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DNA FINGERPRINTING

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ABSTRACT

DNA fingerprinting is an emerging forensic technology that has made a lasting impact on society in general, especially the judicial system. Similar to past complex technologies, society has shown skepticism for using DNA for various purposes. Recent advances in DNA collection, storage, and analysis has made this evidence more widely accepted in the courtroom. This project explores this technology by defining the main concepts behind DNA fingerprinting, its uses, DNA databases, and the technology's eventual acceptance in the courtroom.

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PROJECT OBJECTIVE

This project was undertaken to explore the new technology of DNA fingerprinting, and to document its great impact on forensic science, the court system, and society. Although DNA fingerprinting has the potential to change forensic science as we know it, controversy still surrounds this complex technology in the courtroom. Through meaningful and extensive research, we will examine how this powerful technology arose, how it is utilized, the advances made in DNA collection and storage, and reflect on current legal and ethical concerns encompassing this new technology.

CHAPTER 1 – DESCRIPTION AND TYPES OF DNA FINGERPRINTING

Introduction

When more than 99% of human DNA is alike (Human Genome Project Information, 2004), the 1% difference in DNA establishes the variation observed in each human being. This variation between each person can be extremely beneficial, especially when utilized in a technique called DNA fingerprinting. These genetic differences between individuals can be exploited with DNA fingerprinting, which are advantageous when it is necessary to identify a specific person or other organism. Unlike traditional fingerprints found on the tips of a person's fingers, the DNA sequence cannot be easily altered. This is helpful in certain situations, for instance, crime forensics and paternity testing, when the identity of a specific person is needed. The purpose of this chapter is to discuss the types and uses of DNA fingerprints, along with advantages and disadvantages of each type. To begin, it is important to understand the significance of DNA to completely comprehend the concept of DNA fingerprinting.

Background on DNA Structure

The chemical structure of each individual's deoxyribonucleic acid, or DNA, is identical, except in the case of identical twins. However, it is the sequence of this structure that distinguishes one person from another (Brinton and Lieberman, 2007). Each person has a unique DNA sequence, which makes each person different on a molecular level. This is an important feature utilized with DNA fingerprinting.

All living organisms, from the bacteria at the bottom of the ocean to the adjacent person, contain DNA in each cell. The cell is the most fundamental unit of an organism (Carpi, 1999). Different cells come together to develop a functioning organism. Cells have differences depending on their location and function. As an example, the cells found in the human stomach and brain are different due to the location and functions of these organs. However, there are similarities evident in each cell. One of these similarities includes the organelles found in these cells. An organelle is a differentiated structure present in eukaryotic cells that performs specific functions for the cell (Voet et al., 2006).

The structures found in a standard animal cell are shown in Figure 1.1. This figure displays the organelles present in each animal cell of an organism.

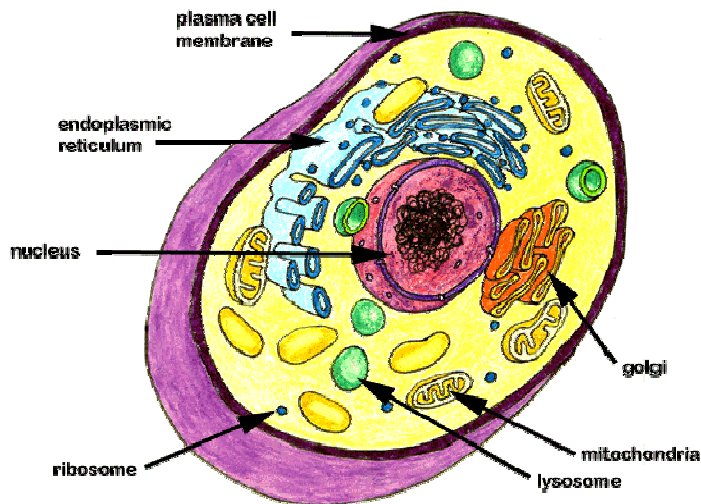


Figure 1.1 Diagram of an Animal Cell. Note the nucleus (red in diagram center) and the mitochondria (yellow) the organelles that contain DNA (Capri, 1999).

A very important organelle found in the cell is the nucleus. The nucleus is the location of the chromosomes and DNA for each cell. These structures, within the nucleus, are responsible for containing the genetic information of the cell.

The concept of the structure and function of DNA is critical to fully comprehending DNA fingerprinting, since DNA is a significant key factor. DNA is composed of molecules that contain the genetic information for all functions present in a cell (Some DNA..., 2007). This

DNA is assembled to form a chromosome (Figure 1.2). Chromosomes are structures that package and store DNA for future uses, such as replication (DNA and Chromosomes, 2007). Figure 1.2 reveals how the genetic information of a cell is stored and packaged in the nucleus. The manner in which the chromosome packages the DNA in the nucleus is significant since the structure of DNA is maintained and available to provide genetic information when necessary.

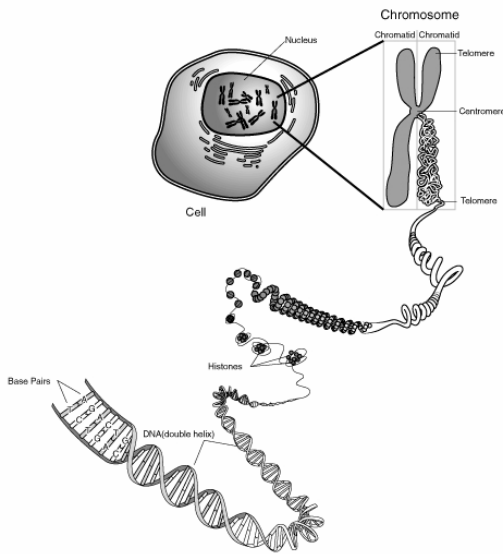


Figure 1.2 Organization of DNA into Chromosomes. The DNA double helix (lower left) is wound into higher order helices (diagram center) that are mixed with protein to make chromosomes (upper right) (Chromosome, 1999).

The structure of DNA is composed of nucleotides, also called bases, which bond together in a specific manner to form a double helix (Figure 1.3). These nucleotides include adenine (A), cytosine (C), guanine (G), and thymine (T). In this structure, adenine base pairs with thymine and cytosine base pairs with guanine to construct the DNA's double helix.

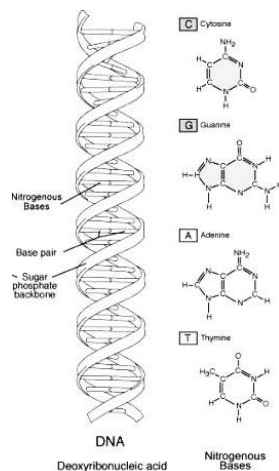


Figure 1.3 The Chemical Structure of DNA. Note the double helical structure (left), and the four nucleotides that form the precursors to DNA during replication (right) (DNA Basics, 2007).

The length of the fragment will depend on the length between the restriction sites. If the restriction sites are close together, there will be a larger number of short fragments generated, and vice versa. Such precision enables the opportunity to observe and compare two samples of DNA depending on the fragment lengths generated. These fragments can be separated and observed by mean of a Southern blot (Figure 1.5).

There are disadvantages to using the RFLP technique. One of these disadvantages includes the need for a large amount of high quality DNA. Also, the analysis of RFLP is a time-consuming procedure that examines the DNA one piece at a time (Collins, 2002). These disadvantages provide the reasons why RFLP analysis is not a frequent practice with most forensic proceedings.

Southern Blot

Named after Edward M. Southern, the Southern blot procedure was designed to separate and identify a specific DNA fragment of interest from an assortment of DNA. Southern blotting is used in RFLP and VNTR analysis (discussed below) to distinguish a desired sequence of DNA. Southern blotting contains a variety of steps in order to successfully isolate the desired DNA fragment, which can be observed in Figure 1.5.

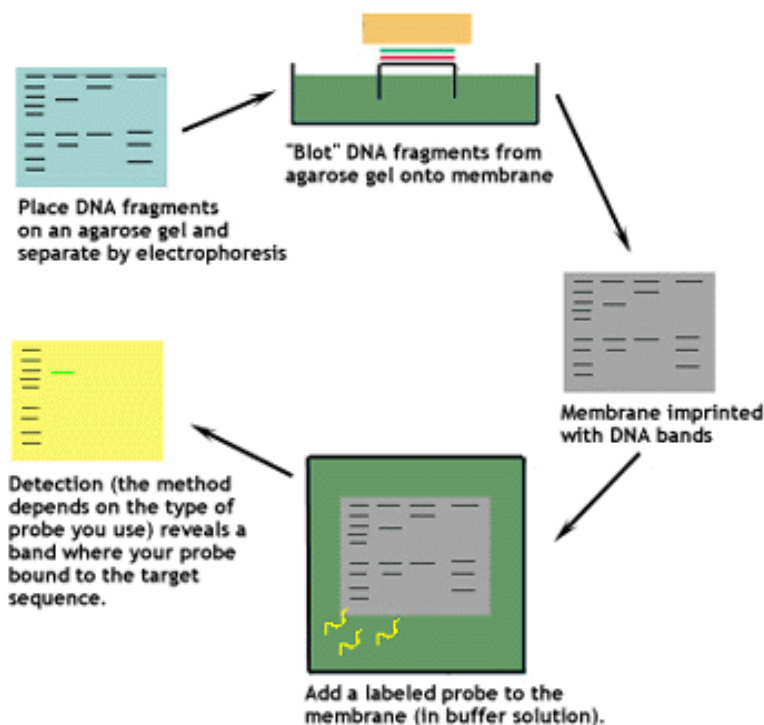


Figure 1.5 Diagram of a Southern Blot. In the first step, the DNA is separated by using gel electrophoresis. Once the DNA is isolated by size, the gel is placed against a nylon membrane to transfer DNA. A specialized probe is introduced to the membrane, which attached itself to the targeted DNA sequence (Khalsa, 2004).

When performing a Southern blot, the first step is to introduce the DNA sample into the wells of an agarose gel in order to carry out a gel electrophoresis. An electric current is established in order to separate different sized fragments of DNA. Due to the phosphate backbone of DNA, the molecule has an overall negative charge. When an electric current is induced, DNA will migrate through the small holes of the agarose gel towards the positive end. The larger fragments of DNA will not be able to navigate through the agarose gel as easily as the smaller fragments, separating the DNA fragments solely based on size. These smaller fragments will move farther down the gel than the larger DNA fragments. Following the gel electrophoresis, the gel is soaked in an alkaline solution, which transforms double-stranded DNA into its single-stranded form. The gel is then covered with a membrane. The single-stranded fragments of DNA are transferred from the agarose gel to the membrane. A solution is introduced to the membrane with a probe that contains the complementary DNA sequence to whichever locus is being

analyzed in that particular experiment. Once hybridization occurs, the probe will bind with the DNA of interest to reveal its location on the gel.

VNTRs

The main idea behind DNA fingerprinting is every individual has a different sequence of base pairs in his or her DNA, which can be used to identify a person. Not all DNA encodes important proteins for use in cell function, some DNA is considered “junk” (although we now know that most DNA serves some kind of function). The junk DNA varies between individuals, so is that portion analyzed in DNA fingerprinting. A significant portion of junk DNA consists of specific repeating sequences, which are called variable number tandem repeats (VNTRs). The repeat length can range from twenty to one hundred base pairs long (Brinton and Lieberman, 2007) and be found repeated in lengths of 500 to 20,000 base pairs within the DNA (Collins, 2002). The technique is somewhat similar to the mechanism of RFLP with DNA fingerprinting, except with RFLPs you can probe for any specific sequence of interest, while with VNTRs the probe is specific for a repeating sequence. With VNTRs, specific restriction endonucleases are used to cleave the DNA into fragments, and then a Southern blot is used to determine the length of the VNTR locus, to determine whether the VNTR fragments correlate with a given sample of DNA. VNTRs provide a more accurate way to gauge individual differences, but the same technique disadvantages still remain as stated previously with RFLPs.

STRs

“Approximately 3% of the human genome consists of highly repetitive DNA sequences...” (Voet et al., 2006) called short tandem repeats, or STRs. These repeats are

believed to be randomly generated during DNA replication where the template strand moves unexpectedly. Parts of DNA will have the same sequence due to the movement of the DNA template, which will produce a prominent degree of polymorphism in the human population. This has been proven to be an extremely valuable asset in DNA fingerprinting because STRs are short enough to be analyzed by PCR instead of the more laborious DNA blotting methods.

The concept behind STRs is very similar to VNTRs, except the length of the repeated sequence is shorter. Where VNTRs usually occur in lengths of 500 to 20,000 nucleotides (Collins, 2002), STRs are much smaller with lengths of 2 to 7 nucleotides. Since STRs are small in length, Taq polymerase can read through them during PCR, which will be discussed in the following section. The process is very sensitive and can be completed in a few hours, so this is currently one of the most commonly used procedures for analyzing DNA.

Amplification is possible through another technique, polymerase chain reaction or PCR. This technique will be discussed in the following section. By using PCR, there are several advantages over utilizing Southern blots with RFLPs and VNTRs. One of the main reasons STRs are popular in DNA fingerprinting is that the quality and quantity of DNA is less of an issue. Since the repeats are short in length, PCR can be used to amplify the amount of DNA present in order to produce a larger amount of short repeating sequences. This can be beneficial at a crime scene where there is degradation of DNA and/or when there are trace amounts of DNA present.

PCR

Polymerase chain reaction, or PCR, is a technique used to amplify small amounts of a particular DNA sequence. In order to synthesize the specific DNA sequence, it is necessary to

develop DNA fragments (termed primers) which will flank the desired targeted sequence, in this case, an STR region. A reaction mix is created, which contains a large volume of these synthesized primers, along with the target DNA and a thermostable DNA polymerase.

There are three main steps in PCR, which can be illustrated in Figure 1.6.

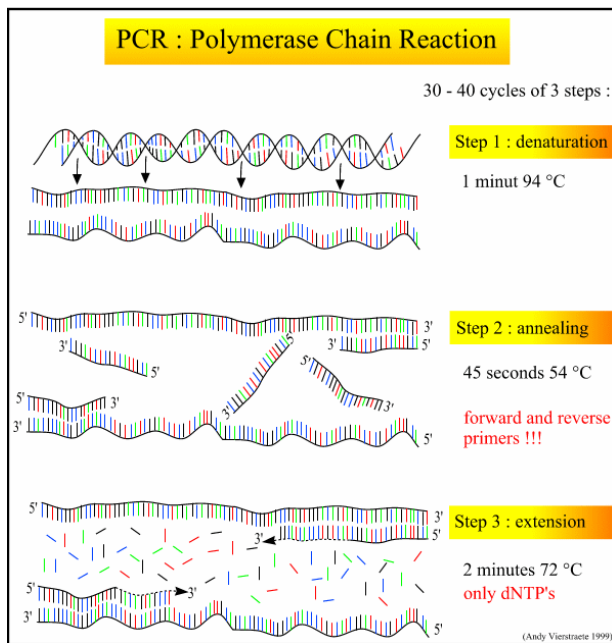


Figure 1.6 The Main Steps of PCR. The first step is denaturation, where double-stranded DNA is denatured by high temperatures, such as 94°C. The second step is annealing in which the primers bind to the DNA. The last step is extension in which Taq polymerase extends the primer sequences to make the target DNA sequence longer (Vierstnete, 1999).

First, the target DNA is denatured by heat in order to separate its complementary strands. When the temperature is lowered, the primers anneal to the target DNA on both sides. There is an excess of primers found in the reaction mix and this prevents the two original strands of the DNA from annealing to each other during the cooling period. If there is a large volume of primers present, the probability of the primers annealing to the target DNA is high. Finally, *Thermus aquaticus* (Taq) DNA polymerase lengthens the primers and synthesizes more copies of the target DNA. At the end of this cycle, both strands of the targeted DNA sequence have been copied (Prescott et al., 2005). The amount of DNA will double each time a PCR cycle is run, which means that it does not take a significant amount of time to reach a practical amount of

DNA. The ability to amplify a small amount of DNA has been shown to be extremely useful in STR analysis.

Applications of DNA Fingerprinting

DNA Forensics

Advances in methods used with obtaining knowledge from DNA have played an important role in society, especially with DNA forensics. According to the Merriam-Webster dictionary, forensics can be defined as the “application of scientific knowledge to legal problems, especially scientific analysis of physical evidence (as from a crime scene).” With this concept, DNA taken from a crime scene can be analyzed and then tested against alleged suspects associated with a specific crime.

To facilitate crime solving, most U.S. states currently required people convicted of violent crimes to donate a DNA sample to the FBI’s Combined DNA Index System (CODIS). This database contains the DNA profiles of hundreds of thousands of individuals, and DNA profiles obtained from a crime scene can be scanned against CODIS to see if a hit occurs. This national database widely adopted by forensic DNA that is based on thirteen STR loci present in DNA, shown in Figure 1.7 (University of Arizona, 2006).

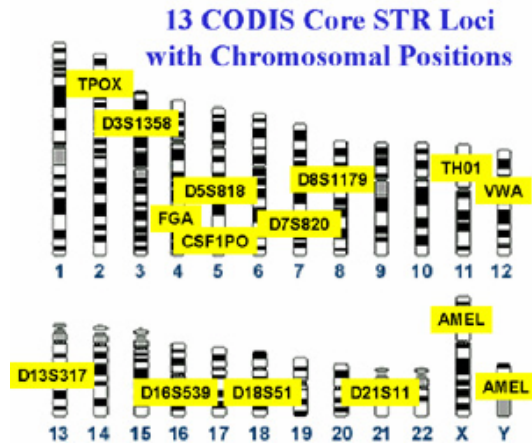


Figure 1.7 Note the thirteen STR loci used in CODIS. These markers are currently the most frequently used in order to identify a specific person (CODIS..., 2006).

Each of these repeating four base-pair sequence gives a specific genotype, along with the frequency of obtaining one of the specific genotypes. A more in-depth explanation of CODIS can be found in Chapter 5. By using these features, it is sometimes possible to distinguish an innocent suspect from a guilty one.

Analyzing DNA extracted from a crime scene has proved to have an incredible development in the forensics community. With DNA, it is possible to compare two individuals on the microscopic molecular level. The opportunity to catch the correct suspect is increased enormously by using DNA, since each individual contains a specific sequence of genetic information. Before DNA was widely used, evidence samples, such as hair and blood, would be compared on the macroscopic level. For example, if a black strand of hair was present at the crime scene, it was possible to narrow the search down to people with black hair. However, if there were more than one suspect with black hair, this piece of evidence would not be able to single out which individual committed the crime. The use of traditional fingerprinting added more accuracy to forensic analysis, but fingers can easily be covered by gloves during crimes. The use of general blood typing (A, B, O, etc) also provides some accuracy, but far less than with DNA typing.

Paternity Testing

Another application of DNA fingerprinting is paternity testing. During fertilization, the sperm and the egg come together, forming the first new cell of an organism. This event gives the new organism half the DNA from the father and the other half from the mother. This is important with a paternity test. DNA samples from the mother, child, and assumed father can be compared and analyzed to see if there are similarities on the genetic level, as shown in Figure 1.8 (DNA Fingerprinting, 2007).

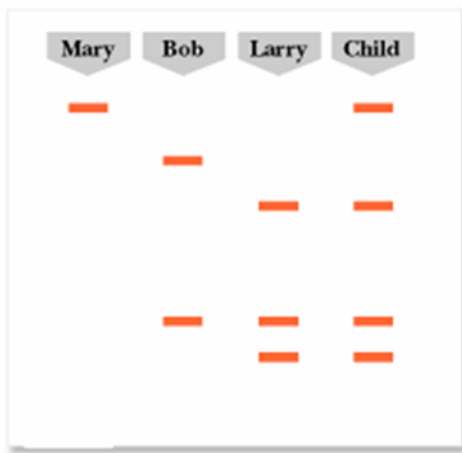


Figure 1.8 Example of a Paternity Test. The two candidates as father are Bob and Larry. By observing the figure, it is possible to determine that Larry is the father when comparing his DNA with the child's DNA since that DNA shares the most bands with the child (Sha, 2004).

The main comparison would be between the DNA of the child and the suspected father. If the man was the child's father, there would be similarities in DNA between the child and the father. However, if the man was not the father, there would not be any genetic similarities between the two individuals. In the case shown in Figure 1.8, Larry is determined to be the father, the mother's DNA bands are subtracted from the child's profile since it is already known that she is the mother.

Inherited Disorders Research

All the genetic information for an individual is found with its DNA. As stated previously, an individual will obtain half of the DNA from the mother and the other half will

come from the father. If there is an inherited disorder present in the DNA of either parent, it is quite possible to pass this trait onto the child, which is illustrated in Figure 1.9.

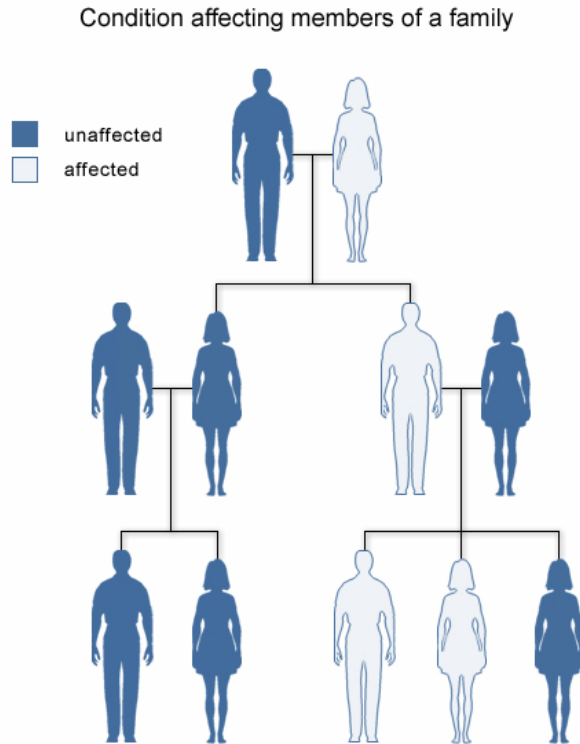


Figure 1.9 How an Inherited Disorder Can Be Passed Through a Family. Using DNA fingerprinting, it is potentially possible to obtain more information about a specific disorder (Genetics Home Reference, 2007).

U.S. National Library of Medicine

Using DNA fingerprinting, it is feasible to study the DNA patterns associated with the disease by comparing the DNA from an individual with the disorder and one without the disorder (Betsch, 2007). Gaining information about the genetics of a disorder can lead to a better understanding of the disorder, along with the possibility of acquiring a cure. In these cases, genetic screening can help lower the disease incidence.

Molecular Archaeology

Molecular archaeology is an emerging, new field of archeology that uses the knowledge and understanding of DNA to become more aware of the past (Christianson, 2000). Depending on the state of the uncovered organism, it is possible to recover DNA to examine, even from

ancient samples. This discovered DNA can be compared against other DNA sources to obtain information concerning the past. The mummies of Egypt are one example of utilizing molecular archaeology. By obtaining DNA from these mummies, it is possible to determine the lineage of the royal family. In addition, significant genetic information about the deceased individual can be obtained, such as whether they had a crippling disorder. Molecular archaeology presents the opportunity to gain additional knowledge concerning ancient civilization and its people, along with its differences to present day individuals, solely based genetic information.

CHAPTER 2 – DNA FORENSICS

Advances in DNA Forensics

It may be hard to believe at the present time, but DNA fingerprints were not widely acknowledged as credible evidence approximately twenty years ago. This was due to multiple reasons, including the lack of legal precedents for accepting complex DNA evidence in U.S. courts, the general public's lack of understanding of DNA, and factors related to DNA handling (contamination and degradation). The purpose of this chapter is to discuss the latter topic, advances in how to control DNA contamination and degradation.

DNA fingerprinting was first introduced to forensic science in 1985, but it was not until 1992 that the National Research Council stated that “DNA testing was a reliable method to identify criminal suspects” (Burns, 2006). The concept behind DNA fingerprinting underwent seven years of criticism prior to becoming a serious implement in the U.S. court system.

Contamination and degradation of DNA was a main reason DNA evidence was not allowed in many early trials, so advances were made in this area to ensure that DNA discovered at a crime scene can be used in court. Techniques were developed for minimizing contamination, or if it is present for minimizing it. Techniques were also for tracking chain of custody of the samples, and for proper methods of storage to help prevent degradation. (Meeker-O'Connell, 2007).

Sources of DNA at a Crime Scene

There are two main cellular sources of DNA found at a crime scene utilized in forensic analysis; these include nuclear DNA (nDNA) and mitochondrial DNA (mtDNA). Nuclear DNA

is found in evidence such as blood, semen, saliva, body tissues, and hairs with tissue at its roots. Mitochondrial DNA is found in naturally shed hairs, hair fragments, bones, and teeth (Handbook of Forensic Services, 1999). When biological samples have become older and begin to decompose, mitochondrial DNA is especially important. Nuclear DNA will perish over time, whereas mitochondrial DNA degrades much less. Mitochondrial DNA can be helpful in investigations that have been unsolved for years because this DNA comes from the mother's egg cell, hence transferring the same mitochondrial DNA onto the offspring ("DNA Forensics," 2006). This can be valuable in older cases since the mitochondrial DNA can be compared to the potential maternal relative, without the complicating genetic recombination changes that occur with nuclear DNA.

It is also imperative to know where these DNA sources come from. At a crime scene, DNA can be collected from almost everywhere; it depends on the location in which the investigator searches. Table 2.1 displays examples of evidence, the probable location of DNA on the evidence, and the source from which the DNA came from. Note in the table the large variety of physical evidence that is likely to have DNA on it.

Evidence	Possible Location of DNA on the Evidence	Source of DNA
Baseball Bat or Similar Weapon	Handle, End	Sweat, Skin, Blood, Tissue
Hat, Bandanna, or Mask	Inside	Sweat, Hair, Dandruff
Eyeglasses	Nose or Ear Pieces, Lens	Sweat, Skin
Facial Tissue, Cotton Swab	Surface Area	Mucus, Blood, Sweat, Semen, Ear Wax
Dirty Laundry	Surface Area	Blood, Sweat, Semen
Toothpick	Tips	Saliva
Used Cigarette	Cigarette Butt	Saliva
Stamp or Envelope	Licked Area	Saliva
Tape or Ligature	Inside/Outside Surface	Skin, Sweat
Bottle, Can, or Glass	Sides, Mouthpiece	Saliva, Sweat
Used Condom	Inside/Outside Surface	Semen, Vaginal or Rectal Cells
Blanket, Pillow, Sheet	Surface Area	Sweat, Hair, Semen, Urine, Saliva
“Through and Through” Bullet	Outside Surface	Blood, Tissue
Bite Mark	Person’s Skin or Clothing	Saliva
Fingernail, Partial Fingernail	Scrapings	Blood, Sweat, Tissue

Table 2.1 Sources of DNA Evidence (President’s DNA Initiative, 2007)

Documenting Chain of Custody

The chain of custody of a sample is “a written record of all evidence transfers from the crime scene to possession of the court or the clerk of the court” (Schiro, 2001). A lack of chain of custody provides gaps in the ownership of a sample where someone could tamper with the evidence, so establishing a continuous chain of custody from the crime scene to court officer is important. One precaution to help establish chain of custody of the sample is to correctly label the package in which evidence is transferred. This can be as simple as classifying the day, time, location found, and a brief description of the evidence, as seen in Figure 2.1. Also, placing labels on the evidence containers, such as “evidence” or “biohazard,” can minimize the

credibility of any DNA evidence by minimizing the risk of contamination at the crime scene and in the laboratory. The prevention of contamination is one of the main goals of biological evidence collection. To ensure that this goal is achieved, it is very important that the evidence sample does not come in contact with any other biological source. This would compromise the evidence, which could prevent its ability to be shown in court. The best way to avoid cross-contamination is to properly package each piece of evidence without introducing any other DNA to the sample (Spear, 2004). This can be done by wearing latex gloves and a face mask when collecting evidence at a crime scene. Limiting the amount of people present at the crime scene would also minimize the possibility of contamination of a sample (Crime Scene Investigation: A Guide for Law Enforcement, 2000).

When removing a sample from the crime scene, it is recommended that biological evidence is collected from the source without harming or contaminating the sample. Using sterile, one-time use instruments is best. The nature of the evidence will demonstrate the best method in which to collect, but the overall goal when collecting is to ensure that this evidence does not interact with other objects. If the evidence is present on an immovable surface, such as carpet, it is necessary to cut out the sample for analysis. The evidence may also be present on a surface in which it is possible to cut out the sample, such as a concrete floor. The best method to sample this evidence is by running a damp cotton swap over the evidence, or by scraping off a sample and placing the evidence in an individual sterile container (Spear, 2004). It is also necessary to take a control sample of the surrounding area to determine if contamination occurred.

Once the evidence samples have been collected in an orderly manner, it is necessary to correctly package them to send to the laboratory for analysis. The manner in which the evidence

is packaged plays a large role in minimizing biological contamination. Evidence should be placed in “paper packaging that will protect the item against loss and contamination” (Spear, 2004), along with establishing the chain of custody and the description of evidence. Prototypes of paper bag storage are shown in Figures 2.2 and 2.3.



Figure 2.2 Paper Evidence Bags.
Used for large samples of evidence
(Arrowhead Forensics, 2007).

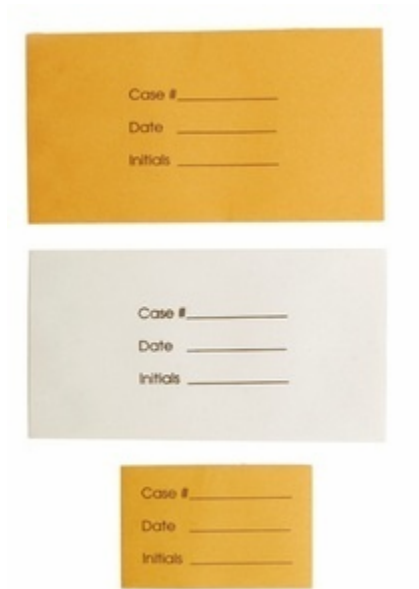


Figure 2.3 Paper Evidence Bags.
Used for small samples of evidence
(Arrowhead Forensics, 2007).



Figure 2.4 Plastic Evidence Containers.
Used for tissue samples containing moisture (Arrowhead Forensics, 2007).

If the biological evidence contains moisture, it is necessary to place the sample in a sterile, unused plastic container to prevent contamination, as shown in Figure 2.4. This type of evidence

should also be collected and analyzed in less than two hours to minimize microbial growth and contamination on a microscopic level (Schiro, 2001).

Blood is one type of moisture-inhabiting biological evidence that needs to be collected and analyzed in a quick, but meticulous manner. Along with being placed in a sterile plastic container, it is a common practice to introduce chemical solutions to prevent harm and degradation to the sample. Ethylenediamine tetraacetic acid, more commonly known as EDTA, is a chemical compound frequently used to prevent biological DNA degradation (Spear, 2004). This chemical serves as an anticoagulant, which inactivates metal-dependent enzymes that could degrade DNA in a sample. Blood samples should be stored in the refrigerator to ensure the stability of the sample. The same procedure occurs with other samples that could retain moisture, such as saliva or semen. When the sample is needed for analysis, it is good procedure to bring it to a secured clean area to thoroughly air dry it. Once this is done, it is possible to examine the sample for DNA.

Once the evidence has been located, collected, and packaged, it is transported to a laboratory to be analyzed. This is the last location of possible contamination. The FBI has issued specific standards for laboratories to lessen the probability of contamination in the laboratory. According to the standards presented by the FBI, contamination can be prevented by providing a team of trained and experienced laboratory personnel, “controlled and limited” access to all laboratories, separate working areas for analyzed and unanalyzed samples, and the laboratory should be cleaned and sterilized once a procedure is completed (Standards for Forensic DNA Testing Laboratories). By adhering to these standards, it is possible to examine a piece of evidence in a manner that has a decreased risk of contamination.

Prevention of DNA Degradation

Combined efforts between crime scene investigators and laboratory technicians may be appropriate to prevent contamination of a biological sample, but this can still lead to DNA degradation if the evidence is not properly handled. A prime example of an occurrence such as this is the use of distilled water at a crime scene. Distilled water is used to swab surfaces with cotton, such as cement and walls, to obtain DNA samples, but this can also lead to DNA degradation if too much water is used. One of the consequences of introducing distilled water to a sample is the growth of bacteria (Spear, 2004). Bacteria can grow in moist surroundings, which do not exclude a sample of biological evidence. A warm, humid environment will also play a role in DNA degradation. Other factors that contribute to DNA degradation include chemical contact, ultraviolet light exposure, and time (Luftig and Richey, 2001). The manner in which biological evidence is handled from the crime scene to the laboratory is crucial to maintain the integrity of evidence.

DNA Storage

Once the evidence is collected, it is important to store these important sources of DNA in a dry, cool environment protected from air to considerably slow the rate of DNA degradation (Kaye and Sensabaugh Jr., 2000). For short term storage, it is possible to preserve evidence samples at room temperature. Certain liquids, such as blood, should be stored in the refrigerator for short periods of time. For long term storage, it is recommended to place evidence samples in the freezer at temperatures ranging from 4°C to -20°C (Spear, 2004). When storing samples at such a low temperature, it is advised to introduce a buffer to the DNA sample to prevent breakage or degradation. A buffer containing Tris-EDTA (TE) is commonly used when freezing

samples to prevent hydrolysis of DNA during storage. When storing a blood sample, a buffer including EDTA is recommended to prevent coagulation (DNA Purification Services, 2007).

Chapter Conclusion

It is the responsibility of each person involved from individuals doing the collection to those doing the analysis of all biological evidence to ensure its integrity. Following the guidelines and standards established by the FBI will reduce the probability of DNA contamination and degradation in all fields of forensics analysis, and will increase the court's confidence in the DNA evidence.

CHAPTER-3: LANDMARK DNA COURT CASES

1923, Frye v US

The case *Frye vs. United States* in the District of Columbia Circuit Court in 1923 was a murder case. On November 25th, 1920, in Washington D.C., a young black man named James Frye was said to have shot and killed Dr. Robert W. Brown. Brown was murdered in his office at about 8:45 PM. At the time of the shooting another physician was in the office and witnessed the event. According to the witness, Frye ran out of the office chased by the witness. However because the witness had never seen Frye, the police did not know his identity at that time. Coincidentally, on August 21, 1921, Frye committed an armed robbery, which led to his arrest. When the police questioned him about the robbery, “he confessed to it and the murder of Doctor Brown” (Fisher, 2004).

Frye’s murder trial began on July 17th, 1922, in Washington D.C. before Judge William McCoy. The defense was based upon Frye’s alibi witnesses and William Marston’s then new Lie Detector Test. Although Frye passed the lie detector test which showed the admission of guilt was coerced, according to Judge McCoy the lie detector evidence was not admissible due to its questionable accuracy. If Marston’s new test was permitted, it would have concluded that Frye was coerced into his confession of Doctor Brown’s murder. In addition, it was believed that four days after the trial began, Frye’s alibi witnesses were scared off, therefore contributing to Frye’s sentence. Because the argument over admissibility of Marston’s lie detector test was performed in front of the jury, the jurors lessened the sentence from first degree murder (which would have resulted in the death penalty) to second degree murder which resulted in a life sentence.

Subsequently, in 1923, Frye's lawyer appealed in the Circuit Court of Appeals in the District of Columbia, on the grounds that the lie detector results should have been allowed. Utilizing Marston's lie detector results, Frye's lawyer presented the case to appellate Judge Van Orsdel. But Marston's scientific principle was questionable due to a lack of general acceptance of lie detectors in the field. During the 1920s, the courts believed that evidence based on polygraphs were still between the experimental stage and the demonstrative stage. It was argued that expert testimonies would be utilized if the principle or discovery was recognizable and acceptable in the particular field in which it belonged. The fact Marston's systolic blood pressure deception test was not eminent among physiological and psychological professionals, Judge Van Orsdel upheld Judge McCoy's earlier sentence of second degree murder (Fisher, 2004). James Frye served 18 years in the District of Columbia Prison at Lorton, Virginia until June 17, 1939, when he was granted parole. He later died in 1953 at the age of 58. To this date, lie detector results are still not allowed in U.S. courts.

Frye vs. United States resulted in the establishment of the *Frye standard*, which set a legal precedent "regarding the admissibility of scientific examinations or experiments in legal proceedings" (Frye Standard, 2007). In reference to Frye's appeal, the court stated that

Just when a scientific principle or discovery crosses the line between the experimental and demonstrable stages is difficult to define. Somewhere in this twilight zone the evidential force of the principle must be recognized, and while the courts will go a long way in admitting experimental 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 vs. United States*).

The Frye standard created a foundation for any new technology, experiments or discoveries used as evidence in any legal proceedings. Although this case did not use DNA evidence, it set precedence for lawyers whom later began to use DNA analyses in their trials. Therefore, unless

a new scientific theory was “generally accepted” by scientists within its field, it would not be considered probable in any court proceedings. The Frye standard established a basis for allowing technical evidence that changed U.S. courts.

Colin Pitchfork, 1986



Figure 3.1 Colin Pitchfork. This individual was the world’s first person convicted for murder with DNA evidence. He was found guilty for the murders of two teenage girls, (Wikipedia 2007).

The first murder conviction on DNA evidence happened in 1986. In 1983, Lynn Mann at the age of 15 was found raped and murdered in her hometown of Narborough, Leicestershire. The only evidence in custody was a semen sample pulled from the victim. It was concluded that the killer was a type A blood group, and with an enzyme profile which matched 10% of the adult male population in Leicestershire. Due to the lack of evidence, the murder was put aside until the unfortunate death of 15 year old Dawn Ashworth in 1986. A 17 year old boy, Richard Buckland was the prime suspect, however with the help of Drs. Alec Jeffrey, Peter Gill, and Dave Werrett who had just invented their technique for creating DNA profiles, Buckland was cleared. After the Buckland case was thrown out, the police decided to test the DNA type of the 10% of the Leicestershire population with blood type A, but none of the 500 donors matched the evidence. Luckily for the authorities, Ian Kelly did not know how to keep his mouth shut. He was heard boasting about providing his friend Colin Pitchfork with a sample of his blood to give to the cops in place of his own. With this new information, the police arrested Pitchfork, took his

blood, and finding it matched the profile of semen DNA, closed both murders (Colin Pitchfork, Wikipedia 2007).

Drs. Jeffreys, Gill, and Werret were the first to clear a suspect of any charges (Buckland), and the first to convict a suspect of murder (Pitchfork) with their DNA profile technique. In 1985 through their work at the Forensic Science Service, they published the first paper that demonstrated that DNA could be obtained from crime stains, and that DNA was capable of being analyzed in specific loci to reveal identity. With their findings they were able to prove that Buckland was indeed innocent. And with their same technique they were able to bring Lynn Mann's and Dawn Ashworth's deaths to justice. Because the DNA testing was found to be flawless, Pitchfork confessed to the murders, and the cases did not ever have to go to trial.

By developing the ability to test and match DNA, the doctors of the FSS have saved a lot of innocents and put away a lot of guilty parties. And since the technique can be applied to old stains, the technique provides hope that old crimes will eventually be solved.

Dr Gill said: "I was responsible for developing all of the DNA extraction techniques and demonstrating that it was possible after all to obtain DNA profiles from old stains. The biggest achievement was developing the preferential extraction method to separate sperm from vaginal cells – without this method it would have been difficult to use DNA in rape cases" (Forensic Science Service, 2007).

Although it is unfortunate to say, rape crimes have increased dramatically since in the 80's. Not only did the DNA testing aid in the justice of the two girls, but in rape cases today many have been put away solely on the basis of DNA, even with no other physical evidence. This provided cases with more to offer as evidence. DNA has become the most important piece of evidence in countless number of cases today. With the ability to test clothing, hair, and semen, etc., the ability to find the guilty has increased. Without DNA testing, Buckland could have been

founded guilty solely on his confession, and Colin Pitchfork could have walked away from two murders.

People v. Castro

The case of the *People v. Castro* (1989), the defendant was on trial for the death of two people. On February 5, 1987, Vilma Ponce and her two year old daughter were killed in the Bronx, NYC. With the help of neighbors and bloodstains found on his watch, Jose Castro was arrested. In this case however, the DNA evidence underwent the most complex attack to date by the defense attorneys. They argued the technique was not performed correctly by Life Codes (Valhalla, NY), and that proper markers and controls were not used. The judge agreed, and the outcome was the development of a new three prong standard for use at pretrial hearings to determine whether to allow DNA evidence at trial: (1) is there a scientific principle stating that individuals differ in their DNA? (2) Does a reliable technique exist that allows this difference to be tested? (3) Did the specific testing facility follow all correct procedures in analyzing these particular forensic samples?

These three prongs were utilized to determine whether to allow the DNA evidence against Castro. Prongs 1 and 2 passed, but prong-3 failed (Life Codes did not use controls), so the DNA evidence was not allowed at trial. The court also needed sworn documentation stating that Life Codes could prove that the bands matched. Another problem found was that the autorads were misread; Life Codes ignored three bands, discounting them as “of non-human origin.” In conclusion, the evidence was thrown out, however it was not needed due to Castro’s confession of the crime, therefore there was no need for an appeal (Patton,1990).

The importance of the *People v. Castro* case is the very use of an extension of the Frye standard with the new Three Prong analysis. The Prong I analysis deeply reviewed the theory of DNA analysis, and the court found the DNA theory and test reliable and accepted in the scientific community. The court explained that DNA is unique to the individual, and can not be manipulated, therefore the court deemed the testing reliable. In the Prong II analysis the court reviewed the RFLP test, and found the “DNA forensic identification tests to determine inclusions and exclusions are reliable and meet the Frye standard of admissibility.” Finally, with Prong III, the court reviewed the reliability of the tests performed by Life Codes. The court found that Life Codes did not follow the necessary procedures with their experiments, techniques, and their use of controls. The court made it clear that every case should use Prong III along with the Frye test to ensure that these labs are using the right procedures (Patton, 1990).

Although the Frye test is extremely useful, one must not forget that labs and tests are performed by humans who are not perfect. Overlooking a simple three or four bands or the use of a certain probe could change the outcome of the evidence.

Daubert v. Merrell Dow Pharmaceuticals

In the case of *Daubert v. Merrell Dow Pharmaceuticals* (1993), Jason Daubert and Eric Schuller believed that the drug, Bendectin caused their birth defects, so the family sought to sue the manufacturer Merrell Dow Pharmaceuticals Inc. in the state court of California. Merrell Dow had the case moved to a federal court, and submitted documents showing that there was no way to prove that Bendectin caused the defects. Daubert and Schuller also had their own evidence based on several doctors’ experiments with Bendectin and animals. However the district court concluded there was no strong evidence proving Bendectin caused birth defects, so granted

summary judgment to Merrell Dow, therefore leading Daubert and Schuller to appeal to the Ninth Circuit Court.

The Ninth Circuit found that the district court came to right conclusion. The Ninth Circuit believed that the evidence seemed to have been created just for litigation. The court believed that the plaintiffs did not have evidence that could definitely prove that Bendectin was the direct the cause of their birth defects.

However, Daubert and Schuller did not quit, they took their case to the Supreme Court. The Supreme Court looked over the evidence and the appellate court's reasoning on its decisions. The Supreme Court found that although the defendants did not meet the Frye standard of general acceptance (it was not generally accepted in the scientific community that Bendectin caused birth defects), there was a new standard known as Rule 702 which they felt supersedes the Frye standard. The Supreme Court reopened the case and demanded it be retried in the district court using the Rule 702 Federal Rules of Evidence. The very fact that the previous appellate court trial overly relied on the written word, dismissed the scientific experts of Daubert and Schuller (*Daubert v. Merrell Dow Pharmaceuticals*, 1993).

The legal precedence set by the *Daubert v. Merrel Dow Pharmaceuticals* was the interpretations of the rules and tests utilized in past cases. Although the case of *Frye v. U.S.* declared the necessity of more than one scientific expert for any particular new way of finding evidence, the subsequent Rule 702 was created to make sure that courts did not dismiss cases based solely on the harsh general acceptance standard. It is stated under Rule 702, "the expert's testimony pertains to 'scientific . . . knowledge,' since the adjective 'scientific' implies a grounding in science's methods and procedures, while the word 'knowledge' connotes a body of known facts or of ideas inferred from such facts or accepted as true on good grounds" (*Daubert*

v. Merrell Dow Pharmaceuticals, The Supreme Court Case, 1993). This means that although something has not yet gained general acceptance, it could still potentially be true and accepted in court if several experts agree. Therefore, this case opened doors for many subsequent cases that used scientific experts agreeing with each other in place of a general acceptance standard.

People v. Paul Eugene Robinson



Figure 3.2 Paul Eugene Robinson. A picture of the first man to be convicted of a crime based solely on his DNA with no other physical evidence (Delsohn, 2001).

In August 1994, Paul Eugene Robinson raped a 24 year old woman in Sacramento, California. The crime was similar to several other rapes performed by the so-called “Second Story Rapist”, but there were no eyewitnesses, and no physical evidence other than semen, so semen was frozen, and the crime went unsolved (Delson, 2001). Subsequently, Robinson was convicted of a string of burglaries, and served part of a 64-month sentence, but no DNA was taken at the time. However in November 1998, he was arrested for violating parole (prowling and loitering, authorities now believe looking for his next victim). After pleading guilty to the parole violation, authorities took his DNA on the basis of the then recently passed "DNA and Forensic Identification Data Base and Data Bank Act of 1998", and sent it to the state

Department of Justice Crime Lab in Berkeley, where the DNA profile was placed in the database.

On August 24, 2000, as the six-year statute of limitations approached for the rape, the Sacramento detective assigned to the case, Peter Willover, sent out an arrest warrant without a name, picture, or tangible evidence, but which included the DNA profile extracted from the semen left on the victim. The filing of the “John Doe” warrant stopped the statute of limitation, which gave the case more time to be solved. In addition to the warrant, Laurie Earl, a sex assault prosecutor filed a case labeled *People v. John Doe*. Three weeks after the filing of the John Doe warrant (and sending the crime scene DNA profile to Berkeley), on Sept. 15, 2000, Detective Willover got a call from a state criminalist informing him of a "cold hit." The warrant DNA matched that of Paul Eugene Robinson in the database. It was the first time that a John Doe warrant was used in court, as well as the first arrest in America solely based on DNA (Delsohn, 2001). Eugene was tried for 5 counts of sexual assault, and sentenced to the maximum of 65 years (Scully, 2003).

12
13 THE PEOPLE OF THE STATE OF CALIFORNIA,
14 vs.
15 JOHN DOE ,unknown male with Short Tandem
16 Repeat (STR) Deoxyribonucleic Acid (DNA) Profile
17 at the following Genetic Locations, using the COfiler
18 and Profiler Plus Polymerase Chain Reaction (PCR)
19 amplifications kits: D3S1358 (15,15), D16S539
20 (9,10), THO1(7,7), TPOX (6,9), CSF1PO (10,11),
21 D7S820 (8,11), vWa (18,19), FGA (22,24),
22 D8S1179 (12,15), D21S11 (28,28), D18S51 (20,20),
23 D5S818 (8,13), D13S317 (10,11), with said Genetic
24 Profile being unique, occurring in approximately 1 in
25 21 sextillion of the Caucasian population, 1 in 650
26 quadrillion of the African American population, 1 in
27 420 sextillion of the Hispanic population
28

Figure 3.3 The “John Doe” Warrant. This warrant was issued to extend the rape case’s statute of limitations when they had the DNA profile but no suspect (Delsohn, 2001).

There was no need for an appeal, however the case opened many doors for rape cases. In 2001, California's six-year statute of the limitations was eliminated where DNA evidence is available. Across the nation, rape cases now utilize the John Doe warrant approach for unsolved sexual assault cases, to lengthen the statute of limitations, and to identify assailants solely on their genetic code (Cooper, 2000). The use of DNA has solved countless number of cases. Because of the legal system, most states now require convicted felons and violent misdemeanors to give their traditional fingerprints and a DNA swab sample. Unfortunately, when no suspects exist, unless the guilty is in the database system it is nearly impossible to solve the crime. DNA has opened doors for many victims and law force agencies. The fact that the DNA testing by itself proved successful in the Robinson case set a legal precedence that allows similar cases to be closed based solely on DNA evidence.

CHAPTER 4: SENSATIONAL DNA COURT CASES

The purpose of this chapter is to remind the reader of important famous trials in which DNA evidence played a strong role. Although these cases set no legal precedents, they do point out the power of DNA evidence.

O. J. Simpson Trial

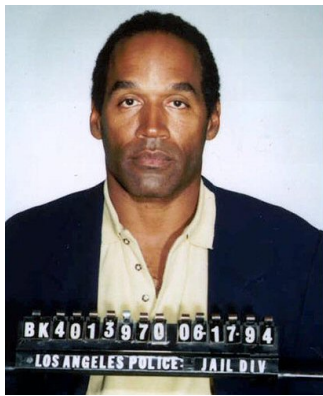


Figure 4.1 Orenthal James “OJ” Simpson. Picture of OJ’s arrest after the LA police found his ex-wife and her friend, Ronald Goldman dead (CNN.com, 1995).

On Monday, June 13th 1994, Nicole Brown Simpson and Ronald Goldman were found murdered outside Ms. Brown’s condominium in LA, California at 12:10 AM. Noon that same day O.J. Simpson was handcuffed and brought down to the LA Police Department. He was later released, but a week later on June 17th due to evidence released to the public O.J. Simpson turned himself in after a famous “slow car chase”. Simpson’s first court date was June 21, where he pleaded not guilty to the acquisitions. However, because of the excessive news coverage, the grand jury chosen was dismissed due to influence that media might have already had. On July 7th, a California court superior judge ruled that there was enough evidence to try Simpson for both murders. Once again on July 23rd, O.J. Simpson pleaded not guilty (Linder, 2007).

O.J. Simpson was born on July 9th, 1947. He is most known as a former NFL running back. On February 2, 1985 Simpson married his second wife, Nicole Brown Simpson. They had two children and lived happily until their divorce in 1992.

A total of 150 witnesses gave their testimony during the eight-month trial. Simpson hired six lawyers totaling \$4 million dollars in expenses, including F. Lee Bailey, Barry Scheck, Robert Shapiro, Robert Jardashian, Alan Dershowitz, and Johnnie Cochran (CNN.com, 1995). One key witness included Allan Park the limo driver who testified that he picked Simpson at his home at 10:50 PM, that no one opened the door earlier, and that he saw a black man enter the house just prior to the door opening. There was a question of Simpson's car location, however Park did not remember whether he saw the car, therefore that portion was later rejected due to his uncertainty.

Another witness was LAPD detective Mark Fuhrman. Fuhrman was called to the stand where he testified about finding blood marks on the driveway of Simpson's home, and on a black leather glove found at the same location. However cross-examiner by F. Lee Bailey argued Fuhrman was racist and may have planted the evidence. It came out that Fuhrman had used the word "nigger" to describe black people in the ten years prior to his testimony. Later the defense brought evidence of tape recordings of Fuhrman's use of the word, showing Fuhrman's lack of creditability. He pleaded the Fifth Amendment to the acquisitions, but was later indicted for perjury (Linder, 2007).

The black leather glove that was supposedly found on the Simpson ground was key evidence against Simpson because the sister glove was found at the crime scene with blood on it. Cochran wanted prosecutor Christopher Darden to prove that the glove that they found was indeed Simpson's. The prosecutorial team decided that they would not ask Simpson to try the

glove on due to the fact that it was drenched in blood, but Darden made his own decision. When Simpson tried the glove on with a latex glove over his hand, it did not fit. However, Darden expressed to Judge Lance that Simpson “has arthritis and we looked at the medication he takes and some of it is anti-inflammatory and we are told he has not taken the stuff for a day and it caused swelling in the joints and inflammation in his hands” (CNN.com, 1995). They also argued that since the glove was soaked in blood, it shrunk the glove. Prosecutors believed the glove was covered in blood from a cut on Simpson’s finger that occurred during the murder of Ronald Goldman. But the defense pointed out that there were no cuts in the glove itself. It was also pointed out that there was blood on the glove, however there was blood found on the property. With respect to the glove evidence, the now famous phrase “if it doesn’t fit you must acquit” played a strong role in placing doubt in some juror’s minds, but whether the gloves were really OJ’s ignores the obvious point that one was found on OJ’s property, and the other was found at the crime scene, which links OJ to the crime scene.

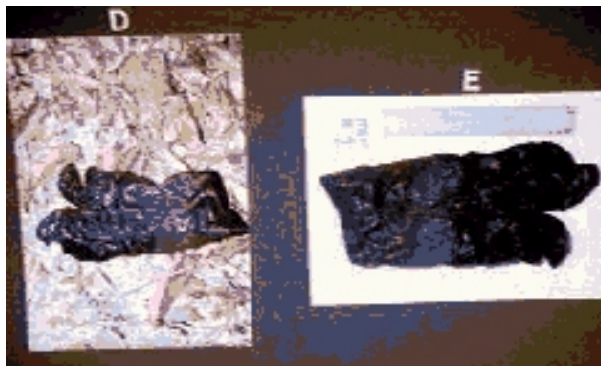


Figure 4.2 The right and left hand leather gloves of the OJ trial. One was found at the murder scene while the other was found at O.J. Simpson’s home (CNN.com, 1995).

The DNA evidence consisted of the blood found in, on, and near Simpson’s Bronco. It revealed traces of Simpson’s, Nicole’s, and Goldman’s blood. DNA analysis of bloody socks found in Simpson’s bedroom had Nicole’s blood. And DNA analysis of blood on the left glove found outside of Nicole Simpson’s home was proven to be a mixture of Simpson’s, Nicole’s, and Goldman’s. Bloodstains were found throughout the entire crime scene. Blood was found on

Simpson's foyer, a paper at the crime scene, bloody footprints, blood on Simpson's sidewalk, and blood on the fence near Goldman's body. DNA was extremely important in the case against Simpson. Although the DNA evidence overwhelmingly placed OJ at the crime scene, the defense used the fact that the blood was contaminated and could have been planted as a conspiracy against Simpson. Both sides had witnesses confirming their beliefs on the DNA samples taken (CNN.com, 1995).

DNA has been utilized throughout many cases before O.J. Simpson case, many of those cases have been found guilty solely based on DNA evidence. The DNA evidence in this case was extremely visible and found everywhere. The LA crime lab processed all the DNA related evidence and came to the conclusions that the blood of Simpson, Nicole, and Goldman were all found in countless pieces of evidence. However, can the contamination of blood skew the evidence? And how was it possible for the LAPD to plant Simpson's blood in his car, driveway, glove, and other pieces of materials found, when multiple officers would have to be involved? Many of these questions still cannot be answered, but we do know one thing for sure, DNA does not lie.

Other key evidence included Goldman's hair and Simpson's Bronco's carpet fibers found within the gloves. Simpson's Bronco also had blood stains found on the door handle, and a partial footprint on the carpet, as well as some on the headrest. The arrest record indicated Simpson was previously charged with beating his wife. There was a dome light that had been removed from its position with blood smears on it, but it was never checked for whose DNA. A set of Nicole's house keys had also been missing and she had been worried that O.J. had taken them. It was also stated that O.J.'s girlfriend had broken up with him on the day of the murders, therefore providing a possible reason for OJ being upset that day. The prosecutors proved that

Simpson did own a pair of the same gloves found, as well as a pair of shoes whom prints were found at the scene. And the knife that was used in both murders was the same as a knife that Simpson had purchased six weeks before the murders, they had receipts that confirmed the allegation (Linder, 2007).

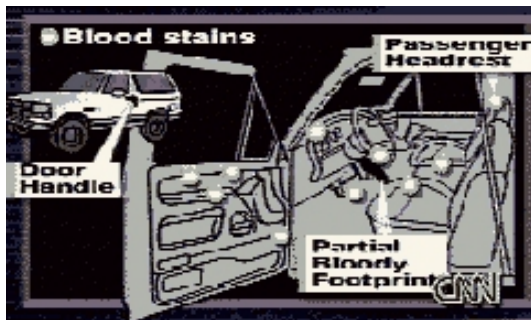


Figure 4.3 The Vehicle evidence found in O.J. Simpson's White Bronco (CNN.com, 2007).

On top of the tangible evidence, the prosecution had fifteen key testimonial witnesses that took the stand, and the defense had nine key witnesses. Both sides had witnesses that aided the physical evidences and the actions of O.J. Simpson the day of the murder.

After eight months of an agonizing, televised trial at 10 AM on October 3, 1995 after only three hours of deliberation, the jury returned with a verdict of not guilty. Although Simpson was released due to the verdict of not guilty, he was later sued in civil court for wrongful death by the survivor's family and was found accountable. He was ordered to pay \$33.5 million dollars in damages. Simpson tried to appeal; however the California Supreme Court rejected his bid (CNN.com, 1995).

The Boston Strangler

The famous Boston Strangler case occurred during the early 1960s. The death toll came to 13 within just a two-year time period. The victims included, with dates found:

June 14, 1962: Anna E. Slesers, 55, sexually molested with unknown object and strangled with the cord on her bathrobe.

June 28, 1962: Mary Mullen, 85, died from a heart attack but in the confession was said to have collapsed as the strangler grabbed her.

June 30, 1962: Nina Nicols, 68, sexually molested and strangled with her nylon stockings,

June 30, 1962: Helen Blake, 65, sexually molested and strangled with her nylon stockings.

August 21, 1962: Ida Irga, 75, sexually molested and strangled.

August 30, 1962: Jane Sullivan, 67, sexually assaulted and strangled with her nylon stockings

December 5, 1962: Sophie Clark, 19, sexually assaulted and strangled with her nylon stockings.

December 31, 1962: Patricia Bisette, 23, sexually assaulted and strangled with her nylon stockings.

March 3, 1963: Mary Brown, 69, stabbed and beaten.

May 8, 1963: Beverly Samans, 23, stabbed to death.

Sept 6, 1963: Evelyn Corbin, 58, sexually assaulted and strangled with her nylon stockings.

Nov 25, 1963: Joann Graff, 23, sexually assaulted and strangled.

Jan 4, 1964: Mary Sullivan, 19, sexually assaulted and strangled with dark stockings. (Boston Strangler, Wikipedia).

From June 14th, 1962 to January 4th, 1964, these 13 women were murdered in the Boston area. Most of them were not only killed but sexually assaulted. There was no evidence of forced entry so the women were assumed to have known or trusted the assailant. Police believed that the murders had not been carried out by one man.

On October 27th, 1964, a man entered a woman's home pretending to be a detective. He tied his victim to the bed and raped her while apologizing to her as he left. The woman's description lead the police to find Albert DeSalvo, who was well known to Boston police from his ongoing trial for being the "measuring man", who talked his way into women's apartments claiming to be a model agent, took their measurements, then claimed his assistant would call them.

A couple of years before the strangling murders began, there were a series of strange sex offenses that occurred in the Cambridge area. It was believed to be a man in his late twenties who would knock on the door of an apartment and "if a young woman answered, he would introduce himself: 'My name is Johnson and I work for a modeling agency. Your name was given to us by someone who thought you would make a good model'" (Crime Library, 2007). He told them that the modeling would be just of evening gowns and swimsuits. He told them that his job would be to get her measurements and other information if she was interested. Many women believed his scam and gave him the information needed. Some felt uncomfortable and notified the police, so he became known as the "Measuring Man."

On March 17, 1961, Cambridge police caught DeSalvo trying to break into a house. Not only did he confess to breaking and entering, but he confessed to being the "Measuring Man." The judge of his case, felt sympathetic for DeSalvo due to his role as a bread-earner, and therefore reduced his sentence to 18 months. With good behavior, DeSalvo was released in April of 1962, which was 2 months before the first victim of the Strangler was found (Crime Library, 2007).

Albert DeSalvo was born in Chelsea, Massachusetts, on September 3, 1931. He was in the Army from 1948 through 1956, and was stationed for awhile in Germany. There he met his

wife, Irmgard Beck, an attractive woman from a respectable family, and they had two children. He was promoted to Specialist E-5, but later was demoted to private, and received an honorable discharge. In 1955, he was also arrested for fondling a young girl, but the charge was dropped. Between 1956 and 1960, he had several arrests for breaking and entering. Each time, he received a suspended sentence. During all this time he worked as a press operator at American Biltrite Rubber (Crime Library, 2007).



Figure 4.4 Alberto DeSalvo, the photo released by the Cambridge Police Department (Wikipedia, 2007).

On November 3, 1964, DeSalvo was brought in for questioning on rape charges, after one of the victims of another case gave police a description resembling the "Measuring Man." DeSalvo's confession to a series of rapes forced authorities to put him in the Bridgewater State Hospital, where he was committed for observation, and where he was befriended by George Nassar, a convicted murderer. With their private discussions and visits from police, it led the authorities to DeSalvo's full confession to the "Boston strangler" crimes. In his confession, DeSalvo also confessed to two "new" victims, never previously linked by the authorities. One, 85-year-old Mary Mullen, who was found dead at her home on June 28, 1962, DeSalvo said that

Mullen had collapsed from the shock of his invasion. Also to Mary Brown' death, age 69, she was stabbed and beaten in her home on March 9, 1963 (Boston Strangler, Geocities, 2007).

He went in to full detail of some of deaths, however there were some inconsistencies. Inconsistencies such as confessing to all 13 killings, when only 11 of them were killed, and if DeSalvo was driven by a mother-fixation, as his psychiatrists claimed, why did he choose young women as five of his last seven victims? More importantly, the strangler's sole surviving victim, assaulted in February 1963, couldn't pick Albert out of a lineup, and neither could other witnesses who sighted a suspect near the Graff and Sullivan murder scenes. Also some of the blood found on the women did not match DeSalvo's blood type. One of his victims might have not died by strangulation like DeSalvo said (Albert DeSalvo- The Boston Strangler, 1994). Some believed that his lawyer convinced him to confess to the stranglings in order to be sent to a psychiatric hospital instead of a federal prison. Others believe DeSalvo's cellmate Nasser committed all the crimes, and simply told the details to DeSalvo. Although DeSalvo was never tried for the Boston Strangler case, he was tried and convicted for the crimes of robbery and sexual offenses for the "measuring man", which led to his life sentence in 1967 (Boston Strangler, Geocities, 2007).

In the same year, he escaped with two fellow inmates from Bridgewater State Hospital. DeSalvo left a note saying that he wanted to address the conditions of the hospital and his situation. The next day he turned himself in. He was then transferred to maximum security Walpole State Prison where six years later he was murdered on the day he was to speak to a reporter about the strangler case.

There were doubts within the Boston Police Department as to whether DeSalvo was the Boston Strangler. Many believed the "Strangler" consisted of several killers rather than one. It

was said that the last victim was in 1964, however there was also evidence of other victims after that date. Also following DeSalvo's death, journalist Whitfield Sharp assisted the families in a media campaign to obtain DNA from the government to explain the truth of who the Boston Strangler really was (Boston Strangler, Geocities, 2007). The outcome of that DNA testing was DeSalvo's DNA did not match that of evidence left on Mary Sullivan the last victim.

If the courts really want to do the families justice, then why won't they exhume the other 10 bodies besides Mary Sullivan's, to do DNA analysis to determine whether there was more than one strangler, and whether any crime scene DNA matches that of any of Nasser's relatives? Obviously DNA testing did not exist in the 1960's, but DNA is the best evidence for rape victims, therefore it should have been utilized in all 13 cases if the DNA had been saved and stored correctly. Because there has never been anyone put on trial for the murders and sexual assaults, with a person who confessed but was never convicted, the Boston Police Department should have never rested. Each of the 13 women had evidence that could help find the truth, the question remains as to whether any of that evidence remains intact enough to test. DNA testing is now readily available and should be utilized to truly bring justice to each of the victims. Unfortunately in the case of the Boston Strangler, there was no trial, no outcome, and no justice. However, with the tools available today, it is possible to find out the truth. The use of DNA analyses are extremely valuable, but can not always guarantee victory.

CHAPTER-5: DNA DATABASES

Introduction

The purpose of this chapter is to discuss what are DNA databases, why do we need them, what do its critics think, who should contribute to them, and what are the privacy issues involved? In this chapter, the science of DNA fingerprinting meets head to head with ethics and privacy rights, making this topic well suited for an evaluation of technology on society.

DNA Databases and Their Importance

To answer the questions mentioned above, one must first take a look at DNA databases, how the individual DNA is collected, and why it is important that we create larger DNA databases to increase their accuracy. “Any type of organism can be identified by examination of DNA sequences unique to that species, but identifying individuals within a species is less precise at this time” (DNA Forensics, 2002). But as DNA sequencing and fingerprinting technologies have progressed farther, we can now perform direct comparisons of very large DNA segments, can perform rapid STR analysis of short DNA repeat loci for identifying individuals, and can even sequence whole genomes. As discussed in Chapter-1, DNA fingerprinting is a process in which a laboratory creates a profile from 13 carefully chosen DNA loci. That profile is then compared with that of other DNAs, such as those collected from a crime scene, or those collected in advance from individuals entered in a database.

There are two main reasons we need DNA databases. First, we use them to perform “cold hits”. In these instances, a DNA profile from a crime scene sample (from an unknown

suspect) is compared to all entries in a database to see if any previous offenders have committed a crime again. One of the most groundbreaking cases involves the Night Stalker cases.

According to the U.S. Department of Justice Office of Justice Programs:

In 1990, a series of brutal attacks on elderly victims occurred in Goldsboro, North Carolina, by an unknown individual dubbed the “Night Stalker.” During one such attack in March, an elderly woman was brutally raped and almost murdered. Her daughter’s early arrival home was the only thing that saved the woman’s life. The suspect fled, leaving behind materials intended to burn the residence and the victim in an attempt to conceal the crime. In July 1990, another elderly woman was brutally raped and murdered in her home. Three months later, a third elderly woman was raped and stabbed to death. Her husband was also murdered. Their house was burned in an attempt to cover up the crime, but fire/rescue personnel pulled the bodies from the house before it was engulfed in flames. When DNA analysis was conducted on biological evidence collected from vaginal swabs from each victim, authorities concluded that the same perpetrator had committed all three crimes, but there was no suspect. For 10 years, both the Goldsboro Police Department and the crime laboratory refused to forget about these cases. With funding from the National Institute of Justice, the crime laboratory retested the biological evidence in all three cases with newer DNA technology and entered the DNA profiles into North Carolina’s DNA database. This would allow the DNA profile developed from the crime scene evidence to be compared to thousands of convicted offender profiles already in the database. In April 2001, a “cold hit” was made to the perpetrator’s convicted offender DNA profile in the database. The perpetrator had been convicted of shooting into an occupied dwelling, an offense that requires inclusion in the North Carolina DNA database. The suspect was brought into custody for questioning and was served with a search warrant to obtain a sample of his blood. That sample was analyzed and compared to the crime scene evidence, the results confirmed the DNA database match. When confronted with the DNA evidence, the suspect confessed to all three crimes. (U.S. Dept o f Justice, 2002)

The second reason we need DNA databases is we use them to assign “allele frequencies” to each locus analyzed on the DNA. This helps us calculate the probability of a random match occurring. For example, say a suspect has genotype 35 at locus-1. We need to know how many other individuals in the general population also have genotype 35 at this locus. In our example say its frequency is determined to be 1/10. Also assume the suspect has genotype 25 at locus-2, and its frequency is 1/10. If we analyze both loci in our fingerprint, then the probability of a random individual in the population having genotypes 35 and 25 are 1/100. The larger the

database of samples, the more accurate the probabilities can be assigned. Consequently, the more accurate the match, the more likely the data will get accepted into the courtroom.

When we analyze someone's DNA forensically, we don't actually sequence it from beginning to end; we analyze specific loci (locations) on the DNA. The more loci analyzed, the more we can multiply each of their individual probabilities together to increase the overall probability. In the U.S., the standard for identification requires a comparison of 13 carefully chosen so called "core loci". According to the Electronic Privacy Information Center (EPIC, 2007) "reliable identification requires that samples be handled carefully to prevent contamination, that a sufficient number of segments be compared, and that researchers set an appropriately high threshold (usually 1 in a billion) for acceptable probability of a match."

"The widespread acceptance of DNA typing by court systems around the country has led many states to pass laws requiring people convicted of sex offenses and other crimes to be DNA typed and included in statewide offender databases. Currently, US Law enforcement officials have integrated the FBI and various state DNA offender records into a single national database known as CODIS (Combined DNA Index System) that allows for the rapid comparison and matching of known offenders with genetic material recovered from crime scenes. These profiles contain the analysis of 13 core loci (representing segments of non-coding DNA that do not contain information about medical predispositions). This technology is authorized by the DNA Identification Act of 1994. According to Dwight Adams of the Federal Bureau of Investigation (2001), "The DNA Identification Act of 1994 provided the statutory authority for creation of the National DNA Index System (NDIS) and specified the type of data that could be included in this national index. Only the following types of DNA data may be stored in the national index

administered by the FBI Director:

- DNA identification records of persons convicted of crimes;
- analyses of DNA samples recovered from crime scenes;
- analyses of DNA samples recovered from unidentified human remains; and
- analyses of DNA samples voluntarily contributed from relatives of missing persons. See 42 U.S.C.S. §14132(a).

In accordance with the DNA Act, the FBI recommends that states include all felony offenders and misdemeanor sex offenders within the scope of their database laws". All 50 states have laws requiring that DNA profiles of certain offenders be sent to CODIS (to be discussed below). As of January 2003, CODIS contained more than a million DNA profiles in its Convicted Offender Index, and about 48,000 DNA profiles collected from crime scenes (but which have not yet been connected to a particular offender) (Biotech Industry Organization, 2003). The US CODIS database is now the world's largest DNA database, and has contributed significantly to our understanding of allele frequencies, and match probabilities.

According to James Schumm (1996), "The O.J. Simpson trial brought the use of DNA analysis for personal identification into sharp public focus. The U.S. Crime Act of 1994, and similar legislation in Canada, the United Kingdom, and many other countries, has paved the way for the development of DNA databases which will hold "DNA fingerprints" for large numbers of individuals previously convicted of violent crimes."

Criticisms of DNA Databases

Some critics believe that a DNA fingerprint may not yet be reliable enough to use in the court system. They question how accurate a DNA fingerprint is, and its cost. They believe that it

is not very accurate because only a segment of DNA is analyzed, not the complete strand. A DNA fingerprint may not be unique (EPIC, 2007). They argue that until we sequence more individual's DNAs entirely, a confirmation of uniqueness has not been established. Although such comments were prevalent when DNA profiling first started out, and little information was available on locus frequencies, with the recent adoption of the very well researched 13 core loci for standard analysis, whose frequencies are widely accepted, this argument is no longer used in US courts.

Early critiques also included that the process of DNA fingerprinting is done in private laboratories, so the exact testing standards may not be followed (EPIC, 2007). Prior to the standardization of the DNA methods established by the Technical Working Group on DNA Methodology (TWGDAM) following the *People v Castro* (1989) trial, companies did not always use proper quality controls. Human error can provide false results if protocols are not followed properly. But now that the TWGDAM guidelines have been established, and the courts require their use prior to DNA evidence admission, this criticism applies less.

Other critics also argue that DNA testing is very expensive, and if the accused can't pay for the testing then they will not be able to defend themselves using the results of the test. Although this argument has become less important as the cost of DNA testing declined with the advent of STR testing, and the states have agreed to pay for it for all defendants.

One strong criticism is "will people misuse the process"? According to Addler and McCormick (2007), "A misuse that scares them is the unauthorized use of the database to identify individuals with a genetic disease by looking up their personal profile without their permission." This misconception is quite prevalent on most privacy rights website, but in fact, no medical predispositions can be obtained from an analysis of 13 core forensic loci (to be

discussed below). Collected samples are stored, and many state laws do not require the destruction of that DNA sample, so in theory medical information could be obtained from that stored sample (although not from the 13 core loci). So there is a chance that a person's entire genome may be available --criminal or otherwise. Although the DNA used is considered "junk DNA", in the future this information may be found to reveal personal information such as susceptibilities to disease and certain behaviors. Because of this fact, one recommendation of this IQP author is to destroy the original DNA samples once the 13 core loci have been analyzed, and before any other loci can be viewed.

Another problem some have with DNA analysis involves a process that takes place in the womb during fetal development. In the journal *Nature* (EPIC, 2007), it was reported that in some rare cases, DNA can be different in different tissues of one individual. However because this is very rare, this situation does not negate the correct use of DNA fingerprinting in the vast majority of cases, and moreover would make no difference whatsoever to the analysis so long as the *same* tissue is taken from the suspect that was left at the crime scene. So for example, if the suspect had one DNA type in his blood, and another type in his liver, so long as blood was left at the crime scene from the suspect and that profile was compared to the blood of the captured suspect, then the analysis would be correct.

A final criticism involves the mishandling of DNA evidence. The OJ trial taught the world the importance of chain of custody, and preventing contamination by controlling the DNA samples. According to EPIC (2007), "the high confidence placed in DNA matches makes it particularly important that biological evidence be handled carefully to avoid contamination and other evidence be available to link the individual to the crime. DNA evidence has been challenged in several courts in different countries because of improper handling during evidence

collection or testing.” However, following the Simpson case, the protocols for handling DNA and controlling chain of custody have improved substantially.

Who Should Contribute DNA to Databases?

Who is chosen for DNA sampling is the public’s main concern with DNA databases. In the United Kingdom, for example, all suspects can be forced to provide a DNA sample, even if not convicted of a crime. This is somewhat similar to the current US practice of taking conventional fingerprints for anyone suspected of DUI. All arrestees, regardless of the degree of the charge, and the possibility that they may not be convicted, can be compelled to comply. This empowers police officers, rather than judges and juries, to provide the state with intimate evidence that could lead to "investigative arrests."

In the U.S., arresting people on less than probable cause just to obtain DNA evidence raises the question of Fourth Amendment violations against unreasonable search and seizure. In addition all 50 states require that sex offenders provide DNA samples, and some states even require samples from all felons and in some cases juveniles. These samples are retained indefinitely. The following table was collected from the National Conference of State Legislatures (2005) which displays who gives DNA in each state.

State	All Felonies	Other	Juveniles
Alabama	X		
Alaska	X		X
Arizona	X	Includes residential and criminal burglary.	X
Arkansas	X	Includes those persons committed for mental defect or disease for qualifying offense; and also some misdemeanor sexual offenses.	X (violent crimes only)
California	X	All convicted felons were added as a result of Proposition 69 in 2004, as were adults arrested for or charged with a felony sex offense, murder or voluntary manslaughter, or attempt of these crimes. Starting in 2009, arrestee sampling is expanded to arrests for any felony offense. California statute includes those not guilty by reason of insanity for qualifying offense; those convicted of terrorist activity in violation of weapons of mass destruction provisions; and those convicted of a qualifying offense in another state.	X
Colorado	X	Includes any person who has a duty to register as a sex offender, including probationers, habitual offenders as condition of parole, and those released without parole supervision.	X
Connecticut	X	Includes those not guilty by reason of mental disease or defect for qualifying offense; and includes persons on probation or parole prior to discharge from supervision.	
Delaware	X	Includes offenders convicted of child endangerment or abandonment.	
Florida	X	2001 legislation incrementally adds crimes in 2002 and 2003 and, effective 2004, includes all forcible felonies, contingent on appropriations. Includes those excluded from penal responsibility due to mental disorder, defect. Also includes persons on probation, parole, release or supervision following conviction of certain offenses.	X
Georgia	X		X
Hawaii	X	Includes people who are mentally unfit. Includes qualifying persons in prison, on probation or parole, parole violators.	X
Idaho		Most felons are included.	X
Illinois	X	Includes people held under civil commitment under sexually dangerous those law, those found guilty but	X

State	All Felonies	Other	Juveniles
		mentally ill for a sex offense, persons seeking transfer to state under interstate compact, stalking and residential burglary.	
Indiana	X	Includes qualifying offenders on probation or parole.	
Iowa	X	Includes qualifying parolees and offenders on work release; includes those found not guilty by reason of insanity, those receiving a deferred judgment of felony.	X
Kansas	X	Includes any crime covered under offender registration law, many serious felonies, some drug offenses and certain misdemeanors in which the victim is under age 18.	X
Kentucky		Includes those convicted of unlawful transaction with a minor, promoting sexual performance of a minor, burglary I and II and class A and B felonies involving death or serious injury to the victim.	X
Louisiana	X	Arrestee sampling authorized to extent funding is available.	X
Maine	X	Includes all Class A, B, C serious crimes.	X
Maryland	X	Includes some misdemeanors.	X
Massachusetts	X		X
Michigan	X		X
Minnesota	X		X
Mississippi	X		
Missouri	X		
Montana	X		X
Nebraska			
Nevada		Includes all class A or B felonies or a category C felony that involved use or threatened use of force; also includes some drug offenses.	
New Hampshire		Includes violent crimes.	X
New Jersey	X	Includes those found not guilty by reason or insanity for a qualifying offense.	X
New Mexico	X		X
New York		Includes many serious felonies and some controlled substance offenses.	
North Carolina	X	Includes those found not guilty or responsible by	

State	All Felonies	Other	Juveniles
		reason of mental disease or defect for a qualifying offense; and persons on community supervision.	
North Dakota	X	Many serious felonies, including burglary.	
Ohio	X		X
Oklahoma	X	2001 law requires planning to incrementally add qualifying felonies to the database, to include all felony offenses by 2006.	
Oregon	X		X
Pennsylvania		Includes violent and sexual offenders.	X
Rhode Island	X		
South Carolina	X	Includes qualifying offenders on community supervision.	X
South Dakota	X		X
Tennessee	X	Includes those persons seeking transfer to the state under interstate compact who have committed qualifying offense.	X
Texas	X	Expanding to all felons contingent upon federal funds. 2001 law provides for <i>post-indictment</i> samples in certain sex crimes.	X
Utah	X	Includes persons convicted in another state or under federal law and those committed as mentally incapable, both with a qualifying offense.	X
Vermont	X		
Virginia	X	A 2002 law requires a DNA sample be taken from every person <i>arrested for</i> a violent felony, including destruction of that sample upon dismissal of charge or acquittal.	X
Washington	X	Includes those who have been convicted out of state or under federal law of a violent offense.	X
West Virginia	X		
Wisconsin	X	Includes those found not guilty or responsible by reason of mental disease or defect for a qualifying offense.	X
Wyoming	X		X

Currently most states require felons convicted of violent or sex-related felonies to submit DNA. On 11-13-03, then Governor Mitt Romney of Massachusetts signed a bill requiring ALL

convicted Massachusetts felons to submit DNA. Declaring that “the long arm of the law just got a little longer,” Governor Mitt Romney visited the State Police Crime Lab to sign legislation requiring all convicted felons (but not those merely arrested) to provide DNA samples to the state’s database (The Encyclopedia Mittanica, 2006). According to Romney himself, “I want to make sure that our law enforcement officials have the best possible tools at their disposal to do their jobs and keep our neighborhoods safe,” Romney said. “The state’s DNA database is one of the most important tools they have.” The new law requires every convicted felon in the Bay State, including those now incarcerated or on parole, to provide a DNA sample to the state database. The prior law only required felons convicted of 33 sex-related and violent crimes to submit such samples. Studies indicate that by the time a defendant is convicted of one of these designated offenses, he or she has already committed 34 other crimes on average (The Encyclopedia Mittanica, 2006). The current Massachusetts database has approximately 20,000 samples. With the expanded law, the number is expected to grow to 100,000 in just a few years. Romney said 28 other states have similar laws in place, helping law enforcement officers compare crime scene evidence against DNA samples for known offenders. Virginia’s all-felon DNA database has resulted in 1,100 “cold hits.” Only 15 percent of those cases would have been solved if the Virginia database had been limited to violent offenses (The Encyclopedia Mittanica, 2006).

Genetic Privacy

But what are the ethics of databases? The public is concerned that such databases violate their right to privacy. Opponents raise concerns with how long the samples are kept on file, how such a sweeping collection might violate the civil liberties of the offenders, and the margin for

human error. Even with a phase-in period where new technicians are trained, opponents say there is still a clear possibility that DNA evidence may be misread or misfiled, eventually leading to wrongful convictions. DNA databanks must also have appropriate safeguards for the storage of the physical sample, DNA databases, and security to protect the links between. This creates several points at which individual DNA privacy can be violated. Supporters, however, feel that DNA can be such a strong crime-fighting tool that the decision to use it should be obvious. However, convicted felons may have fewer privacy rights; they may still have the right to be housed in semi-private facility, but not to withhold their DNA that could help solve a crime, when psychologists maintain that certain criminals are likely repeat offenders. After all, some argue that the convicted offenders should give up some of their privacy rights (the right to withhold DNA) the moment they commit the crime.

Another important issue is storage. In some cases, DNA is sometimes collected from witnesses and family members to exonerate them from the crime. However, if such samples are included in databanks, then the databanks will contain peoples DNA who have not convicted any crimes. The public is also concerned that insurance companies or prospective employers will gain medical information on individuals from the database. However, you can't really obtain medical information from the allele information obtained from the 13 core loci entered into a forensic database that lists only forensic allele types because, as discussed before, the DNA used is considered "junk DNA". Thus this information even if released into the hands of an insurance agency or employer could not be used to reveal personal information such as susceptibilities to disease and certain behaviors.

An analysis of *non-forensic* loci in DNA can indeed provide some medical information. Philip L. Bereano (2000) is a professor in the College of Engineering who points out several

examples of this type of discrimination in an article in ActionBioscience. Examples of such discrimination include:

A pregnant woman, whose fetus tested positive for cystic fibrosis, was told by her health maintenance organization (HMO) that it would be willing to cover the cost of an abortion but would not cover the infant under the family's medical policy if she elected to carry the pregnancy to term. A healthy woman, who casually mentioned to her family doctor that her father had been diagnosed with Huntington's disease, and that she herself was at risk for inheriting this genetic disorder, was later denied disability insurance. The insurance company rejected her because they found a note about her father's diagnosis written in the margin of her medical records. A healthy boy, who carried a gene predisposing him to a heart disorder, was denied health coverage by his parents' insurance company, even though the boy took medication that eliminated his risk of heart disease. One healthy man in his 20s with a gene for the degenerative brain condition Huntington's disease was refused life insurance. His older brother, on the other hand, tested negative and was able to reduce his premium which had been previously set on a family history of the disease. Another case involved a well woman in her 30s whose genetic test indicated a 70 to 90 per cent risk of developing cancer. Despite having regular screening for cancer, her superannuation was reduced and the life coverage component refused (Bereano, 2000).

In a statement at the National Institutes of Health, President Bush called on Congress to pass legislation to protect genetic privacy, so that 'medical research can go forward without an individual fearing personal discrimination' (EPIC, 2007). A genetic privacy bill, which passed the Senate in 2003 but died in the House, was reintroduced in the House on January 16. The bill seeks to establish a national standard to prohibit genetic discrimination by health insurance providers and employers. Under the bill, these entities cannot require genetic testing, cannot determine premiums or eligibility for insurance or employment based on genetic information, and are limited in their collection and use of genetic information" (EPIC, 2007).

CONCLUSION

The goal of this IQP was to discuss the important role of DNA fingerprinting technology to society. Discussed was the technology of how fingerprints are performed, new methods for collecting and storing DNA (to increase acceptance in courtrooms), landmark court cases (to analyze how technical information is presented in U.S. courts, sensational cases (to remind the reader the power of DNA evidence, and DNA databases (to discuss privacy rights ethics). With respect to DNA databases and who should be forced to provide DNA samples, each state currently sets their own standards on who must provide DNA to a database. In Massachusetts, currently all convicted felons, violent misdemeanors, and juveniles must provide DNA. Most other states require only those convicted of certain violent or sex crimes, however some states are considering requiring all *arrested* individuals to provide DNA. The authors of this IQP chapter believe that the Massachusetts standard is a good one because it includes all felons and juveniles, but not those merely arrested of a crime. This belief stems from the information that most felons are repeat offenders, and having all those individuals in a databank that any state can reference increases the accuracy of all DNA fingerprinting (increasing our knowledge of allele frequencies) and increasing the ability to solve crimes which otherwise might have gone unsolved. As for issues of privacy and critics of DNA fingerprinting, there are many issues which have attracted much criticism with DNA fingerprinting, we believe most have disappeared over time with improvements in the technology and its standardization, and any remaining negatives are greatly out-weighted by the positives. Therefore, it is our opinion that DNA databases are an essential tool in fighting and solving crimes, and the technology should be accepted in all courts of law.

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