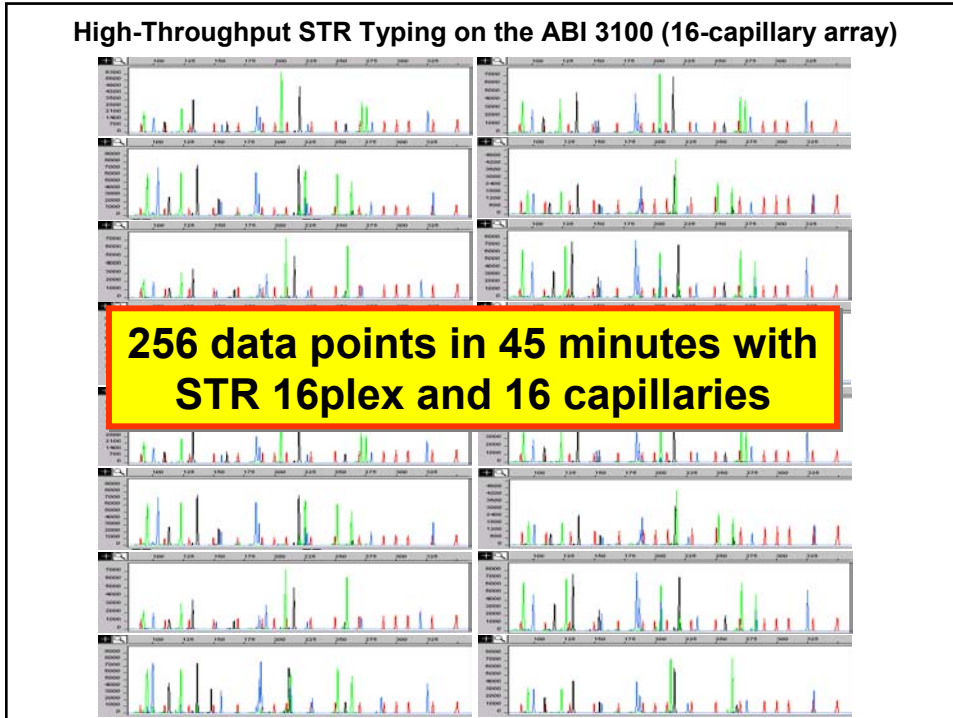


Multiplex by Dye Color



Multiplex by Number of Capillaries





Product Rule

For heterozygous loci

$$P = 2pq$$

P = probability; p and q are frequencies of allele in a given population

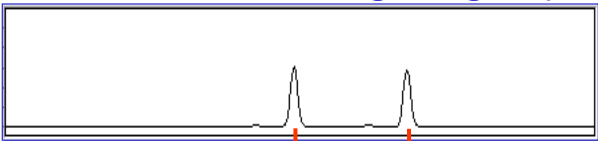
Example: For the locus D3S1358 and individual is 15,18 with frequencies of 0.2825 and 0.1450 respectively

$$P = 2(0.2825)(0.1450) = 0.0819 \text{ or } 1 \text{ in } 12$$

For 5 loci the

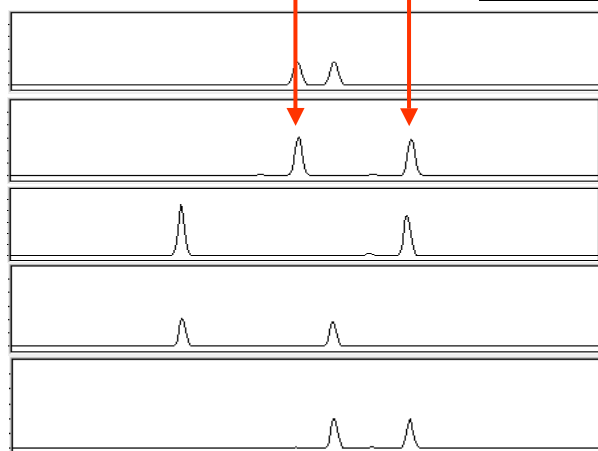
$$\begin{aligned} \text{Profile Probability} &= (P_1)(P_2)\dots(P_n) \\ &= (0.0819)(0.0875)(0.0687)(0.0245)(0.0984) \\ &= 0.000001187 \text{ or } 1 \text{ in } 842,539 \end{aligned}$$

DNA Profiles from a Single Region (Locus)



**“Crime Scene”
Evidence**

DNA Lineup of the “Suspects”



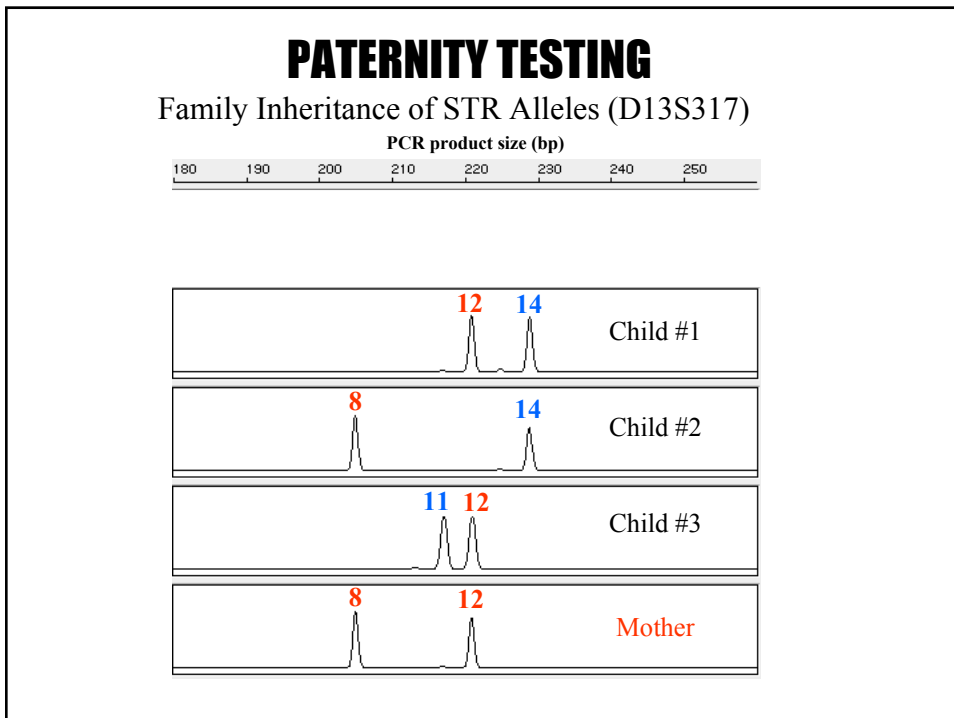
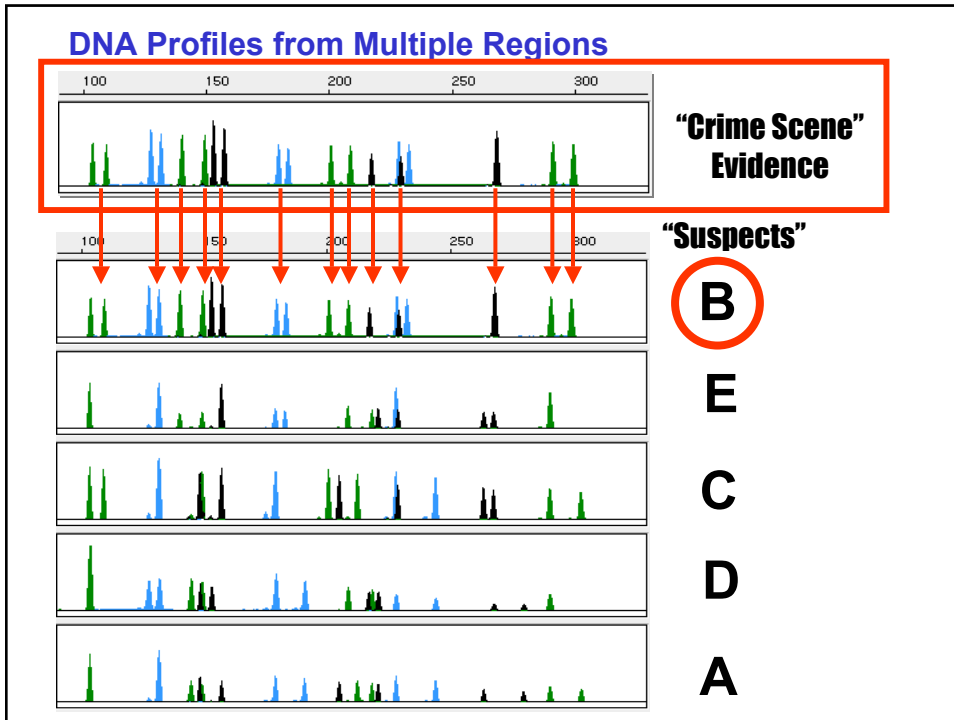
A

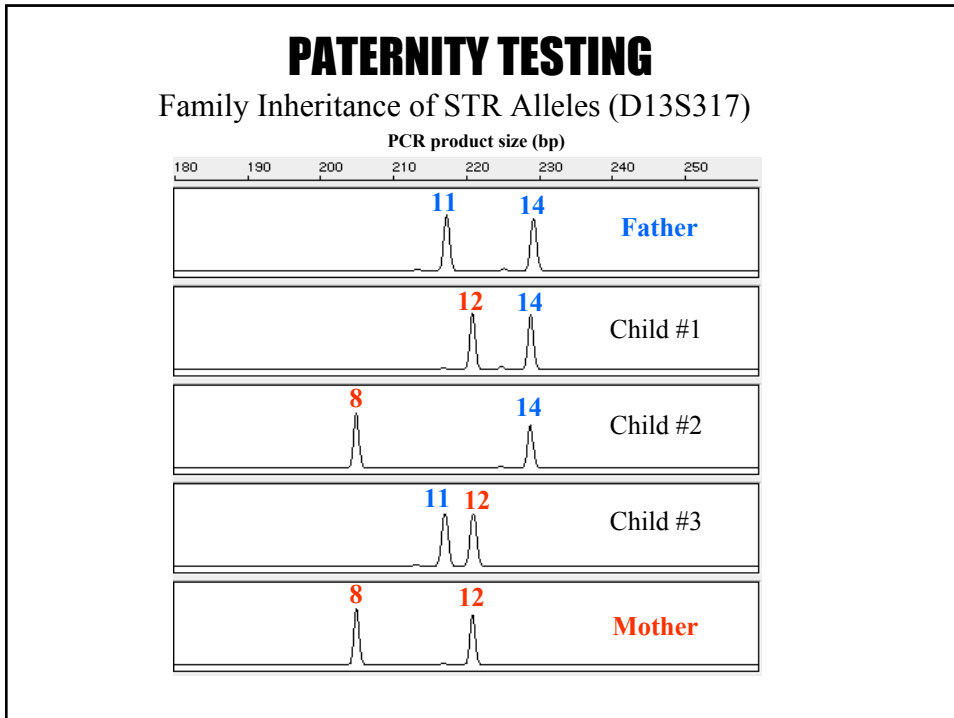
B

C


D

E






FBI database



CODIS DNA Database



Combined DNA Index System

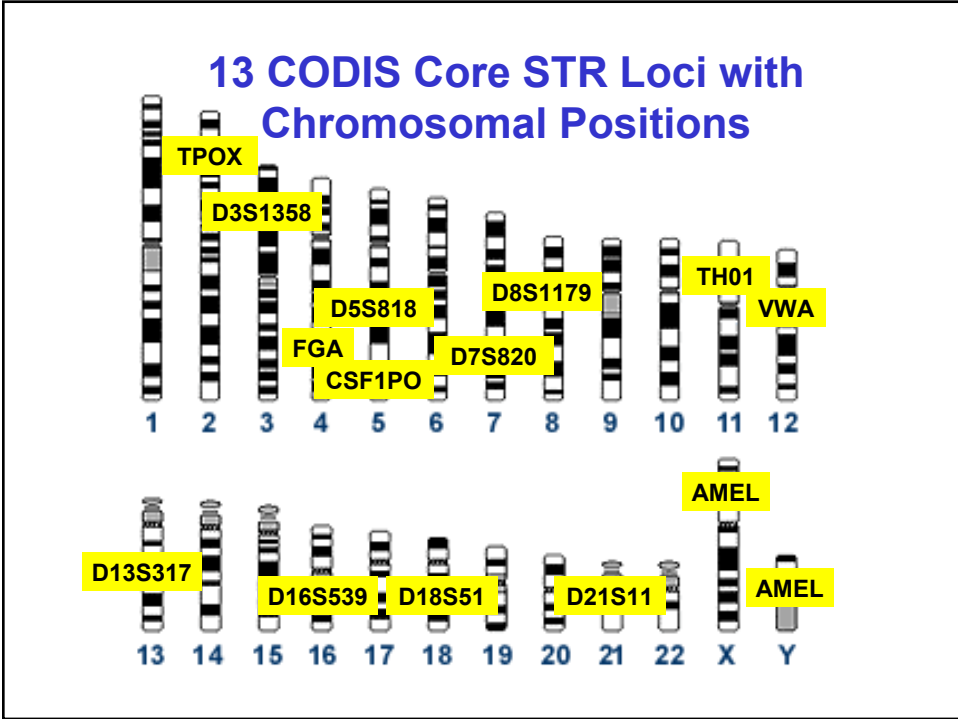
Used for linking serial crimes and unsolved cases with repeat offenders

Convicted offender and forensic case samples

Launched October 1998 and links all 50 states

Requires 13 core STR markers

Current backlog of >750,000 samples (\$15M in FY2002 to reduce backlog)



All 50 states now require convicted offenders to submit a sample for DNA testing purposes



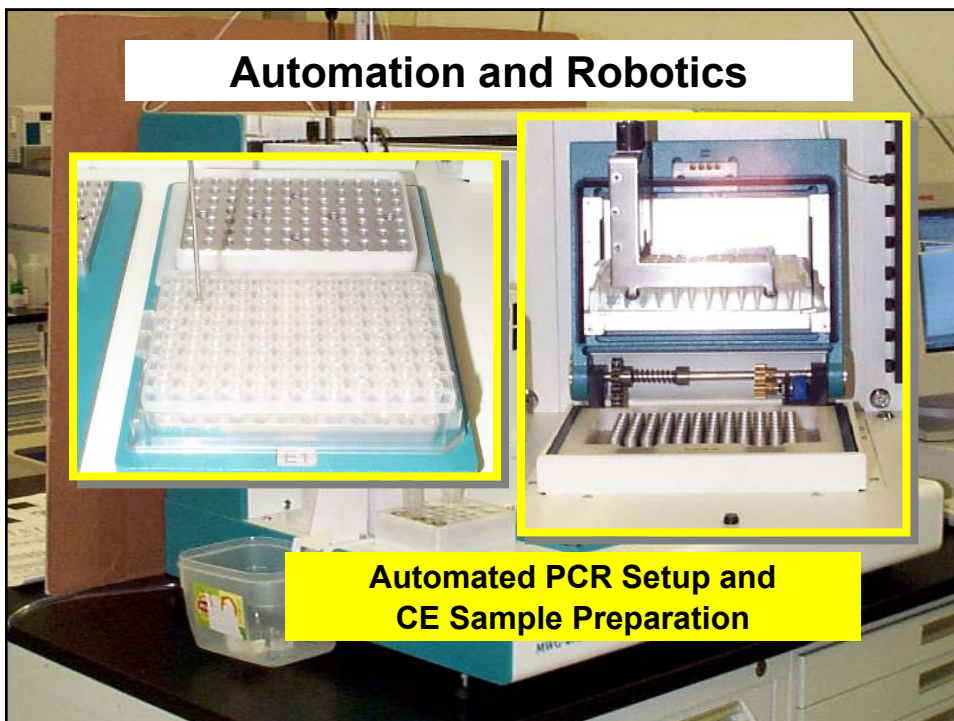
7,788 Investigations Aided through April 2003

As of April 2003 the total profile composition of the National DNA Index System (NDIS) is as follows:

- Total number of profiles: 1,376,749**
- Total Forensic profiles: 54,895**
- Total Convicted Offender Profiles: 1,321,854**

<http://www.fbi.gov/hq/lab/codis/clickmap.htm>

Automation and Robotics



Automated PCR Setup and CE Sample Preparation

The Role of NIST Scientists

- **Develop DNA standards** so that laboratories around the world may compare their results.
- **Conduct tests of laboratories** around the world to insure accurate results in DNA testing.
- **Develop new DNA tests** which are more rapid and efficient than those currently used.
- **Create useful information databases** (STRBase)
<http://www.cstl.nist.gov/biotech/strbase>.
- **Evaluation and development** of new technologies.

NIST Standard Reference Materials (SRMs)

SRM 2390 - DNA Profiling Standard
Meets RFLP Needs

SRM 2391 - PCR-Based DNA Standard
Cell Lines and Genomics

SRM 2392 - Mitochondrial DNA Standard
Cell Lines and Cloned HV1 Plasmid



SRM 2393 - *mtDNA heteroplasmy*

SRM 2395 - *Y chromosome DNA standards*

NIST


SRM 2391: DNA Profiling Standard for Forensic and Paternity Testing Laboratories

- Human identity testing using Polymerase Chain Reaction (PCR) technologies growing rapidly
- PCR techniques diverse, requiring DNA standards that perform under various amplification and electrophoretic methods
- SRM 2391 certified for genetic locus D1S80; expanding for other loci as needs evolve




DNA Quality Assurance recommendations by the DNA Advisory Board were signed by the FBI director on July 15, 1998.

Beginning October 1, 1998, all federally-funded laboratories that conduct DNA testing must verify procedures using NIST SRMs



Chemical Science and Technology Laboratory

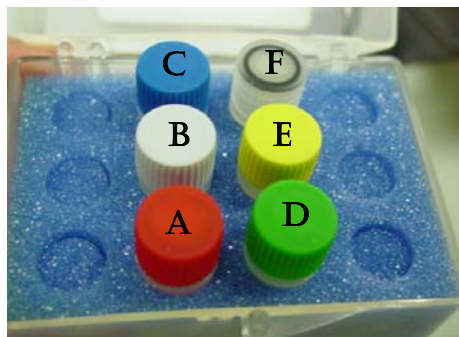


DAB Quality Assurance Standards for Forensic DNA Testing Laboratories

STANDARD 9.5

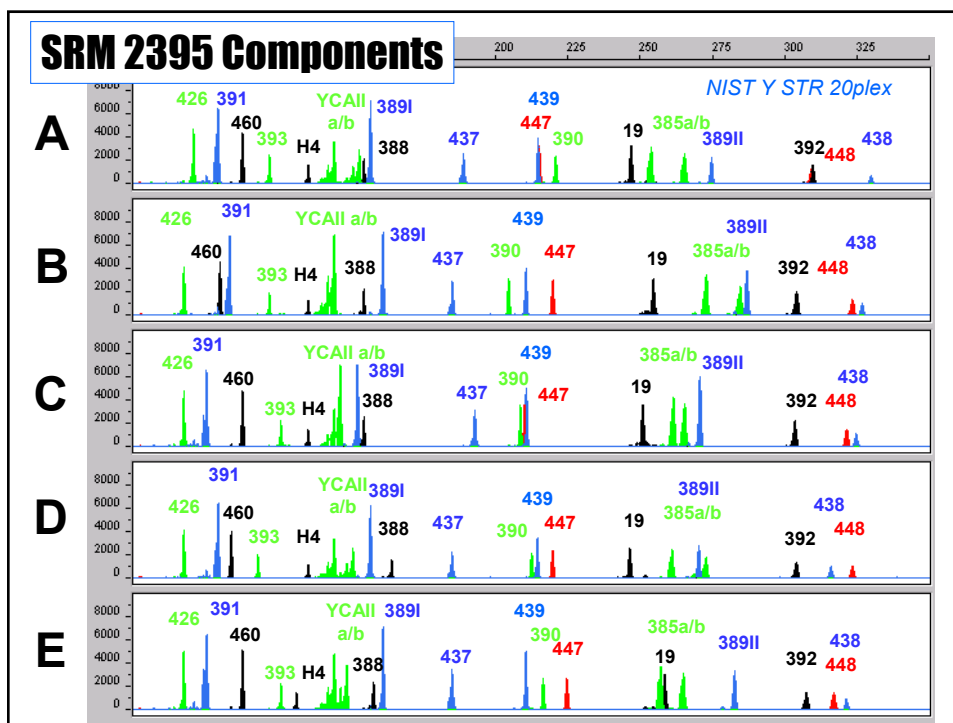
The laboratory shall check its DNA procedures annually or whenever substantial changes are made to the protocol(s) against an appropriate and available NIST standard reference material or standard traceable to a NIST standard.


NIST Y Chromosome Standard



6 genomic DNA samples
5 male and 1 female
Typing Information on 27 Y STRs and 50 Y SNP markers

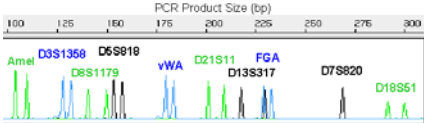
Available as of 07/2003






World Trade Center Towers
(Sept 11, 2001)

DNA typing being used as only possible method to identify over 2,000 victims of this tragedy



Highly degraded DNA; ~20,000 samples recovered; 3 years to complete...



Wreckage at Ground Zero

Identifying Mass Disaster Victims

Medical Specimen (Biopsy sample/bloodspot)

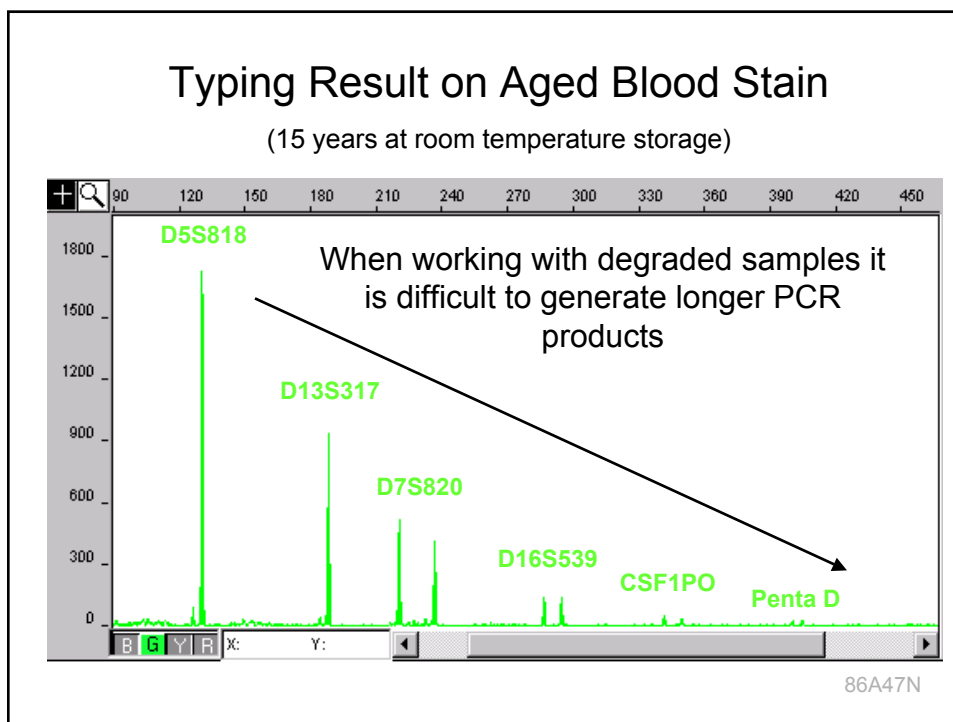
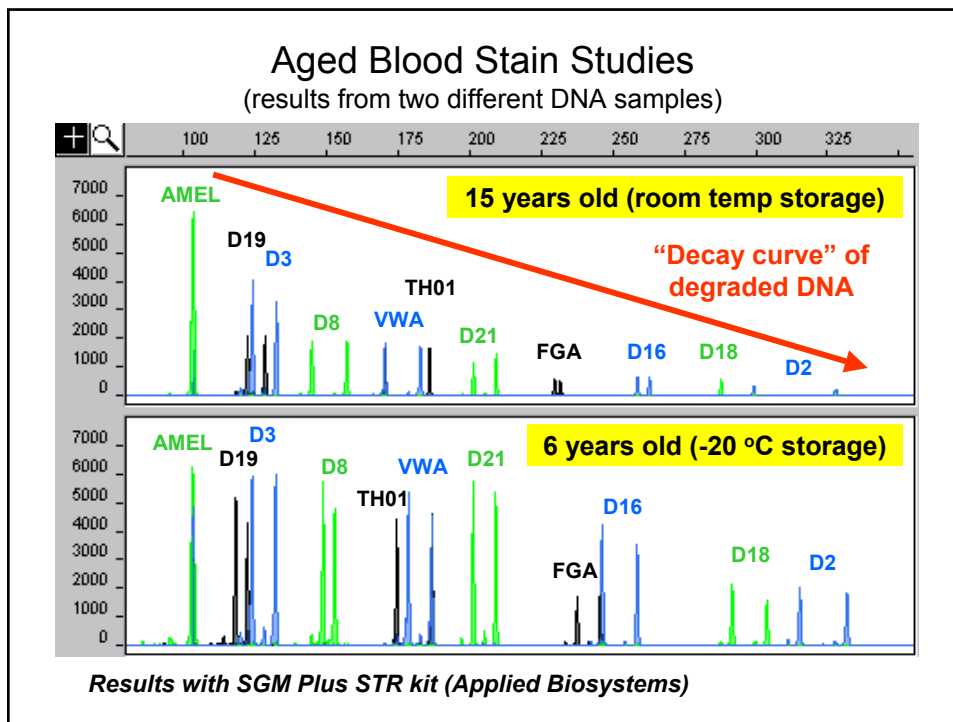
Personal Effect (toothbrush/hairbrush)

Kin (close relative)

Remains (bone/ tissue)

DNA profiles obtained are stored in a database and attempts at identification are made

Challenge lies in typing degraded samples



STR Size Reduction Through Moving Primer Positions Closer to Repeat



Primer positions define PCR product size
Repeat information is independent of amplicon size

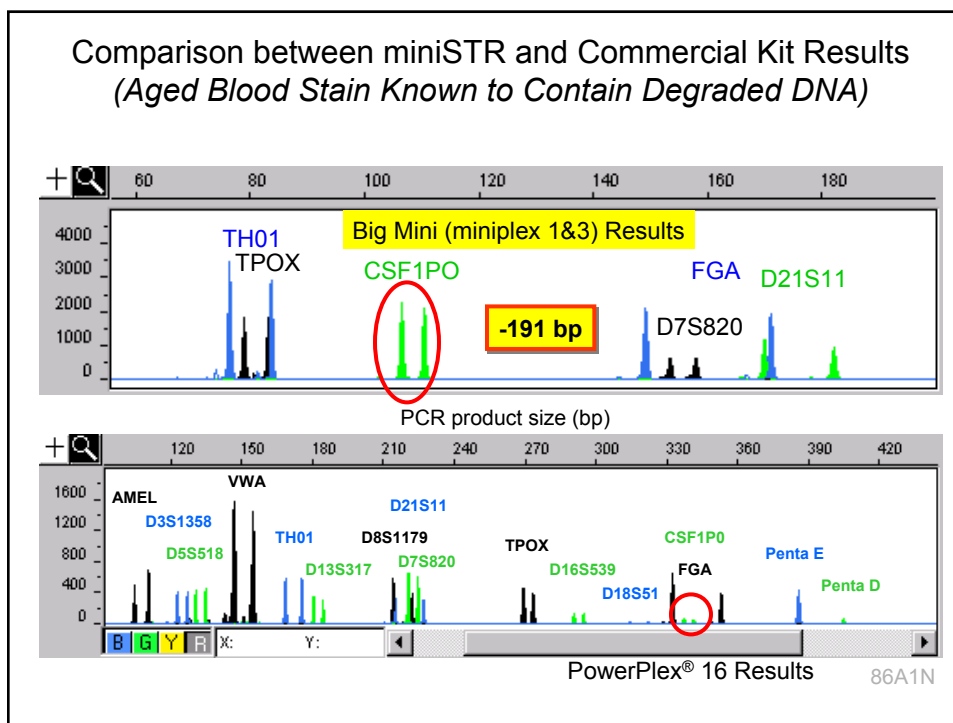
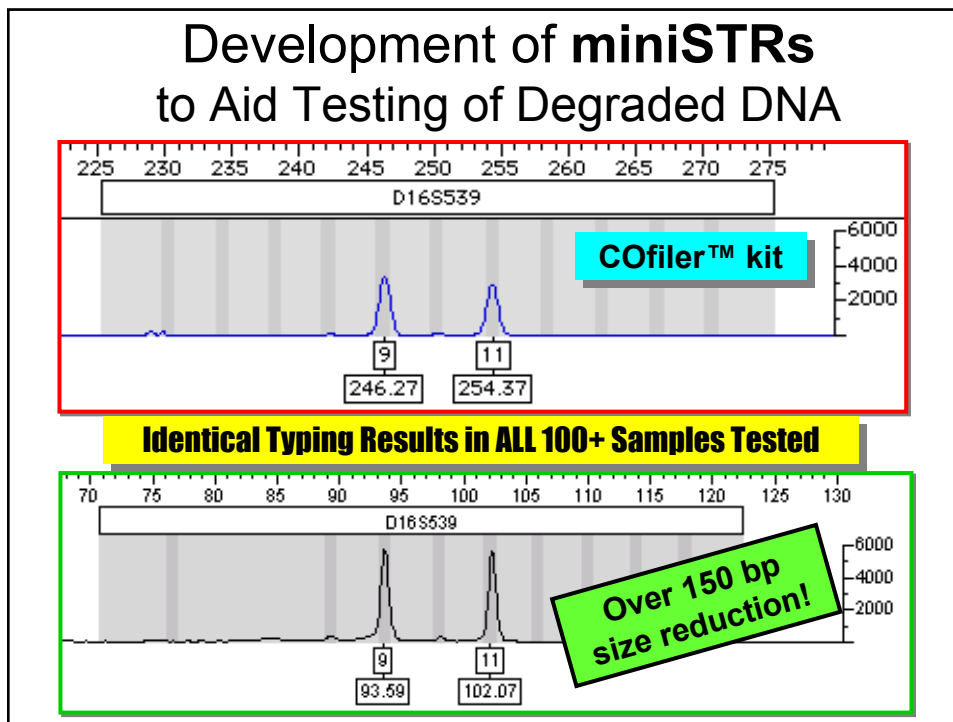
Advantages of Approach:

Size reduction enhances success rate with degraded DNA
Retains same marker information (database compatibility)
Uses highly polymorphic STR loci (high discriminatory power)

Limitation: Lower levels of multiplexing 5-6 plex vs 10-15 plex

Development of miniSTR Assays

- Primers designed to come as close as possible to the repeat region to generate the smallest possible PCR products
- Equivalent genotypes are obtained when compared with commercial STR kits
- Available as singleplexes or miniplexes (usually one locus per dye color)
- Smaller amplicons offer improved chances of success with degraded DNA samples
- Project begun in November 2001 at the request of Bob Shaler to aid WTC DNA identifications



Current Status of WTC Samples

28,251 Total Profiles

Personal Effects 4,903


Kin 6,876

Remains 16,472

2795 reported missing – 1511 Identified

Use of miniSTRs has resulted in ~20 additional identifications


WTC Kinship and Data Analysis Panel

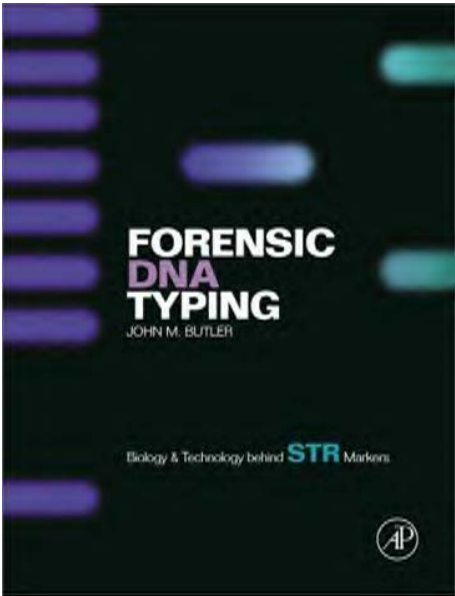


STRBase
Short Tandem Repeat DNA
Internet Database

... working with industry to develop and apply technology, measurements and standards

<p><u>General Information</u></p> <ul style="list-style-type: none"> •Intro to STRs (downloadable PowerPoint) •STR Fact Sheets •Sequence Information •Multiplex STR Kits •Variant Allele Reports 	<p><u>Forensic Interest Data</u></p> <ul style="list-style-type: none"> •FBI CODIS Core Loci •DAB Standards •NIST SRM 2391 •Published PCR Primers •Y-Chromosome STRs •Population Data •Validation Studies 	<p><u>Supplemental Info</u></p> <ul style="list-style-type: none"> •Reference List •Technology Review •Addresses for Scientists •Links to Other Web Sites
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 <http://www.cstl.nist.gov/biotech/strbase>



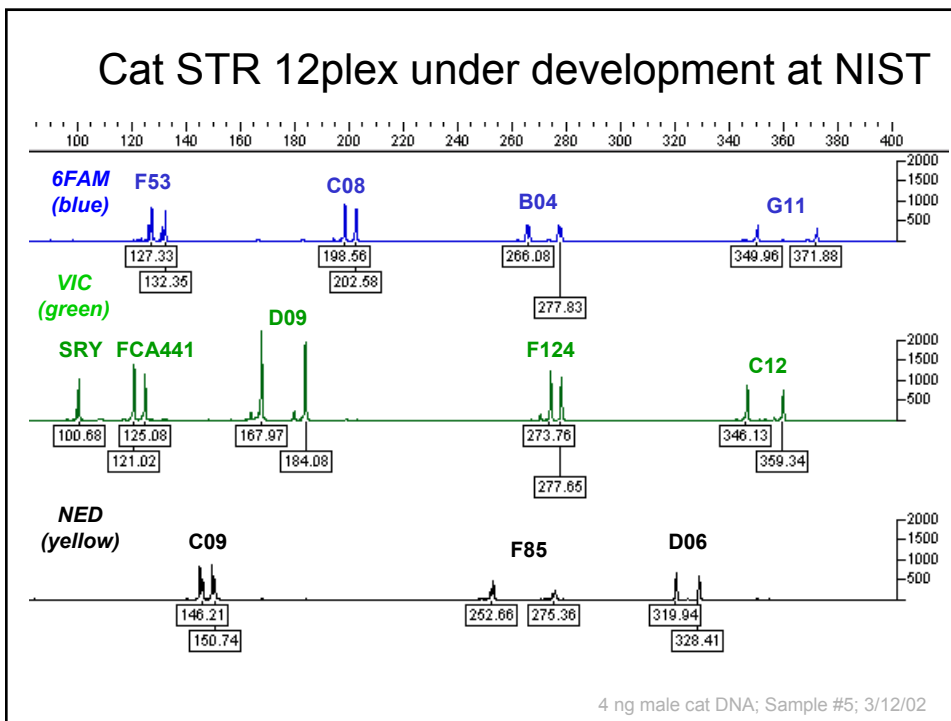
FORENSIC DNA TYPING
Biology and Technology
behind STR Markers

John M. Butler

Listed on amazon.com
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A Harcourt Science and Technology Company

http://www.apnet.com/aps/forensics/for_bio.html



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