Forensic DNA Testing

Basics

Applications

Fun and Games

HUMAN DNA POLYMORPHISM
By the numbers

- $6x10^9$ humans on earth
- $3x10^9$ bp in human haploid genome
- $6x10^9$ bp in human diploid genome
- Therefore 6pg of DNA per cell
- In coding and 5', 3' untranslated regions, ~0.05% difference between individuals on average

HUMAN DNA POLYMORPHISM
By the numbers

- $5x10^{-4}$ probability of base change x $6x10^{9}$ bp in human diploid genome = $3x10^{6}$ differences between two people

- So, people are closely related to each other, but easily told apart at the DNA level

HUMAN DNA POLYMORPHISM
By the numbers

- Furthermore, $5x10^{13}$ cells per person x 6 pg DNA per cell = 300 g DNA per person - really really a lot
- As we will see, a 16-locus standard DNA comparison takes 200 pg of DNA - less than 50 cells
- Lysing an entire human would give enough DNA for 1,500,000,000,000 tests

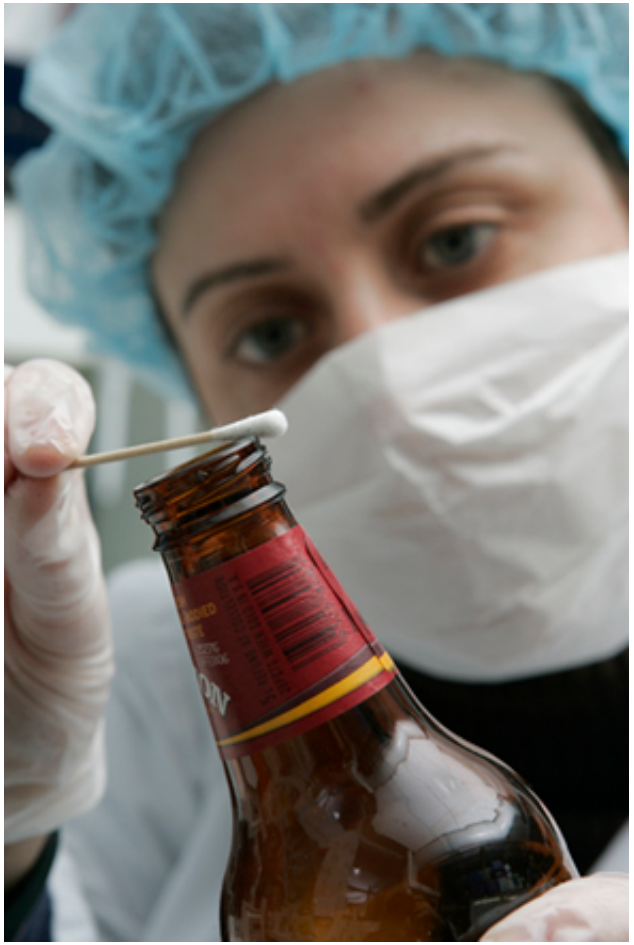
HUMAN DNA POLYMORPHISM
By the numbers

- 200 pg of human DNA can be found in:

- 0.2 microliters of saliva (a spit spray drop)
- 200 microliters of urine (<10 drops)
- 1/4 of a hair root from a shed hair (plucked hair has more)
- 1/1,000 of a 1 cm^2 blood stain

HUMAN DNA POLYMORPHISM
By the numbers

- Conclusions: it is easy to identify a person by DNA, and people shed enough DNA to test everywhere and all the time - a licked stamp, a cigarette butt, an invisibly small blood spot are plenty.



How it is done

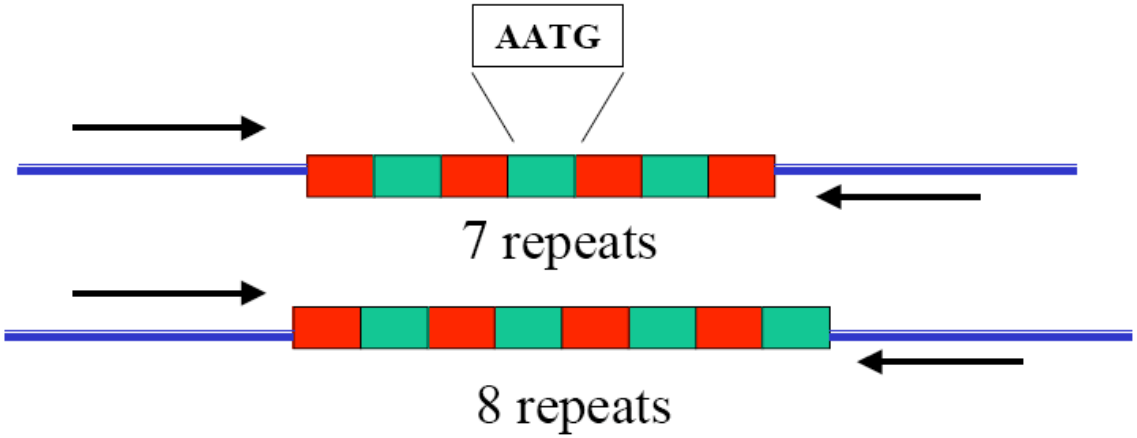
- First, it isn’t done by looking at the single nucleotide differences in or near genes (though this can be done, there are simpler ways)
- It is done using STRs - short tandem repeats

How it is done

- At many non-coding places in the human (or other) genome, there are short tandem repeats like

  gatagatagatagatagatagata
- The number of repeats varies from person to person
- STRs are defined as having repeats of length 2-4 or so [VNTRs more like 15-35]
- The number of repeats does not appear to be under any measurable selection

Short Tandem Repeats (STRs)



the repeat region is variable between samples while the flanking regions where PCR primers bind are constant

Homozygote = both alleles are the same length

Heterozygote = alleles differ and can be resolved from one another

For example

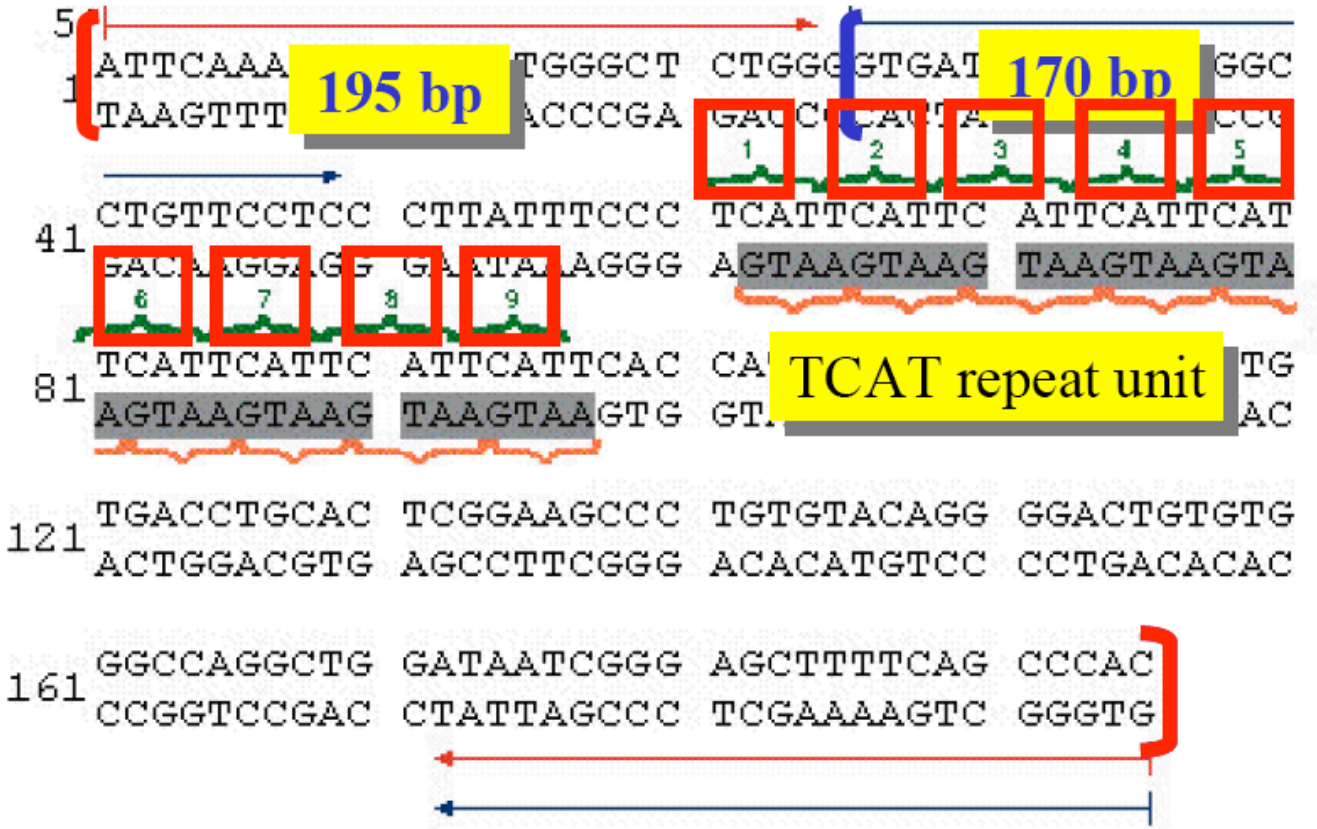
D7S280

D7S280 is one of the 13 core CODIS STR genetic loci. This DNA is found on human chromosome 7. The DNA sequence of a representative allele of this locus is shown below. This sequence comes from GenBank, a public DNA database. The tetrameric repeat sequence of D7S280 is "gata". Different alleles of this locus have from 6 to 15 tandem repeats of the "gata" sequence. How many tetrameric repeats are present in the DNA sequence shown below? Notice that one of the tetrameric sequences is "gaca", rather than "gata".

```
  1 aatttttgta ttttttttag agacggggtt tcaccatgtt ggtcaggctg actatggagt
 61 tattttaagg ttaatatata taaagggtat gatagaacac ttgtcatagt ttagaacgaa
121 ctaacgatag atagatagat agatagatag atagatagat agatagatag atagacagat
181 tgatagtttt tttttatctc actaaatagt ctatagtaaa catttaatta ccaatatttg
241 gtgcaattct gtcaatgagg ataaatgtgg aatcgttata attcttaaga atatatattc
301 cctctgagtt tttgatacct cagattttaa gg
```

HUMTH01 Sequence from GenBank

(Accession D00269)

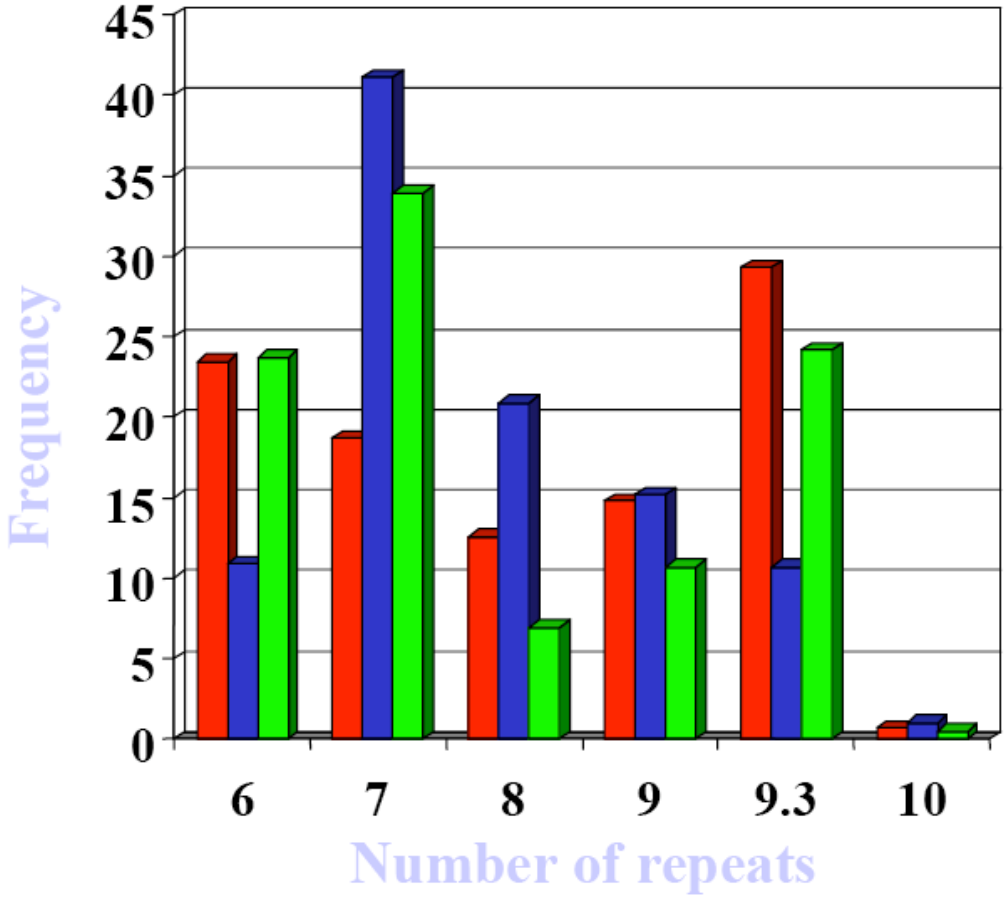


Different primer sets produce different PCR product sizes for the same STR allele

How it is done

- For simple calculations, unlinked STRs are used so there will be no linkage disequilibrium (events need to be mutually exclusive and independent)
- And ones are chosen where average repeat number is less than 10% or 20% allele frequency, and the highest single allele frequency is <30% or so

STR Allele Frequencies



TH01 Marker

Caucasians (N=427)
Blacks (N=414)
Hispanics (N=414)

*Proc. Int. Sym. Hum. ID (Promega) 1997, p. 34

How it is done at the lab level

- Take tissue sample and extract DNA
- Buy a kit for example the Promega PowerPlex® 16 System
- It contains a set of PCR primers that hybridize to unique sequences that flank 15 different STRs, and one other locus (on which more in a moment) with the spacing of the primers such that all alleles of each STR locus are separable from all alleles of all other STRs that use the same primer

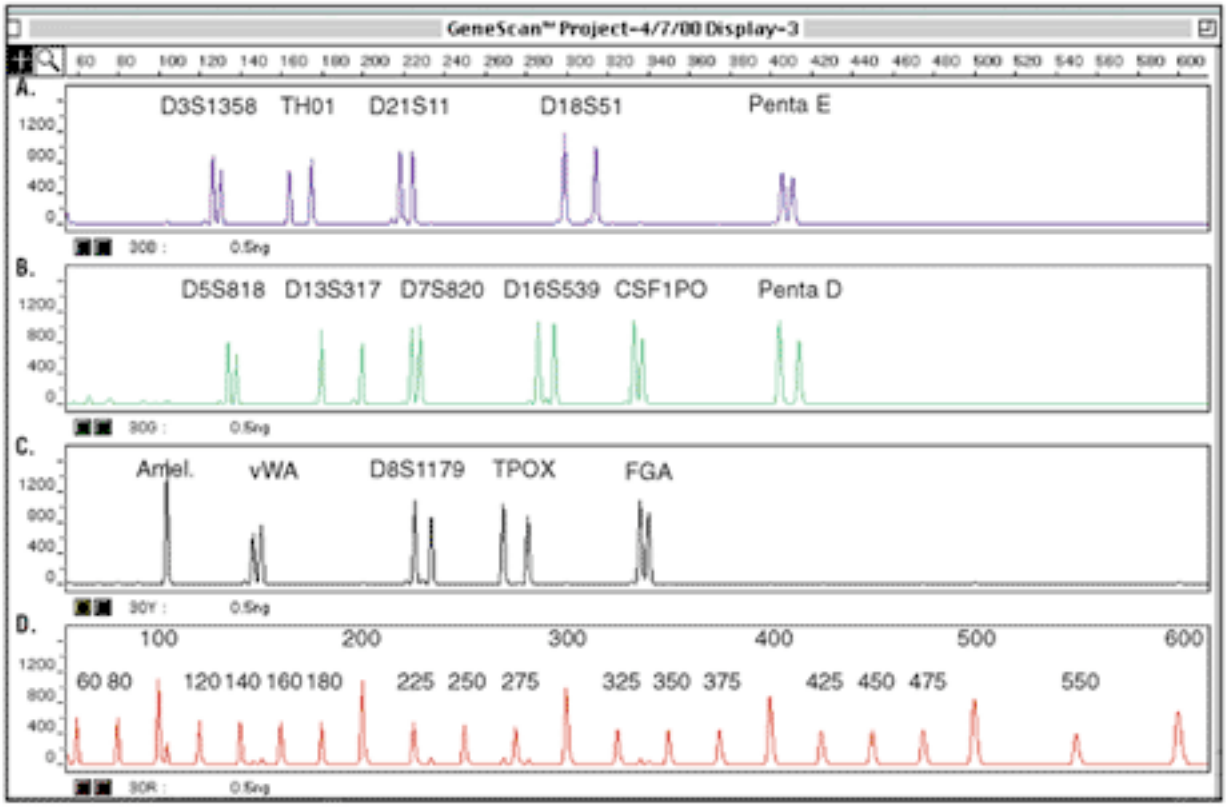
How it is done

- In practice this means that the primers are in three groups, each with a different color dye attached, and each dye type has well-separated loci
- Run amplified DNA in a capillary sequencing machine with a separate size standard (the fourth dye color) and read out the alleles

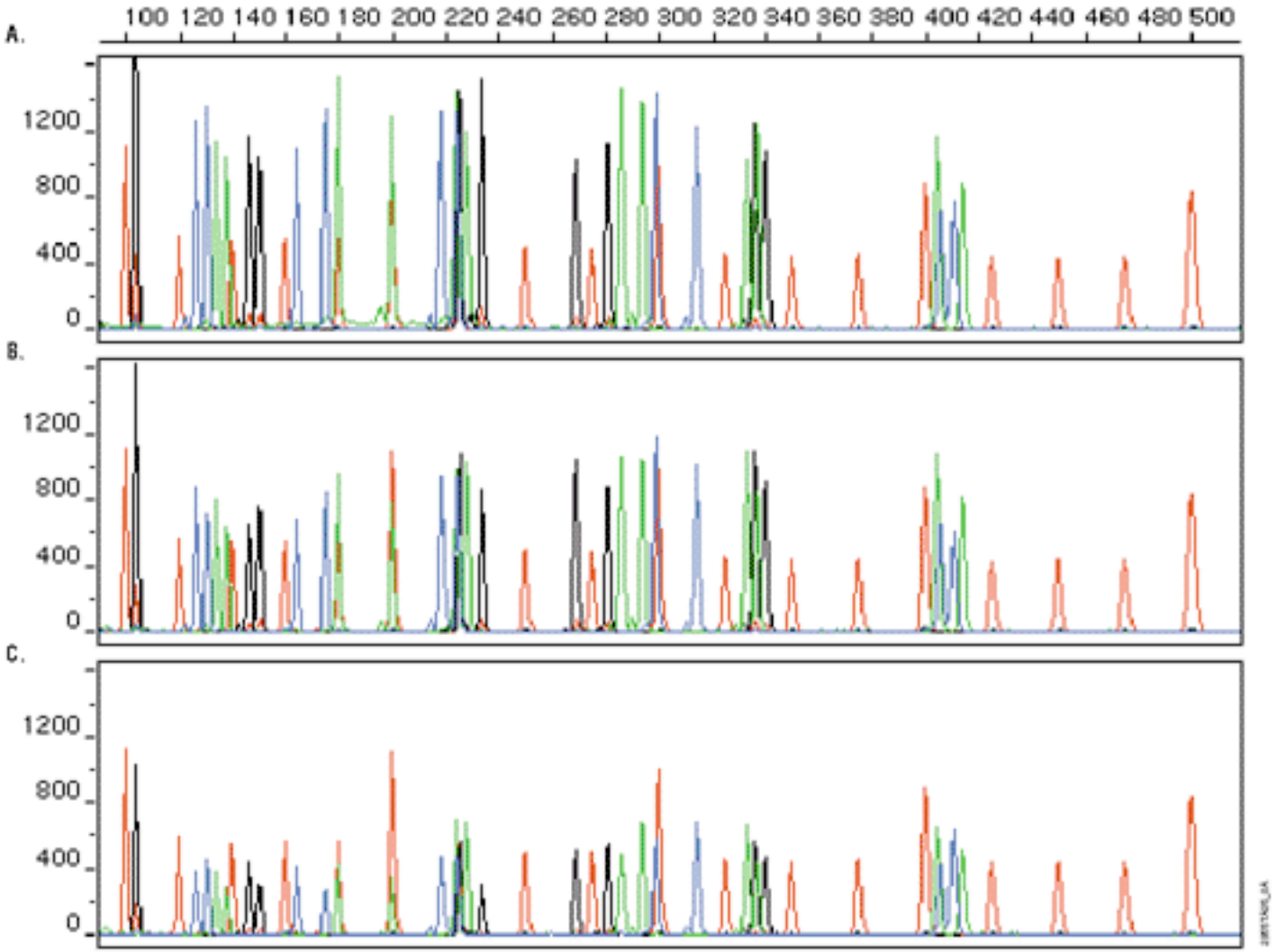
How it is done

- 15/16 primer pairs are for standard STRs with low single allele frequencies
- The last pair amplifies Amelogenin locus, which codes for the major protein component of tooth enamel
- The gene is on the X and Y chromosomes, there is a length polymorphism in the first intron
- Primers for X version give 106 bases, Y version 112
- So two peaks means sample is from a male, one at 106 means it is from a female

Promega result



Promega result: 1ng, 500 pg, 200 pg



What about standards?

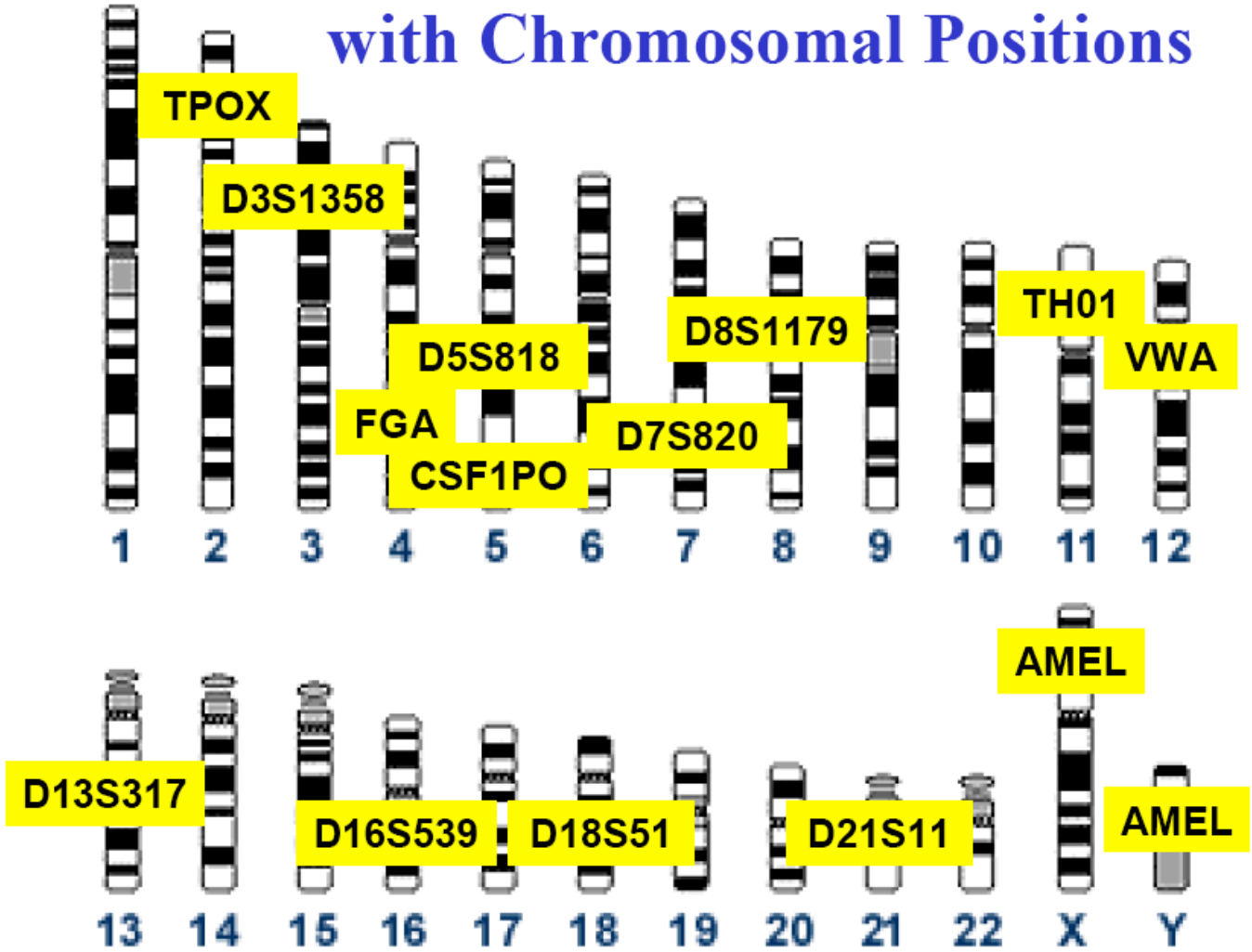
- FBI has defined 13 loci that are used in common in the kits from different companies
- And FBI keeps a database of results from testing of convicts, suspects, etc. called NDIS

FBI's CODIS DNA Database

Combined **D**NA **I**ndex **S**ystem

- Used for linking serial crimes and unsolved cases with repeat offenders
- Launched October 1998
- Links all 50 states
- Requires >4 RFLP markers and/or 13 core STR markers
- Current backlog of >600,000 samples

13 CODIS Core STR Loci with Chromosomal Positions



How it is done

- Probability of a single locus match if a suspect is heterozygous is calculated based on Hardy-Weinberg equilibrium.
- If there are 2 alleles, A1 and A2, then A1A1+2A1A2 +A2A2 = 1
- Proportion of A1A2 heterozygotes in a population is 2A1A2
- This actually holds for a gene with any number of alleles, so proportion of the population that matches = 2AnAm where An is an allele frequency of allele of length n.

How it is done

- Are human populations in Hardy-Weinberg equilibrium? Generally yes, though there are exceptions (some Indian tribes, for example)
- If there is inbreeding in a group, 2AnAm overestimates the match probability because inbreeding decreases proportions of heterozygotes - so using 2AnAm favors the defendant, and is therefore fair

How it is done

- What about homozygotes? Hardy-Weiberg says to use An^2, but there are two problems with this:
  - If the suspect is from an inbreeding subgroup, homozygotes are more frequent than in H-W equilibrium, so we are underestimating the random match probability, which makes the suspect seem, unfairly, more guilty
  - We can't really identify homozygotes anyway - they could be heterozygotes where we missed one allele (mutation in primer site, e.g.)

How it is done

- So the cautious approach that is used is to use 2An - for the allele that we are seeing - and to derive nothing from the one we may be missing.
- So now - how do we calculate?

How it is done

- For many unlinked loci (in linkage equilibrium), the match probability can be calculated by the product rule:
  - 2A1A7 x 2B3B4 x 2C8C9 x 2D7 (apparent homozygote)…
  - And allele frequencies are taken from large databases, and use the highest allele frequency in any breeding group (usually white, black, hispanic done separately).
- Formally, this is a match probability

How it is done

- We can make it a likelihood ratio: the ratio of probability that the suspect matches the sample, to the probability that a random person would match
- Since the suspect matches (or we wouldn't be bothering with calculations), that probability is 1
- The likelihood ratio therefore = 1/match probability

How it is done

- Suppose we had a match probability from 24 alleles (from the 13 CODIS loci) with frequency 0.25, where one locus had only one allele turn up - or $[2(0.25)(0.25)]^{12} \times 2 (0.25) = 7.2 \times 10^{-12}$
- $1/7.2 \times 10^{-12} = 1.4 \times 10^{11}$
- Therefore, the observation of a match is 1.4×10^{11} times more likely if the DNA sample came from the suspect than from a single randomly chosen person

How it is done

- THIS IS NOT to say that it is 1.4×10^{11} times more likely to come from the suspect than from ANYONE else (the prosecutors fallacy).
- To calculate THAT probability we use Bayes' theorem, that the Prior Odds (without DNA evidence) x Likelihood Ration (LR) = Posterior Odds

How it is done

- So what is the prior probability? This is the usual problem with application of Bayes' Theorem.
- Suppose we say that a total of 100 people on earth could have been at the crime scene at the appropriate time, and the suspect was there
- Then the Posterior Odds are 0.01:1 x 1.4 x 10^{11} = 1.4 x 10^{9}:1

How it is done

- What if it is a cold hit, that is, there is no evidence at all that the suspect was at the crime scene?
- Then the prior odds are, at the most extreme limit, 1: 6 x 10^9
- (1/ 6 x 10^9) x 1.4 x 10^{11} = 23:1
- So in a cold hit the odds that the sample came from the matched person in the database are 23:1, or 96%

How it is done

- A more reasonable prior odds might be the adult population of the US (the only population in the database is US felons and US crime samples), ~2 x 10^6, in which case the cold hit odds are 700:1, or 99.9%

- And once the cold hit is found, it still needs to be established that the suspect was in the area of the crime at the time of the crime, which would seal it
- Furthermore, a 15-locus test could be done on crime sample and suspect to make the odds astronomical

How it is done

- Is the person guilty then?
- DNA EVIDENCE DOESN'T SAY - IT ONLY SAYS THAT THE SAMPLE LIKELY COMES FROM THE SUSPECT
- There may be an innocent reason why someone's blood is found at a crime scene - DNA only provides evidence for a MATCH, not evidence of GUILT - which is for a jury to decide.

How it is done

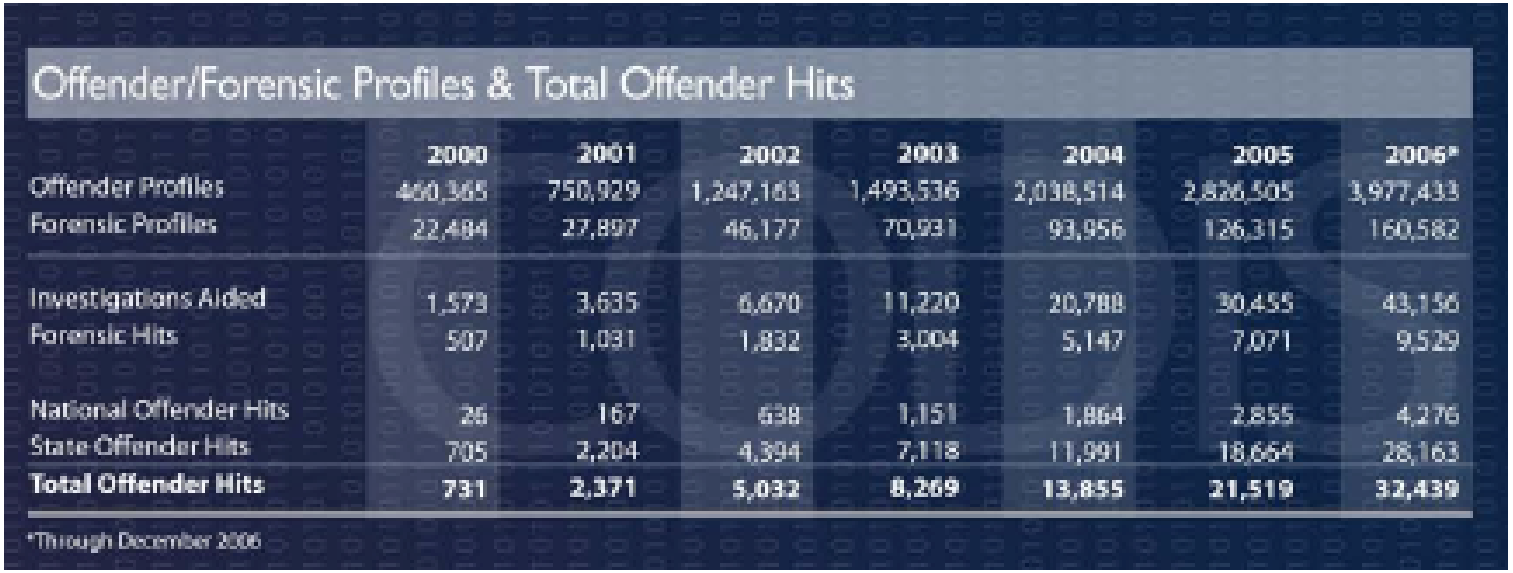
- And don’t forget what could be the most important use of DNA evidence - when the sample does not match the suspect.
- This provides absolute exclusion, and over 200 prisoners, many on death row, have been exonerated in the past decade by testing subsequent to conviction, and freed from prison

NDIS: National DNA Index System

- As of March 2007 the profile composition of the National DNA Index System (NDIS) is as follows:

- Total number of profiles: 4,510,617
- Total Forensic profiles: 170,763
- Total Convicted Offender profiles: 4,339,854

NDIS: National DNA Index System



Offender/Forensic Profiles & Total Offender Hits

	2000	2001	2002	2003	2004	2005	2006*
Offender Profiles	460,365	750,929	1,247,163	1,493,536	2,038,514	2,826,505	3,977,433
Forensic Profiles	22,484	27,897	46,177	70,931	93,956	126,315	160,582
Investigations Aided	1,573	3,635	6,670	11,220	20,788	30,455	43,156
Forensic Hits	507	1,031	1,832	3,004	5,147	7,071	9,529
National Offender Hits	26	167	638	1,151	1,864	2,855	4,276
State Offender Hits	705	2,204	4,394	7,118	11,991	18,664	28,163
Total Offender Hits	**731**	**2,371**	**5,032**	**8,269**	**13,855**	**21,519**	**32,439**

*Through December 2006

Problems:

- What if there are single nucleotide polymorphisms in primer binding sites?
- ·The AmpFℓSTR® Profiler Plus ® *ID* kit uses the same primers as the proven, reliable Profiler Plus kit and includes an additional single unlabeled primer for the D8S1179 locus. The inclusion of the unlabeled primer addresses a primer binding site mutation observed in a population of Chamorros and Filipinos from Guam, allowing the amplification of those alleles in samples containing this variant.
- Otherwise - get only 1 of 2 alleles, lose (1/ allele frequency) power

Problems:

- DNA degradation
  - Special kits for small DNA
  - Mitochondrial DNA
- DNA mixtures
  - Y chromosome analysis

Problems: Degraded DNA

FOSTER CITY, Calif. – February 13, 2007 – Applied Biosystems (NYSE: ABI), an Applera Corporation business, today announced the world's first commercially available reagent kit for generating genetic profiles from aged, compromised, or damaged DNA samples. The new AmpFlSTR® MiniFiler™ PCR Amplification Kit was developed in response to the growing backlog of samples recovered from crime scene investigations and other instances of DNA collection in which the samples could not previously be identified because of poor sample quantity or quality. The new kit is expected to enable an increase in the number of solved criminal cases, in addition to aiding in the investigation of missing person occurrences.

MiniFiler applies a new approach to standard DNA technology by shortening the fragments used to amplify DNA. These shortened regions are known as short tandem repeat (STR) regions or miniSTR technology. They allow analysis of very small fragments of DNA. STRs are repeated DNA sequences that are variable in length and are widespread throughout the human genome. Such variability allows discrimination among individuals in a population, which is useful for identification in forensic cases.

Problems: Degraded DNA

- Use mitochondrial DNA
  - Much greater abundance
  - No recombination
  - Sequence of D-loop variable region
- BUT - matrilineal inheritance only
- Limited number of informative sites

Problems: Mixed Samples

This kit enables forensic laboratories to identify, segregate, and analyze male DNA from sexual assault samples and other evidence-containing mixtures of male and female DNA.

The Applied Biosystems AmpFℓSTR® Yfiler PCR Amplification Kit co-amplifies 17 Y-chromosome STRs in a single PCR reaction. The kit includes the core European Minimal Haplotype set of loci recommen by the Scientific Working Group on DNA Analysis Methods (SWGDAM), plus six additional highly polymorphic loci, significantly increasing the kit's ability to discriminate and analyze haplotypes.

USES

- Suspect matches
- Cold hits
- Missing persons
- Scattered remains
- Historical questions
- Paternity testing (**1-800-Who's the Father)**
- Innocence project
- Fun with geneology, family history

Cold Hits

https://coldhit.doj.ca.gov/dna/stats.asp

State of California
5 / 16 / 2007

Profiles in State Offender Databank:	455,348
Cases Inventoried:	10233
Cases Screened:	9624
Cases Profiled:	6293
Cases Uploaded:	4412
Cold Hits:	758
Case-to-Case Matches:	380
Cold Hit Tracking System Users:	270

Arlington County Police Department
Your Case # 970212004
FS Lab # M97-1490
August 4, 1997

CONCLUSIONS:

Based on the above test results, the DNA profile obtained from the sperm fractions of the "left upper chest" swabs (Item 1), the crotch area stain from the underpants (Item 1) and the rear panel stain from the underpants (Item 1) as well as the DNA profile obtained from the "bitemark right upper back" swabs (Item 1) is consistent with the DNA profile of Marvin Albert. Therefore, Marvin Albert cannot be eliminated as a possible contributor of the genetic material isolated from these samples.

The probability of randomly selecting an unrelated individual with a matching DNA profile (HLA DQA1, PM, CTT and D1S80) as obtained on the crotch area and rear panel stains from the underpants (Item 1) and the "bite mark right upper back" swabs (Item 1) is approximately:

1 in 2.6 billion in the Caucasian population

1 in 670 million in the Black population

1 in 1.1 billion in the Hispanic population

Cold Hits

Oakland Tribune, Jan 3, 2006 by Malaika Fraley, STAFF WRITER

REDWOOD CITY -- San Mateo County's first trial based on "cold hit" DNA evidence is under way with opening statements set to begin this week.

Former Menlo Park resident Jose Luis Villeda, 24, faces life in prison without the possibility of parole for allegedly raping a woman on Halloween in 1999 in Menlo Park.

The case remained unsolved until 2004, when the state's DNA data bank of genetic samples from convicted felons produced what is called a cold hit and matched Villeda to seminal fluid collected after the 1999 rape.

Villeda was required to submit a genetic sample to the data bank in 2003 upon his arrival at Pleasant Valley State Prison, where he was serving a three-year sentence for an attempted rape of a woman in May 2002 Redwood City.

In that case, Villeda dragged a woman walking to the Caltrain depot behind the Sequoia Station Safeway. The attack was stopped by store employees who heard the woman's scream

DNA convicts man of rape
Oakland Tribune, Jan 7, 2006 by Malaika Fraley, STAFF WRITER

REDWOOD CITY -- A jury convicted former Menlo Park resident Jose Luis Villeda on Friday of rape, kidnapping and robbery in a six- year-old case solved using DNA evidence.

USES: Missing Persons

Customer Focus

Applied Biosystems

California Missing Persons DNA Program Challenged with Identifying Thousands of Human Remains

John Tonkyn, Ph.D.

Director, Missing Persons DNA Program
Department of Justice,
California

Application:

- Testing Solutions
- Human Identification

Applied Biosystems Technology:

- ABI PRISM® 3100 Genetic Analyzer
- ABI PRISM® 310 Genetic Analyzer
- AmpFℓSTR® PCR Kits
- ABI PRISM® GeneScan® Software
- ABI PRISM® Genotyper® Software

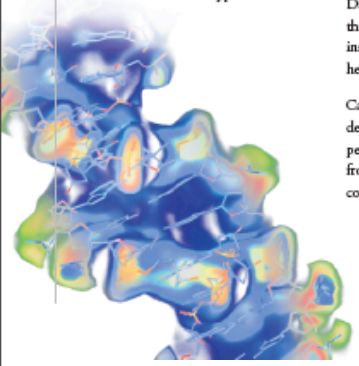
Each year in California the identity of approximately 100 deceased people cannot be made. Currently the state has records of 2,100 such remains, some dating as far back as 1959. It is the task of John Tonkyn, Ph.D., who directs the new Missing Persons DNA Program at the California Department of Justice (DOJ), to apply modern DNA technology in an attempt to solve these cases. If successful, the program will provide a measure of closure to the families of the deceased as well as assist ongoing police investigations.

Dr. Tonkyn, a molecular biologist, has worked at the DOJ for almost eight years. He is also the supervisor in the Convicted Offender DNA Databank Program where he worked to develop and validate Short Tandem Repeat (STR) DNA typing for both casework and convicted offender databank analysis. He has trained forensic scientists throughout California and other states on the use of STR typing for forensic analysis. In 2002, Dr. Tonkyn began directing the newly formed Missing Persons DNA Program.

Identification of missing persons is challenging. *"There have been about 3,000 long-term missing persons reported in California since 1972. Approximately 150 individuals are categorized as high-risk missing persons each year—those missing as a result of stranger abductions, suspicious circumstances, or have been missing more than 30 days,"* Dr. Tonkyn reports.

The DOJ program aims to use DNA analysis for identification whenever possible. Dr. Tonkyn and his staff rely on a whole suite of Applied Biosystems products for this work. Applied Biosystems donated a new ABI PRISM® 3100 Genetic Analyzer instrument and $150,000 worth of DNA reagents for human identification to help fund this worthwhile program.

California legislation now requires coroners to take tissue samples from unidentified deceased persons for DNA testing. Genotyping results from unidentified missing persons are stored in one database. A second database stores genotyping results from relatives of the missing persons. The DOJ makes the identification by comparing the two databases and finding a match.



For more customer stories, go to www.biobeat.com

Many of California's crime labs have standardized on Applied Biosystems technology—AmpFℓSTR kits for STR amplification, with analysis on the validated ABI PRISM® 310 or 3100 Genetic Analyzers and data analysis software.

The AmpFℓSTR® PCR kits amplify STRs, combining PCR-based testing and fluorescent detection to provide the highest possible discrimination. The kits are designed for laboratories analyzing forensic casework, establishing DNA databanks, processing paternity samples, and matching specimens.

Analysis of the PCR products is performed on one of Applied Biosystems newest capillary electrophoresis instruments. The ABI PRISM® 3100 Genetic Analyzer is a 16-capillary system operating in parallel to analyze hundreds of samples every day. Like its predecessor, the ABI PRISM® 310 Genetic Analyzer, the 3100 instrument is validated for forensic casework. ABI PRISM® GeneScan® and Genotyper® software analyze the data.

The DOJ also uses Applied Biosystems human identification technologies in their Convicted Felon DNA Data Bank to compare DNA evidence from crime scenes against the DNA of approximately 200,000 convicted criminals. Established in 1994, the databank has identified over 300 suspects.

California Senator Jackie Speier commended Applied Biosystems for its donation of the instrument and reagents in a resolution, which in part stated *"…Applied Biosystems DNA equipment and materials are used in nearly every crime lab in the nation and throughout the world, and crime labs have used Applied Biosystems equipment to help solve thousands of otherwise unsolvable rapes and homicides, and to help identify missing persons…"*

Science

iScience. To better understand the complex interaction of biological systems, life scientists are developing revolutionary approaches to discovery that unite technology, informatics, and traditional laboratory research. In partnership with our customers, Applied Biosystems provides the innovative products, services and knowledge resources that make this new, Integrated Science possible.

Applied Biosystems

Mass Fatalities: http://massfatality.dna.gov/

SEPTEMBER 2006

Lessons Learned From 9/11: DNA Identification in Mass Fatality Incidents

PRESIDENT'S DNA INITIATIVE

www.DNA.gov

Preface

On September 11, 2001, 2,792 people were killed in terrorist attacks on the World Trade Center (WTC) in New York City. The number of victims, the condition of their remains, and the duration of the recovery effort made the identification of the victims the most difficult ever undertaken by the forensic community in this country.

In response to this need, the National Institute of Justice (NIJ), the research, development, and evaluation agency of the U.S. Department of Justice, brought together a group of experts to provide advice and support throughout the identification effort. Called the Kinship and Data Analysis Panel (KADAP), the group made recommendations on new forensic technologies, tools, policies, and procedures to help identify those who perished in the WTC attack.

This report contains the KADAP's "lessons learned," particularly regarding DNA protocols, laboratory techniques, and statistical approaches, in the DNA identification of WTC victims. It is written primarily for the Nation's forensic laboratory directors and other officials who may be responsible for organizing and managing the DNA identification response to a mass fatality incident.

Although New York City's mass disaster plan on 9/11 contained lessons learned from the 1993 terrorist bombing of the WTC, it did not contain policies or procedures for identifying mass disaster victims through DNA analysis. Had this been part of the city's plan in 2001, many of the issues that arose after the attacks could have been more quickly resolved.

This report discusses the incorporation of DNA identification into a mass fatality disaster plan, including how to:

- Establish laboratory policies and procedures, including the creation of sample collection documents.
- Assess the magnitude of an identification effort, and identify and acquire resources to respond.
- Identify reference and kinship samples.
- Create a comprehensive laboratory management plan, including technology management and quality assurance.
- Establish lines of communication between agencies, departments, victims' families, and the press.

Although this report does not address every aspect of a mass fatality DNA identification effort, it does stress intentional testing redundancy as a way to monitor a system's effectiveness. The report also discusses how decisions made in the first 48 hours after a mass fatality event shape the scope of the identification effort.

Designed to augment another NIJ publication, *Mass Fatality Incidents: A Guide for Human Forensic Identification* (http://www.ojp.usdoj.gov/nij/pubs-sum/199758.htm), this guide will help the Nation's forensic laboratories—whether called upon to identify victims of a major natural disaster, transportation accident, or terrorist attack—prepare for a mass fatality incident.

Historical Cases

Honor guards carry coffins containing the supposed remains of Czar Nicholas II and his wife Alexandra to St. Peter and Paul Cathedral in St. Petersburg on July 16, 1998. The bones were flown to the country's old imperial capital and readied for burial, 80 years after the monarch was forced into Siberian exile and executed.

DNA Test Confirms Dead Czar's Identity

A new genetic analysis may finally allow former Russian Czar Nicholas Romanov II to rest in peace. On the night of July 16, 1918, a firing squad of Bolshevik soldiers executed the Russian royal family, including Nicholas, and buried the bodies in a hidden mass grave. The burial site finally came to light in 1989, and 2 years later nine skeletons were excavated.
Though forensic analyses of the bones, clothing, and other material from the grave have provided strong evidence that some of the skeletons belonged to the czar and his family, attempts to confirm the identifications by analyzing DNA smaples have provoked controversy. When researchers compared DNA from bones presumed to be those of Nicholas II with DNA from two living relatives, they found an unusual mismatch.

DNA is composed of long sequences of building blocks called nucleotides, which come in four forms that geneticists label A, C, G and T. The bits of DNA from the skeleton and Nichlas II's relatives matched perfectly except at one position. At a nucleotide site where both living relatives had a T, some of the DNA samples from Nicholas' bones had a T but others had a C. Such a variation is a rare condition called heteroplasmy.

Despite the difference, investigators proclaimed that Nicholas had been identified. Yet the Russian Federation government and the Russian Orthodox Chruch, which is considering canonizing the entire Romanov family, demanded further proof. In July of 1994, researchers resorted to exhuming the body of Georgij Romanov, Nicholas' younger brother, who had died of tuberculosis in 1899.

Like Nicholas's DNA, Gerogij's had either C or T present at the controversial site, report Pavel L. Ivanov of the Russian Academy of Sciences in Moscow and a team from the Armed Forces DNA Identification Laboratory in Rockville, Md., led by Thomas J Parsons. The team describes its findings in the April Nature Genetics.

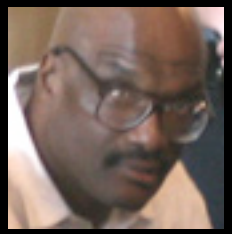
Innocence Project

http://www.innocenceproject.org/

The Innocence Project is a national litigation and public policy organization dedicated to exonerating wrongfully convicted people through DNA testing and reforming the criminal justice system to prevent future injustice.

DNA testing has proven that 201 innocent people
spent nearly 2,500 years in prison for crimes they didn't commit

Breaking News: Byron Halsey's Conviction Overturned After 19 Years in NJ Prisons



Innocence Project

After 19 Years in Prison for One of the Most Heinous Crimes in NJ History, Byron Halsey Is Proven Innocent through DNA

DNA indicates that another man – who testified against Halsey two decades ago – is the actual perpetrator; Halsey's conviction set to be vacated today

(ELIZABETH, NJ; May 15, 2007) – New DNA tests prove that Byron Halsey, who narrowly escaped the death penalty when he was convicted in 1988 of the brutal sexual assault and murders of two young children, is innocent and should be released from prison, the Innocence Project said today. At a hearing today in New Jersey state court, a judge is expected to grant a joint motion to vacate Halsey's conviction filed by the Innocence Project and the Union County District Attorney's Office.

The motion to vacate the conviction says that DNA testing on several key pieces of evidence used to convict Halsey actually indicates the guilt of another man, Cliff Hall, who is already in prison for several other sex crimes in New Jersey and who testified against Halsey during his trial. In March 1988, Halsey was convicted of several charges stemming from the November 1985 murders of a seven-year-old girl and an eight-year-old boy he was raising with his girlfriend; Hall, who lived next door to the family, had dropped Halsey off across town and then returned home on the night the children were brutally killed.

"Today, we can say with scientific certainty that Byron Halsey is innocent. Every piece of physical evidence connects Cliff Hall, not Byron Halsey, to these murders," said Vanessa Potkin, Staff Attorney at the Innocence Project, which is affiliated with Cardozo School of Law at Yeshiva University. "It has taken more than two decades, but DNA has finally revealed the truth in this case."

The physical evidence that was subjected to DNA testing over the last 14 months includes key evidence that was used at Halsey's trial (when advanced DNA testing was not available):

- Semen on the seven-year-old girl's underwear (which was stuffed into her mouth during the rape and murder); the prosecution said during the trial that the semen came from someone with the same blood type as Halsey, but DNA testing now shows that the semen was from Cliff Hall.
- Semen at the crime scene, which was also matched to Halsey's blood type but is actually from Cliff Hall, DNA shows.
- A cigarette butt found at the crime scene, which was central to the initial police investigation of the crimes. DNA testing shows that the cigarette butt was Cliff Hall's.

DNA Paternity Testing.

Get the truth.

There is only one truth about paternity: either he's the father (inclusion) or he is not (exclusion). It takes just minutes to collect a simple swab sample from inside the mouth, and you'll receive conclusive results in just 3 to 5 business days. With Genetrack's technical support team, you'll receive full technical support every step of the way. Find out the truth that will last a lifetime.

Click here to order kit

$125 US - Results in 3 to 5 days.

Home Paternity Test Kit Fee Schedule for Year 2007

Results in 3 to 5 working days

Test Type	Private Kit	Court Admissible Kit
1 child, 1 alleged father	$125 US	$230 US
2 children, 1 alleged father	$210 US	$315 US
3 children, 1 alleged father	$295 US	$400 US
1 child, 2 alleged fathers	$210 US	$315 US
1 child, 1 alleged father, 1 mother	$125 US	$230 US
2 children, 1 alleged father, 1 mother	$210 US	$315 US
3 children, 1 alleged father, 1 mother	$295 US	$400 US
1 child, 2 alleged fathers, 1 mother	$210 US	$315 US

ORCHID GENESCREEN

GENETIC TEST REPORT

SAMUEL H SLOAN
1664 DAVIDSON AVE
APT 1B
BRONX, NY 10453

GS Case/Test Set: 934245 / 694004
Customer Number: EAC0311752442
18803

	Race Description	Specimen ID	Specimen Collection
Mother: KIMURA, KAYO	Asian	1558401	08/31/2005
Child: SLOAN, SANDRA KIMURA		1558402	08/31/2005
Alleged Father: SLOAN, SAMUEL H	Unspecified	1558403	08/31/2005

Combined Paternity Index = 36,590 to 1
Probability of Paternity = 99.99%

Conclusion

The alleged father, SAMUEL H. SLOAN, cannot be excluded as the biological father of SANDRA KIMURA SLOAN. Based on the genetic testing results, the probability of paternity is 99.99% when compared to an untested random man of the North American population. (Prior Probability = 0.5) At least 99.99% of the North American population is excluded from the possibility of being the biological father of the child.

System	Mother	Child	Alleged Father	Paternity Index
D3S1358	15, 16	16	16	3.04
vWA	18, 19	17, 19	16, 17	1.85
FGA	23, 25	21, 23	21	5.65
D8S1179	13, 14	13, 14	10, 14	0.76
D21S11	30, 31	30, 32.2	31, 32.2	4.72
D18S51	14	13, 14	13, 18	3.97
D16S539	9, 10	9, 11	11	3.14
TH01	6	6, 9.3	7, 9.3	1.66
D2S1338	23, 26	23, 25	19, 25	4.17
D19S433	12.2, 15.2	13, 15.2	13	2.72

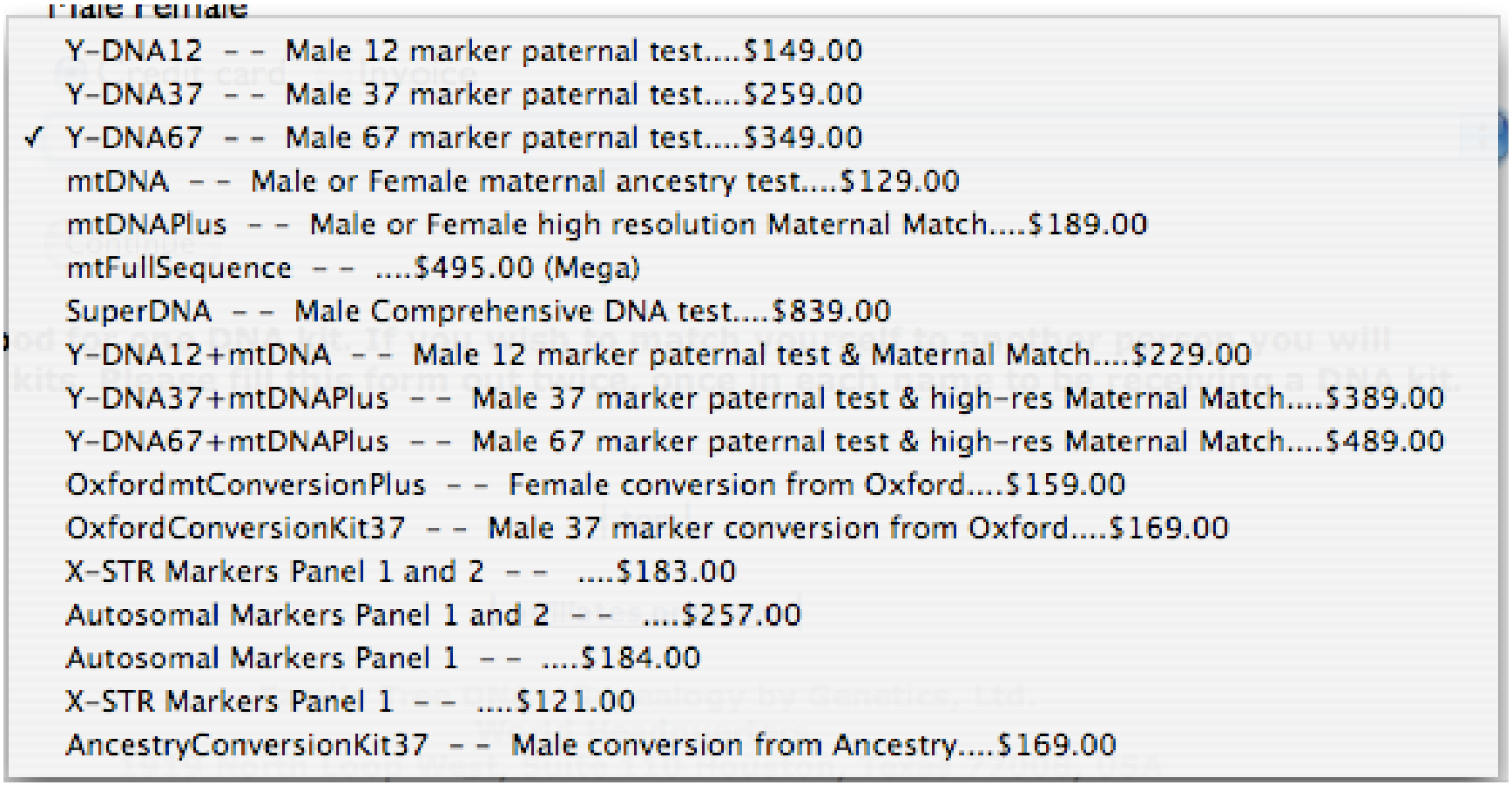
Subscribed and sworn before me on September 06, 2005
in Ingham County, Michigan

Notary Public, State of Michigan,
County of Ingham, Exp

I certify that the foregoing testing was conducted in accordance with the standard protocol and the results contained herein are true and correct to the best of my knowledge.

Marco Scarpetta, Ph.D., Laboratory Director

familytreedna.com



Carpenter Cousins Y-DNA Project

To join: http://www.familytreedna.com/surname_join.asp?code=S82066

This page last updated: 2007 May 4
Web page maintainer: John F. Chandler

Table of Contents

Background

This Y-DNA project was started in September 2002 after a Carpenter discussion group had been held in Clearwater, Florida. One item of discussion was how Y-DNA research could help Carpenter genealogy. Some of the most important questions where Y-DNA testing could help were:

- Were the two William Carpenters who came to America in the 1630's related? The answer is YES. Groups 2 and 3 respectively reflect these two ancestors.
- Could similar Y-DNA markers from an unknown ancestral lines help researchers contact others on the same line? The answer is YES. This project has already shown some Carpenter researchers with no previously known connection that they are related and prompted them to compare notes.
- Could we determine that some Carpenter lines are unrelated to others, such as the Carpenters of English ancestry and those of German/Swiss ancestry? The answer is YES. This project has identified many genetically distinct Carpenter lines, both English and German, and all of the German lines have proven to be different from all of the English lines and from each other.
- Could we connect emigrant lines to Carpenters or Zimmermans still living in the homelands? The answer is presumably yes, but we have not yet recruited many European participants. Stay tuned for future developments.
- Could the Y-DNA research cause many more questions to be asked? The answer is YES. The more we learn the more questions we have!