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DNA FINGERPRINTING

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DNA FINGERPRINTING

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ABSTRACT

Within the last two decades, the arrival of new technologies such as DNA fingerprinting and databases, have strongly affected society and our judicial system. In criminal cases, different types of DNA fingerprinting techniques have evolved to the point of becoming standard and reliable procedures of personal identification. However, using the best DNA fingerprinting technology is useless if the evidence is contaminated or degraded, so adequate methods of collecting, transporting, and storing DNA are required. This project explores this interesting technology, and also shows the legal path DNA has undergone until finally been accepted as technical evidence in courtrooms. The project also investigates the purpose of DNA databases and their accompanying privacy issues.

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PROJECT OBJECTIVES

This project aims to analyze the technology of DNA fingerprinting, and document its effect on the judicial system, forensics, and society. The concept of DNA is introduced, along with which sections of the molecule are analyzed during fingerprinting methods. The main methods for DNA profiling, and its applications in both forensics and medicine are also discussed. The research then focuses on the legal aspects surrounding DNA, including a discussion of the landmark DNA court cases, and describes other cases sensationalized by society where DNA has played a role either incriminating or excluding suspects. How DNA sequences are stored in databases, the purpose of these databases, and the ethics encompassing the use of such systems are also explained. The authors finally contribute their own conclusions on DNA fingerprinting technology based on the information obtained in this Interactive Qualifying Project.

CHAPTER- 1: DNA FINGERPRINTING, DESCRIPTION AND TYPES

Nicolas Rodriguez

A variety of biological parameters have been used for years to aid identification in the forensic and medical fields. For example, the human leukocyte antigen (HLA) test is used to determine tissue compatibility for organ transplantation (Best, 2012), and blood serology testing has been used to analyze blood samples collected at crime scenes (Lerner and Lerner, 2008). However, for identification purposes, accuracy and specificity are extremely important. So, in recent years, scientists have developed new methods of identification using DNA that many claim are the greatest advances in the history of forensic sciences. "DNA identification analysis, identity testing, profiling, fingerprinting, typing, or genotyping refers to the characterization of one or more relatively rare features of an individual's genome or hereditary makeup" (Kirby, 1993). The purpose of this chapter is to introduce the basics of DNA fingerprinting, discuss the different types of this technique, and learn why DNA profiling has become one, if not the most, revolutionary tool utilized for identity testing.

Introduction to DNA

Cells are dynamic, moving, living systems that carry out particular functional tasks for the organism they belong to (Campbell et al., 2009). All living things, including human beings are made of cells. Cells can vary in features and functions depending on the organism. In lower forms of life such as bacteria (prokaryotes), the cell may be the bacterial organism itself. It is surrounded by a membrane and contains a cytoplasm, but it lacks the rest of internal structures that belong to higher eukaryotes (DeBaldo, 2008). However, both types of cells share common

characteristics (**Figure-1**). They are both bounded by a plasma membrane, and both use deoxyribonucleic acid (DNA) as their genetic material, although the DNA is contained in a nucleoid in bacteria and in a nucleus in eukaryotes (Campbell et al., 2009).

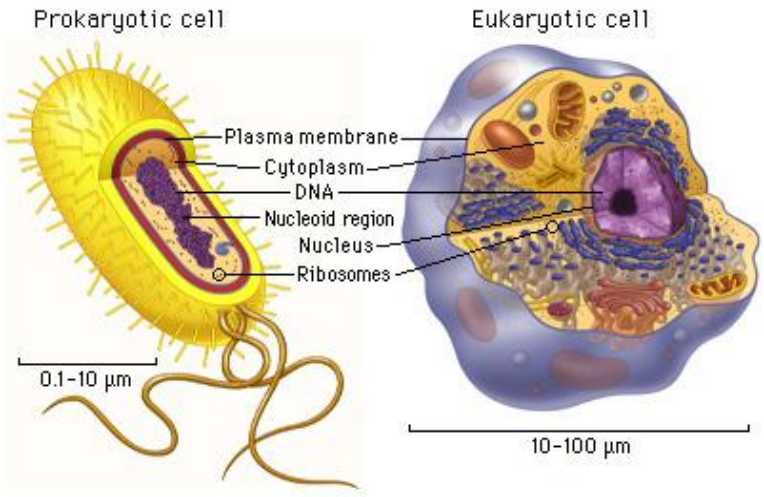

Figure-1: Common Features Between Prokaryotic and Eukaryotic Cells. Diagram shows a prokaryotic cell representing lower organisms (left) and a eukaryotic cell representing higher organisms (right). Both types of cells are surrounded by a membrane, and contain cytoplasm, ribosomes, and DNA. (The Biology Place, 2012)

The key distinguishing feature of eukaryotic cells is the presence of a *nucleus*. The main genomic DNA of higher organisms is contained within this organelle (other DNA is located inside the mitochondria), and is divided into *chromosomes* (Becker et al., 2009). Chromosomes are thread-like structures that contain DNA. During the interphase portion of the cell cycle, the DNA structure is dispersed which allows DNA replication or expression. But during the mitotic phase of the cell cycle, the DNA condenses into chromosomes that allow the DNA to separate more easily into each daughter cell (Campbell et al., 2009). In human beings, chromosomes are in a diploid state (two sets of chromosomes per cell) in all cells except the gametes (egg and sperm) where they are haploid (one set per cell). In humans, there are 22 pairs of autosomal

(non-sex) chromosomes, and one pair of sex chromosomes. The female pair is denoted XX and the male by XY (Kirby, 1993).

The DNA found within chromosomes contains the genetic information that dictates the properties of a cell (or organism) (Becker et al., 2009). Through the information contained in its sequence, DNA orchestrates the formation, growth, operation, and reproduction of cells. The structure of DNA is a double helix made up of two complementary strands of polynucleotides (Watson and Crick, 1953). Polynucleotides consist of independent units called *nucleotides*, which are composed of a phosphate group, a sugar (deoxyribose), and a nitrogenous base. There are four different DNA bases, divided into two groups. The group of purines is made up of adenine and guanine containing 2-carbon-nitrogen rings, and the pyrimidine bases (cytosine and thymine) contain a single carbon-nitrogen ring. Due to the chemical structure and the locations of hydrogen bonds formation in their rings, adenine pairs with thymine, forming two hydrogen bonds, while cytosine pairs with guanine forming three hydrogen bonds (**Figure-2**). This hydrogen bonding between the bases of opposite strands (red dotted line in the diagram) gives DNA its complementary characteristic, and stabilizes the double helix (DeBaldo, 2008). A key characteristic of the DNA macromolecule is the anti-parallel orientation of its two strands. To illustrate, a DNA strand that starts with a free carbon atom in the fifth location (5') on its first nucleotide will also have a free carbon atom in the third location (3') of its last nucleotide. This orientation would be denoted as 5' to 3' (i.e. the lower strand in the diagram). Its complementary strand will exist in the opposite 3' to 5' direction (Becker et al., 2009).

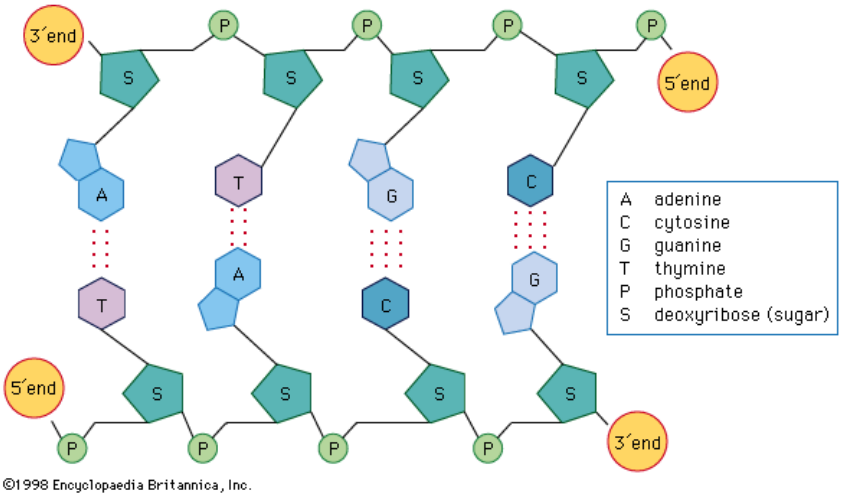

Figure-2: The Major Components of DNA. Shown is the DNA structure, including the nucleotide bases: cytosine (C), thymine (T), adenine (A), and guanine (G) (middle of diagram), linked to a backbone of alternating phosphate (P) and deoxyribose sugar (S) groups (upper and lower strands in the diagram). Two separate sugar-phosphate chains are paired through hydrogen bonds (dotted red lines) between bases A and T, and between G and C, forming the double-stranded double helix of the DNA molecule (Encyclopedia Britannia Online, 1998).

The phosphate/sugar backbone of the DNA helix curves around on itself every 10 base pairs (DeBaldo, 2008) (**Figure-3**). These twists lead to the formation of major and minor grooves in the helix. The presence of more hydrogen bonds exposed in the major grooves allows for proteins to bind to these sites more easily. Some proteins recognize specific DNA sequences helping to regulate its expression (Becker et al., 2009).

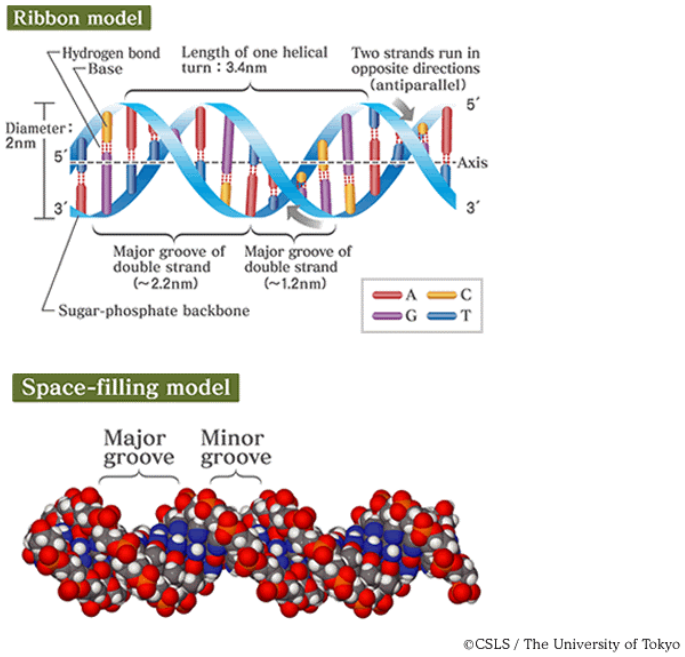

Figure-3: The Double-Stranded Structure of DNA (B-Form). Upper figure shows the structure of the DNA helix, including the hydrogen bonds between the bases (colored rungs on the ladder), and the major and minor grooves in the helix. Lower figure shows a different perspective of the major and minor grooves that play important roles for binding proteins that control DNA expression. (What Kind of Molecule….2010).

With respect to DNA fingerprinting, an important aspect of the DNA structure is that the sequence of bases in a molecule constitutes its genetic information. Their type and order dictates which type of protein is encoded by segments in the molecule termed *genes*. A copy of each gene, known as an *allele*, is located in the same position or locus in each homologous pair of chromosomes (Kirby, 1993).

Repeating DNA Sequences (VNTRs, RFLPs, STRs)

The protein coding sequences of a DNA molecule are often conserved between human beings, and cannot vary much or they become non-functional. The DNAs of all human beings is approximately 99.8% identical. So, with respect to DNA fingerprinting when the goal is to distinguish one individual from another, analyzing conserved coding sequences that are identical between individuals makes no sense. However, DNA sequences that do not encode proteins can vary between individuals, as these sequences are able to vary while still remaining functional. Non-coding sequences comprise about 30% of the DNA molecule, and consist of repeated sequences (DNA Fingerprinting….2010). Repeating DNAs differ from each other in their overall length, the sequence of the repeat, and the length of the repeating unit itself.

One type of repeating DNA unit is termed Variable Number of Tandem Repeats (VNTRs). The repeating cassette can be as short as two bases long but is more often 8-10 bases long. The overall length can extend up to forty repeats, and varies between individuals. Moreover, a person may inherit a given number of repeats from the mother at a certain locus, and a different number of the same repeat from the father at the same locus on the homologous chromosome (Chantler, 2004) (**Figure-4**). For example, in the diagram, individual-1 has 2 and 5 repeats at locus-A, while individual-2 has 3 and 4 repeats at the same locus. As a result, VNTRs can be highly variable from one person to the next, so their analysis is very useful in DNA fingerprinting analysis (Budowle, 1998).

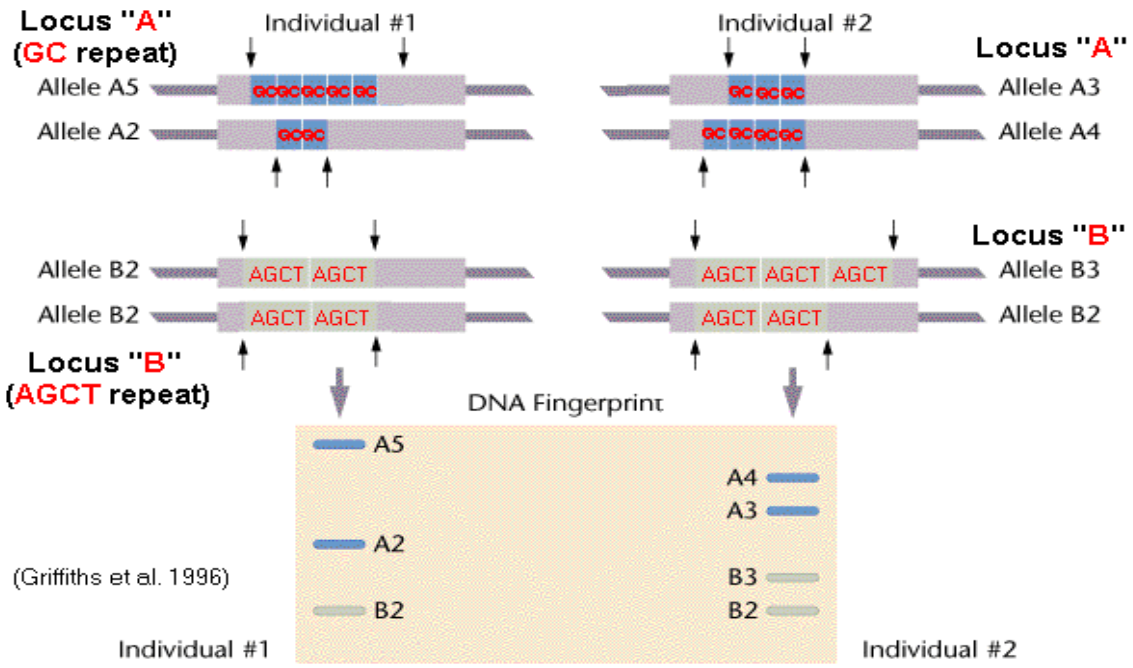

Figure-4: Diagram of Variable Number of Tandem Repeats (VNTRs). Upper picture shows two different individuals with a various repeating elements of the dinucleotide GC at locus A. The number of repeats for one individual can differ as derived from the mother and father. For example, individual-1 shows 2 and 5 GC repeats at locus-A, while individual-2 shows 3 and 4 GC repeats at the same locus. At locus B, individual-1 shows 2 repeats of AGCT on both alleles, while individual-2 has 2 and 3 AGCT repeats at the same locus. The lower picture shows the DNA fingerprint analysis of these VNTRs. Note that the pattern of DNA bands is easily distinguished between the two individuals. (Griffiths, 1996)

Another type of variable DNA sequence is a Restriction Fragment Length Polymorphism (RFLP). RFLPs are produced by cutting DNA with restriction enzymes (Becker et al., 2009). The length of a particular DNA fragment depends on the distance between the two cut sites. The fragments may differ between individuals based on the number of repeating elements within each. If a restriction enzyme is used that cuts infrequently, the RFLPs can be as long as 35,000 bases (DNA Fingerprinting….2010).

A third type of repeat is termed Short Tandem Repeats (STRs). These repeating elements are the smallest of all three types, and range from two to seven base-pairs in length. Due to their short length, STRs are easily amplifiable by PCR, while VNTRs and RFLPs are not (Budowle et al., 1998). Because STRs are easy to analyze by PCR, a rapid technique discussed below, the STR-PCR type of DNA analysis has become standard in the industry. The federal law known as "The DNA Identification Act of 1994" allowed the Federal Bureau of Investigation to establish a biological index to determine an individual's DNA profile (Budowle et al., 1998). This resulted in the establishment of the world's largest DNA database, the Combined DNA Index System (CODIS) where the FBI stores DNA profiles for specific types of crimes (discussed in a later chapter). The standard CODIS analysis is for 13 core loci, analyzed by STR (DNA Fingerprinting….2010; CODIS, 2012).

DNA Fingerprinting Types

The techniques used to analyze DNA can be divided into those that do not amplify the DNA, and those that do. Since DNA's first use in forensics in 1985 (Jeffreys et al., 1985a), the first technique used to analyze DNA for forensics is a well-known type of non-amplifying analysis termed a Southern blot. Named after Edward Southern who invented it (Southern, 1975), this form of analysis requires more DNA than the PCR process, but it is less prone to contamination. Southern blots (or their equivalents) are used to analyze VNTRs and RFLPs because those repeating DNAs are too long to be amplified by PCR. In a Southern blot, the DNA is isolated from a tissue, and then is cut into fragments using restriction enzymes. The fragments are then separated by size using electrophoresis. During electrophoresis, a DNA sample is layered onto one edge of an agarose gel, and a charge is placed across the gel with the

negative cathode closest to the DNA sample. DNA is negatively charged due to its phosphate residues, so it migrates towards the positive anode, with the smaller DNA fragments traveling the farthest (they are hindered the least by the gel). The pattern of DNA fragments are then transferred from the gel to a membrane, which allows the DNA to be hybridized to a labeled probe complementary to a DNA locus of interest to the fingerprinting. The position of the labeled probe on the membrane is visualized by exposing the membrane to x-ray film, which allows the size of the VNTR or RFLP to be determined (Becker et al., 2009). Probe mixtures can also be used to analyze several loci at one time. This type of analysis was the original procedure used for DNA analysis in forensic cases (Jeffreys et al., 1985; Human Genome Project….2009).

The major disadvantages of this non-amplifying method are that degraded DNA samples cannot undergo analysis, and a fairly large amount of DNA is required (10-50 ng) for analysis (Kirby, 1993).

The second type of DNA analysis *amplifies* the DNA using Polymerase Chain Reaction (PCR) to make copies of short segments of STR DNA. PCR was developed by Kary Mullis in 1986 (Mullis et al., 1986), and won him the Nobel Prize in Chemistry in 1993. PCR can replicate millions of copies of an STR from tiny amounts (pico or nanograms) of DNA samples (Budowle et al., 1998; Human Genome Project….2009), so it is very sensitive. PCR is a multi-step process (**Figure-5**) performed in a thermocycler that allows the temperature of the reaction to be variably programmed. The DNA sample is first heated to 95˚C to separate the two DNA strands. Next, the temperature drops to between 37-72˚C, to allow the primers to anneal upstream and downstream of the STR locus being analyzed. Then, the temperature is elevated to 72°C which is the optimum temperature of the special DNA polymerase added to the reaction,

Taq polymerase. Taq polymerase was originally isolated from underwater bacteria *Thermus aquaticus* (Taq) that grow well in hot thermal columns. This unusual polymerase can survive multiple cycles of near boiling temperatures of the PCR reaction. These three main steps: denaturation, annealing and extension, constitute one PCR cycle. The thermocycler is programmed to repeat the cycle from 28 to 36 times, so the DNA fragments are amplified exponentially (Budowle et al., 1998).

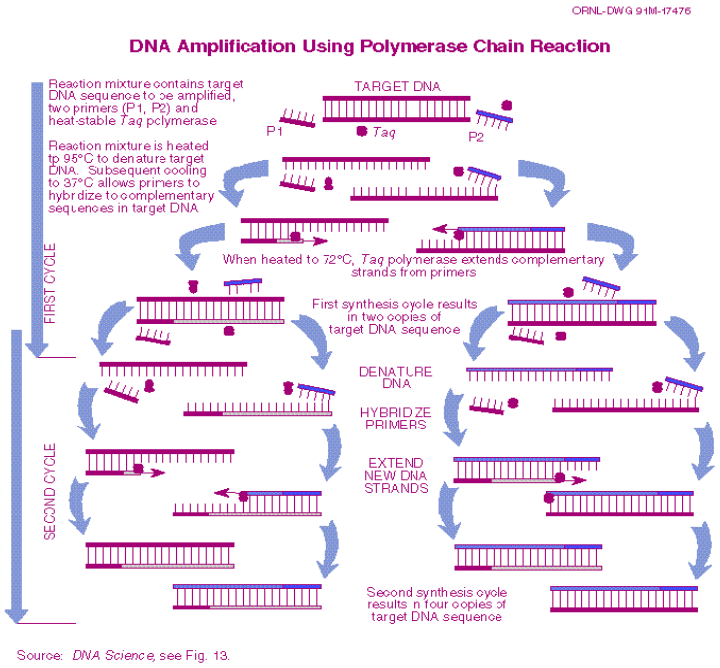

Figure 5: Diagram of Polymerase Chain Reaction. The picture shows the main three steps of PCR, including denaturation, primer annealing, and primer extension, in this case for two amplification cycles of a DNA target sequence. (PCR...2012)

The main advantage of PCR is its sensitivity. It can even amplify STRs from the DNA of a single cell left at a crime scene. Another advantage is that contaminating DNA from fungi or bacteria present in forensic samples will not amplify if the primers are designed specifically for human sequences. However, if the genetic sample is contaminated with human DNA from other

sources, or the buffers contain human DNA from previous reactions, a false positive result is obtained (Kirby, 1993). PCR is usually used to analyze STRs, because they are short enough to be amplified in the reaction, while VNTRs and RFLPs are too long. The combination of PCR-STR analysis has become the industry standard. This combination can be extremely effective for rapidly analyzing a large number of samples (Budowle et al., 1998). As mentioned above, the current standard analysis for the FBI's CODIS database is thirteen core standard STR loci (Human Genome Project….2009).

Fingerprinting Application Examples

DNA fingerprinting can be used for a variety of applications, including paternity cases, identifying unknown remains, identifying criminals, and even molecular archaeology. The very first use of the then new DNA fingerprinting analysis was a 1985 paternity case in England (Jeffreys et al., 1985b). Since then, paternity testing has become the most popular use for DNA technology. In Sweden, for example, Ragnar Johansson had claimed for 55 years that he did not father a daughter back in 1948 (Boyes, 2003). The Supreme Court in Sweden finalized the longest-going paternity dispute in the history of the country when Johansson, at the age of 79, proved he was right. Thanks to DNA profiling which showed Johansson was not the father, the Supreme Court overturned a 1949 ruling based on crude blood tests that earlier forced him to pay child support to the girl's mother (Boyes, 2003). For paternity analysis however, DNA has some limitations in proving paternity when monozygotic twins are involved whose DNAs are identical or very similar. Although chemical markers called epigenetic factors attach to genes and can affect their expression, the genetic codes of identical twins appear to be the same (O'Connor, 2008). In 2007, identical twins Richard and Raymon Miller from Missouri appeared in court

several times. Both denied the paternity of a girl, at that time three years old, and neither of them wanted to pay the child's alimony. The mother of the child, Holly Marie Adams, admitted to having sex with both men within hours of each. DNA tests were taken of both twins after Raymon's request, but because they are identical twins, both of their profiles showed a 99.9 % of probability of being the father of the girl. Judge Fred Copeland ruled Raymond Miller as the legal father of the child. The judge added that DNA was not the sole evidence he had to consider, but he also used the mother's testimony (Burke, 2007).

One of the first cases where DNA profiling was applied to *criminal forensics* was in 1987, in the Narborough Village murders case in the United Kingdom (Colin Pitchfork, 2007). In 1986, a seventeen year old suspect was accused of raping and killing a school girl, and was also indicted for a killing-raping case in 1983. The semen samples collected in both crime scenes matched each other, but to everyone's surprise did not match that of the main suspect, so the teenager was consequently discharged. So, in criminal cases, DNA was actually first used to exonerate someone not convict them. Further evidence in the case suggested that the author of the crimes lived in the same district where the victims were murdered, so 5,500 blood samples were collected from male district dwellers by the police for analysis. Out of this number, forty percent could not be excluded through regular blood analysis, so they were DNA typed. But none of the DNA samples matched the semen found on the victims. One of the patrons at a regional pub referenced the case by saying that he donated two blood samples. The extra one was in the name of his coworker, Colin Pitchfork, who was not able to donate. This information was relayed to the police who had Pitchfork's DNA tested. His DNA matched the crime semen specimens. The suspect confessed to the crimes and was sentenced to life in prison (Kirby, 1993).

Using fingerprinting for archeological purposes has also proved to be fruitful. In an experiment to test the hypothesis that modern humans originated in East Asia, 12,127 male individuals from 163 different populations where selected, including locations from Southeast Asia, Oceania, East Asia, Siberia, and Central Asia. These men were tested for three different markers on two alleles of the Y chromosomes. The results showed that every individual carried a mutation in one of these three sites. This mutation, named M168T, originated in Africa about 35,000 to 89,000 years ago. Thus, the hypothesis that *Homo sapiens* or modern humans arose from East Asia and not Africa was not supported by the Y chromosome typing (Ke et al., 2001).

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Chapter-2: DNA Forensics

Emily Machlin

Using the best techniques for analyzing DNA (discussed in the previous chapter) becomes totally useless if the collected DNA is degraded or contaminated. Without performing very careful collection of DNA evidence, and using well established procedures, the DNA evidence can become inadmissible in court, and let a guilty party walk free. This chapter will focus on where DNA can be found at a crime scene, the right way to collect it, and the right way to transport and store it.

Collecting DNA properly has been an issue since the advent of DNA testing in 1985 in England (Jeffreys et al., 1985). To be used in the courtroom, DNA must have been collected carefully to prevent contamination and degradation, and must have been transported and stored properly. Following landmark DNA court cases such as *People v Castro* (1989) that mandated protocol standardization (discussed in Chapter-3), over the years standards have been put in place for proper evidence collection and its analysis, and these protocols keep improving over time as we learn more about DNA.

General Crime Scene Control

When an officer first arrives at a crime scene, saving people's lives is the first priority. But after having determined medical needs, the next step is to secure the crime scene and control it. This is done by first securing the scene then by restricting the scene to only essential personnel to avoid contamination (Byrd, 2000). Once the scene is secure, there are three basic levels of containment that must be achieved to protect the evidence and the investigators (**Figure-1**). The first, most basic, containment is the inner-most layer (yellow in the diagram).

This containment consists of yellow crime scene tape placed around the immediate area of the crime, such as around a dead body. This level is usually determined quickly, and contains all places where DNA evidence might be found. It is important for this level to include any place the perpetrator might have entered and exited the area. While the first level of containment covers the immediate crime scene, the second level (red in the diagram) expands the level-1 to include a larger buffer zone for equipment, vehicles, and personnel meetings. The third level (black in the diagram), also known as the perimeter containment, is where a perimeter is created with barricades and police vehicles set up surrounding level-2. For example, roads may be blocked to keep out vehicles and foot traffic. The purpose of level-3 is to keep the first and second levels of containment secured (Dagnam, 2006).

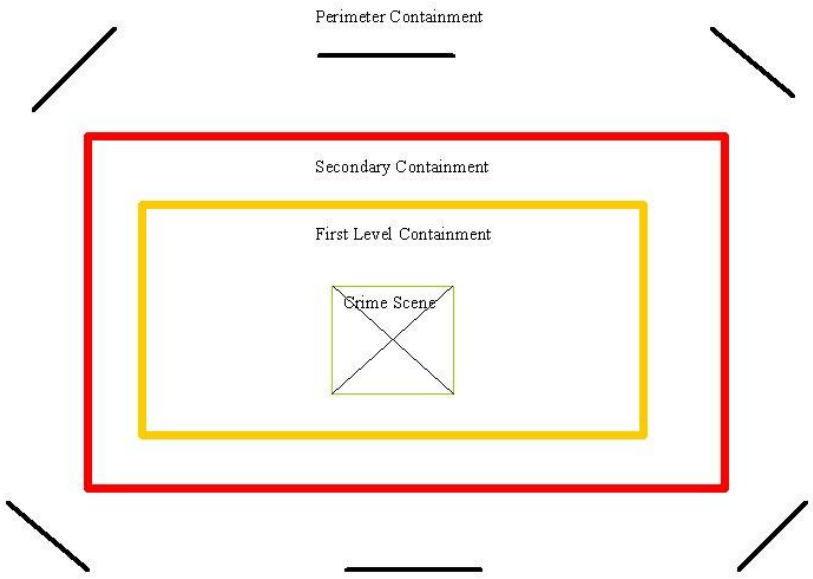

Figure-1: The Three Basic Levels of Containment for a Crime Scene.
Crime scene control is established immediately using a series of overlapping zones. The inner-most zone is closest to the crime, and is the most restricted to personnel. (Dagnan, 2006).

Tissues Containing DNA

At a crime scene, DNA can be found on a variety of evidence, and is present in a variety of fluids and tissues. **Table-I** shows several examples of the amount of DNA present in some tissues, and the average PCR success rates for that evidence. Examples of biological evidence containing DNA are: blood, saliva, semen, skin cells, hair, urine, fecal material (National Institute of Justice, 2012). DNA can also be obtained by swabbing items thought to have been *handled* by a perpetrator, such as a doorknob, although the PCR success rate is relatively low for this type of indirect evidence (Table, lowest row). The evidence likely containing DNA is inspected visually for integrity, and then may be further analyzed by alternative light sources or chemical enhancements such as luminol. Certain types of biological evidence is quite rich in DNA (such as blood and semen), while other tissues have relatively small amounts of DNA (such as hair shafts without the roots).

Table-I: Amounts of DNA Present in Common Crime Scene Evidence and the PCR Success Rates for its Analysis.

Sample Type	Location	DNA Content	PCR Success
Blood	Stain 1 cm x 1 cm	200 ng	>95%
	Stain 1 mm x 1 mm	2 ng	
Semen	Post-Coital Vaginal	0-3,000 ng	>95%
Saliva	On cigarette butt	0-25 ng	50-70%
Hair	Root end of pulled hair	1-750 ng	
	Root end of shed hair	1-12 ng	
	Hair Shaft	0.001-0.04 ng/cm	
Urine		1-20 ng/mL	
Skin Cells	From socks, gloves		30-60%

	Doorknob		<20%

ng = nanogram, or 1/1,000,000,000th of a gram
mL = milliliter; cm = centimeter; mm = millimeter
PCR genetic test success rate estimates from the New York City Office of the Chief Medical Examiner, Department of Forensic Biology.
Adapted from (Kaye and Sensabaugh, 2000, page-564)

DNA Locations at a Crime Scene

DNA can be collected from almost anywhere at a crime scene. As previously stated, nuclear DNA is found in any type of cell (except for a red blood cell which lacks a nucleus), and mitochondrial DNA is found in all human cells. Some locations might surprise you; for example, a murder case was solved when the suspect's DNA taken from saliva in his dental impression mold matched the profile of the DNA swabbed from a bite mark on the victim (What Every, 1999). **Table-II** shows various types of crime scene physical evidence, the likely location of DNA on that evidence, and the likely biological source of the DNA. About DNA Evidence (1999).

Table-II: DNA Location on Crime Scene Evidence and It's Likely Biological Source (What Every…1999).

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

Preventing DNA Contamination and Degradation

When collecting and preparing crime scene evidence that may contain DNA, it is essential that the investigator prevent his/her own DNA from contaminating the evidence (although in some instances his profile can be computer subtracted from the evidence profile). The collector should wear gloves (and change them often), use disposable instruments and/or clean the instruments thoroughly before and after handling samples, avoid touching the area where DNA may exist, avoid talking, sneezing, and coughing around evidence, avoid touching his face, nose, and mouth when collecting and packaging evidence, air-dry evidence thoroughly before packaging, and put the evidence into new paper bags or envelopes, not into plastic bags (which can collect moisture and cause DNA degradation or grow microbial contaminants), and especially not use staples (to prevent possible stabs which would bring blood into the evidence) (What Every, 1999). The collector should only use plastic bags for the transportation of biological evidence when there are excessive body fluids and possible contamination of other people and other evidence items, otherwise use paper bags to avoid moisture accumulation. It is important to never package wet or moist body fluids in plastic bags for long periods of time as this helps bacterial growth and evidence contamination, which can lead to DNA degradation.

Transportation and Storage of DNA

Biological evidence can be significantly degraded due to environmental factors before and/or after evidence recovery. The amount of evidentiary value of a sample is inversely related the duration and intensity of exposure to the following conditions: presence of living organisms (bacteria, molds, insects, animals), weather conditions (temperature, humidity, rain), the chemistry of a hostile environment (soil pH, bio-degradable evidence), and time of exposure (National Institute of Justice, 2012)).

When transporting and storing evidence that may contain DNA, once the evidence has been placed in paper bags or envelopes it must be kept dry and at room temperature. It should be sealed and then labeled with valuable information such as time, date, collectors name, evidence location, etc. This accurate labeling constitutes its *chain of custody*. Any officer, lawyer, or scientist that handles the evidence from that point forward signs his/her name, time, date, and reason for examining the evidence. This provides lawyers with an accurate record of any person who touched the evidence for any reason. This topic is also discussed below. Direct sunlight and warmer conditions also may be harmful to the DNA, so investigators avoid keeping evidence in places that may get hot, such as a police car (What Every, 1999).

The general procedure for packaging biological evidence includes using dry tools, labeling all metal and glass evidence items to be stored at room temperature, air-drying all wet swabs as soon as they are collected, packaging each swab individually in separate containers, and labeling all packaged as biohazard. Anytime material is transferred for collection, is should be inventoried and packaged to prevent cross-contamination prior to leaving the scene. Both the package and the evidence itself should be marked. If the evidence cannot be tagged (such as

soil, hair, and stains) it is placed in a container or envelope. The packaging container should then be tagged, and the tag should list the agency case number, the item number, the recovered and received dates, and the investigators initials (National Institute of Justice, 2012).

Extracting DNA from Crime Scene Evidence

The next step in forensic DNA analysis is the purification of DNA from an evidence item, also called a substrate, on which the DNA is deposited. This is called DNA extraction. There are many types of DNA extraction, all of which function to separate the cells containing DNA away from the substrate on which they are embedded, break open the cells to release DNA and other cellular material, and separate the DNA from the cellular components and any DNA degrading enzymes that might be present. The goal of DNA extraction is to produce purified DNA in an aqueous solution that can be used for profile analysis.

Some methods used for DNA recovery are better at purifying DNA, increasing maximum DNA yield, and decreasing processing times. Specific extraction techniques may work better for a specific type of evidence sample (Gefrides, 2011). It is the forensic laboratory's responsibility to use the best DNA extraction technique for each sample. New techniques are being developed all the time in an attempt to make DNA extraction more streamlined with a higher DNA yield. Regardless of which type of DNA extraction is being performed, or which type of chemicals that are being used, all DNA extractions attempted in forensic laboratories must be processed alongside each other with a blank. A blank is a sample that goes through the extraction process without an evidence substrate being added to it to monitor for contamination in the extraction solutions used. In this sense, "contamination" refers to the presence of foreign DNA in a sample

that did not reside on the original evidence sample. Blanks should never give any DNA result. If DNA is detected in a blank, it can either mean that DNA contamination is present in the chemicals or plastic containers used in the extraction process, or that an event occurred during the extraction process to introduce foreign DNA like adding DNA from a pipette. If this happens, the DNA extraction for all the samples processed with that reagent must be repeated from the beginning, unless the laboratory can show that the contamination event was isolated to only the blank sample. It is very important that blanks are treated just like every other sample in the reaction process so that they can monitor for contamination (Gefrides, 2011).

Physical procedures for extracting DNA from the evidence range from taking the entire piece of evidence back to the lab (like a toothbrush), to cutting or scraping a piece of the evidence to take back to the lab (like scraping dried fluid from a floor), or simply taking a swab if there is very little evidence to work with. Cutting is used to remove a section of evidence containing the stain using a sterile or clean cutting device. Wet absorption of the stain can be used for a substrate too large to bring back to the lab (a house floor) or for evidence too large on a hard or soft surface. A sterile swab, gauze pad, or cloth slightly moistened with distilled water is used to absorb the stain from the substrate. The stain is usually concentrated in the center of the swab or pad, or at the tip of a swab. The collection device is pressed or rubbed into the stain and then allowed to air-dry. Some laboratories recommend following a wet collection with a second dry swabbing to help ensure a thorough sample collection. Both swabs are retained and submitted for analysis. Scraping is another method used to obtain evidence from a hard surface. The sample is scraped with a clean razor blade or scalpel into a clean piece of paper that can be folded and packaged. This is a method to be used in a controlled environment (i.e., no wind or traffic) where the scrapings produced will not contaminate other nearby evidence. An optional

method for collecting dried blood stains on a nonabsorbent substrate surface is using fingerprint tape. The fingerprint-lifting tape may be placed over the stain and lifted off, transferring the stain to the tape, which is then secured on a clear piece of acetate for submission to the laboratory. When using this method, the collector must ensure the fingerprint tape is not contaminated with other biological materials (National Institute of Justice, 2012).

In forensic casework, it is not good laboratory practice to use an entire biological sample during DNA extraction. Typically, only half of a sample should be processed for each extraction to leave enough sample for retesting if necessary. Retesting is important if the original extraction becomes contaminated, or the final results are inconclusive. Then the extraction can be repeated by the laboratory. For items in which no DNA profile was obtained, saving a portion of the sample can be important so it can potentially be processed in the future when new technology becomes available. Another reason for testing only a portion of the sample is to allow another lab to test it for confirmation if necessary (Gefrides, 2011).

DNA Sample Chain of Custody

As discussed briefly above, it is important to establish very accurate records for each piece of evidence to aid its use for solving the case, and to help it gain acceptance in courts. The "chain of custody" is an accurate representation of a variety of important information including who collected the original sample, its location at the crime scene, and the time and date of collection. The chain of custody also includes the name, time, and date of any person examining the evidence after its original collection.

The first person to collect an item of evidence will sign their initials and date either on the item itself, on its packaging, or both. This label will clearly mark the item and will ensure

there are no mistakes if the packaging gets separated from the evidence. Occasionally, some types of evidence, such as bullets or bloodstains, cannot be physically marked itself, so its packaging material is labeled. Evidence typically goes from the crime scene to the forensic lab for examination where the receiving officer will sign the evidence package and date it. From then on, everyone who handles the evidence does the same until the analysis is complete. After all the testing is complete, the evidence is given back to the police for storage until it is used in court. If viewing the evidence is necessary in court, the prosecuting attorney takes custody of the evidence and signs the chain of custody label. If the chain of custody procedure is handled correctly, the case can proceed and the evidence is allowed in court. The judge and jury are then allowed to view the evidence, along with witness statements and other information (Lerner and Lerner, 2006).

Chapter-2 Conclusions

As shown in this chapter, without proper technique and carefully followed crime scene procedures, valuable DNA evidence might not make it into court. DNA can be the difference between convicting the guilty, or exonerating the innocent. But if not collected, transported, stored, extracted, and handled properly, the power of the DNA profile becomes meaningless. Over the years, standards in response to several landmark DNA court cases (discussed in the next chapter), have been put into place to increase the amount of information the DNA provides in the profile, and equally importantly to ensure the profile itself can be accepted in court.

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Chapter-3: Landmark DNA Court Cases

Kevin White

Due to the explosion of technological advances over the past century, the birth of DNA fingerprinting has drastically impacted judicial systems all over the globe, providing the most powerful method available for identifying individuals. Although DNA is now frequently used as evidence, and usually plays a pivotal role in the outcome of trials, this was not always the case. Complex technology is not easily accepted in courts; it is not always apparent how *accepted* the specific technology is in the scientific community, or how *reliable* the technique is when performed under specific conditions. The admissibility of DNA evidence within the courtroom has developed over time from a series of landmark court cases that established precedents for accepting complex technology in a courtroom. The technique must be proven to be accurate and reliable to help jurors and judges reach accurate conclusions. The purpose of this chapter is to describe some of the landmark court cases that eventually helped DNA fingerprinting technology gain acceptance in U.S. courts. The following cases do not all involve the use of DNA, but they do involve setting precedence for admitting complex technical evidence in the courtroom. The outcome of these cases was the realization that the system needs standards and rules to make the admissibility of DNA evidence reliable and consistent when incorporated within a trial.

1923, Frye v United States

On November 25th, 1920, an African-American man by the name of James Frye allegedly murdered a physician named Dr. Robert W. Brown (Bloosberg Law, 2012). Another physician, a co-worker of Brown was in the office at the time of the homicide and witnessed the crime.

Although he chased Frye out of the office, he eventually got away, leaving the police with no leads other than the description given to them by the witness.

Months later, Frye was arrested for being involved in an armed robbery, and eventually confessed to both crimes. But he later retracted his confession, so the case went to trial in the District of Columbia (*Frye v US*, 1923). Frye's defense was based on his alleged alibi, and a then new 'systolic blood pressure deception test', in which an "expert" measured Frye's blood pressure following a series of questions. The expert testimony was held inadmissible by the lower court due a lack of *general acceptance* in the scientific community for this new technology. After 4 days of trial, in 1923 in the District of Columbia, Frye was convicted of second-degree murder for killing Robert Brown, with a life sentence. The debate over the lie detector test in front of a jury likely saved Frye's life, as it prevented a guilty verdict for first degree murder (Bloosberg Law, 2012).

Frye decided to appeal the decision to the Appellate Court, but again the judge agreed with the lower court judge that the lie detector test had not gained general acceptance from psychological and physiological authorities, so the test was deemed inadmissible. The *general acceptance* precedence that this landmark court case established became the *Frye Standard.* (Bloomberg Law, 2012), and became an important standard for decades for scientific evidence in the courtroom. Scientific techniques were often presented as testimonial evidence in an attempt to persuade jurors into believing, in most instances, that the appellant was innocent. Yet, who is to say that those techniques are valid.

1975, Federal Rules of Evidence 702 (Rule 702)

During the twentieth century, as science and technology continued to advance, the legal system attempted to develop coherent tests for the admissibility of scientific evidence (USLegal, 2010). Following *Frye v United States*, and the implementation of the Frye Standard, which stated that in order for a scientific technique to be used as evidence within a trial it must be generally accepted in the scientific community, it quickly became apparent that the Frye Standard is hard to actually achieve. How does one prove "general acceptance" in any community. So, in the mid-1970's the judicial system established the Federal Rules of Evidence that attempted to allow "expert" witness testimony to assist the court to understand complex technical evidence. "An expert witness is one allowed to provide opinion testimony at trial based upon his or her specialized knowledge, training or experience, if the opinion is *reliable, relevant* to the issues in the case, and will help the fact finder to reach a decision. An expert witness need not have knowledge of all the facts of the case, but must be prepared to defend the technology as reliable and relevant. In state and federal courts, experts and their opinions must meet the admissibility standards of Rule 702 of the Federal Rules of Evidence (and its state law analogs) that serve to define the opinion witness" (Hutchinson, 2009).

On January 2nd, 1975, Rule 702 was established as an amendment in the court system, to be used when the help of a scientific expert would have a direct influence pertaining to the outcome of a specific trial (Federal Rules of Evidence, 1975). The first version of Federal Rule of Evidence 702 provided that:

> "If scientific, technical, or other specialized knowledge will assist the trier of fact to understand the evidence or to determine a fact in issue, a witness qualified as an expert by knowledge, skill, experience, training, or education, may testify thereto in the form of an opinion or otherwise, if:
> (1) The testimony is based upon sufficient facts or data
> (2) The testimony is the product of reliable principles and methods

(3) The witness has applied the principles and methods reliably to the facts of the case." (USLegal, 2010)

With the adoption of the Federal Rules of Evidence, the older Frye Standard became more updated and useful, as it allowed courts to allow new technologies based on expert testimonies of the reliability and relevance of a technology, which was easier to achieve.

1987, Colin Pitchfork Case in England

The Case of Colin Pitchfork was the first murder conviction in the world based on DNA profiling evidence. During November 1983, a young girl Lynda Mann was found raped and killed in a town in England. "Forensic examination of semen sample showed that it was a type found in only 10% of men, and was from someone with type A blood" (Elvidge, 2011). No suspects were found. Three years later, another girl, Dawn Ashworth, was found in a similar fashion with traces of the same semen from the previous murder. A local boy later confessed to one of the murders, but when his DNA was tested, it did not match the semen from the crime scene. The local boy, Richard Buckland, was found innocent and became the world's first murder exoneration using DNA testing.

With no suspect in hand, law officials decided to initiate one of the first mass DNA testing projects. They took saliva and blood from over 4,000 men in town hoping to find a match. But no match was found between any of the men and the crime scene evidence, so the case went cold again. Later a man was overheard talking about giving a sample for another person for cash. The man who did not provide his DNA sample was found to be Colin Pitchfork. Pitchfork was arrested, his DNA was taken, his samples matched those from both victims, and he was sentenced to life in prison (Rankin, 2005).

The Pitchfork case provides evidence that DNA can in fact help convict the correct person of murder and other various crimes. This case also expanded our knowledge of DNA sampling and forensics in general, as members of an entire community were tested.

1989, People v. Castro

"Castro is one of the first cases in the relatively short history of DNA fingerprinting in which a court conducted an exhaustive evaluation of both the DNA procedure and the application of traditional admissibility rules" (Patton, 1990). In 1987, a woman named Vilma Ponce and her two year old daughter were found stabbed to death in New York. When questioning suspects in the case, the police noticed a blood stain on a watch owned by a man named Jose Castro, a maintenance man in Ponce's building. Samples were sent to Lifecodes for analysis, and they declared the blood on the watch matched Vilma Ponce. The prosecution wanted the test results admitted as evidence (Patton 1990, pg. 228), but the defense strongly questioned whether DNA testing was ready for the courtroom. The prosecution and the defense battled for a long time, both using expert witnesses. The judge realized a more complex standard was necessary, and a three pronged test was developed to determine whether DNA evidence should be admitted for a specific trial:

> 1. Is there a generally accepted theory in the scientific community which supports the conclusion that DNA forensic testing can produce reliable results?
> 2. Are there techniques or experiments that currently exist that are capable of producing reliable results in DNA identification, and which are generally accepted in the scientific community?
> 3. Did the testing laboratory perform the accepted scientific techniques in analyzing the forensic samples in this particular case? (Patton, 1990)

When the judge applied the new 3-prong standard to the Castro DNA evidence, he ruled that the evidence agreed with the first two prongs, but not the third, as the testing in this particular trial

omitted some key controls. So the DNA evidence was not admitted. The DNA omission proved to be moot, as a trial was never held, and Castro later confessed to both murders. But a new standard had been set for allowing DNA evidence in courts. After the trial, the judicial system mandated that the FBI develop a standardized protocol for DNA testing, so the Technical Working Group on DNA Analysis Methods (TWGDAM) was established to develop the procedures. The Castro case further reinforced the need for more strict and concise standards when approaching DNA evidence.

1990, Two Bulls v United States

In 1990, Matthew Sylvester Two Bulls was put on trial for sexual abuse for raping a 14 year old girl in South Dakota. Using DNA profiling, a semen sample taken from the girl's underwear was compared to a blood sample from Two Bulls, and it was concluded that it was probable that Sylvester raped the girl (US v. Two Bulls, 1990). Two Bulls and his council made a motion before the trial for a suppression hearing, challenging the admissibility of the DNA evidence. During this motion hearing, the judge concluded that the evidence was acceptable on the basis of Federal Rules of Evidence 702, and admitted it at trial where Two Bulls was found guilty.

However, Two Bulls appealed his case, asserting that the more rigorous Frye Standard should have been used instead of Federal Rules of Evidence. The Appellate Court actually set about to prepare a new 5-prong standard that utilized Castro and Frye. Castro focused on whether the DNA testing was done properly for this particular trial, while Frye focused on the general acceptance of the technology. As a result of Two Bulls v United States, a new five pronged standard was initiated:

1. Is DNA testing generally accepted?
2. Is the testing procedure used here generally accepted?
3. Was the test performed correctly here?
4. Is the evidence more prejudicial than probative, and if so, disallow it.
5. Is the statistics of the DNA match more prejudicial than probative? If so, disallow it. (US v. Two Bulls, 1990)

Using the new 5-prong standard, the Appellate judge reconsidered the Two Bulls DNA evidence, and concluded that the evidence was admissible. So, the original Two Bulls guilty verdict was upheld, and Two Bulls was sent back to prison. This new 5-prong standard was quite rigorous, and reminded both prosecutors and defense attorneys alike to make sure DNA testing was done properly in each case.

2000, People v Robinson

The case of *People v Robinson* took place in California in the year of 2000. It was a landmark trial in United States history because it resulted in the first conviction of someone based solely on a DNA profile. In 2000, Paul Eugene Robinson was convicted of five separate accounts of sexual assault that occurred in 1994, six years earlier. Allegations were made by Deborah L., a woman who was threatened and raped one night in her apartment. Once the man fled the crime scene, Deborah was rushed to the hospital where a "rape kit" was prepared, and semen was collected to create a genetic profile of the assailant. But no suspects were identified at that time and the case began to go cold.

The case was unusual because the authorities did not physically apprehend Robinson until *after* the six-year statute of limitations had elapsed, but in 2000 just prior to the lapse, had stopped the clock by filing a then new 'John Doe' warrant. Days before the six year statute had expired, a 'John Doe' DNA arrest warrant was issued for the arrest of the suspect known only by

his DNA profile. Unlike a traditional warrant, it did not contain a name or a physical description. Rather, it contained a DNA profile created by the California Department of Justice (DOJ) that was formulated from the rape kit from the night of the incident. Throughout the ongoing investigation, from time to time, the state California would scan the John Doe profile against CODIS. Over the years, as the database included additional samples, a "cold hit" to the original 1994 DNA profile finally occurred that directly linked Paul Eugene Robinson to the crime scene (Sucherman, 2011).

During his trial, an expert witness for the prosecution testified that, based on the genetic profile created from the collected semen, Robinson's DNA matched that of the perpetrator "at all 13 loci." The witnessed further testified that the:

> "Probability that two people would share identical DNA patterns at each of the 13 loci tested is one in 650 quadrillion . . . in the African-American population, one in six sextillion . . . in the Caucasian population, and one in 33 sextillion . . . in the Hispanic population" (Sucherman, 2011).

The combination of the expert's DNA testimony and the forensic evidence gathered at the scene provided extraordinarily persuasive evidence that he was indeed the assailant from that night in 1994. This case is historic and unusual for a number of different reasons. Not only was it the first time a DNA profile by itself led to a conviction, but the case involved a "John Doe" DNA arrest warrant that did not include a name or a physical description of the alleged criminal. This case is proof that the creation of DNA profiling can play an immense role in the outcome of sexual assault and murder convictions. By being able to gather DNA from crime scenes, it allows police officials to place specific individuals at the scene of a crime. Although DNA evidence provides the means of determining a person's true identity, it can shed light on whether the person making

that DNA was at a crime scene. Beyond the DNA facts, the entire judicial system steps in and helps establish justice and due process.

Chapter-3 Conclusions

"In recent years there has been much discussion on the use of scientific evidence in the courtroom. Parties increasingly ask the courts to admit the expert testimony of research scientists, physicians, psychologists, and other technically-trained people. Paralleling this increased demand for the admission of scientific evidence is a growing awareness that current legal methods of reviewing and weighing such evidence are insufficient and should be reconsidered" (Patton 1990, pg. 223). This quote from 1990 occurred after *People v Castro*, but before *Two Bulls v US*, so since that time DNA testing has undergone very close analysis in courts with the development of very rigorous standards for admission. As the DNA revolution emerges to be one of the most powerful ways to determine the outcomes of specific crimes, the judicial system has realized that standards and regulations are essential to ensure justifiable outcomes. Because DNA evidence is so new, and the potential prejudice to the defendant is sufficiently great, it is imperative that the court satisfy itself that there exists a sufficient foundational basis as to the overall admissibility of the evidence for each specific trial. As time progresses and more complex trials occur, such as the 2000 trial of Eugene Robinson who was found guilty solely on the basis of a John Doe warrant, new regulations may have to be implemented to increase forensic evidence's credibility. By establishing continuous standards, the government is attempting to make the overall system improved to maintain accurate outcomes. The judicial system must continue to define which procedures should be used to test and analyze DNA to insure they are accurate, reliable, and properly controlled.

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CHAPTER-4: SENSATIONAL DNA CASES

Nicolas Rodriguez

DNA profiling is thought to be the most powerful technology for identifying an individual in the history of forensic science. DNA molecular biology techniques were first applied to identifying individuals in a 1985 paternity case (Jeffreys et al., 1985), and were first brought to U.S. courts as an identification method in 1987-88 in a multiple rape trial in Florida (*Andrews v State of Florida, 1988*). But in spite of the power of the technology, it had to undergo rigorous testing in a series of landmark court cases (discussed in Chapter-3) before solidifying its role in helping convict the guilty or exonerating the innocent. Following a standardization of the technology mandated by the landmark cases, eventually DNA testing proved to be a clear, effective means for identifying individuals present at a crime scene, when performed properly. The technique is now generally accepted in the scientific community, with occasional debates about best practices, and allele frequencies. Nowadays, its use in courts is generally more probative than prejudicial in criminal procedures (Ramsland, 2008).

Despite the importance of landmark court cases in helping establish the general acceptance of DNA identification in courts, and the standardization of DNA testing, the public often is often completely unaware of the landmark cases. But, the public is often well aware of some sensational cases that used DNA. This chapter will discuss three sensational cases that involved DNA, focusing especially on the role that DNA evidence played in each case.

O.J. SIMPSON CASE

The most publicized court case in the history of the United States might be that of Orenthal James "OJ" Simpson. This former football player considered one of the greatest

running backs in football history, was indicted of killing his former second wife and mother of his two youngest children, Nicole Brown Simpson, and her friend Ronald Goldman (OJ Main Page, 1995). With a trial lasting eight-months, and 20 million dollars in defense costs, OJ's case became the longest ever held in the state of California, and one of the most expensive litigations at that time in the state. Its verdict, in addition, was not only the object of comments and opinions based upon racial arguments, but also called into question the ethics and fairness (given the circumstantial evidence) of the American Justice System (OJ Main Page, 1995; Jones, 2004).

Orenthal James Simpson was born in San Francisco in 1947. During his college years he was a relevant football player earning All-America honors at the University of Southern California. In 1968, he won the Heisman Trophy as the top U.S. college football player. He retired from football in 1979 to work as a sports commentator and actor (OJ Main Page, 1995). On the night of Sunday July 12, 1994, Simpson's ex-wife Nicole Brown and her friend Ronald Goldman were brutally stabbed to death at Nicole's place located on South Bundy Drive in Los Angeles. Suka Boztepe, Brown's neighbor, found both of the bodies hours later, around 12:30 AM on July 13. Blood traces were shown by the distressed behavior of Nicole's pet, an Akita dog covered with the blood from the corpses (OJ Main Page, 1995). Simpson, who flew to Chicago on a business trip later the same night the murders were committed, was notified of the murders by West Los Angeles Division Homicide Detective Ron Philips in the first hours of July 13. Philips and his partner, Detective Mark Fuhrman, were among the first high division LA police personnel encountering and analyzing circumstantial evidence in this polemical case. Detective Third Grade Phil Vannatter was officially assigned by LAPD Homicide Division Head Captain William O. Gartland as one of the two detectives (the other being Tom Lange) to lead the Simpson case. Vannatter had already drafted a search warrant on Simpson's home before the

suspect arrived (Linder, 2000). Simpson, flying back from Chicago, arrived at his residence around 11 AM (OJ Main Page, 1995). At this point Simpson was only a potential suspect, and though mistakenly handcuffed by patrol officer Don Thompson, he noticed that Simpson's middle finger was bandaged as he released him (Jones, 2004). He was then taken to the Headquarters of LA Police Department for questioning and blood drawing for analysis (OJ Main Page, 1995). On July 17, Marcia Clark, lead prosecutor on Simpson's case, along Detectives Lange and Vannatter prepared an arrest warrant against Simpson. The suspect did not turn himself in to the authorities and so he was chased down by police patrols and helicopters in a famous televised slow-speed pursuit whose high levels of audience exceeded those watching the landing on the moon in 1969 (Jones, 2004). After one hour of pursuit and another of negotiation, OJ Simpson surrendered, and was finally arrested at his Brentwood residence at 8:45 PM (Jones, 2004). Two days later, on July 19 he was arraigned and pleaded not guilty to both homicide charges. OJ Simpson was confined at Los Angeles County Jail until his trial began on January 25, 1995 (**Figure 4.1**).

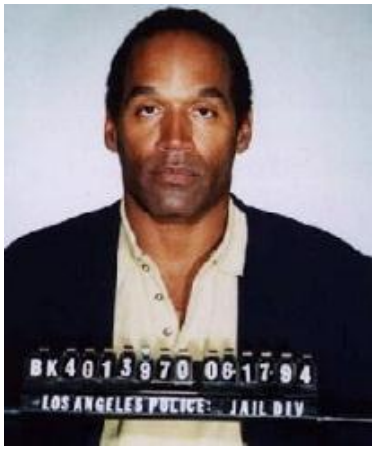

Figure 4.1: OJ Simpson's Mug Shot at LAPD. On July 17, 1994 Simpson was arrested for the murders of his ex-wife Nicole Brown Simpson and her friend Ronald Goldman. (Linder, 2000).

The polemical trial set records for viewing, and became the most followed event in the United States at the time (Linder, 2000). During the trial, 50,000 pages of trial transcript pages were processed, of which 10,000 referred to genetic information. Also, 150 witnesses were summoned to render testimony. The jury, represented by nine African-Americans, 2 Hispanics and one White person, was sequestered in a hotel in downtown L.A. during the trial from January to October of 1995 (Jones, 2004). After the evidence was collected and genetically analyzed, none of it would exonerate Simpson from committing the crimes. Blood DNA was the vast majority of evidence. Out of 54 blood stains that underwent DNA analysis, 10 underwent Southern Blotting for RFLPs, and 44 were analyzed by PCR. Evidence collected from OJ's Rockingham property included blood stains found at his foyer, on a pair of socks found in his bedroom, and on a right leather glove. The glove, found behind Brian "Kato" Kaelin's (Simpson's state housekeeper) bungalow next to the main house at Simpson's property was seen by Det. Mark Fuhrman on the morning following the crimes. RFLP tests were also performed from blood found at the entrance of Brown's home and on Ronald Goldman's boot **Figure 4.2** (Jones, 2004).

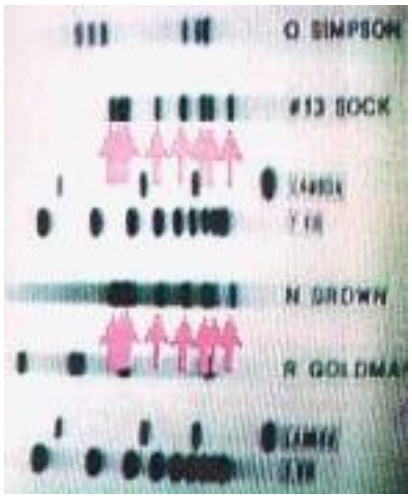

Figure 4.2: DNA Profiles on Blood Evidence in Simpson's Case. The DNA results obtained after PCR and electrophoresis revealed that the blood found on Simpson's socks (second lane from the top) matched that of Nicole Brown (5th profile from top) (Linder, 2000).

In addition to DNA, further criminal evidence also linked Simpson to the murders, including: Simpson's hair on a knit cap and on Goldman's shirt at the Bundy residence, cotton fibers from the Ford Bronco found on the right glove left at Rockingham Avenue and on the cap at Brown's residence, and shoe prints from a size 12 Bruno Magli shoe at the Bundy residence and on bloody prints on the Bronco's carpet (Linder, 2000). All of these pieces of evidence, except for one blood stain found on the center console of Simpson's bronco, were analyzed by PCR. The 44 stains included drops of blood spotted the night of the crime at South Bounty back gate but collected from the property on July 3, three weeks after the murders (Jones, 2004). Given that PCR analysis was faster than RFLP, a greater number of loci on every single drop of blood were tested using this method (Linder, 2000). Besides the DNA evidence, there was also the testimony of Allan W. Parker. Parker was the limousine driver supposed to take the suspect to the airport the night of the crimes. The driver arrived at Rockingham Avenue at 10:25 PM. He tried to communicate with the house to alert them that he was waiting on Simpson, but had no success. After seeing a man wearing black (matching Simpson's stats) crossing the driveway and entering the house at about 10:50 PM (right after the crimes were committed according to the prosecution) Park used the gate telephone and called the house again. Simpson answered the phone claiming he overslept. When he came out, Simpson was profusely sweating and agitated according to Parker.

The prosecution was convinced that the amount of incriminating data against Simpson would indict him as the murderer. The defense, however, led by Johnnie L. Cochran, claimed all to be a racist hoax prepared by the police to frame his innocent client (Jones, 2004). Thus, Cochran accused Fuhrman of having planted the glove the detective had found behind Kato's bungalow at Rockingham Ave. However, records showed that Fuhrman was the seventeenth

officer that came into the crime scene, and all the other officers also saw one glove at the crime scene (Jones, 2004). Accusations against Fuhrman were based on racist comments he made against African-Americans heard on a tape made during a previous trial. In the tape he refers to members of a black gang using racial epithets (Cosme, 2012). Furthermore, Thano Peratis, the male nurse who drew Simpson's blood at LAPD Headquarters the day after the murders, testified that he had drawn about 8 cc of blood and put it in a vial containing ETDA to preserve the blood. Scientific Identification Division accounted only for 6.5 cc in the vial. The defense argued that the missing blood was used to taint evidence incriminating Simpson (OJ Main Page, 1995). Prosecutor Hank Goldberg explained to the jury that the missing 1.5 cc of blood might have resulted from particles stuck to gloves and lab equipment during analysis. The defense then summoned Fredric Reiders, a forensic toxicologist who claimed that EDTA was found on Simpson's blood as well as in the blood spots in Nicole's property back gate. With this fact the defense supported its thesis to the jury that the blood on the evidence was planted from the vial containing Simpson's blood. EDTA is also found in detergent and paint. This was the reason why the prosecution stated that it was found on the pair of socks and the painted gate (Jones, 2004).

Dennis Fung, an LAPD evidence technician, was in charge of gathering evidence from both the crime scene and Simpson's place. His testimony on April 4th reduced jury confidence in the prosecution's case. Defense Attorney Barry Scheck, a specialist in DNA fingerprinting, questioned why the Ford Bronco driven by Simpson had not been sealed off as evidence, why Fung had been the only criminalist working at both places, and how covering Nicole Brown's body with a blanket could have corrupted the evidence. Scheck also accused Fung of destroying evidence by concealing the time when he received the vial with Simpson's blood, and of

contaminating evidence by not using gloves when holding it. He denied this last accusation. But a picture showing him holding the envelope brought by Ron Goldman to the crime scene with his bare hands proved he was lying. Fung admitted that Andrea Mazzola (Fung's assistant) collected essential evidence at the crime scene and at Simpson's estate, and that evidence may have been corrupted after Detective Lange covered Brown's body with a blanket from the house. Fung showed, however, the mislaid original checklist that proved that he received the vial at the time he stated it, discarding the possibility of his destroying the evidence. Videos presented by the prosecution showing Mazzola carrying Simpson's blood sample into the truck confirmed the fact. The criminalist accepted, on the other hand, that blood collected at Rockingham Avenue was left in plastic bags in a truck that did not have a working refrigerator, which might partially degrade it. Fung added that it is most important that the blood vial was correctly closed and sealed in an evidence envelope, not how it was carried to his LAPD vehicle (Jones, 2004; OJ Main Page, 1995).

On October 2nd, 1995 the Jury, from which only six original members remained since the beginning of the trial, deliberated for four hours the verdict of the "The State of California versus Orenthal James Simpson" case. On the day of the verdict, the commotion was so great outside of the Courthouse police helicopters, police squad cruisers and hundreds of extra police officers were stationed around downtown. On October 3rd at 9:45 AM, the Jury's foreperson Amanda Cooley read the verdict declaring O.J. Simpson "not guilty" of the crimes of murder (Jones, 2004).

In the end, DNA typing proved its point to be accurate in matching the evidence with the suspect. The case, on the other hand, got a different nuance when the defense alleged that the evidence had been tampered with or even added to two crime scenes. Although the defense

never proved that the blood evidence *was* contaminated, they convinced the jury that the evidence *might* have been contaminated, which provided them with enough doubt to declare the not guilty verdict. OJ was later found liable for the two deaths in a civil court case where the verdict was based on the "preponderance of the evidence", not on the "without doubt" standard of a criminal trial. OJ Simpson's case is an example that although DNA is a powerful tool, it is useless if the evidence is not collected and stored properly (discussed in Chapter-2). DNA by itself is not usually a determining element in the outcome of a case.

THE BOSTON STRANGLER

Thirteen single women in the Boston area were murdered between June 14, 1962, and January 4, 1964. The women ranged between 19 and 85 years of age, and were murdered in their apartments without signs of forced entry. The Modus Operandi of the assassin included sexually molesting or raping the victims, killing them with articles of clothing (stocking, pillowcase, robe belt) and usually laying their bodies nude as if on display for a pornographic shot in the end. The killer would also use the clothing piece to tie an ornamental bow around the neck of his victims (Fisher, 2000). These crimes were committed by either a single serial killer or possibly several. However, due to their very similar MO, eleven of the thirteen murders were attributed to the Boston Strangler (Bardsley and Bell, 2003).

Anna Slessers, a 55 years old petite divorcee living on Gainsborough Street in Boston, was the first to die, strangled with the cord of her bathrobe on June 14, 1962. A 68 years old widow, Nina Nichols was murdered in her apartment in Brighton on June 30. The killer strangled her with a nylon stocking. The very same day, Helen Blake, age 65, was found dead with a stocking and bra knotted around her neck. On August 19, a very shy and retiring widow, Ida

Irga, fell victim of the strangler. She was seventy five years old and lived in an apartment at 7 Grove Avenue in the Boston's West End. Jane Sullivan, 67, was found dead after a week, on August 20. She had her face submerged and her body slumped over the edge of the bathtub. She was strangled with her own stockings (Bardsley and Bell, 2003). The killer seemed to have changed his killing trait when he murdered an African American young lady, twenty year old Sophie Clark who was murdered in her apartment on Huntington Ave on December, 5, 1962. She was strangled with three of her own nylon stockings. A week after, on December 31, Patricia Bissette was found dead in her apartment on Park Drive in the Back Bay area. Patricia was covered with a blanket to her chin instead of the usual graphic display the killer usually showed. Mary Brown, in early March 1963 was found beaten to death in her apartment in Lawrence. She had also been raped and strangled. On May 6, 1963 twenty three year old Beverly Samans was been stabbed to death 22 times in her Back Bay apartment. This was the first time the killer had used a knife as a murder weapon. Then, strangler seemed to have switched back to his original pattern by killing Evelyn Corvin, 58, in Salem, on September 8, 1963. However, two new younger victims were murdered after Corvin. Joann Graff, 23, was found dead on November 23 in her apartment in Lawrence. There were teeth marks on her breast, and her vagina was bloody and lacerated (Fisher, 2000; Bardsley and Bell, 2003). The last victim, found on January 4, 1964, was nineteen year old Mary Sullivan. Besides being the last victim, Sullivan was probably the woman killed in the most grotesque way. She was in a sitting position on her bed, a bow tied to her neck and a broomstick handle was rammed into her vagina. In addition, all of the victims were assassinated in their own apartments without the killer having to force his way in. It was apparent that the victims either knew the assassin, or they let him in voluntarily (Bardsley and Bell, 2003).

Ten months after the last murder, Albert De Salvo (**Figure-4.3**), a press operator in a rubber factory, was arrested on unrelated sexual assault charges (Boston Strangler, 2012). De Salvo was born in Chelsea, MA in 1931 and was raised in an abusive and violent home. He joined the army at the age of 17, and was stationed in Germany. There he met his wife, Irmgard Beck, with whom he had two children: Judy, born in 1955, who had a pelvic disease physical handicap (impacting De Salvo's homelife), and Michael, born in 1960 (Bardsley and Bell, 2003). A couple of years before the strangler's killing began, Desalvo had a record of felonies and misdemeanors, and a sex offender history, under the nickname "Measuring Man". As the Measuring Man, he pretended to be recruiting fashion models. He would knock on the doors of young ladies' apartments, and present himself as a model agent. De Salvo would take measurements and information to see if the prospect models were considered suitable by the agency (Boston Strangler, 2012). Apparently a number of women were flattered and allowed De Salvo to measure them. De Salvo confessed to being the Measuring Man after Cambridge Police caught him trying to break into a house on March 17, 1961.

Figure 4.3: Photograph of Albert De Salvo, "The Boston Strangler." Albert De Salvo confessed to have committed the eleven official murders attributed to the Boston strangler, and in addition also confessed to two other murders. Nevertheless, the only evidence linking him to the crimes was his confession. (Bardsley and Bell 2003)

Albert went to prison, and was released after eleven months, in April of 1962. This happened two months before the first strangler's victim, Anna Slesers, was found (Bardsley and

Bell, 2003). Almost three years after De Salvo had been released from jail, police started receiving complaints about "the Green Man," a maintenance worker who would talk his way into women's apartments and then would assault them. Susan Kelly, novelist and author of "The Boston Stranglers" who researched this case for her book commented that De Salvo would be very polite to his victims and they would be let him in their apartments. He then would make an overture to his victims. If his advances were repelled he left, otherwise, Albert would make love to them. Apparently his assaults became more aggressive, and that is when he got caught in November of 1964 (Boston Strangler, 2012). De Salvo was arrested and sent to Bridgewater State Mental Hospital, where Dr. Ames Robey was the medical director. Here, Albert De Salvo became friends with George Nassar. This was an inmate with an IQ approaching genius level who had viciously killed a gas station attendant (Bardsley and Bell, 2003). Dr. Robey recognized the need of being someone important to De Salvo. Robey said that the inmate would brag about almost anything. Although De Salvo did not say it, Robey had a feeling that the Salvo wanted badly to be "the Boston Strangler" (Boston Strangler, 2012). De Salvo indeed confessed to being the Boston Strangler to F. Lee Bailey, Nassar's lawyer. Besides confessing murdering the eleven "official" victims, Albert De Salvo confessed killing Mary Brown in Lawrence and another elderly woman who died of a heart attack before he could strangle her (Bardsley and Bell, 2003).

Although De Salvo confessed to committing the murders, he never went to trial for them. Instead, De Salvo stood trial for robbery and other unrelated sexual offenses that were easier to prove. He was found guilty on these charges and sentenced to life in prison in 1967. While pending his appeal for his numerous rapes, De Salvo was being held at Massachusetts State Mental Hospital. On February 24, 1967, he fled and was caught in Lynn, MA the next day. He

was stabbed to death in the infirmary of Walpole State Prison in November of 1973 (Boston Strangler, 2012).

Whether De Salvo was the Boston Strangler has never been proven. The only thing that connected De Salvo to the murders was his confessions, but not a shred of physical evidence. Robert Ressler, a criminologist for the FBI expressed that it is unlikely that one person could be responsible for all of the murders. Ressler added that it is inconceivable behaviorally that all these different killing patterns could fit one individual (Burns, 1994). Furthermore, Kenneth Rowe, who lived on the floor above Joan Graff's apartment, spoke to a stranger who was looking for Joan's apartment just before she was killed. When Rowe was shown a picture of De Salvo, he did not recognize De Salvo as the guy he talked to. Another eye witness, Marcella Lulka, who lived in the same building as Sophie Clark, had an encounter with a man called "Mr. Thompson" right before Sophie Clark was murdered. The guy, who claimed to be a painter sent to her apartment by the super of the building, left as soon as Lulka told him that her husband was sleeping in the next room (Bardsley and Bell, 2003). Surprisingly, when Lulka was brought to prison to ID the possible murderer, she did not remember De Salvo as the guy who came into her apartment when she saw him. Nassar, on the other hand, made a shocking impression on her. Susan Kelly and Dr. Robey point out that thanks to the exceptional memory that Albert De Salvo possessed, this man was capable of retelling the details of the murders with extreme precision, even though he did not commit them. De Salvo could have read and memorized the information presented in newspapers, or visited the places where the assassinations were committed after police investigations were done, or he might have even talked to the actual murderer who passed on the details to him (Bardsley and Bell, 2003).

The most important piece of evidence planting doubt that Albert De Salvo committed all of the crimes was DNA. In October 2000, the remains of the last victim of the killer, Mary Sullivan, were exhumed for DNA testing. Forensic molecular biologist, Dr. David Foran, took part in the DNA analysis process. Foran isolated a DNA sequence found in seminal fluid found on the victim's body and compared it to Albert De Salvo's genetic material using his brother's, Richard De Salvo, DNA. The indisputable results showed that DNA found on the victim was not De Salvo's (Boston Strangler, 2012). To corroborate this, Albert DeSalvo's body was exhumed the following October, and his own DNA was compared to the evidence found on Sullivan. The results, reported on December 13, 2001, confirmed that DeSalvo's DNA and the DNA taken from the evidence on Mary Sullivan's body did not match (Bardsley and Bell, 2003).

JACIE TAYLOR CASE

On June 4, 1994, Jacie Taylor, 19, was found dead and her body brutally beaten in the bathtub of her Grand Junction apartment in Colorado. After having her body examined by a forensic doctor, evidence was found that she was sexually assaulted before she was strangled by a nylon dog leash that was found wrapped around her neck (Massie, 2012). Robert Dewey (**Figure-4.4**), a motorcycle enthusiast, became a suspect in Taylor's murder when a relative of his told the police that Dewey had been hiding in a closet in Taylor's apartment during the time of the murder. Although this lady retracted her statement later on, Dewey admitted he had been at the victim's house prior to the murder. Police also learned that Jacie had told several people that she was afraid of Dewey, whom she met through friends in common (Massie, 2012). Dewey was incriminated when he gave a false name to the police trying to hide from authorities for unrelated issues (Paulson, 2012).

Figure 4.4: Photograph of Robert Dewey. Robert was accused of killing Jacie Taylor in 1994, but was set free after reanalyzing DNA evidence. Dewey spent almost 18 years in jail for this crime that he did not commit (Ripley, 2012).

During a second interrogation at the apartment where Dewey was living at the time, Police recovered a t-shirt with blood stains on it that Dewey was wearing around the time of the killing. A scientist from a lab in Texas, performed a primitive type of DNA analysis, and testified at his trial that the blood was a mixture of two types, and some blood might have come from Taylor (Fender, 2012). In addition, more DNA testing was done on evidence at the victim's home, including a semen stain on a blanket, and from DNA found underneath Taylor's fingernails. But the crude profiles did not match that of Dewey's.

Prosecutors, however, decided to continue with the trial, alleging that Robert Dewey and an unidentified second perpetrator had attacked and killed Jacie Taylor (Paulson, 2012). In April 1995, Colorado authorities arrested Robert Dewey on charges of first-degree murder and sexual assault. His trial would not start until September of 1996 (Miller, 1996). On October 17, 1996, Dewey was found guilty and sentenced to life in prison.

Over the years, the evidence containing DNA was kept in a California Laboratory; the Mesa County Sheriff's Office sent the bloody stained t-shirt and the semen–stained blanket to a temperature and moisture-controlled storage unit to prevent degradation. In 2000, the Colorado Bureau of Investigation (CBI) began to upload DNA profiles to the federal CODIS database

(Fender, 2012). During the period between 2009 and 2010, Danyel Joffe, Dewey's post-conviction attorney had the stored evidence samples retested. The results showed that the blood on the working t-shirt belonged to Dewey only, and was not a mix of two individuals. Joffe passed the information on to the Attorney General John Suther. In 2011, Julie Selsberg with the Colorado Justice DNA Review Project took up the case (Fender, 2012). The Review Project, established in 2009, aims to review DNA evidence in cases where innocent people may have been convicted (Paulson, 2012). On December 20, 2011 new tests were done by the CBI on Dewey's case evidence. Besides confirming that Taylor's blood was not on Dewey's shirt, a full DNA profile on the semen stain on Taylor's blanket partially matched that of evidence found under her nails and on the leash used to strangle her (Fender, 2012). The semen DNA typing was loaded to the CODIS database and it matched that of Douglas Thames who is serving a life sentence for the murder and rape of Susan Doll in Fort Collins, CO. So on the basis of this new evidence, Thames was charged with the Taylor murder, and Dewey was exonerated. On Monday April 30, 2012, fifty one year old Robert Dewey walked out of a Mesa County courtroom as a free man after spending almost eighteen years in jail (Ripley, 2012).

Although happy to regain his freedom, Dewey re-enters society with few resources. Colorado is one of about half the states in the union that do not provide compensation or services for those who have been wrongfully convicted. Robert Dewey became the first person exonerated through Colorado's Justice Review Project, and the 290th person released by post-conviction DNA testing (Paulson, 2012).

This case demonstrates how the interpretation of DNA results, as well as the correct application of the DNA technology can have a major impact on getting at the truth in a court case. In this case, the initial crude DNA analysis that did not properly exclude the suspect cost a

man eighteen years in prison. Moses Schanfield, who led a genetic-testing lab in Denver at the time of Robert Dewey's trial, criticizes the methods used by scientists who analyzed the blood on the Dewey's shirt at the Texas lab. Schanfield states that scientists failed at ruling out DNA that might have been on the shirt before Robert Dewey's blood stained it (Fender, 2012). Also, the analyst who profiled the DNA on the blood evidence in 1996 showed the blood to be consistent with Dewey's and Taylor's, unfortunately that type also matches about 45% of the entire Caucasian population (Paulson, 2012). Hopefully, this type of exclusionary mistake is less common now in view of the current practice of analyzing 13 core loci for identification purposes. Thus, Professional scientific judgment is imperative when it comes to determining the freedom or conviction of a suspect. Crude data with such a high percentage of uncertainty should not be considered relevant in any present day trial.

CHAPTER-4 BIBLIOGRAPHY

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Chapter-5: DNA Databases

Kevin White

Over the past few decades, DNA fingerprinting has drastically changed the way criminal investigations are performed. Advancements in technology have allowed investigators to extract useful data from crime scenes, and scientifically link them to the correct perpetrator. The process of transforming DNA "fingerprints" into usable forensic profiles has proved to be the most powerful method available for identifying individuals. DNA fingerprinting has an incredible ability not just to help convict the guilty but also to exonerate the innocent. As DNA evidence emerged as the most powerful forensic tool, the need to organize and scan the accumulated DNA profiles also increased. The purpose of this chapter is to discuss what DNA databases are, describe how they are used, explain why we need them and the problems associated with them, and discuss why the creation of DNA databases is ethically controversial.

Introduction

As discussed in previous chapters, DNA profiles are derived at crime scenes from discarded or extracted human material: blood, hair, semen, skin cells, etc., all containing genetic information. When forensic investigators arrive at a crime scene, nothing is to be touched, altered, or manipulated before they undergo their process of carefully analyzing the scene for the previously mentioned human materials, without contaminating it with their own DNA. If tampered with or degraded, the genetic information may be lost. If a usable sample of DNA is discovered, it is collected and transported to the lab using means to prevent degradation and contamination, then the technicians use STR-PCR or VNTR DNA fingerprinting technology (discussed in Chapter-1) to determine how many repeat sequences that individual has at specific

locations in the DNA molecule. Numbers are assigned at each locus representing the number of repeats (two types of repeats may be present, one from each parent). "Focusing on thirteen core loci, technicians use these numbers to create a profile that is virtually unique to that person. Because DNA profiles are unique, they prove to be extraordinary crime-solving tools when available and, when encoded, they are well suited for collection in databases" (Sucherman, 2011).

What Are DNA Databases?

A DNA database, or databank, is a collection of DNA profiles, collected for forensic databases from crime scenes and convicted offenders, and for medical databases from the general population. The databases, whether private or public, can be used for various purposes, including analyzing genetic diseases, identification of criminals, paternity analysis, genealogy, identification of unknown remains, etc. The difference between a forensic DNA database (such as CODIS) and a genetic database (such as the Icelandic DNA database; Hloden, 2000) is "that the DNA used for the forensic identification purposes actually does not contain genes, and thus provides no genetic information about a person, 'Junk DNA' they call it" (Stencel, 1999), while a medical DNA database can include a person's entire genome. This difference in the type of information entered into forensic versus medical databases provides different ethical issues (discussed below).

When discussing what a DNA database is, it is best to understand what problem or desired outcome the collection of particular DNA is trying to solve. In regards to a forensic database, our country needs a DNA database to help link crime scenes and to help identify offenders, to act as a crime deterrent, and to serve as a platform to uphold justice. Crime is inevitable, therefore we need to continue to enhance our current databases and continue to

develop new scientific techniques to help our authorities keep murders and rapists off the streets. A database full of DNA profiles from previous *convicted* offenders helps solve crimes from repeat offenders, and serves as a great resource for law enforcement officials to attempt to crack cold cases. In the future, possibly implementing a system in which *everyone* gave a DNA sample would help further decrease crime, but would open up some privacy rights issues. Is it right to ask innocent people to contribute their DNA to a database?

CODIS Forensic DNA Database

The DNA database era in American history started in 1998 when the Federal Bureau of Investigation (FBI) implemented CODIS (Combined DNA Index System), the largest DNA database in the world. CODIS was developed to allow local, state, and federal law enforcement agencies to electronically compare and exchange DNA profiles. The database was originally created to catalog the DNA profiles of sex offenders, but it eventually developed into a broader forensic database that exists as today, containing profiles from various felons and misdemeanors, and from crime scenes. By 2010, CODIS contained over 8,646,417 offender profiles, 328,067 forensic profiles, and aided 119,764 investigations (FBI.gov, 2011). CODIS's main goal is to sustain a credible and organized DNA profile index that can help law enforcement officials nationwide identify perpetrators and to work together to try and prevent future crimes from taking place. The DNA Identification Act of 1994 paved the way for the FBI to establish a National DNA Index System (NDIS), a single entity of CODIS (Vercillo, 2012). "The NDIS is responsible for developing, providing, and supporting the CODIS program to federal, state, and local crime laboratories in the United States and selected international law enforcement crime laboratories to foster the exchange and comparison of forensic DNA evidence from violent crime investigations" (FBI, 2012). The FBI developed a technique to systematically collect, analyze,

and store DNA information, with the goal of data sharing among law enforcement agencies, in a collaborative effort to compare one target DNA profile with a large pool of DNA samples.

The software system that makes up the CODIS network is a distributed system. The hierarchy works at three levels, Local Forensic Labs (LDIS), State DNA Index System (SDIS), and National DNA Index System (NDIS). Because the entire process initiates with local forensic labs, they have the primary responsibility for entering the data correctly. After local forensic labs create a new DNA profile by assigning numerical values to the 13 core loci, they enter those values into their database, creating a unique profile entry. When a detective with access to CODIS wants to run a search, "the detective will search their local or state databases of convicted offender and arrestee profiles, contained within the Convicted Offender and Arrestee Indices, if that state is authorized to collect and database DNA samples from arrestees" (FBI, 2012). If there is a match, the lab will confirm it and the perpetrator will be arrested. The offender index is able to identify suspects by matching DNA found at a crime scene to an existing offender DNA profile previously entered into the database. The sample is also searched against the state's Forensic index of crime scene DNA profiles. If a match is found, it links to crimes to each other. Law enforcement agencies would then collaborate to analyze the multiple crime scenes and the criminal's *modus operandi*, to develop additional leads. CODIS demands strict protocols that must be enforced to ensure the privacy and credibility of the system. The FBI conducts regular seminars and training programs in the various laboratories that generate profiles for CODIS (FBI, 2012).

CODIS and Match Probabilities

In order for DNA evidence to be useful in courts, scientists must understand how rare that specific profile is. They must determine the odds of a *random* match occurring to the database entry. To determine this, scientists must know how often a particular repeat pattern occurs at each locus (termed the allele frequency). Databases facilitate this process by helping scientists determine how frequent specific patterns are in large populations. So for example, if an individual is found to have a 4,5 pattern of repeats at locus-1 (4 repeats from his mother and 5 repeats from his father), how often in the general population does a 4,5 pattern occur. The larger the database, the more accurately scientists can calculate the frequency in a given population. Determining that a 4,5 pattern occurs in about 1% of the population is a more accurate statement if several million samples have been screened than 100. The frequencies of each pattern are then multiplied together to determine the overall probability. For CODIS, when all 13 core loci are analyzed, the chance of a random match occurring is one in several billion (FBI.gov, 2011). One thing is clear, with the size of CODIS constantly increasing, the allele frequencies can be assigned far more accurately than in the past.

Whose DNA Should be Recorded in a Database?

Within the U.S., each individual state determines whose profile gets entered into CODIS. Most states require the profiles for convicted sex offenders and convicted felons (National Conference on State Legislatures, 2010). After that, the states diverge; some states record DNA for misdemeanor crimes, while other states require all violent and non-violent crimes to be entered. Some states give a break to young offenders, but some make juvenile delinquents enter the system. The state of Massachusetts currently requires *convicted* felons and some *convicted*

juveniles to submit their DNA profiles. Only 15 states currently require *arrestees* to submit their DNA samples (National Conference of State Legislatures, 2010). Most states take their DNA from cheek swabs, but some states including Massachusetts take blood samples as it provides more DNA:

> "Authority for the Commonwealth to participate in CODIS is governed by Massachusetts General Law, Chapter 22E. As of February 10, 2004, this legislation requires all individuals convicted of a felony offense to submit a blood sample to the Massachusetts State Police Crime Laboratory" (Mass.gov, 2012).

With the various levels of CODIS present, it is important for each level to communicate efficiently with the other levels to help solve crimes. Overall, Massachusetts appears to have a reasonable standard for whose DNA should be entered, and the 15 states that require profiles from *arrested* individuals appear to be on the edge of the ethical curve.

DNA Database Ethics

With respect to ethics, it is important for the public to understand the key difference between forensic DNA databases and medical DNA databases. As previously discussed, the former contains only information on junk DNA repeat sequences at 13 core loci which encodes no medical information, while the latter can contain medical predisposition information.

CODIS Ethics

Theoretically, let's imagine CODIS being at full capacity, meaning every individual's DNA in the country was recorded in the database. If a crime was committed where DNA evidence was discovered, the profile would be compared to the large database and a match would likely occur 100% of the time because everyone's profile is in there, and the criminal would be

brought to justice. This type of large database could in theory be created by taking cheek swabs from every individual at time of birth. However, many people are against the idea of innocent people's DNA profiles being in a database for fear of *false* matches to those profiles. So the fear is that a false match to an innocent person that never committed a crime would result in that person's arrest until it could be cleared up with authorities. It is understandable to think that people will argue that their DNA is their own property, and it is, but if something this extraordinary could help solve crimes, should society consider this? Obviously this idea is extreme, and currently no state in the U.S. requires this.

Although CODIS does not contain medical predisposition information, some people are worried that the *original* DNA chemical sample that resides in a lab's freezer does contain confidential information. However, this criticism is relatively easy to solve by mandating that each lab destroy all original DNA samples after making sure an accurate CODIS profile is obtained.

"Law enforcement officials today insist that the state and FBI DNA databases pose no real risk to privacy rights. They insist that the DNA profiles are strictly safeguarded, and in any event, are nothing more than junk DNA that contains no sensitive information about a person's health or background" (Stencel, 1999). Although CODIS likely contains no information of use to any medical insurer, some people have stated their concerns:

> "The U.S. has failed to employ comprehensive privacy regulations that would prevent the government from sharing DNA profiles in a DNA database with other groups, such as insurance companies, employers, or academia. DNA database statutes can be grouped into broad categories based on authorized uses of both DNA profiles and raw DNA samples: 1) statutes that allow access to DNA for non-law enforcement purposes, 2) statutes that allow access to DNA information to public officials other than law enforcement, 3) statutes that allow law enforcement to use DNA evidence for purposes other than identification, and 4) statutes that do not require expungement of DNA records upon reversal" (Roman-Santos, 2011).

So with CODIS, the main issues are to ensure that only authorized individuals have access to CODIS, that only persons mandated by law to provide their profile be forced to give it, and that states reconsider the use of arrestees DNA when they have not been convicted of any crime. Rigorously enforcing these standards will help strengthen the overall index system. CODIS has already helped in over 199,000 investigations (2010 numbers), and has proved its worth, but authorities must always remain vigilant when armed with this power to arrest individuals. DNA databases do a lot more good than they do bad, but our control and oversight of the systems can always continue to improve.

Medical Database Ethics

Medical databases are an entirely different story, as they can indeed contain huge amounts of genetic information, including medical predispositions. For medical databases, "DNA carries a person's identity. It also carries a vast amount of other information about that person's biology, health and, increasingly, psychological predispositions" (The Economist, 2012). This information has medical value, and could potentially be abused by insurers, employers, politicians, and civil servants. Although this may be true, there are always two sides of an argument. Medical databases can be quite useful; the Icelandic database was recently used to identify a mutation in amyloid precursor protein (APP) that prevents an individual from getting Alzheimer's disease, even when that individual contains other mutations the predispose them to the disease (Jonsson et al., 2012).

But what if this database was hacked by an insurance company in Iceland trying to determine who should be fully covered by medical insurance. These databases deserve our highest security for separating a person's genome information from that person's real identity,

even separating that information into different databases. And individuals' contributing their DNA to medical databases should do so only with informed consent.

Chapter-5 Conclusions

"The Godfather" of DNA fingerprinting, Professor Sir Alec Jeffreys said it best, "The national DNA database is a very powerful tool in the fight against crime, but recent developments such as the retention of innocent people's DNA raises significant ethical and social issues. When the DNA database was initially established, it was a database for criminals so if they re-offended, they could be picked up" (News Medical, 2008). DNA databases were created for the greater good, to keep some of the worst criminals in the world behind bars, but the use of arrestee data indeed comes with ethical concerns, so individual states should reconsider how this information is used, realizing they could be handling DNA from a totally innocent person. The public should be more aware that CODIS does not contain information on genes, but on junk DNA, and thus provides no genetic information about a person. We have the largest DNA index system in the world, and technological advances are happening on a daily basis. Ensuring that only approved individuals have access to CODIS, destroying the original DNA samples themselves, and re-assessing the use of arrestee DNA, are all very worthwhile. Overall, expanding CODIS will continue to help solve more crimes, exonerate innocent people wrongly convicted, and reduce the need to reverse previous miscarriages of justice.

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PROJECT CONCLUSIONS

DNA fingerprinting has allowed for great advancements in forensic science. DNA analysis is the most powerful method for determining an individual's identity, and has been applied to a variety of situations, such as paternity testing, criminal forensics, or identifying human remains. DNA fingerprint analysis focuses on specific locations (loci) in an individual's DNA. The 13 core loci tested for CODIS entries vary considerably from person to person, but can be similar to a low percentage of other individuals. These locations contain repeating DNAs that vary by the length of the repeating elements, the nucleotide sequence of the repeats, and the overall number of repeating elements at that site. Repeating DNA domains are often classified as variable number of tandem repeats (VNTRs) or short tandem repeats (STRs) depending on their overall lengths. These repeating DNAs can be analyzed by non-amplifying or amplifying assays. The non-amplifying assay is based on an earlier Southern blot technique, which is a method applied to DNA fragments that are cut at specific nucleotide sequences by restriction enzymes. Such DNA fragments are called Restriction Fragment Length Polymorphism (RFLP). The Southern Blot technique is now somewhat obsolete due to the increase in inexpensive DNA sequencing technologies, the fact it required a considerable amount of DNA in order to be used, and the several weeks it took to analyze a single DNA sample. Although the technique proved to be tedious, the results were not strongly affected by contamination. The amplifying technique uses polymerase chain reaction (PCR) to make copies of STR DNA. STRs are short enough to be amplified by PCR. Because PCR is rapid and sensitive, the PCR-STR method of DNA testing is now the industry standard for the FBI's CODIS database. When all 13 CODIS loci are analyzed, the chance of a random match to the database is one in one in several billion. PCR is

prone to contamination, so when DNA evidence might be contaminated, sometimes an RFLP is also run.

No matter how valuable modern DNA analysis is, the sample will be useless if the DNA is contaminated or degraded during collection, transport, or storage. So without proper technique and carefully followed crime scene procedures, forensic evidence that could affect the outcome of individual trials may be lost. DNA can be the difference between convicting the guilty, or exonerating the innocent. But if not collected, transported, stored, extracted, and handled properly, the power of the DNA profile becomes meaningless. Complex technology is not easily accepted in courts; it is not always apparent how *accepted* the specific technology is in the scientific community, or how *reliable* the technique is when performed under specific conditions. The admissibility of DNA evidence within the courtroom has developed over time from a series of landmark court cases that established precedents for accepting complex technology in a courtroom.

As the DNA revolution emerged it proved to be one of the most powerful ways to determine the events of specific crimes, and the judicial system realized that standards and regulations are essential to ensure justifiable outcomes. Because DNA evidence is so new, and the potential prejudice to the defendant is great, it is imperative that the court satisfy itself that there exists a sufficient initial basis to admit the evidence for each specific trial. The current standard for admitting DNA evidence was established in 1990 by the case of *Two Bulls v Wyoming*, that established a 5-prong standard to determine in a pre-trial hearing whether there is a general acceptance in the scientific community of the DNA testing used, whether the testing is reliable, whether the testing was performed properly with controls in this particular case, and whether the information obtained is more probative than prejudicial.

As time progresses, and more complex trials occur, such as the 2000 trial of Eugene Robinson who was found guilty solely on the basis of a John Doe warrant, new regulations may have to be implemented to increase the credibility of forensic evidence. By establishing new standards, the government is attempting to improve the overall system to maintain accurate outcomes. The judicial system will continue to define which procedures should be used to test and analyze DNA to insure they are accurate, reliable, and properly controlled.

Following the standardization of the technology mandated by the landmark cases, eventually DNA testing proved to be a clear, effective means for identifying individuals present at a crime scene, when performed properly. Despite the importance of landmark court cases in helping establish the general acceptance of DNA identification in courts, and the standardization of DNA testing, the public often is often completely unaware of the landmark cases, but instead are often aware of some sensational cases that used DNA.

DNA databases are computers containing a collection of DNA profiles. The world's largest DNA database is the FBI's database, known as the Combined DNA Index System (CODIS). CODIS contains DNA profiles from large numbers of crime scenes, and from previous offenders of other crimes. DNA databases have helped solved numerous crimes by matching forensic evidence with previous offenders. They have also helped determine that several crimes are in fact related. With respect to whose DNA profiles should be entered into the CODIS database, it is important to distinguish the CODIS database (which contains only information from the 13 core loci and helps solve crimes) from medical databases such as the Icelandic database (which contains entire genome sequences). CODIS is a very powerful tool in the fight against crime, and it was created to keep some of the worst criminals in the world behind bars, but the use of arrestee data indeed comes with ethical concerns, so individual states

may need to reconsider how this information is used. Recently, the retention of innocent citizens DNA has sparked a variety of ethical and social issues. The public should be more aware that CODIS does not contain information on genes, but on junk DNA, and thus provides no genetic information about a person. We have the largest DNA index system in the world, and technological advances are happening on a daily basis. Even though the current Index System has had an immense positive impact on the current legal system in general, there is always room for improvement. Guaranteeing that only approved individuals have access to CODIS, destroying the original DNA samples once a profile has been created, and possibly implementing a nationwide standard solidifying which particular convictions and arrests will meet the criteria for entry into the database are highly recommended. Overall, expanding CODIS will continue to help solve more crimes, exonerate innocent people wrongly convicted, and reduce the need to reverse previous miscarriages of justice.