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DNA Fingerprinting E08

Jason Krug
Worcester Polytechnic Institute

Randi Nicole Pawson
Worcester Polytechnic Institute

William J. Lyons
Worcester Polytechnic Institute

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DNA FINGERPRINTING

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By:

Jason Krug	William Lyons	Randi Pawson

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APPROVED:

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Prof. David S. Adams, Ph.D.
Project Advisor

ABSTRACT

The purpose of this IQP was to inform the reader about the growing technology of DNA profiling, and to discuss how this powerful technology affects today's society and our justice system. As background, this IQP described each step of creating DNA fingerprints. Also, procedures on how to find, collect, and store DNA evidence were described. DNA court cases that laid the foundation for the inclusion of complex technology in the justice system were explained, as were a few sensational cases which has made the process of DNA fingerprinting famous. Last, this IQP discusses the controversies caused by DNA databases and the ethics of DNA fingerprinting.

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PROJECT OBJECTIVE

This project's goal was to extensively research DNA fingerprinting, the technology behind it, and the future of this revolutionary forensic tool, to help determine its impact on society. The usefulness of DNA fingerprinting in forensic science is endless. With this technique, crime in today's world could be investigated more fully, with higher rates of conviction of the guilty, and exoneration of the innocent. To achieve this goal, DNA collection procedures, DNA testing practices, and court protocols were studied. The legal and ethical aspects of privacy rights in DNA fingerprinting were also broadly researched.

Chapter-1: DNA Fingerprinting, Description and Types

DNA fingerprinting is used in forensic investigations as a means to identify persons by comparing DNA evidence found at the crime scene to that of a suspect. Although two humans do have much of their DNA in common (which makes us human), there are certain variable sections of DNA that two unrelated people are not likely to share. DNA profiling exploits these varying DNA segments in distinguishing between persons, to provide a tool that has been termed the greatest tool in the history of forensic science.

Cells

Let's begin by studying where DNA originates. The smallest living unit of an organism is called a cell. A human cell contains many individual parts, each with its own function. The cell membrane is a semi-permeable substance that can protect the cell by allowing, partially allowing, or not allowing, certain substances to enter or exit the cell. The cytoskeleton (Figure 1.1, item 7) gives the cell its shape and keeps each of the organelles in place. Ribosomes (Figure 1.1, item 3) build proteins for the cell. Cytoplasm (Figure 1.1, item 11) is a gelatinous substance that holds necessary materials and the other organelles. Mitochondria (Figure 1.1, item 9) provide energy to the cell by means of a chemical reaction known as respiration. The endoplasmic reticulum (Figure 1.1, item 5 [rough] and item 8 [smooth]) is used to transport specific substances where they need to go in the cell. The Golgi apparatus (Figure 1.1, item 6) is used to process large molecules (macromolecules), such as proteins, to transform them to something useful to the cell. Lysosomes (Figure 1.1, item 12) are like the stomach of the cell, in their function of digesting food particles, but it also digests extra organelles along with viruses

and bacteria. Vacuoles (Figure 1.1, item 10) are storage space for food and waste within the cell. Vesicles (Figure 1.1, item 4) are small sacs that store substances to be processed elsewhere in the cell. The centrosome (Figure 1.1, item 13), composed of two centrioles, organizes the cytoskeleton and dictates how substances pass through the endoplasmic reticulum and the Golgi apparatus. With respect to this IQP, the nucleus (Figure 1.1, item 2) contains the genetic material that we are interested in for DNA fingerprinting.

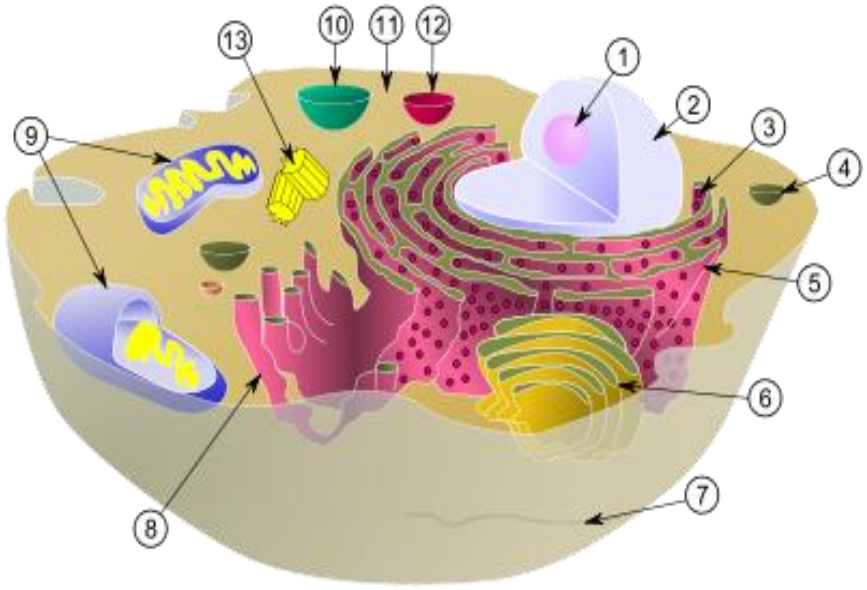

Figure 1.1 – Diagram of an Animal Cell
(Biological Cell, 2006)

Nuclei

The nucleus of a cell (Figure 1.2) is protected from the rest of the organelles by the nuclear envelope, which consists of an inner and outer membrane that stops macromolecules from transferring between the cytoplasm outside of the nucleus and the nucleoplasm inside. Nuclear pores are made of proteins, together called nucleoporins, and they allow for small

molecules to pass freely in and out of the nucleus. Larger molecules that need to pass through the nuclear membrane require the use of special proteins called karyopherins, which act as transport proteins. During cellular interphase, the part of the cell cycle when the cell is not dividing, genetic material is found in the chromatin, with the chromatin separated into the heterochromatin and the euchromatin. Euchromatin contains chromosomes that are transcribed more often than those found in the heterochromatin. The process of transcription copies DNA to create RNA that is used in the production of proteins. During mitosis when the cell is dividing, the DNA is found in chromosomes.

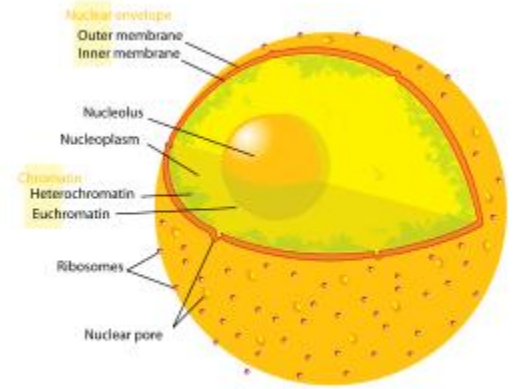

Figure 1.2 – Diagram of a Cell Nucleus
(Cell Nucleus, 2007)

Chromosomes

Within the nucleus, a singular chromosome is a singular piece of DNA, which contains the cell's genetic material along with DNA-related proteins used in genetic functions. During cell division, the chromatin becomes denser, and the four arm structure commonly associated with chromosomes arises, as shown in Figure 1.3 below:

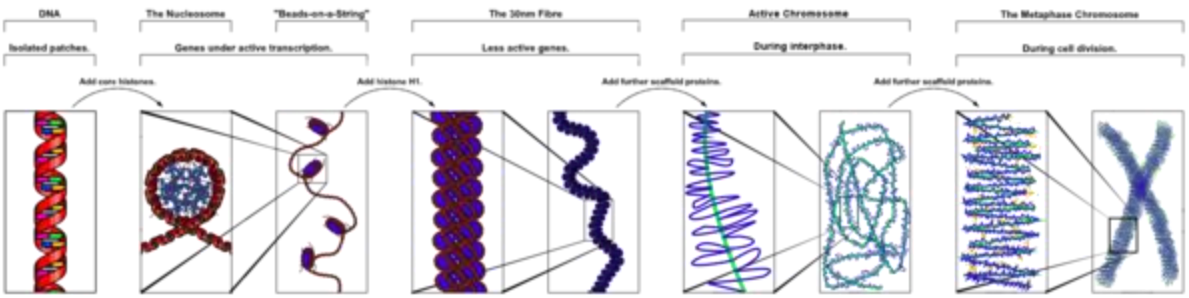

Figure 1.3 – Chromosome Composition
(Chromatin Structures, 2008)

During cell division, the process of transcription stops, and the strands of DNA condense as shown above. In the four arm structure, the point where the strands cross is called the centromere. Around the centromere are the repetitive sequences that are important to DNA fingerprinting. The human species has forty six chromosomes, as shown in this karyogram below (Figure 1.4):

Figure 1.4 – Karyogram of a Male Human
(Genome.gov, 2008)

DNA

DNA is an acronym for deoxyribonucleic acid, a macromolecule whose primary function is to store genetic information. One could say that DNA is the blueprint of life, since one's genes carry the instructions to build proteins, RNA, and other necessities of the cell. DNA is made of repeating nucleotides, each consisting of a phosphate and a sugar as a backbone, and a

base (Figure 1.5). The bonds in the backbone of the polymer are asymmetric, which causes each strand to have a direction. In DNA, the two backbones run in opposite directions of each other, and thus the strands are said to be antiparallel. Four bases make up the section of DNA unique to every creature: adenine (A), cytosine (C), guanine (G), and thymine (T). Chemically, adenine and guanine are fused five- and six-membered rings known as purines. Cytosine and thymine are classified as pyrimidines, six-membered rings with two nitrogen atoms at the one and three positions (separated by 2 bonds).

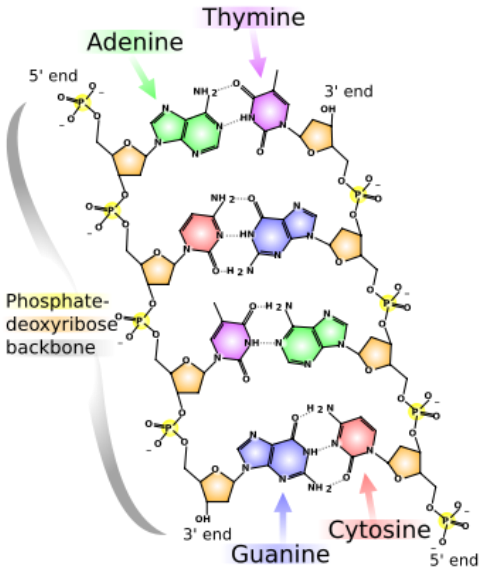

Figure 1.5 – Molecular Structure of DNA
(DNA Chemical, 2007)

The two strands of DNA are not actually covalently bonded together. There is only an intermolecular attraction between the bases called a hydrogen bond. Hydrogen bonds form between molecules when one molecule has an exposed hydrogen atom and the other has an exposed electronegative atom (for the case of DNA, the electronegative atoms are oxygen and nitrogen). The electron rich oxygen or nitrogen attracts the electron poor hydrogen, and thus the molecules are weak (compared to covalent bonds within a molecule) attracted to each other. Due

to their respective chemical geometries, adenine can only hydrogen bond with thymine, and guanine can only hydrogen bond with cytosine, as shown below (Figure 1.6). Each corner in the figure is a carbon atom unless labeled as hydrogen, nitrogen, or oxygen. Solid lines represent covalent bonds between atoms of a molecule. Two solid lines represent a double covalent bond. Curved lines are the bonds between the base and the phosphate-sugar backbone, and dashed lines represent the hydrogen bonds between the bases.

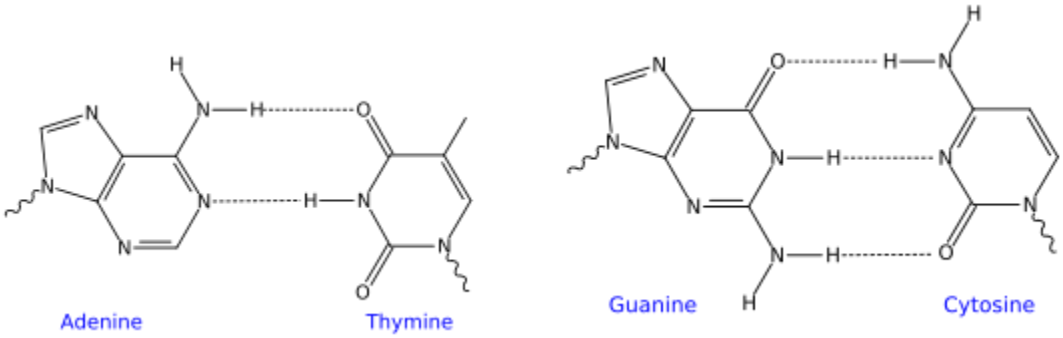

Figure 1.6 – **Hydrogen Bonding Between the Base Pairs of DNA** (left: AT pair, right: GC pair) (AT DNA, 2007 and GC DNA, 2007) (Wikipedia, 2007)

Because the two strands in DNA are only held together by hydrogen bonds, a sufficient force or even a high temperature can easily unzip the DNA molecule. This fact, along with that only one base can bond with one other base, is crucial to DNA replication, and thus also cell replication. This complementary mode of replication, and strand denaturation at elevated temperatures by breaking weak hydrogen bonds, will also be discussed in the section on PCR for forensics. Notice that guanine and cytosine have three hydrogen bonds, while adenine and thymine have only two hydrogen bonds. Thus, DNA chains that have many AT pairs are easily unzipped, while chains that have more GC pairs are harder to separate. In most standard forensic situations, it turns out that DNA strands that need to be opened frequently are rich with adenine and thymine.

DNA Loci

A locus, is a genetic term that denotes a specific location in the DNA strand. An example of a locus is 22q12.2 (Figure 1.7). Twenty two represents chromosome number 22, q represents the long arm (p for the short arm), 12 means band number 12, and .2 is a sub-band. Thus, 22q12.2 means the second sub-band in the twelfth band from the centromere of the long arm of chromosome number twenty two. The ends of the chromosome are called telomeres, and they are represented in the locus as "qtel" or "ptel," such that 22qtel would be the telomere of the long arm of chromosome 22.

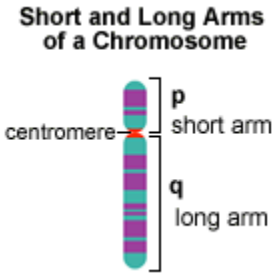

Figure 1.7 – Arms of a Chromosome
(Oak Ridge, 2003)

In the United States, 13 core loci are analyzed during genetic profiling and entered into the CODIS (Combined DNA Index System) database (Figure 1.8). As discussed in more detail in chapter-5, these core loci have been chosen for standard forensic analysis due to their very high levels of uniqueness in human populations, and their ease of testing. Table 1.1 outlines their placement on human chromosomes and the general nucleotide repeating pattern that is observed (Repeats will be discussed later in this chapter).

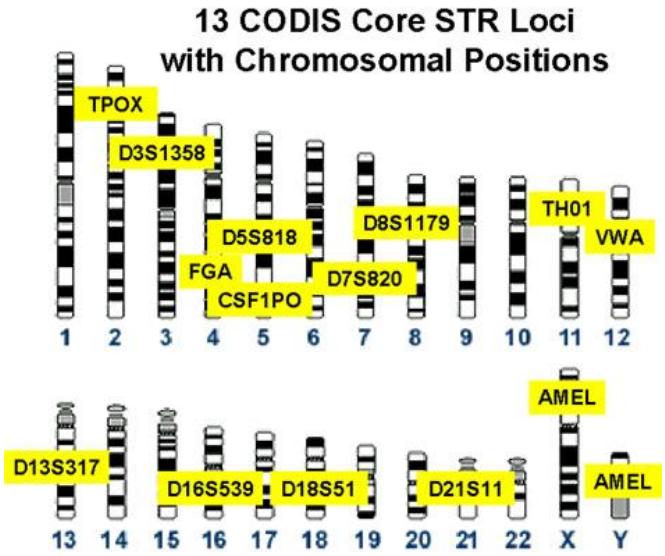

Figure 1.8 – The Now Standard Thirteen Core Loci for the CODIS Database (Butler, 2008)

Table 1.1 – Summary of the 13 Core Loci (Butler, 2008)

Locus Name	Locus Position	Expected Repeat
CSF1PO	5q33.1	[AGAT]
FGA	4q28	$[TTTC]_3TTTTTTCT[CTTT]_nCTCC[TTCC]_2$
TH01	11p15.5	[AATG], [TCAT]
TPOX	2p25.3	[AATG]
VWA	12p13.31	[AGAT], [TCTA] with [TCTG] and [TCCA] inserts
D3S1358	3p21.31	[AGAT], [TCTA]
D5S818	5q23.2	[AGAT]
D7S820	7q21.11	[GATA]
D8S1179	8q24.13	[TATC]
D13S317	13q31.1	[GATA], [TATC]
D16S539	16q24.1	[GATA]
D18S51	18q21.33	[GAAA]
D21S11	21q21.1	[TCTA], [TCTG]

RFLP DNA Analysis

The two main ways for analyzing a DNA fingerprint are amplifying (PCR) versus non-amplifying (RFLP), for viewing short tandem repeats (STR) or longer tandem repeats (VNTR). The non-amplifying techniques are older, and take larger amounts of DNA from a crime scene sample to be successful, but are still in use today for analyzing DNA that might have small amounts of contamination since they are more immune to contamination. An example of a non-amplifying technique is Restriction Fragment Length Polymorphism (RFLP). In RFLP analysis, a restriction enzyme is used to cut the DNA in specific locations where a unique sequence is found (Figure 1.9). Then, agarose gel electrophoresis is used to separate the cut DNA segments by length. In electrophoresis, the DNA sample is placed in a gel, and an electric current passes through, pulling the DNA through the gel in a fashion that allows the smaller segments to move farther through the gel than larger ones. After electrophoresis, a Southern blot procedure (named after Edward Southern) labels specific sequences in the DNA. In a Southern blot, the separated-by-length DNA is transferred to a membrane, and a hybridization probe (labeled either with a dye or radioactivity) is applied. The hybridization probe attaches itself to a pre-determined complementary sequence in the DNA, and that strand of DNA will now be noticeable under a microscope (or X-ray film, depending on the labeling method).

The RFLP method for analyzing DNA is not as currently well known as the PCR-based STR method because the latter is faster and can be done on trace amounts of DNA. So the STR method is often used first on a DNA sample, then if contamination is thought to be a problem, and enough DNA has been isolated, the non-amplifying RFLP method is used.

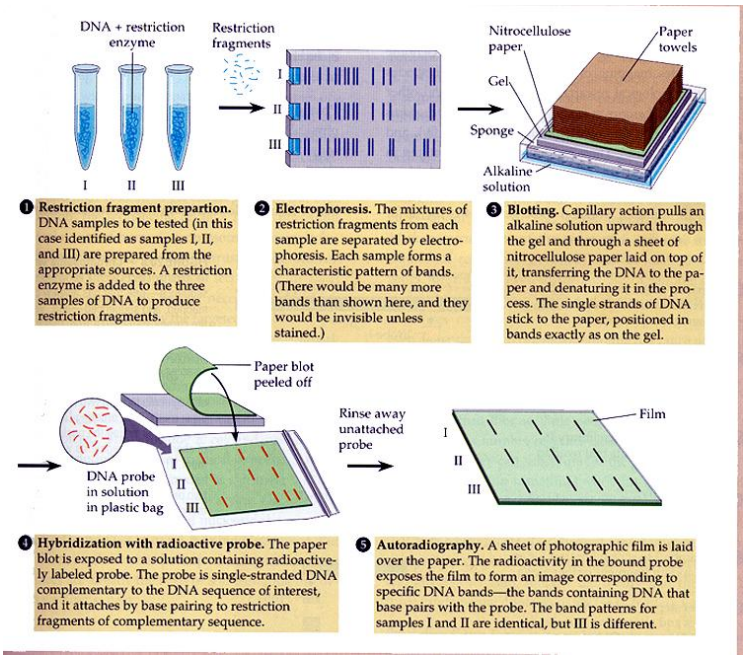

Figure 1.9 – Procedure of RFLP Analysis
(Pawlik, 2008)

With respect to DNA fingerprinting, an RFLP occurs when the hybridized (visualized) labeled DNA fragments are different lengths between persons. An example of an RFLP is pictured below (Figure 1.10). Notice that the one long DNA segment in the right lane for the disease sample does not travel as far as the two smaller segments in the normal sample.

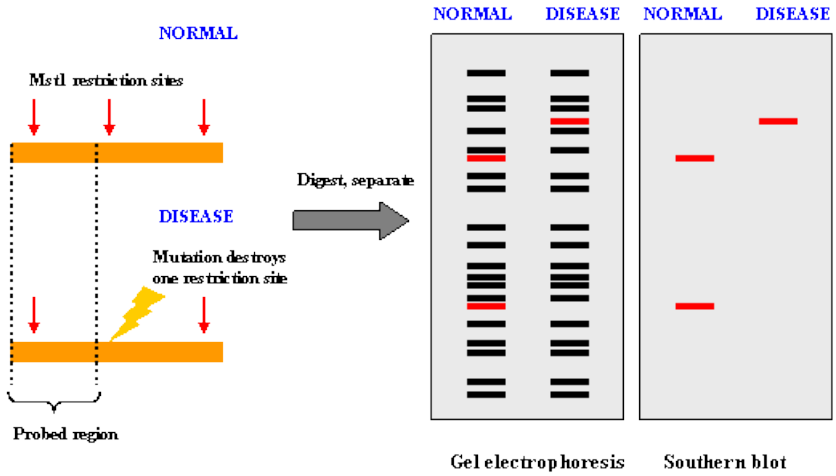

Figure 1.10 – Example of an RFLP Due to Mutation
(Schuler Group, 2008)

VNTR's

Another way the RFLP technique can distinguish between individuals is by variable number of tandem repeats (VNTR's). Shown below is an example of a VNTR, with each of the individual repeats shown as shaded blocks, and the rest of the DNA chain as lines. VNTR's occur in some DNA loci frequently enough to be the basis of DNA fingerprinting. If the segment of DNA to be probed for an RFLP was a section that contained a VNTR, two individuals could have fragments of different lengths because one could have a different number of repeats, thus the labeled strand would travel different distances in the gel. VNTR's follow two rules: they are inherited, and they vary between unrelated individuals, so it is very useful in paternity testing and in criminal forensics. VNTR's are divided into two categories, microsatellites and minisatellites. No rule is set in stone to differentiate between the two except that microsatellites usually contain about five base pairs or less, and minisatellites contain more base pairs.

Figure 1.11 – Example of a VNTR for Four Different Alleles. Note the different number of shaded blocks (VNTR repeats) for each sample, which would create DNA fragments of different lengths (VNTR Example, 2008).

STR's

Short Tandem Repeats (STR's) fall into the microsatellite category, and, combined with the PCR (polymerase chain reaction) technique, can provide a full DNA profile from very small samples of DNA. Short tandem repeats in use today are usually four or five nucleotide repeats

that provide DNA fragments short enough to amplify by PCR. Much longer repeats require the RFLP method of analysis. Shorter repeat sequences are susceptible to errors, while longer sequences degrade more easily and are not easily amplified by PCR. STR's appear in the non-coding region of DNA, making it junk DNA, or DNA where no function has been assigned to it.

PCR Analysis

The polymerase chain reaction (PCR) technique is the more common technique to analyze DNA, as it is able to make billions of copies of DNA from a very small sample of genetic material. A DNA polymerase is an enzyme that can piece together the complimentary strand of DNA from a single strand of DNA template using deoxynucleoside triphosphates (dNTPs) as precursors. A dNTP can be thought of as a single nucleotide that the DNA polymerase uses to put together the new DNA strand. Also required for PCR to work are two primers complimentary and flanking to the DNA region to be analyzed, one for the five prime end, and one for the three prime end. Other reagents include a template that contains the target DNA to be copied; buffer solution, which creates a suitable chemical environment for the reaction; divalent cations, such as Mg^{2+} which serves as a co-factor for the polymerase; and monovalent potassium ions to provide optimal salt concentrations.

PCR starts with denaturing the DNA template by heating the reaction vessel to 94°C (just underneath boiling temperature), which essentially melts the DNA into two separate strands by breaking the weak hydrogen bonds between the bases (Step 1, Figure 1.12). Next, the annealing step cools the reaction to about 54°C, which allows the primers to form hydrogen bonds with their respective ends of the DNA strands (Step 2, Figure 1.12). Third, the extension step is carried out at 72°C, the optimal temperature of the DNA polymerase, where the enzyme pieces

together the DNA strand in the 5' to 3' direction of the primer, and doubles the amount of DNA that the cycle started with (Step 3, Figure 1.12). Multiple cycles continue the exponential growth, where you get $m*2^n$ DNA molecules, where n is the number of cycles, and m is the number of starting DNA molecules (Vierstraete, 1999). To end the cycle, step 3 is held long enough to fully extend any unfinished DNA strands, and then the reaction vessel is held at a cold temperature for storage.

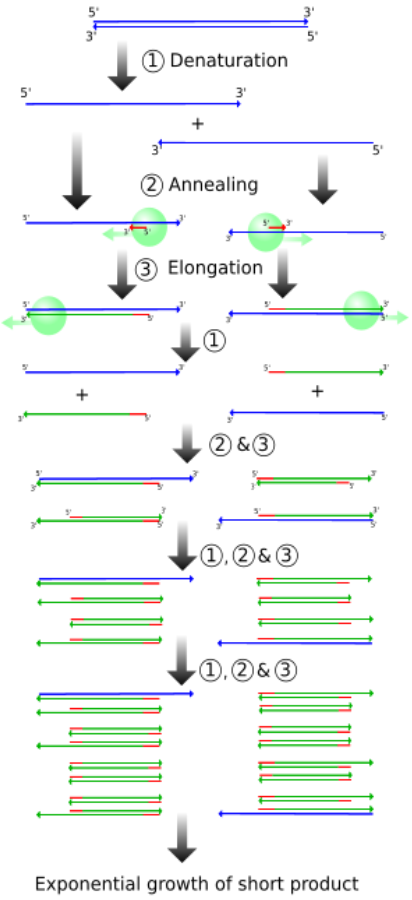

Figure 1.12 – Diagram of the Cycles of PCR. Blue: original DNA, Red: primer DNA, Green: DNA built by dNTPs and DNA polymerase, Green circle: Taq DNA polymerase) (Cycles of PCR, 2008)

PCR reactions need to be checked for accuracy after completion. Using agarose gel electrophoresis, the length of the PCR product is checked against a DNA ladder to check if the copied DNA is of the predicted size (and of only one size) (Figure 1.13). The DNA ladder uses known sizes of DNA (read in number of base pairs). Although this technique is rapid, and can be

used on trace amounts of DNA, PCR reactions can be easily botched by DNA contamination, causing the replication of more than one section of DNA, the wrong section of DNA, or even the wrong DNA entirely. If the DNA is copied successfully, there will be a single band, and the number of base pairs within can be determined by comparing to the ladder of known sizes of DNA.

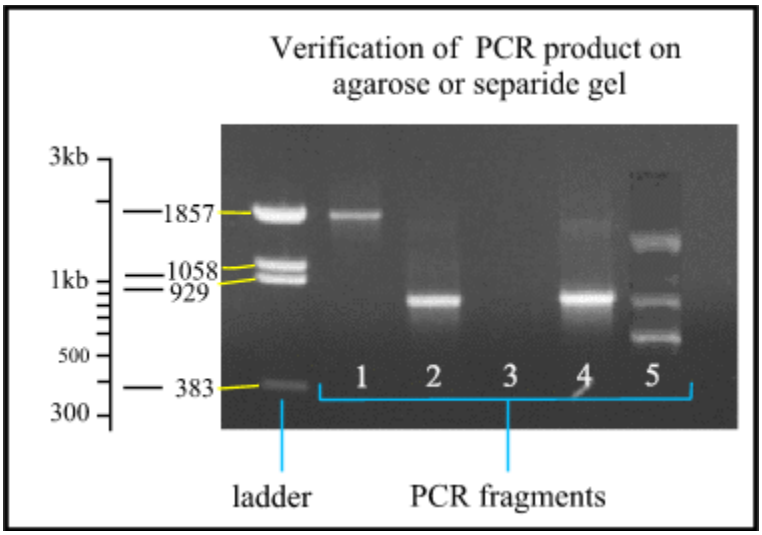

Figure 1.13 – Example of a PCR Electrophoresis Result.
Lanes 1, 2, and 4 show successful products.
(Vierstraete, 1999)

PCR vs. Non-PCR Fingerprints

There are advantages and disadvantages to using each of the two main (PCR-based and non-PCR-based) fingerprinting systems. The RFLP system of generating a fingerprint is not affected much by contamination. It would take a mutation at a restriction site to cause an error, and even so, other sections of DNA could be analyzed to find a match that could be used in court. The disadvantage of the RFLP technique is that a large amount of DNA is required, as the DNA is not amplified to start. Trace amounts of DNA are insufficient for RFLP analysis, and thus can only be used by PCR based analysis. PCR can amplify small amounts of DNA to any

amount required for testing. The only issue with this is that any contamination or error will also be copied, and render the entire fingerprint useless. PCR-based fingerprinting is now the more frequently used procedure, and the RFLP approach is mostly used when contamination is suspected.

DNA Fingerprinting Applications

Paternity Testing

DNA profiling can be used in a variety of applications. In one of its main applications, DNA fingerprinting may be used to find the biological parents of a child. In sexual reproduction, the DNA of the two parents comes together in a way that the child has about half of their mother's and half of their father's DNA at random, as shown in Figure 1.14.

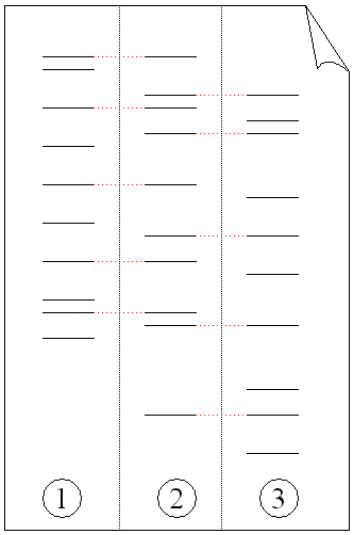

Figure 1.14 – Example of a PCR Fingerprint of a Family. The left and right lanes are the two parents, and the center lane is the child. Note that each band of the child was inherited from one of the parents shown as red dotted lines. (PCR Fingerprint, 2005)

Paternal DNA testing of the Y-chromosome has been used in descendants of Thomas Jefferson and Sally Hemings to determine the possibility of their having a child. Thomas Jefferson was suspected of fathering multiple children with his slaves; Sally Hemings was one of them. The Y-chromosomes of male-line descendants of Field Jefferson (Thomas' paternal uncle, as male-line descendants of Thomas did not exist) were compared to that of male-line

descendants of Eston Hemings (Sally's youngest son), and they matched, proving that someone with Jefferson's Y-chromosome fathered the child. Although Jefferson is the most likely candidate based on the rumors that he was in Sally's vicinity at the time of conception, it remains a possibility that someone from the same male-line as Jefferson could have fathered the child (Foster *et al*, 1998).

Molecular Archeology

Molecular Archeology is the use of DNA testing to analyze ancient archeological finds. For example, it can be used to determine the species of an unidentified animal's remains. Finds such as the Tyrolean Ice-Man and the mummies of Egypt are preserved enough to extract DNA from, as they were found in cold and arid climates, respectively. Analysis of such DNA alongside other archaeological finds can glean information related to how these being's lives were different than it is today.

Criminal Justice

DNA fingerprinting is most closely associated with the criminal justice field. A suspect can be incriminated or proven innocent through comparison of his/her DNA fingerprint to that of DNA found at a crime scene. DNA can be found in many forms at a crime scene, in the form of blood, semen, and hair to name a few. The DNA found at the crime scene is then compared to DNA given by the suspect, which is usually acquired by a buccal swab, a painless procedure where cheek cells are taken from in the mouth. If the DNA provided by the suspect matches that found at the crime scene, then that places the suspect at the scene of the crime. Likewise, DNA that does not match the suspect or the victim can be used as proof of innocence. The O. J.

Simpson case, discussed in Chapter-4, relied on forensic evidence, but the evidence became heavily doubted due to collection and handling errors. The next chapter will discuss what we learned from the OJ case regarding the now standard techniques for handling DNA evidence and the procedures to insure that the evidence will hold up in a court of law.

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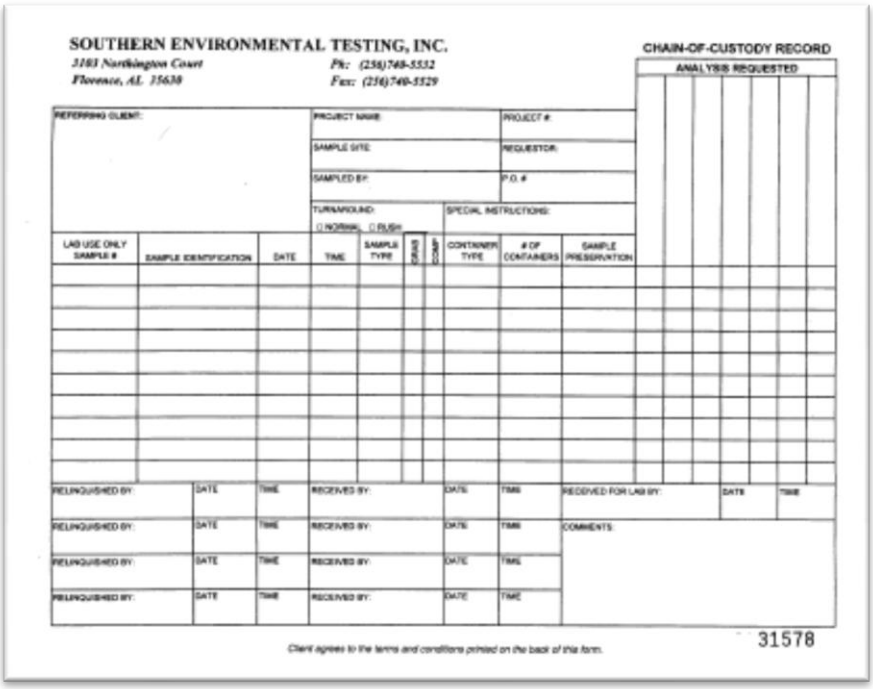
Chapter 2: DNA Forensics

Deoxyribonucleic acid (DNA) forensics has become a very critical piece of evidence collection over recent years. This key evidence, termed by some as the greatest forensic tool in the history of forensic science, can be the cause of an accused person being proven innocent or guilty in a court of law. In the past, cases have arisen where an innocent person has been sent to prison due to the lack of technology needed to test the DNA at the crime scene and prove their innocence. Only recently have we been able to do these tests on DNA samples collected either fresh or in the past, and see whom it matches. Also, many members of the public remember the outcome of the O.J. Simpson trial, in which DNA (blood) samples were potentially mishandled, mislabeled, or contaminated. Since that infamous case, in the last 10 years there have been many advances in methods for the collection of DNA evidence to prevent contamination, documenting its chain of custody to prevent mishandling, and storing the DNA to prevent degradation. Unfortunately, if certain steps are not taken correctly, the DNA findings will not hold up in a court of law. To help the DNA findings to be accepted in a court, certain restrictions have been put in place to assure authenticity of the findings. This chapter will discuss some of these advances, why they are in place, and how they help bring the truth into the courtroom.

Chain of Custody

One major advance in DNA forensics is documenting the chain of custody of the evidence. The chain of custody refers to a paper trail of who had access to the evidence. It is necessary that the seizure, custody, control, transfer, analysis, and disposition of the evidence are all recorded. These records can be physical (see Figure-2.1) or electronic, but must include

every step of how the evidence was obtained, where it was obtained, and who tested it among any other things done with the evidence. The chain of custody is used to avoid later allegations of tampering or misconduct, and it is absolutely needed or it can compromise the case.



SOUTHERN ENVIRONMENTAL TESTING, INC.
3103 Northington Court
Florence, AL 35630
Ph: (256)740-5532
Fax: (256)740-5529

CHAIN-OF-CUSTODY RECORD
ANALYSIS REQUESTED

REFERRING CLIENT:
PROJECT NAME:
PROJECT #:
SAMPLE SITE:
REQUESTOR:
SAMPLED BY:
P.O. #
TURNAROUND: ☐ NORMAL ☐ RUSH
SPECIAL INSTRUCTIONS:

LAB USE ONLY SAMPLE #	SAMPLE IDENTIFICATION	DATE	TIME	SAMPLE TYPE	GRAB	COMP	CONTAINER TYPE	# OF CONTAINERS	SAMPLE PRESERVATION

RELINQUISHED BY:	DATE	TIME	RECEIVED BY:	DATE	TIME	RECEIVED FOR LAB BY:	DATE	TIME
RELINQUISHED BY:	DATE	TIME	RECEIVED BY:	DATE	TIME	COMMENTS:		
RELINQUISHED BY:	DATE	TIME	RECEIVED BY:	DATE	TIME			
RELINQUISHED BY:	DATE	TIME	RECEIVED BY:	DATE	TIME			

Client agrees to the terms and conditions printed on the back of this form.

31578

Figure 2.1: Example of a Chain of Custody Form for DNA Evidence (Murray, 2008).

The chain of custody first starts with the police officer or detective who documents the collection. In the original documentation, information including what the evidence is, how they acquired the evidence, and when it was collected are a must. Then it is also required to keep a list of who handles the evidence, why they handled it, and where it has travelled. This is to prove that only authorized people have been in contact with the evidence, and thus it was not tampered with. Then when the evidence is at the lab, the analysts must record who they are and what they tested the evidence for. After the testing, the evidence has to be stored, and that information is also included in the chain of custody to insure that they know where the evidence can be found and so to prove it was stored correctly.

Evidence Collection

However, in order for this collection and testing process to get underway, it starts with the collection of evidence at the crime scene. The first people at the scene must secure the area and keep it blocked off from anyone who is not authorized to work there. In order to do this, the area is usually marked with crime scene tape (Figure-2.2) and then patrolled by the police to make sure that nobody goes over the tape.

Figure 2.2: Crime Scene Tape
(Bailey, 2008).

After the area is secured, crime scene investigators must go through every inch of the area to collect all possible evidence. In order to do this, they tend to form straight lines and go straight across the area if it is possible. This helps to make sure that evidence will not be over looked since there are many eyes looking in a small space. Once the evidence is collected, it is taken back to the lab. The next step is for the evidence to be processed, but unfortunately this

step can take a while due to the amount of evidence to be tested and the long time it usually takes. In the meantime, the evidence must be stored in a safe location.

Evidence Storage

One of toughest steps in this overall process is how to store the evidence to prevent contamination or degradation. Since the evidence has to be stored until the court date, and even past that date, it is very important to make sure that it is sealed away from anything that can hurt the evidence. It is also important to understand what could harm the different kinds of evidence, such as physical evidence versus digital evidence. For DNA evidence, it is best to store the sample in paper bags (Figures-2.3 and 2.4), not plastic, since the latter retains moisture allowing DNA degradation.

Figure 2.3: Tamper Indicating Evidence Bag
(Evidence Collection, 2007)

Figure 2.4: Paper Evidence Bags
(Evidence Collection, 2007)

Another important fact is to work with only a portion of the original sample in case a mistake is made, although in some cases that is not possible for small samples. With most digital photograph or x-ray evidence, such as information on a computer hard drive, a copy should first be made and then the lab technicians can work with the copy and not jeopardize the original.

Figure 2.5: Example of a DNA Collection Kit
(Evidence Collection, 2007)

Physical evidence can be contaminated in many ways, including being collected already contaminated. One of the most common contaminations that can be easily detected is when the analyst's DNA accidently mixes with the forensic sample. Since many labs require a DNA profile of their analyst, it his/her DNA can be detected quickly and fixed. It is also helpful that the analyst can sometimes use PCR to replicate DNA from a very small amount to obtain millions of samples. This insures that only a small portion of the original evidence has to be used at one time and then can be safely stored.

However, when the DNA is contaminated through other samples in the lab, it can be a bit more problematic because it is hard for a lab to detect low-level contamination with another sample without knowing whose DNA is in the samples. Since contamination can be a huge problem, laboratories have put in place strict protocols to prevent contamination accidents, such as constantly wearing gloves, as well as changing the gloves often, and wearing masks to prevent contamination from the collector's coughing, etc.

In order to further detect and prevent DNA contamination in the lab, a "reagent blank" control (Bessetti and Sundquist, 2005) is used to determine whether a positive signal is obtained from the reagents by themselves (Figure-2.6). "A 'reagent blank' control consists of all reagents used during sample processing" (Bessetti and Sundquist, 2005), but the test will not contain an added DNA sample. Therefore, if a positive reaction does occur, the analyst knows that the reagents could be contaminated with DNA.

Figure 2.6: Reagent Blank vs. sGAG
(Blyscan™, 2007)

Avoiding DNA Degradation

However, contamination is not the only thing that can discredit DNA evidence. It is very likely to have DNA degrade if it is not stored carefully. DNA tends to degrade faster in warm or moist environments. It is very important when handling and testing DNA to not let it degrade since the tests will not be accurate after it has degraded. Some procedures that have been put in place to reduce DNA degradation are to store DNA in paper sacks or envelopes instead of plastic bags. The evidence should also be air dried before it is packed, and once packed it should be sealed in the container. Then the container should be refrigerated or frozen (Figure-2.7).

Figure 2.7: Giant Freezer holding DNA
(More Drugs, 19 Nov. 1998)

As discussed in chapter-1, there are many different ways to analyze DNA. The two main ways are known as restriction fragment length polymorphism (RFLP) and polymerase chain reaction (PCR). RFLP requires large amounts of DNA and the DNA must be completely undegraded. Once the DNA is even slightly degraded RFLP can no longer be used to test the DNA. However, one advantage of the RFLP method is that it can tolerate small amounts of contamination. If degradation occurs, the most effective way to test DNA is to use PCR which requires a smaller amount of DNA and can work with partially degraded DNA in order to amplify it.

Using these procedures can tell analysts pretty much anything they need to know forensically. Since everybody, except identical twins, have unique DNA, like their nearly unique fingerprints, analysts can determine a lot about the human source, such as hair and eye color. Even more amazingly, the sources which provide analysts with DNA such as hair, white blood cells, skin, and semen can also provide the analysts with other factors about the human source. The hair follicles collected at a crime scene is especially important because scientists can find traces of things such as poison or hair dye which can help in a court case.

Despite all of these advances, contamination or degradation accidents can still happen, but if the procedures for collecting, testing and storing evidence are executed properly, the evidence is more likely to get accepted in a court of law. The chain of custody assures the court that the evidence has not been tampered with, and the testing and storage procedures allow repeated testing if needed.

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Chapter-3: Landmark DNA Court Cases

The use of DNA fingerprinting analysis as court approved evidence has many protagonists and antagonists, and the seesaw battle of clarification and acceptance of this type of evidence is still ongoing. When DNA testing first hit the U.S. criminal justice system in the late 1980s, prosecutors hailed it as an infallible tool for putting criminals behind bars. It was the new fingerprint, foolproof. It could pinpoint a suspect down to a billion-to-one ratio, or it could also clear a person who was innocent (Shellem, 2003). "Since the discovery of traditional fingerprinting at the turn of the 20th century, science has assumed an increasingly important and powerful role in the decision making process of our judicial branch" (Biancamano, 1996), and to this date, we are still evaluating the full judicial potential of this technological breakthrough. In either civil and criminal cases, DNA evidence may prove to be the deciding factor.

Antagonists of this new technology and methodology saw a variety of issues worth focusing on, including the initial lack of standardization of the technique, and an ongoing lack of continuity in the process by which evidence is collected and analyzed (discussed in Chapter-2). The initial lack of a standard and uniform method for DNA testing resulted in a variety of techniques introduced in U.S. courtrooms (Biancamano, 1996), and eventually in a series of landmark DNA court cases, standard collection and analysis procedures were created to allow DNA to become the gold standard for technical evidence.

This chapter will review several landmark cases which set the standard for DNA evidence to be accepted within U.S. courtrooms. These cases address the reliability and general scientific acceptance of DNA technology, in an effort to show the validity of these techniques

when properly instituted. Not all of the cases discussed in this chapter involve DNA; some cases examine precedents for the general acceptance and admittance of technical evidence in general.

Frye v. United States, 1923.
Determining Standards for the General Acceptance of Technical Evidence

To determine the outcome of any court case, the evidence presented is of paramount importance. When weighing the evidence, those on the jury must determine the credibility of what has been presented. This jury-based method for determination of evidence reliability was in effect until 1923 when a new scientifically unproven "lie detector" technique was used to attempt to enter evidence, mandating a new procedure for accepting technical evidence.

James Alphonzo Frye was arrested and charged with second degree murder in Washington D.C.. Frye denied the accusations against him, and hoped that his innocence would be proven through the use of an expert witness by his lawyers. As revealed in the court transcript, "counsel for the defendant offered an expert witness to testify to the result of a deception test made upon the defendant" (Frye v. United States, 1923). The intent of this strategy was rooted in the belief that the test would subsequently prove Frye's innocence. A more common name for this "deception test" is a polygraph/lie detector test, and although very common today (but still unacceptable as court evidence), this was new technology in 1923.

In an effort to put together the best possible defense for their client, Frye's lawyers reached out to the inventor of this new and possibly revolutionary technology.
They asked William Marston (from Harvard), to administer his new test to Frye. Marston agreed and it was his determination through test results that Frye was telling the truth with his denial of the murder. Aiming to prove Frye's innocence, the defense felt that Marston's high ranking

reputation in his scientific community rendered the test results valid enough to be admissible to the court as evidence. However, it was the high court's ruling that "we (the court) think the systolic blood pressure deception test has not yet gained such standing and scientific recognition among physiological and

psychological authorities as would justify the courts in admitting expert testimony deduced from the discovery, development, and experiments thus far made" (Frye v. United States, 1923). Thus the defendant's lie detector evidence was not allowed, and Frye's guilty verdict stood. To this date, lie detector evidence is not allowed in U.S. courts.

In what would later become known as the "Frye Standard", the court established in this case "that somewhere in this twilight zone the evidential force of the principle must be recognized, and while courts will go a long way in admitting expert

testimony deduced from a well-recognized scientific principle or discovery, the thing from which the deduction is made must be sufficiently established to have gained general acceptance in the particular field in which it belongs" (Frye v. United States, 1923). In more general terms, this standard declares that in order for scientific evidence to be admitted in the court room, it must have the general acceptance within the scientific community in which it applies.

The key outcome of this landmark case was that a new standard was set in terms of evidence that could be admitted in U.S. legal proceedings, evidence that lacks a general acceptance of the scientific community would not be allowed in the courtroom. This Frye standard remained intact for decades, as more cases encountered the task of admitting other new technological advances as accepted evidence. However the standard of *general acceptance* was sometimes difficult to achieve in real court cases, thus in 1975 a different more lenient standard was introduced.

Federal Rules of Evidence 702 (Rule 702), 1975.
Testimony by Experts: Loosening the Frye Standard

In 1975, Congress signed into law Federal Rules of Evidence, Rule 702, which was enacted to replace the rather vague and difficult Frye Standard. Regarding testimony by experts, Rule 702, states: "If scientific, technical, or other specialized knowledge will assist the trier of fact to understand the evidence or to determine a fact in issue, a witness qualified as an expert by knowledge, skill, experience, training, or education, may testify thereto in the form of an opinion or otherwise, if (1) the testimony is based upon sufficient facts or data, (2) the testimony is the product of reliable principles and methods, and (3) the witness has applied the principles and methods reliably to the facts of the case" (Expert Article Library, 2008). The result of Rule 702 was that, in a case where the jury finds the testimony of an expert witness to be helpful in rendering their verdict, the court may deem the evidence as admissible, even if it has *not* been generally accepted within the scientific community. With this rule in place, many courtrooms subscribed to the more liberal interpretation that Rule 702 allowed, rather than the stringent interpretation the Frye Standard held legal counsels to.

Rule 702 plays a key part in facilitating the rise of DNA fingerprinting as accepted evidence, as it was eventually applied in the 1980's to the then new non-generally accepted DNA technology that did not withstand the rigid interpretations of the Frye Standard. Had the Frye Standard continued to apply, it is very possible that today DNA evidence could still be in the infant stages of acceptance.

Colin Pitchfork, 1986.
First Murder Conviction on DNA Evidence also Clears the Prime Suspect

Alec Jeffreys in England developed the technique we now recognize as DNA fingerprinting in 1984, and since that year, a myriad of cases have been solved, thrown out, or overturned due to this amazing technique. The first DNA fingerprinting conviction took place in England involving "two schoolgirls who were murdered in the small town of Narborough in Leicestershire in 1983 and 1986, that sparked a murder hunt that was only to be resolved by an intelligence-led screen, eventually leading to the conviction of a local man - Colin Pitchfork" (Casefiles, 2007).

In 1983, Lynda Mann, a fifteen year old girl was discovered along on off beaten path, raped and asphyxiated to death. Sadly, at the outset, authorities were not able to gain any leads. Although there were only 150 men in the town, none of them were considered suspects. The evidence consisted of a small sample of semen from the rapist recovered at the scene and stored for what they hoped would be later use.

In 1987, in the same area, another fifteen year old girl was raped and murdered. When Dawn Ashforth's body was discovered, the police again described her as being "strangled and sexually assaulted" (Casefiles, 2007). Both girls were found in an area called The Black Pad, leading those with knowledge of the case to deem the murderer "The Black Pad Killer" (Autopsy, 2004).

Piecing together the similarities of the situations, police determined that it must have been the work of the same man. The police apprehended a possible suspect, John Buckland who had admitted to Dawn's murder, but he denied any involvement in Lynda's death. Learning about DNA fingerprinting, the police inquired whether Dr. Jeffreys would try the new technique, but they discovered that Buckland's DNA was not a match in either murder case, so he was

discharged. Thus the first court application of DNA fingerprinting was to exonerate an innocent person.

Moving forward to try to find the real killer, the legal authorities decided that "all unalibied local men between the ages of 16 and 34 were requested to give authorities a DNA sample - drawn from their blood - to compare to the killer's" (Autopsy, 2004). But a problem arose when no match came back as positive with the suspect's DNA, and critiques of the method began to pour in. That was until "a woman who worked in a local bakery told investigators that while drinking in a pub with some co-workers, one of them claimed he'd taken the blood test for another man" (Autopsy, 2004). Ian Kelly had taken the test for Colin Pitchfork, and when questioned about it, Kelly led them to Pitchfork. "Pitchfork had convinced Kelly he couldn't take the test because he'd already helped out someone else - a friend with a police record for flashing - by giving a sample for him. Pitchfork claimed to be afraid that if he gave another sample he'd be arrested for the deception. As it turned out, Pitchfork's reason for wanting Kelly to take the test for him was much less convoluted than that: he was the murderer" (Autopsy, 2004).

Pitchfork pleaded guilty to the murders, and the case never actually made it to the courtroom. Pitchfork had been caught through the use of DNA evidence, the first conviction based on DNA evidence. Not only was this case a breakthrough for advances in DNA fingerprinting and its ability to find someone guilty, it also proved it could be used to determine innocence.

Andrews v Florida, 1988: DNA Makes Its Way Into a U.S. Courtroom

After making a revolutionary impact abroad, DNA fingerprinting was ready to come to the courtrooms of America. This happened in 1988 in Orlando, FL with the case of Tommy Lee

Andrews. Based on traditional evidence, Andrews was convicted of rape in one of several rape cases in the Orlando area, resulting in a 22 year sentence (Andrews v. State of Florida, 1988). However, authorities wanted to compare the DNA from each rape case to see if they were committed by one person. The testing at Lifecodes lab concluded that all the DNA samples were a match; each woman was a victim of the same man. Once this information was compiled, the next step was to compare the DNA from the victims to Andrew's DNA, and again a match was made, so Andrews was charged with the rape of all the victims.

The authorities wanted this charge to stick in a court of law, but with DNA testing in the infant stages of acceptability, the court required a pretrial hearing to determine the validity of the DNA evidence being proposed. This review of evidence was critical because if this evidence was admitted Andrews would be charged with all counts of rape, however if it was determined to be invalid he would only be charged with one count.

Following a long and difficult pre-trial hearing, the judge ruled in favor of the prosecution, allowing the DNA evidence to be admitted. Andrews' sentencing was adjusted from the 22 year sentence to a sentence of 115 years. DNA evidence was now in United States courtrooms, but was it here to stay?

The People v. Castro, 1989, New York: Introducing The Three Pronged Test

It was the hope of DNA fingerprinting proponents that the ruling of the 1988 Andrews case would streamline the acceptance of the technology for subsequent cases. But only one year later, the 1989 case of Joseph Castro v. the State of New York, would provide DNA fingerprinting with its toughest challenge to date. "The first case that seriously challenged a

DNA profile's admissibility was People v. Castro; the New York Supreme Court, in a 12-week pre-trial hearing, exhaustively examined numerous issues relating to the admissibility of DNA evidence. Joseph Castro was accused of murdering his neighbor and her 2-year-old daughter. A bloodstain on Castro's watch was analyzed for a match to the victim" (Frontline, 1996).

Based on the Andrews case, it was thought that this would be an easy conviction for the state of New York. However, the Supreme Court of New York wanted to delve deeper into the standards and techniques of DNA fingerprinting. It was the goal of the court to determine the necessary steps that would result in accepted outcomes for DNA fingerprinting evidence. Once they had these steps established, they aimed to set a procedure that would need to be followed exactly. A "Three Prong Test" was developed which the high court believed would undoubtedly allow the courts to determine which evidence would be deemed acceptable. This test included:

1. Is there a generally accepted scientific theory stating that DNA testing can be reliable?
2. Do techniques exist that can produce reliable DNA results?
3. Did the testing lab perform these accepted DNA tests in this trial?

For the Castro case, it was the courts ruling that:

> "- DNA identification theory and practice are generally accepted among the scientific community.
> - DNA forensic identification techniques are generally accepted by the scientific community.
> - Pretrial hearings are required to determine whether the testing laboratory's methodology was substantially in accord with scientific standards and produced reliable results for jury consideration" (Frontline, 1996).

The main piece of evidence in play for the Castro case was the stain on Castro's watch, which was analyzed and matched to one of the victims. The court ruled that in this instance, the analyzed DNA could only show exclusion, not inclusion. It could determine whether the DNA was Castro's or not, but it could not determine whether it was the DNA of the victim. The case

came to a close when Castro eventually confessed to committing the murders, so it did not go to trial. Had his confession not occurred, the DNA evidence would *not* have been allowed for this case, due to the fact that the third requirement of the "Three Prong" test was not met by the Lifecodes lab who did not follow acceptable practices when it tested the Castro sample (People v Castro, 1989).

The pre-trial hearing also resulted in a demand for a standardization of DNA testing. In 1991, the U.S. Federal Bureau of Investigation developed the Technical Working Group on DNA Analysis Methods, more simply referred to as "TWGDAM", in an effort to develop stricter, more defined guidelines for DNA analysis (Miller, 1991). The overarching impact of the Castro case in the DNA world is that for the first time DNA methods were seriously questioned and standardized techniques were put in place.

Two Bulls v US, 1990: Amending The Three Pronged Test to Five Prongs

The three prong test of 1989 Castro did not last long. In 1990, Matthew Sylvester Two Bulls was charged with the rape of a fourteen-year-old girl on the Pine Ridge Indian Reservation in South Dakota. The FBI analyzed DNA from the semen in the victim's underwear, and compared it to Two Bulls' DNA, their main suspect. The FBI concluded the DNA samples were the same (United States v. Two Bulls, 1990). This case took a close view at a number of DNA cases and pooled them together to create a five pronged pre-trial approach. It was courts belief that this new five prong testing was needed because, "It would ease the burden on trial lawyers and triers of fact to make proper implementation a threshold issue for the admissibility of DNA typing tests. Before the test offered by a particular laboratory is admitted, there should be a

showing, during an evidentiary hearing, that the specific protocol employed by the laboratory is accepted as reliable by disinterested scientists familiar with the procedure. In routine cases, the attorneys could focus their attention on the tractable question of whether an accepted protocol was accurately followed instead of the enormously more difficult question of whether the protocol itself is good or bad" (United States v Two Bulls, 1990).

As they tried to amend previous rulings to make a better standard, it was determined that Castro's three-prong test was too narrow, however Rule 702 and the Frye Standard were considered correct in their application and interpretation. This new test would blend all of these to create what was labeled the Five Prong Test to be used at DNA pre-trial hearings:

1. Is DNA testing generally accepted (Frye)?
2. Is the testing *procedure* used here generally accepted (Castro)?
3. Was the test performed correctly here (Castro)?
4. Is the evidence more prejudicial than probative, and if so, disallow it (Rule 702).
5. Is the statistics of the DNA match more prejudicial than probative? If so disallow it (Rule 702).

Clearly the first prong in this new testing originated from the Frye Standard. It served the purpose of determining whether the technology of DNA fingerprinting has been accepted, or has gained general acceptance in the scientific world. The second and third prongs stemmed from the Castro ruling and its "Three Prong" approach, with a less restrictive interpretation to question the acceptance of *testing techniques* of the DNA evidence and make sure they are technologically and scientifically accurate for the given case. Prongs four and five are based on Rule 702 and the Federal Rules of Evidence, and brought into focus the awareness that the evidence and information gained from the testing of DNA evidence should in no way prejudice or bias either side.

Miles v Illinois, 1991: FBI's TWGDAM Called On and Verified

Following its creation after the Castro case, the functionality of TWGDAM had not been fully called upon. That changed in 1991 during the case of Reggie Miles v The state of Illinois. Miles, charged with rape, had his DNA recovered from bed linens at the crime scene. Investigators who found the sheet sent it to the labs at Cellmark to have the DNA evidence examined. Cellmark was an interesting choice since it had previously had some evidence examined at its labs denied admittance on several prior occasions. These rejections stemmed from Cellmark's inability to comply with the standards put in place by TWGDAM. But in the Miles case, Cellmark made the necessary adjustments to qualify for compliance of all TWGDAM's standards. Cellmark's work was deemed acceptable through the evaluation of the FBI's special task group. Cellmark's work showed extremely accurate statistics that aided in the conviction of Miles being upheld. These results showed that for the DNA on the linen not to be Miles, it would have to be a one in hundreds of thousands coincidence (People v Miles 1991), so the original guilty verdict was upheld. The ruling also allowed proponents of DNA evidence to affirm confidence in the methods and preciseness of the results achieved from DNA fingerprinting, and pushed critics to begin to accept its methods.

The ruling also improved the credibility and confidence in TWGDAM and their policies, and strengthened the use of the Two Bulls Five-Prong test. The longest lasting impressions from this Miles case boosted confidence in DNA evidence, and allowed DNA testing to be seen as an accurate piece of evidence.

Paul Eugene Robinson, 2003: First Sole DNA Conviction

Six years passed of unsuccessful investigation of two unsolved sexual assault cases, in 1993 and 1994, so as the cases were about to expire from the six year Statute of Limitations for sex crimes, a warrant was issued for the arrest of "John Doe". These sexual assaults which took place in the Cal Expo area of California, had been a series of dead ends for the District Attorney's office as they tried to zero in on the suspect. The investigators had DNA evidence from the crime scene, but were unable to find a match to any previously convicted felon in the FBI CODIS database, therefore they issued a warrant for what was described as "the individual belonging to the victim's semen samples", even though they had no idea who that individual was.

Eventually, as more DNA samples entered the CODIS database, the original rape evidence was matched to Paul Eugene Robinson's DNA (Scully, 2003). "If investigators had not issued a DNA warrant in the case, they would have been unable to arrest Robinson because the statute of limitations is six years" (Associated Press, 2000). As a result of this positive match, in 2003 Robinson was convicted on five counts of sexual assault in the area. Following the convictions District Attorney Jan Scully announced…that "Paul Eugene Robinson was sentenced to the maximum term of 65 years in state prison for five counts of sexual assault occurring in August 1994" (Scully, 2003).

This was the first case in history in which someone was convicted of a crime solely on DNA evidence, without any other corrorborating physical evidence. However it is hoped that this case will serve as a precedent to resolve other cases such as Robinson's. " 'This is all new territory, but hopefully in 10 years, it will be an everyday thing,' said Sacramento Police Detective Peter Willover" (Associated Press, 2000). In 2000, California granted $50 million

from the State Office of Criminal Justice Planning, to be given to police offices in an effort to have DNA fingerprinting analysis used to re-investigate old sexual assault cases (Associated Press, 2000).

This chapter's collections of landmark cases show the progression of DNA fingerprinting technology's use and acceptance in the U.S. courts through the years. The technology and methods have made great leaps in accuracy, standardization, and ultimately, acceptance. And the acceptance is not limited only to the scientific community, but also into courtrooms across society. The cases discussed laid the groundwork for the admittance of multifaceted scientific evidence in legal preceedings. Although these cases have had great importance on accepting DNA evidence in U.S. courts, they are not well known in the public. The following chapter will discuss some sensational cases well known to the public in which DNA evidence played a role.

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United States v. Two Bulls, 918 F.2d 56 (8th Cir. 1990) http://www.altlaw.org/v1/cases/466746

Chapter 4: Sensational DNA Cases

Although there have been many advances in the past 10 years with respect to handling and analyzing DNA evidence, it is possible to argue that these advances did not come soon enough. In this chapter we will explore some of the famous court cases the public is likely already familiar with, where DNA evidence played a role, or is about to play a role. In one case where the DNA evidence was dismissed, it is possible that the verdict would have been very different if the DNA evidence was properly handled. In another case, the person admitting to the crime, may have been shown to be innocent if DNA testing was in place at the time of the trial, allowing the real criminal to be found.

Case 1: O.J. Simpson

The first case to be discussed is the murders of Nicole Brown Simpson and Ronald Goldman, on June 12, 1994, when they were stabbed to death. The accused murderer in this case was Orenthal James (O.J.) Simpson (Figure-4.1) who was famous for being an ex-NFL football star.

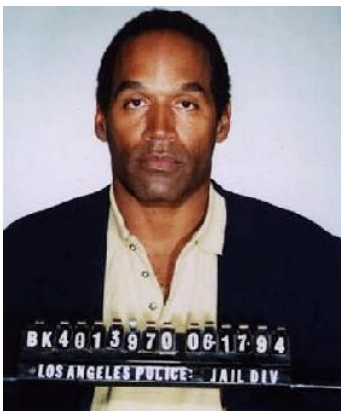

Figure 4.1: Photograph of O.J. Simpson (Linder, 2000)

Nicole's and Ronald's bodies were found in front of Nicole's condominium in Brentwood, surrounded by bloody footprints. Later, O.J. Simpson was notified of the deaths

while on a business trip in Chicago. At the time, O.J. Simpson and Nicole Brown Simpson were divorced. There was a lot of significant evidence that while married, the two were not happy, including a statement from Nicole's sister, Denise, saying the O.J. abused Nicole. O.J. has also stated that he was not happy with Nicole openly flirting with other men in front of their two children, and admitted to being angry with her on June 12, 1994, the day that the murders took place.

At the crime scene, there were quite a few pieces of DNA evidence found. First, there were hairs consistent with O.J. Simpson found on a cap at the Bundy Residence where bodies were found and also on Ronald Goldman's shirt. Along with the hair evidence, there were also cotton fibers consistent with the carpet of the Bronco which O.J. presumably drove to the Bundy Residence, on a glove found at O.J. Simpson's house, and on the cap at the Bundy Residence. Along with this evidence, there were also two Aris light gloves (Figure-4.2), size extra large, found. One was found at the Bundy Residence and the other at O.J.'s residence. Records also show that Nicole bought the same exact brand and size of gloves at Bloomingdale's in 1990, and photographs showed that O.J. had worn the gloves before. However, on May 15, 1995, Simpson tried on one of the bloody gloves in court and it did not seem to fit.

Figure 4.2: Gloves found at crime scene (left) and O.J.'s residence (right) (Linder, 2000).

There was also shoe evidence at the crime scene from the bloody footprints around the bodies. These prints were found to be from a size 12 Magli shoe. Although it is not known if O.J. was wearing a Magli shoe, it is known that he wears a size 12 shoe. The Magli shoes also

left an impression on the Bronco carpet. Crime scene investigators also found plenty of blood evidence. The blood found at the Bundy residence was the same type as O.J. Simpson's, but it can also match 0.5% of the population, so that type evidence alone cannot determine that he is the killer. Also, there was blood found in the Bronco and in the foyer and master bedroom of the Simpson's house and driveway. One of the most interesting pieces of evidence is blood found on two socks in O.J.'s home which matched Nicole's (Figure-4.3).

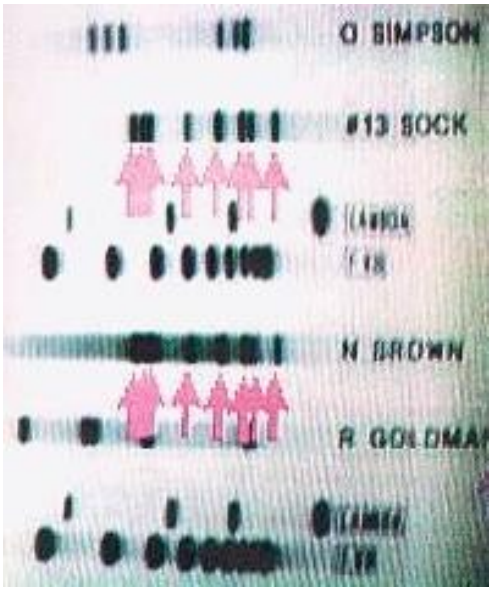

Figure 4.3: DNA testing results of bloody socks (Linder, 2000)

However, both socks were put into one bag upon collection and were still wet with blood, thus allowing transfer. Dr. Henry Lee and one of the defense attorney's Barry Scheck, discussed this problem during the court hearing:

> DR. LEE: I notice that both socks are in one bag, in one envelope. I made a comment, I said why are those two socks in one envelope.
>
> MR. SCHECK: And what is the significance of putting both socks in one envelope--in terms of forensic procedure?
>
> DR. LEE: Start that initial moment, you pick up the socks, put in one envelope, you already contaminate both socks. You have a cross-contamination. It's no longer its virgin state.
> (Linder, 2000)

Since the socks could have been cross-contaminated, they were no longer a good source of evidence. This is proof that the procedures that we have in place now in terms of evidence collection are there for a reason. O.J. Simpson was found not guilty by the jury on October 3, 1995. However, on October 23, 1996, O.J. Simpson's civil trial started, using the more lenient "preponderance of the evidence" standard for civil trials. It ended February 4, 1997, with the jury finding Simpson liable for the two deaths, and awarding the plaintiffs 8.5 million dollars. They also ordered Simpson to turn over his assets. The main outcome of this famous trial in forensic science was a re-investigation of current protocols for collecting evidence from a crime scene to prevent contamination or degradation, and documenting the evidence's chain of custody to prevent possible evidence tampering.

Case 2: The Boston Strangler

Thirteen women (Table-4.1), with ages ranging from 19 to 85, were raped and murdered in the Boston, Massachusetts area in the early to mid-1960's. These murders happened from about June 1962 till January 1964, and then they seemed to stop for a bit even though the killer had not been caught. All of the victims lived alone, and there were no signs of forced entry

into their homes. During these trying times, the Boston females were very scared and started to isolate themselves no longer going out at dark or if they did, they always had a friend with them.

Name	Age	Died	Comments
Anna Slesers	55	14th June 1962	Discovered by her own son; Found to be strangled with her belt.
Mary Mullen	85	28th June 1962	Killer left a New Year's greeting card wedged between the toes of her left foot.
Nina Nichols	68	30th June 1962	
Helen Blake	65	30th June 1962	Forensic psychiatrists called in by police to help profile killer.
Ida Irga	75	19th August 1962	
Jane Sullivan	67	20th August 1962	
Sophie Clark	20	5th December 1962	Suspicions of a 'Mother-Killer' on the rampage are squashed by the latest killing.
Patricia Bissette	23	31st December 1962	
Mary Brown	69	9th March 1963	
Beverley Samans	23	6th May 1963	
Evelyn Corbin	58	8th September 1963	
Joann Graff	23	23rd November 1963	
Mary Sullivan	19	4th January 1964	

Table 4.1: List of the 13 Boston Strangler's Victims. (DeSalvo, Albert – The Boston Strangler)

On the evening of October 27, 1964, Albert DeSalvo (Figure-4.4) posed as a motorist with car troubles when he broke into a home in Bridgewater, Massachusetts. The owner of the home, however, fired a shot at him but he escaped. DeSalvo was not suspected at the time of being the Boston Strangler. However, later that same evening, DeSalvo posed as a detective and entered a young woman's home, tied her up, and sexually assaulted her. Then he suddenly left, saying an apology to the woman. The woman came to police with her description of the man which matched DeSalvo, so he was arrested. Although he originally denied his involvement in any murders, DeSalvo did confess to breaking into homes and rape. Albert was then sent to a mental

hospital, where he eventually confessed to being the Boston Strangler. "In total, he spent 50 hours confessing to 13 murders, two of which were not even suspected crimes of the Strangler" (Mitchell, 2006). However, since he was in a mental hospital, the confession could not be used, so he was charged with other crimes, and received a lifetime imprisonment based on those instead of the strangler crimes. DeSalvo died six years later in prison, stabbed in the heart, according to some sources on the day before he was to provide information on the strangler to a reporter (Bardsley and Bell, 2003).

Figure 4.4: Photograph of Albert DeSalvo (Wuebeen, 15 Feb 2008)

Some in the law enforcement community have their suspicions that DeSalvo's confession was a lie to provide his family with money from the sale of a book on the strangler (Bardsley and Bell, 2003). Susan Kelly, author of *The Boston Stranglers*, is one person of many who believes that DeSalvo did not commit those murders. "The newspapers were an excellent source of information – and it's very interesting to me that the details that Albert got wrong in his confession were identical to the details that the newspapers got wrong" she states (Kelly, 1995). Moreover, DeSalvo was never linked to any of the crime scenes via physical evidence.

Nowadays, some family members are still looking for answers. Diane Dobb, sister of the last victim Mary Sullivan, does not believe that Albert DeSalvo was the Boston Strangler, and pressed the state to reexamine her sister's body. A forensic expert, James Starrs, performed the second autopsy on Mary Sullivan on October 26, 2001, at York College in Pennsylvania, and on December 13, 2001, stated that the DNA evidence taken from Mary Sullivan's remains did not match Albert DeSalvo. The new findings included DNA analysis on a head hair from the pubic region which they did not expect to find. The new findings may also provide doubt about DeSalvo's statement that he strangled the victim with his bare hands, since Starrs' autopsy showed the hyoid bone in Sullivan's neck (which would have most likely broken if the strangulation had occurred) was not broken.

Although the real Boston Strangler might not have been caught, the state might open up the long dormant case, and according to CBS news, the state of Massachusetts recently announced that it did find new evidence and will test it. So far the state has refused to share this new evidence. Also, a gag order was placed on the media for this case based on complaints from some family members. However, some families want to be present when the testing is done.

Case 3: Anastasia

Grand Duchess Anastasia Nicholaevna (Figure-4.5) had a very interesting, but short, life. Her father, Nicholas II, was the last tsar of Russia, and her childhood ended abruptly when she was murdered in the basement of a farm house they were exiled to, with her parents, three sisters, and brother, at the age of 17.

Figure 4.5: Photograph of Anastasia Nicholaevna
(Marie, 2008)

However, not everybody believes that Anastasia died on that night. Many believe that a solider took pity on her and helped her to escape. The murderers of Anastasia's family tried their best to destroy the bodies by throwing them down a mine shaft, tossing grenades into it, and then removing the bodies, burning or dousing them with acid before throwing them into a pit. For decades, those who knew where the bodies of the last imperial family were kept quiet in fear, although rumors arose that one or more of the children had survived.

One of many suspects who claimed to be Anastasia was Anna Anderson (Figure-4.6). Anna Anderson was rescued after jumping off a bridge in Berlin, and when taken to a mental hospital, she had no identification on her. At the hospital somebody believed that they recognized her as Tatiana, one of Anastasia's sisters. From there, Anna was given a list of the tsar's daughters and she crossed off everyone but Anastasia. Unfortunately, at the time, DNA testing technology did not exist, so Anna could not be tested to see if she was related to surviving tsar relatives.

Figure 4.6: Anna Anderson
(Atchison, 2008)

Although Anastasia's family members and friends were torn on whether Anna Anderson was Anastasia, there were many similarities. Some of these similarities were that Anna was about the correct age that Anastasia would be if she had lived, she had a foot deformity like Anastasia's, and anthropologists who have studied their photographs have found their faces to be very similar. Also, when Prince Sigismund, a childhood friend of Anastasia, asked Anna a list of questions, Anna's answers convinced him that she was in fact Anastasia.

However, it was also suspicious that Anna Anderson refused to speak Russian. It was speculated that Anna didn't even know any Russian, which Anastasia would obviously have known extremely fluently. Anna Anderson was finally brought to a German court in 1938 to prove her identity and to claim part of the inheritance. The case was not concluded until 1970, when the court ruled that Anna Anderson had not proved that she was Anastasia, which is not to be confused with them saying that she was or was not Anastasia. To finally silence this Anna Anderson debate, using DNA testing when it became available in the late 1980's, Anna's son's DNA was found to not match any current tsar relative, but instead matched that of an insane polish factory worker named Franziska Schanzkowska.

To end the Anastasia story, the gravesite of the tsar family was finally discovered. Initially, only portions of nine skeletons could be exhumed. The DNA testing done on these skeletons showed that it was the parents and three of their daughters, but questions remained about the son and one daughter. Eventually, the final two skeletons were discovered at a site about 50 yards from the main gravesite, and DNA testing proved those two skeletons were tsar relatives, so at this time all the family's bodies have been accounted for, and the myth of Anastasia's survival is laid to rest.

Chapter Conclusion

In the three famous cases discussed above, DNA evidence played a role either in the original trial (O.J.), or later after DNA testing became available (Boston Strangler and Anastasia). The O.J. Simpson case shows that even if DNA testing matched O.J. to an unimaginably high probability, the evidence is useless if contaminated or the chain of custody inconsistent to allow potential tampering. The Strangler and Anastasia cases show the power of DNA testing, even when used long after the original trials have been completed to try to obtain the real truth.

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Chapter 5 – DNA Databases

DNA databases are a very useful tool to finding who is responsible for a crime. Without databases, DNA would be tested from a crime scene but there would be no way to find whose DNA it is (assuming the DNA does not match a suspect determined from other crime scene evidence). By having a database, investigators can search the database for anyone who matches the DNA they have found. Unfortunately, this search can still come up with nothing at times, when the person who the investigators are trying to find has not yet been put into the database. It would be nearly impossible to commit a crime (and get away with it) if everybody's DNA was submitted to the database at birth. However, many people do not want that to happen because they believe it infringes upon their rights. In this chapter we will discuss some of the different databases in the country, who is placed in the databases, and the ethics surrounding database use.

Database Legislation and CODIS

The U.S. Federal Bureau of Investigation's (FBI) Combined DNA Index System (CODIS) is the largest DNA database in the world. CODIS is very similar to the Automated Fingerprint Identification System (AFIS) database which allows traditional fingerprints found at a crime scene to be analyzed for a suspect, but instead of fingerprints, CODIS allows DNA profiles to be analyzed. CODIS began as a pilot project in late 1990 by the FBI to try to allow a select few local and state crime laboratories to share their DNA profile information with each other in the hopes of better fighting crime.

In 1994, the DNA Identification Act formally authorized the FBI to set up and run CODIS, as well as to set up the national standards for DNA testing. CODIS itself is a computer

software program that coordinates local, state, and national databases of DNA profiles from convicted offenders, unsolved crime scene evidence, and missing persons (Lotter, 2008). CODIS however, does not contain any personal information, such as social security numbers, date of birth, medical predispositions, or any previous records on the person. The only thing that CODIS stores is the specimen identifier, the DNA profile of 13 core loci, and the laboratory where the profile was made.

There are "three hierarchical levels as part of this project that allows federal, state and local crime laboratories to compare DNA profiles electronically" (Combined DNA, 2006). These three levels (Figure-5.1) are: the National DNA Index System (NDIS) (top of the diagram), which is managed by the FBI to upload DNA profiles from participating states, the State DNA Index System (SDIS) (diagram center) that serves as each state's DNA database collected from local laboratories, and the Local DNA Index System (LDIS) (diagram bottom) where the DNA profiles are usually inputted.

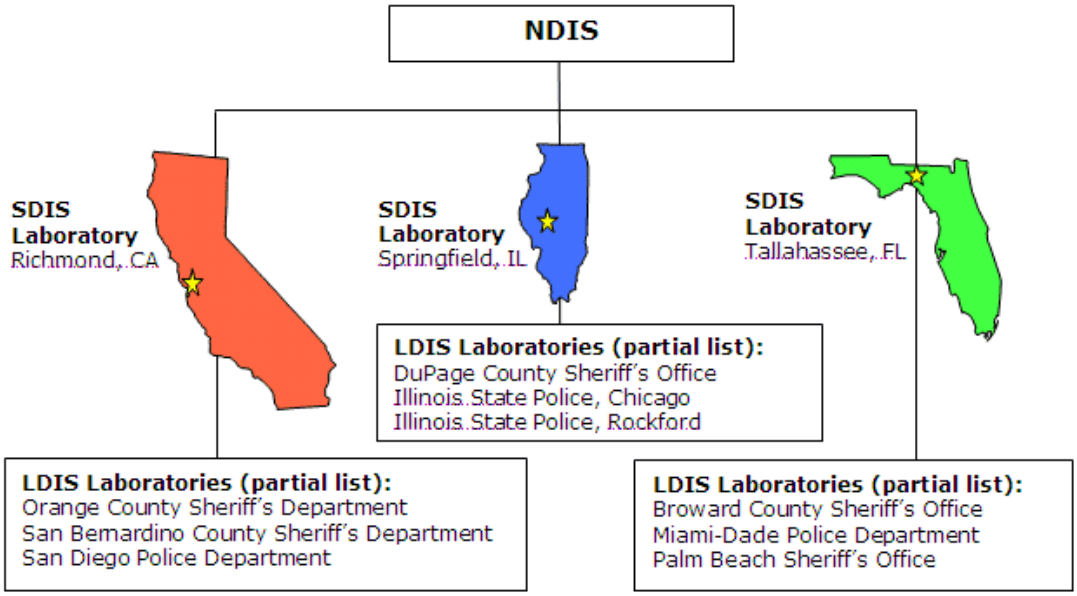
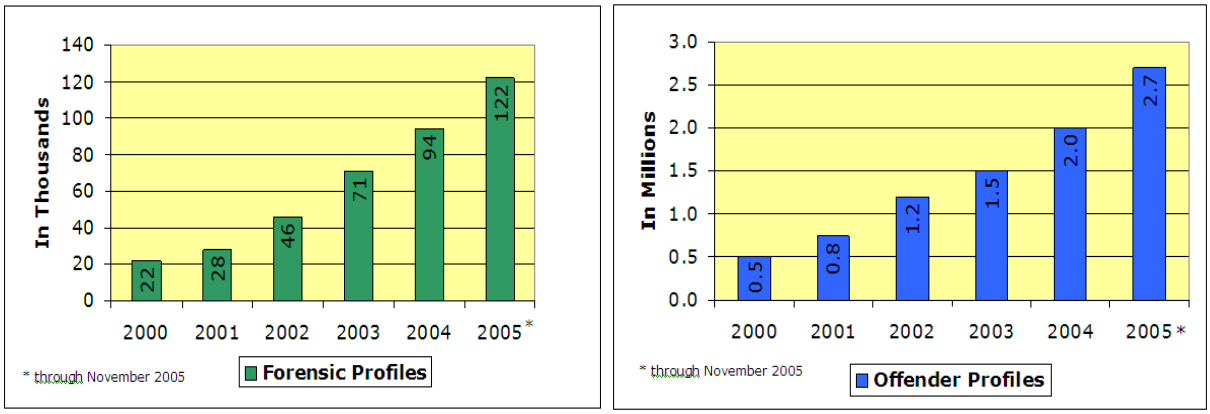


Figure 5.1 – Hierarchy Structure of the FBI's CODIS System. Samples are analyzed at three levels, national, state, and local (Combined DNA, May 2006).

CODIS was up and running by 1998, and has since then has grown (Figures-5.2 and 5.3). By November 2005, the NDIS already contained about 2.9 million profiles from the Convicted Offender database, the Forensic database, the Unidentified Human Remains database, the Missing Persons database, and the Relatives of Missing Persons database. However, only the first two mentioned work together to provide CODIS with its crime-solving capabilities. The other three databases can be searched against each other to help find missing and unidentified persons from around the country.



Figures 5.2 and 5.3 – Dramatic increases of profiles included in NDIS (Combined DNA, May 2006)

It is important for CODIS to keep growing because the larger the database, the greater the chance of obtaining a hit from a crime scene sample. A lesser known fact, is the larger the database, the more accurate match probabilities can be assigned. This is because, as discussed in chapter-1, we do not test a full DNA strand (that would be completely unnecessary and a waste of time and resources); instead we only test certain locations (loci) on the DNA. The more loci analyzed, the more accurate the analysis is. And the more entries in the database, the more

accurately we can assign frequencies to each locus being analyzed. This allows investigators to see how random those loci appear in people.

Proving the Uniqueness of DNA

Knowing the probability of another person having the exact same sequences at each of the 13 core loci analyzed is crucial to having DNA evidence allowed in court. Because each locus is independent of other loci, the probability of two people having the same sequence at each locus can be multiplied. For example, if three loci are tested, A, B, and C, the probability of two people sharing the same sequences at all the loci would be the probability of sharing the same sequence at A, multiplied by the probability of having the same sequence at B, multiplied by the probability of having the same sequence at C, assuming that these probabilities are known.

In theory, when all 13 core loci are analyzed for a sample today, the combined probability of two people sharing the same sequences at all 13 loci is 1 in much-more-than-the-population-of-Earth, thus proving that each human's DNA is nearly unique to themselves, much like their traditional fingerprints (although some sources argue 7 people on the planet can have your same traditional fingerprints if you have no unusual distinguishing abnormalities). A DNA database is like an ongoing collection of information, so by using the database a computer can go through every DNA sample collected and calculate the frequency of all possible sequences at each of the thirteen loci that are stored in the CODIS. Therefore, the more DNA samples that are inputted into CODIS, the more accurate the calculated frequency of each possible outcome will be. For example, a calculated frequency based on one thousand samples will be less accurate than a frequency based on one million samples.

Who Provides DNA Samples to CODIS?

Who provides their DNA to databases is determined by individual states. On November 13th, 2003, the governor of Massachusetts signed a bill that required all current Massachusetts felons to submit a sample of their DNA to a database within a year of the bill passing. This bill also requires all future felons in the state of Massachusetts to submit a DNA sample.

Massachusetts is not the only state requiring these DNA samples either. All 50 states require that *convicted* sex offenders provide the state with a DNA sample, and many states are trying to expand these policies to also include all felons, or at least many serious felony offenders (State Laws on DNA, 2008). To show the progress to July 2008, 46 states now require that all *convicted* felons give a sample of DNA to the state's database. The four states which do not yet require this are Idaho, Nebraska, New Hampshire, and Pennsylvania. However, twelve states have even stricter laws that require all *arrestees* to give DNA samples; other states have varying laws that include requiring DNA samples from minors, people convicted of misdemeanors, sexual offenders, etc.

Databases and Privacy Rights

Since DNA databases have significantly helped solve many crimes and even past crimes (also sometimes referred to as cold cases), many law officials are looking into new ways of stopping crimes all together. With increases to the DNA databases, many would-be criminals would most likely be deterred from committing crimes at all. This is due to the fact that one trace of DNA at a crime scene, such as a drop of sweat or a loose hair, would almost instantly prove their guilt. However, the hopes for stopping crimes all together would require DNA

samples from every citizen. Many citizens, although excited about reducing crimes, believe that this method is also a violation of their rights.

Most of these violated rights come from the fourth amendment in the constitution. The fourth amendment states, "the right of the people to be secure in their persons, houses, papers, and effects, against unreasonable searches and seizures, shall not be violated, and no warrants shall issue, but upon probable cause, supported by Oath or affirmation, and particularly describing the place to be searched, and the persons or things to be seized" (U.S. Constitution, 2008).

One argument for privacy from Tania Simoncelli is that "these databases are starting to look more like a surveillance tool than a tool for criminal investigation" (Weiss, 2006). Another general argument is the collection of DNA for these databases "constitutes a particularly gross violation of privacy" (Etzioni, 2001). In general, citizens who believe that their privacy is violated feel that the databases are turning everybody in the nation into suspects.

A more specific argument has been made about keeping medical predisposition data private. Medical genetics is only now getting to the point of identifying loci capable of predicting certain medical predispositions. Some recent examples include the BRCA genes for breast cancer, and the ApoE gene for Alzheimer's disease. Privacy supporters believe that outside parties, such as insurance companies, could access their DNA information and use the information (such as diseases they are prone to) against them. However, it is not well known in the public that no person has ever shown medical predisposition data from the 13 core forensic loci. So if this core locus information is all that is entered in the database, this argument weakens, unless the original DNA sample is analyzed more fully. This is due to the fact that the FBI normally saves the original sample of the DNA. However even this argument could be

significantly weakened by simply agreeing to destroy the original DNA sample after obtaining the 13 core loci information.

Chapter-5 Conclusions

Despite popular beliefs, a number of people support having a universal DNA database, which would include the entire Earth population. In forensic databases, only thirteen specific loci are tested, and these locations are not known to code for any biological purpose (effectively, these locations are junk DNA). While the original DNA samples are often stored, it is only for the purpose retesting in case of errors. As for the DNA samples getting in the hands of third parties, the original samples should be restricted to only certain law enforcement personnel, much like a patients information at a hospital.

To this IQP author, it makes logical sense to include every person's DNA in a database for criminal justice purposes. Of course, in order to do this it would require time to collect samples and to put in place procedures for collection when a baby is born, but in one generation we would have a complete world DNA database. As for the claim that everyone in the DNA database is a suspect, that is false. Being found as a match by a DNA database would only provide sufficient probable cause and additional information would be needed for a conviction.

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CONCLUSIONS

This project has been constructed in an effort to bring to light the powerful uses of DNA fingerprinting technology, and to document the effects of this technology on society. We started our exposé by looking at the structure and origins of DNA itself, as well as how it is used to create a DNA profile. We then described the applications for this new technology, as well as the two main types of fingerprinting techniques used. The applications discussed included paternity testing, molecular archeology, and criminal justice. The two main ways for analyzing a DNA fingerprint are amplifying (PCR) versus non-amplifying (RFLP) fingerprints. The PCR form of testing was seen to be faster, and needed less DNA for analysis. However this PCR test was also sensitive to contamination which can render the results useless. The RFLP/Southern blot technology was slower, needed larger DNA samples for analysis, was also less prone to contamination, and is more accurate than PCR testing.

Chapter 2 focused on the recommended ways to handle DNA evidence to avoid contamination and increase the likelihood of the evidence getting accepted in a court of law. Most of these techniques came about in the ten years following the O.J. Simpson murder trial, in which DNA evidence was sometimes mishandled. These standards for collecting and storing DNA range from the collection of evidence, to maintaining a chain of custody, to its proper storage.

The third chapter looked at various landmark cases that paved the way for DNA evidence to be used in U.S. courts. These cases were not the well known cases that the general public points to as instances of DNA use, but instead they initiated and guided the formation of outlines for determining whether DNA evidence could be used in individual cases. These cases aided us

in determining that DNA can be an accurate form of evidence when the analysis is performed properly, and it can be the conclusive piece of evidence in many cases. These cases provided us with a set of standards, principles, and precedents for the use, admittance, and evaluation of DNA fingerprinting evidence in the courtroom.

The fourth section of this project looked at three sensational, well known court cases which involved DNA analysis. Although these sensational cases did not set legal precedents, they involved the use of DNA during the cases (O.J. Simpson) or applied the techniques to the case once they became available (Boston Strangler and Anastasia). Some of these cases have now been closed, while others are still ongoing. A highlight of this chapter was the emphasis of the power of the DNA fingerprinting techniques within these cases. The O.J. Simpson case showed that even if the collected DNA evidence was matched to the suspect, the evidence is rendered useless if it has become contaminated or if an inconsistent chain of custody results in the potential tampering of evidence. The Strangler and Anastasia cases show the power of DNA and its techniques, that it can be implemented even long after the original trials have been completed, in an effort to unveil the truth.

The final piece of this project deals with DNA databases and the ethical decisions associated with them. Although large DNA databases increase the probability of finding a match to crime scene evidence, and they increase the accuracy determining allele frequencies from which match probabilities are determined, several questions arise from the possibility of a worldwide, universal database containing DNA for each person in the world. What ethical lines are crossed when we ask each person to provide a DNA sample? How long should this sample be stored? Once the DNA is accurately entered into a database, such as CODIS, should it be destroyed to prevent deeper analysis of genetic predispositions? If so when should it be

destroyed? If all people give a sample, what about the possible use of their DNA to determine their medical predispositions and infringement on their privacy rights? There is also the question of who should have to give DNA samples for a database. Should it be all people? Should it be all people who have been arrested? Should it be convicted felons?

These questions were analyzed by the authors of this project, and different answers were obtained for each of the 3 authors of this report. One author believes *everyone* should have to submit their DNA to a database, as it would deter people from committing crimes. Another author believes that once DNA has been tested for the 13 core CODIS loci, the DNA sample should be destroyed for privacy purposes, such that all that remains is the profile of 13 core loci that contain no medical predisposition data. If the DNA sample needs to be retested, then another sample of DNA can be acquired. This author also believes that people are born with some innate good in them, thus I do not believe that everyone should have to give a sample at birth, but *convicted felons* should, then the DNA sample should be destroyed once the case is finished. However, if this felon upon his release commits another crime, they should have to provide another sample that does not have to be destroyed ever. The destruction of the first sample would allow the government to avoid any accusations of determining someone's medical predisposition. It is also my belief that when someone commits a crime, they forfeit some of their privacy rights which they are entitled to upon birth. The third author agrees that only *convicted felons* should give their DNA. He didn't believe that everyone should because once criminals realize their DNA profile is already in the database that would provide an incentive to determine ways to block its deposition at crime scenes. For example, when traditional fingerprints could be tested, criminals started wearing gloves. It is his belief that DNA should be destroyed one year after testing, which should give enough time to retest it if needed. Even

though a larger database would ideally help solve more crimes and allow for more accurate allele frequencies, the third author feels it would be a crime itself to force everyone to provide a DNA sample upon birth. Living in a free country we are entitled to certain rights. This being said, should one choose to violate the law of our country, then you have chosen to give up a certain privacy rights this country has provided us.

It is the hope of this project that we have shed a significant amount of light onto the power and accuracy of DNA fingerprinting evidence. We have shown the gradual progression of the techniques and standards used to create the DNA acceptance we see today. Without the knowledge of this groundbreaking technology many cases would go unsolved, and more criminals would still be unaccounted for. The use of DNA in court cases and as evidence is still growing, and its full use has yet to be determined. As the uses and functionality of DNA evidence increases, it will undoubtedly bring clarity and correct rulings in courtrooms across the United States of America.