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DNA FINGERPRINTING

An Interactive Qualifying Project Report

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ABSTRACT

The purpose of this IQP was to investigate in the most concise manner possible, DNA fingerprinting and its relationship to society as it currently stands. To accomplish this task, we introduced what DNA Fingerprinting technology is and how it's used, and the collection, preservation and processing of DNA samples. We focused on some of the landmark court cases that helped to establish DNA fingerprinting as not only reliable but a necessary tool for criminologists. Further, we documented some of the sensational court cases likely already known to the reader, reminding them of the role that DNA evidence played. And finally we discussed the controversial topic of DNA databases, with a focus on the FBI's CODIS, showing what it has done for the crime fighting community, the laws surrounding their use, and the moral and ethical debates that continue to rage today on this controversial topic.

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PROJECT OBJECTIVE

Due to television shows like 'CSI' and other forensic based dramas, and the numerous sensational cases that have been recently in the public eye, DNA fingerprinting has been brought to the public eye like never before. Still, there is a mysticism about the technology, and with the advent of DNA databases, more controversies arise about personal privacy. The objective of this project is to bring to light to the average layperson, the techniques involved in creating a DNA fingerprint, document correct sampling and storage procedures, and investigate the court cases that set precedents for accepting complex technical information in U.S. courts. The technology when performed correctly has usefulness not only in fighting crime, but also as a tool to assist identifying missing persons and solving cold cases still on the books.

Chapter-1: DNA Fingerprinting Technology

DNA (deoxyribonucleic acid) fingerprinting has revolutionized the world of forensic science, especially in the areas of law enforcement and human health care research. Using DNA fingerprinting techniques, suspects can be linked biologically to the scene of their crime. Something as simple as sneezing over a counter, leaving a drop of blood on the floor, or losing even a single hair somewhere in the crime scene area can eventually convict you in court. Conversely, suspects deemed guilty have been exonerated utilizing DNA forensics. DNA fingerprinting has also been used in paternity cases to help settle custodial battles, and DNA patterns are being studied to possibly identify adults and children with inherited disorders. Most recently, DNA fingerprinting is being studied to help identify soldiers missing in action.

One of the chief problems identified with this technology however, is the lack of public comprehension of the subject matter. DNA forensics is a complex science for the average person, and that has become a problem in the judicial system. The debate turns to whether or not a jury can make a ruling on evidence that they may or may not understand. Just like any other piece of evidence, how sure can we be that something is true? Does a drop of blood make it certain you were there, or only likely? Is it scientifically possible that someone is not guilty, but perhaps a family member or another person with similar heritage and physical characteristics is the guilty party? These become extremely important questions when we are dealing with whether or not a person will be found guilty or innocent. To understand the science behind DNA testing, we must first start with a basic overview of DNA.

What is DNA?

The discovery of DNA and our ability to use DNA technology has evolved from decades of research and experimentation, with varying degrees of technicality and complexity. In essence, DNA is the genetic blueprint of our very being. DNA is unique to every individual with the exception of identical twins. Our DNA provides our developing body with the instructions on how body parts are to be constructed, and how it is to manufacture necessary proteins to enable us to grow and develop.

Cells are the smallest unit of an organism that is classified as living. The human body is a multi-cellular organism containing anywhere from 10 to 100 trillion cells. Within each cell are several parts that are specific to the cell's needs. There are hundreds of different types of cells in the human body, but common to each cell is the nucleus. This organelle is where the DNA is stored. The DNA is identical in every cell in an individual's body. Inside the nucleus are very long and tightly packed pieces of DNA called chromosomes (Figure-1). A piece of that DNA within the chromosome that dictates a particular trait is called a gene.

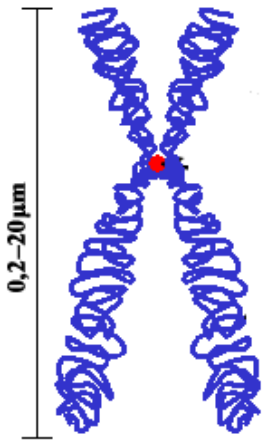

Figure-1: Diagram of a Human Chromosome Containing DNA. Note the highly wound compact DNA structure (blue), and the joining of the two sister chromatids at the centromere (red) (Magnus Manske, Wikipedia).

DNA goes through several stages of compaction and winding throughout different stages of the cell replication cycle, so much so that if you were to stretch it out to one long strand it would be nearly three feet long! (The University of Utah, Genetic Science Learning Center). The two long chains form what is called a double helix (Figure-2), and travel in opposite directions. As shown in the figure, the bases come together in two pairs. Adenine can only attach to Thymine, and Guanine to Cytosine. The sugars and phosphate groups of the backbone strand alternate.

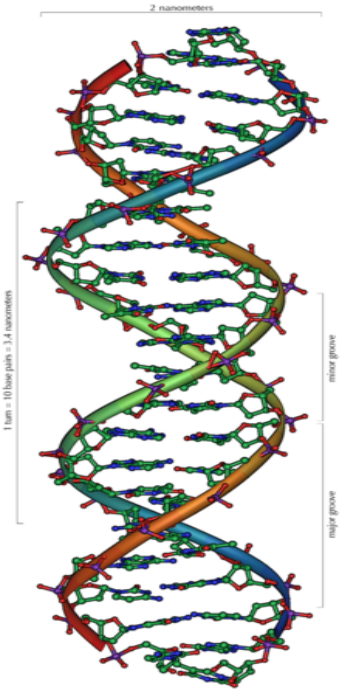

Figure-2: Diagram of the Double Stranded Structure of DNA. The rungs on the ladder denote base pairs whose weak hydrogen bonds hold the two strands together at normal temperatures (Michael Ströck, February 8, 2006).

As for its chemical structure, each strand of the double helix has a backbone made of sugars and phosphate groups, joined by ester bonds. Attached to this backbone is a sequence of chemical bases: adenine (abbreviated A), cytosine (C), guanine (G) and thymine (T). These four bases create a code, a sequence which is essentially the "instructions" our body uses. For example, you could find the sequence T-A-G-T-C, and the DNA strand bound to it would look

like A-T-C-A-G. This sequence of base pairs is the definitive marking which can be used to differentiate one individual's DNA from another.

In general, a base linked to a sugar is called a nucleoside, and a base linked to a five-carbon sugar (deoxyribose) and one or more phosphate groups is called a nucleotide. If multiple nucleotides are linked together, as in DNA, this polymer is called a polynucleotide [Commission on Biochemical Nomenclature (CBN)*]*. The DNA chain is only 22 to 26 Angstroms wide, a mere 2.2 to 2.6 nanometers, but the longest can be up to 220 million base pairs long! (Gregory S, 2006).

The DNA sequence is split between coding and non-coding regions (Figure-3). The coding regions, called exons, are responsible for the instructions on how to produce a particular protein. The non-coding regions are called introns. This series of exons and introns make up a gene. Genes comprise approximately 5% of human DNA, with the other 95% consisting of non-coding regions. The function of non-coding regions is for the most part unknown (Krapp, Encyclopedia of Nursing and Allied Health). The non-coding sequences are not always conserved between individuals, depending on the specific locus analyzed, so these sequences are exploited in DNA testing.

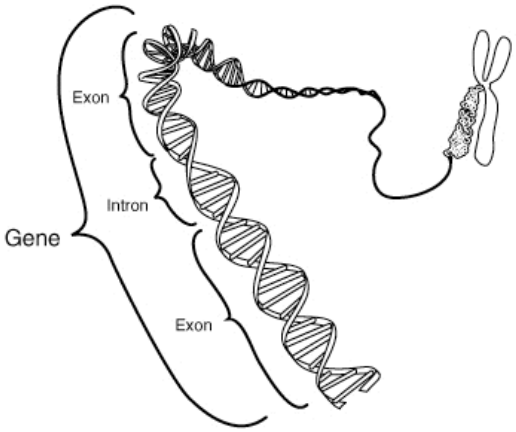

Figure-3: Diagram of a Typical Gene Structure on DNA. Note the alernating exon (coding) and intron (non-coding) sequences (National Human Genome Research Institute).

An important distinction to make with respect to DNA testing, is the difference between an allele and a gene. A gene, like explained above, is a sequence of DNA that codes for a single genetic instruction. This genetic instruction can create proteins, or even turn other genes on or off. An allele is one variant of a gene. Many genes have several different variants. As a basic example, we all carry a gene for hair color. One allele could code for very dark hair color, while the other could come out garbled so that no pigment is produced and the hair comes out white. As another example, the code CCA has no difference from CCC or CCG as each of these code for proline, a non-essential amino acid, meaning we are able to synthesize it. The creation of new alleles and appearances in individuals DNAs is what we call mutation.

Variations occur in the DNA sequence in both the coding and non-coding regions. The two main forms of variation in DNA are sequence polymorphism and length polymorphism. A sequence polymorphism is the difference in the sequence of bases at a particular locus, a specific location on a DNA molecule. Length polymorphisms result from the difference in length at a particular DNA locus. Sequence polymorphisms are most useful in determining differences between two members of the same species, while length polymorphisms are most useful in differentiation between two species, although the latter are also used in RFLP-type DNA testing.

DNA Use in Forensics

The reason DNA fingerprinting is such a powerful tool in forensics is because it can be used to clearly distinguish a suspect from anyone else on the planet. Everyone's DNA is unique unto themselves, but with so many million base pairs it would be impossibly time consuming to analyze the sequence of an individual's entire DNA molecule. Instead, scientists use a faster method for analyzing repeating DNA sequence patterns known as Short Tandem Repeats

(STR's) or for analyzing Variable Number Tandem Repeats (VNTR's). The essential concept of a tandem repeat involves the code produced by a series of nucleotides. Unlike other sections of DNA, a tandem repeat is a section of code in which a pattern of two or more nucleotides is repeated with the repetitions located directly adjacent to one another. For example, in the STR sequence AGATCAGATCAGATC, the nucleotide sequence AGATC is repeated 3 times. STR's generally refer to repeats of 2-10 base pairs, while VNTR's range from 10-98 base pair repeats (Krapp, Encyclopedia of Nursing and Allied Health).

The more DNA loci that are analyzed and matched, the more accurate the findings, and the more likely it can be proven in court to belong to a certain person. Scientists are able to determine then whether two DNA samples are from the same person, from relatives, or from non-related people.

PCR-Type DNA Testing

Once we have obtained a sample of DNA (see Chapter-2 for the various methods of DNA acquisition) we need to analyze it. There are two main ways to test DNA forensically, amplifying (PCR) and non-amplifying (RFLP). The polymerase chain reaction (PCR) technique is the most well known DNA analysis technique nowadays since it is very fast, and can be performed on trace amounts of DNA, so it is often used first to analyze a forensic sample. The RFLP-type method is slower and requires more DNA, but is often used second if contamination is suspected since it is more resistant to DNA contamination.

PCR, or polymerase chain reaction, is a technique used to amplify the number of copies of a specific region of DNA so that we might have enough of it to test. The first step of PCR is knowing what sequence "flanks", or surrounds the genes we are looking for. We are looking for

a sequence before and after an STR. As mentioned previously, some genes can differentiate between species, people, relatives, etc. For the sake of example, let's say we wish to analyze the DNA sentence:

AACCTTGG…….AACCTTGG

We know that the pairing sequence will be:

TTGGAACC…….TTGGAACC

The ……. in between the two nucleotide sequences represents the STR we are trying to analyze. Now scientists need to synthesize primers, of about 20 letters-long. Using a DNA synthesizer machine we can create DNA chains of our design adding a single letter at a time. We create primers which would pair up with the top sequence and bottom sequence, flanking the STR. Adding these produced primers into the sample, as DNA is synthesized using the primers as start sites, we now would have 4 strands of DNA instead of the original two (Figure-4). After repeating this DNA synthesis cycle again, we would have eight DNA strands, then sixteen, and so on. After about twenty cycles there will be approximately one million copies of the original sequence in the reaction tube (Brown, 1995).

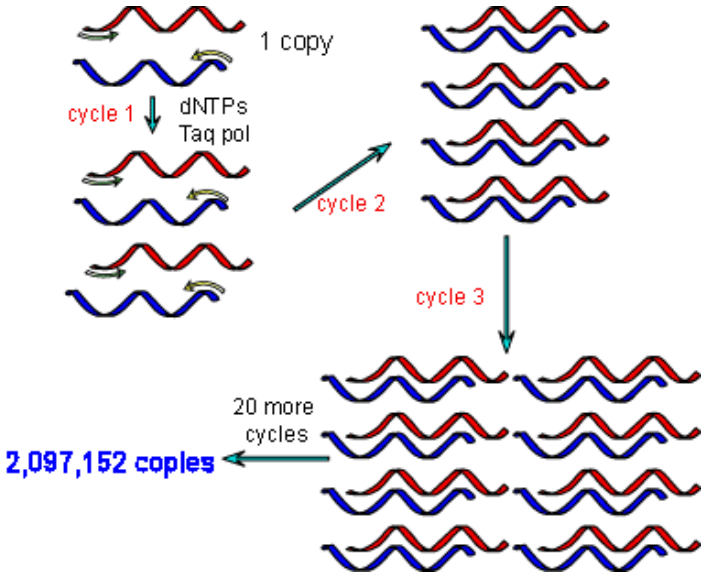

Figure-4: Diagram of a PCR Reaction. This process is used to amplify the amount of DNA for forensic analysis, especially when only trace amounts are found at a crimescene (Bioteach, 2006).

To begin a cycle of replication, the DNA sample is heated to near boiling to separate its paired strands and the primers are added, along with many individual DNA precursor "letters" to be incorporated into the new DNA strands. Because of the large number of primers added, the original DNA strands will always bind to the primers instead of with each other. Next, we add a special enzyme called a DNA polymerase (because it catalyzes the synthesis of new DNA polymers). As we cool the reaction, the primers anneal to their corresponding upstream and downstream locations flanking the STR. The polymerase enzyme then finds the annealed primer sequences to act as beginning points for DNA systhesis, and "read" the letter sentences on the template to incorporate the complementary letters. A useful analogy is a zipper, with each zipper strand being a sequence of nucleotides, the zipper of course being the polymerase. Now the enzyme has synthesized another couple copies of the target DNA region, but importantly only the section we wanted to copy! Repeating this replication process produces two times as many DNA strands of the STR, and can be repeated as many times as necessary (Figure-5).

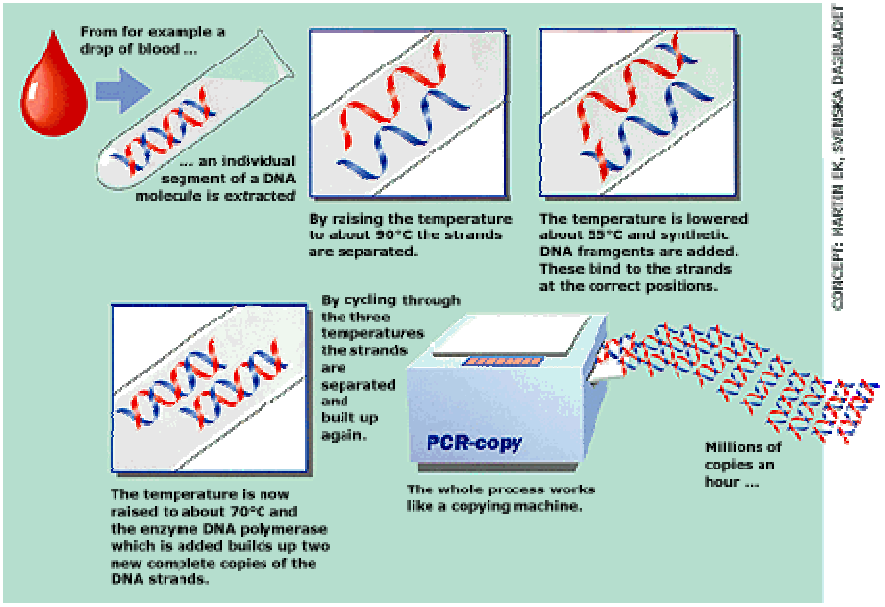

Figure-5: Diagram of the Amplifying Nature of PCR (Nobel Prize, 2006).

The largest advantage to PCR is its ability to be extremely discriminative of which DNA is amplified, and its ability to work with very small quantities of DNA. Unfortunately it is somewhat susceptible to contamination. Any small contaminant is also amplified. Although not all contamination will eliminate a sample, some DNA may be found to be not human at all, and easy to rule out.

RFLP-Type DNA Analysis

The second main method for analyzing DNA is RFLP, Restriction Fragment Length Polymorphism, in which a DNA digestion enzyme is used. The enzyme, a restriction endonuclease, cuts the DNA at a specific sequence known as a restriction endonuclease recognition site. This produces variable lengths of DNA due to the presence or absence of various STRs or VNTRs between the restriction sites. These cut DNA fragments are then separated by size using a technique called gel electrophoresis (Human Genome Project Information, 2008) (Figure-6). Gel electrophoresis is a process which can separate different lengths of DNA. The term gel refers to the matrix used to contain and separate the DNA fragments. The gel is chosen based on the fragments being used, and is usually constructed from a mesh network of polyacrylamide.

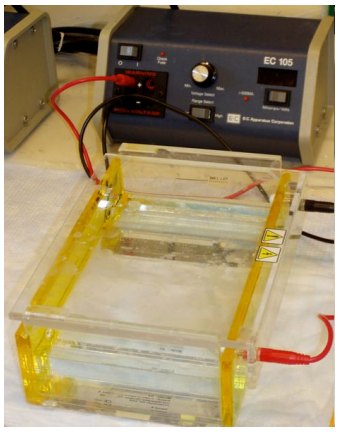

Figure-6: Photographh of DNA Electrophoresis. The gel is shown in the horizontal apparatus. The blue device behind the gel is the power supply used to provide electric curent to the gel to separate the DNA fragments by sizes. (Jeffrey M. Vinocur, 2006).

An electric current is placed across the gel, creating a positive and negative end. DNA samples are placed in wells within the gel, and the DNA molecules migrate towards the positive anode since their phosphate groups are negatively charged. As the molecules migrate through the gel, the shorter fragments of DNA will move the quickest and furthest across the gel because they are hindered less by the sieving effect. The DNA pattern in the gel is then blotted to a membrane, in a process known as Southern blotting, and a particular RFLP of interest is displayed by hybridizing a complementary DNA probe to the membrane. The results are then displayed on x-ray film, and the image is recorded with a computer operated camera, and the intensity of the band or spot of interest is measured, compared against standard or markers loaded on the same gel. The measurement and analysis are mostly done with specialized software (Berg JM, 2002). The final analysis (see Figure-7) looks like bar codes at commercial stores, and differs for each individual.

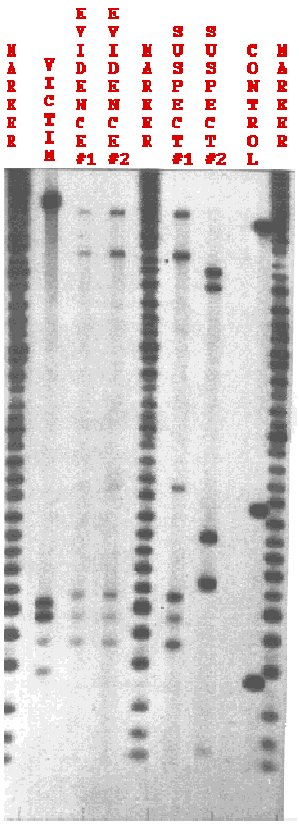

Figure-7: RFLP-Type DNA Analysis. Shown is an example of the resulting "barcode" results from an RFLP analysis. Each column is labeled to identify the different DNA source tested. The DNA evidence in samples #1 and #2 on the left half of the gel appear to be from the same subject, and seem to match that of suspect # 1, and not suspect #2 on the right half of the gel.

The primary weakness of RFLP processing is its requirement for a relatively large quantity of fresh DNA, unlike PCR which can work off extremely little. And the RFLP process takes longer than PCR. However, the RFLP process is less prone to contamination, so the STR process is usually performed first as an initial quick approach, followed by RFLP analysis if sufficient DNA quantities were isolated.

Chapter-1 Bibliography

Berg JM, Tymoczko JL Stryer L (2002) *Molecular Cell Biology*, 5th ed., WH Freeman

Brown JC (2006) What the heck is PCR?
http://www.people.ku.edu/~jbrown/pcr.html

"DNA Typing." Encyclopedia of Nursing & Allied Health. Ed. Kristine Krapp. Gale Cengage, 2002. eNotes.com. 2006. 20 Jul, 2008 http://www.enotes.com/nursing-encyclopedia/dna-typing

Human Genome Program. Wednesday, July 30, 2008.
http://www.ornl.gov/sci/techresources/Human_Genome/elsi/forensics.shtml

The University of Utah, Genetic Science Learning Center.
http://learn.genetics.utah.edu/units/disorders/karyotype/whatarechrom.cfm

What Every Law Enforcement Officer Should Know About DNA Evidence
September 1999 http://www.ncjrs.gov/nij/DNAbro/what.html

IMAGES

Bioteach (2006) Diagram of PCR Amplification of DNA.
http://www.bioteach.ubc.ca/MolecularBiology/PolymeraseChainReaction/PCR.gif

Gel electrophoresis pic- GET INFO.
https://exchange.wpi.edu/owa/?ae=Item&t=IPM.Note&id=RgAAAABMs44Bwh9pQojAdcCsoPMXBwBqTfiQ4FaVToTaxe7xZHCHAAAAB4UNAAATWesieL6RTpgT0kCYybWkAHcqZT3SAAAJ

Magnus Manske, Wikipedia.
http://en.wikipedia.org/wiki/Image:Chromosome-upright.png#filehistory

Chapter-2: The Collection and Processing of DNA

Every forensic investigation initially begins at the crime scene. The success or failure of a prosecutor to win his case often depends on the talents of the law enforcement agency that collects and processes evidence derived from the crime scene. Nowadays, this critical evidence is likely to contain DNA. And once this DNA evidence has successfully been collected, as the world learned in the famous OJ trial, it is critical to establish a chain of custody to prevent any potential tampering, and to handle the evidence so as to prevent degradation or contamination. The purpose of this chapter is to document some of these critical techniques for the collection and processing of DNA evidence.

Initial Processing of the Crime Scene

The entire investigation may hinge on the duties of the first arriving officer whose foremost priority is to isolate the scene. The crime scene is vulnerable to a variety of dangers that could inadvertently contaminate the integrity of the investigation, including evidence accidentally left by other police officers, bystanders, witnesses, suspects, or even animals. All have the potential to become detrimental to the police effort.

The site at which the crime was committed is considered to be the *primary* crime scene. Useable evidence found *outside* the primary crime scene, for example, a car used to transport a body, or a river bank where evidence is dumped, is deemed the secondary crime scene area. Crime scenes are typically divided into 3 tiers (Figure-1). The first tier is created by establishing a physical border around the immediate site of the crime using tape, ropes, or some other form of

restrictive measures. The second tier is created around the first and should be cleared and restricted for authorized personnel. This area is designed for incoming police officers, forensic scientists, and other people directly involved in the criminal investigation. The surrounding areas are perfect for briefing arriving officers, allowing for a break space, or setting up equipment. The third tier is designed to keep non-essential persons and onlookers away from the scene.

A good example of this tiered system is to picture a murder inside a house. The room or rooms in which the murder took place are designated the first tier. The second tier would consist of the surrounding rooms of the house. Finally, the areas outside of the house would be the third tier which restricts access to the public (Mike Byrd, 2000). The purpose of the three tier system is to preserve evidence.

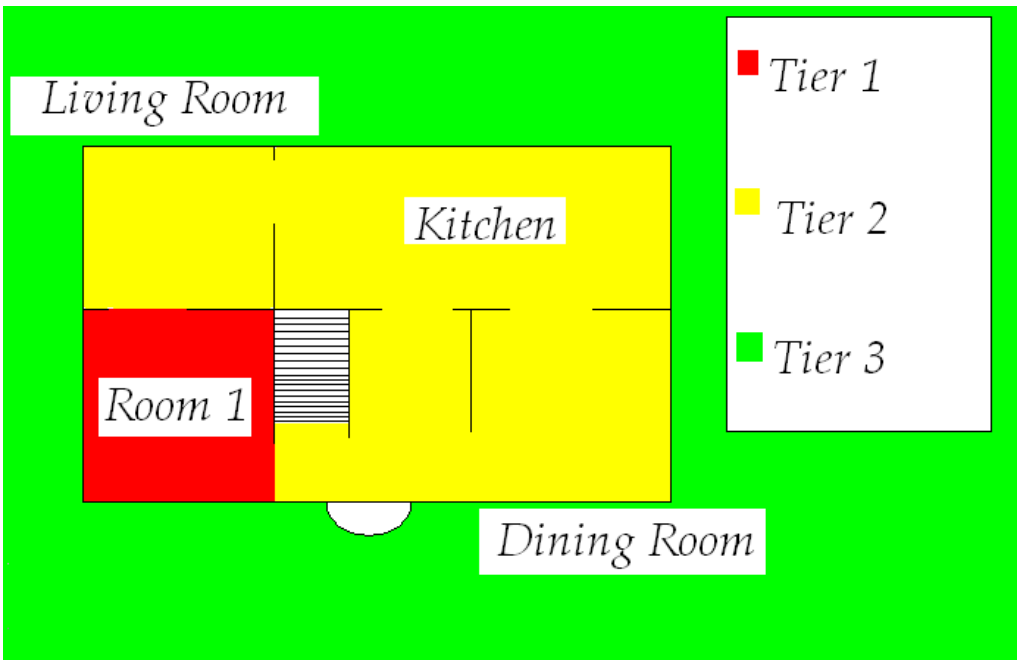

Figure 1: The Three Main Tiers of a Crime scene. Diagramed is a theoretical crime scene in which a murder was committed. Room 1 (red) is where the crime took place. The living room, kitchen, and dining room (Yellow) are the second tier designated for official personnel briefing and break space. The third tier (green) is the outside area, to restrict non-investigative persons from the scene.

Collecting the Evidence

At a crime scene, DNA is found in blood, semen, skin cells, tissue, organs, muscle, brain cells, bone, teeth, hair, saliva, mucus, perspiration, fingernails, urine, feces, etc. From so many sources the chance of finding traces of the perpetrator's DNA at a crime scene is very likely. DNA has been recovered for criminal investigations from saliva on dental molds, ski masks, and postage stamps. Even a hair found inside a victim's throat was used in a capital murder conviction (What Every Law Officer…1999). Even a small hair may contain enough DNA to match a potential suspect.

But great care must be paid to collecting the evidence while avoiding contamination. Contamination occurs from touching evidence without wearing gloves, sneezing, coughing, or a variety of other mishaps. Some DNA contaminating sources can be eliminated, for example, by taking DNA samples from victims or surrounding witnesses, so their DNA profiles can be identified among the collected forensic samples. Police and crime scene units are usually advised to change their gloves often, avoid talking, sneezing, or coughing over any potential evidence. They also use disposable instruments to try and reduce the risk of contamination (What every Law Officer…1999). Using modern techniques, every type of bodily fluid or tissue can potentially yield enough DNA for testing. Fortunately, that means many criminals probably left enough evidence to link him/her to the crime scene. Unfortunately, every individual examining the scene can also leave their own DNA behind as well.

Each type of evidence has its own unique set of collection procedures; however, our primary focus of discussion concerns the forensic evidence that will be collected for DNA testing. The first step prior to physically collecting any sort of evidence is to take photographs of the entire scene, and specific photo shots of each piece of evidence. Each piece of evidence and

the area surrounding it needs to be numbered sequentially, recorded, and photographed to preserve a record of exactly how things appeared before evidence was collected. Only one person should be collecting evidence from a particular source, and a different person should be recording each piece as it is obtained. This helps to prevent contamination, and when ruling out DNA samples from suspects and victims it is helpful to know who handled the evidence. Detailed notes also need to be made about the location and condition of the evidence, the spatial relationships of evidence to the rest of the crime scene, and the condition of the biological evidence.

It was mentioned earlier that samples of an individual's DNA can potentially come from dozens of sources in the human body. That being said, it is unlikely to find all of them at one crime scene. For example, it would be a rare occurrence to find organs at the crime scene, or perhaps pools of perspiration, or even teeth. Since those particular sources are uncommonly found, we will focus the discussion on the primary sources of DNA samples at a crime scene, specifically, blood, semen, saliva, and hair. These substances are generally either involved in the act of committing the crime, or lost in an involuntary and possibly unavoidable manner.

All of the following sources of forensic evidence can provide useable DNA samples for testing. As discussed in detail in Chapter-1, in general there are two types of DNA we can use for testing; chromosomal DNA isolated from a cell nucleus, and mitochondrial DNA (mtDNA) isolated from a cell's cytoplasmic mitochondria. mtDNA is present in greater numbers within each cell (approximately between one hundred and ten thousand copies of mtDNA per average cell) and is generally used for examining older, unidentified skeletal remains. Unlike nuclear DNA, which is inherited from both parents and in which genes are rearranged in the process of

recombination, there is usually no change in mtDNA from parent to offspring, so mtDNA has been useful in tracking ancestry through females (matrilineage).

When used in a forensic laboratory, if possible it is important that mtDNA is not solely used to establish the presence of one individual at a crime scene, because mtDNA generally does not change over generations. It can suggest a strong connection and possibility that a suspect may have been in a certain place. However, when mtDNA is used in conjunction with other forms of evidence, it can be used to positively identify a single human being (Genetics Home Reference, 2008).

Collecting Evidence: Blood

As mentioned previously, each type of evidence requires a different collection procedure. Biological fluids introduce an interesting dilemma in trying to collect them for study. Fluid evidence is often dry by the time police and investigators have arrived at the scene. It may be smeared on a wall or perhaps on an individual's clothing. As an example, let's discuss blood evidence. Blood is perhaps one of the most common clues left at a crime scene, arising in almost any kind of physical altercation. Blood is most often collected in a dried form through a variety of ways, some of which are "dry methods" and require no liquid collection medium, while others utilize liquids to return the blood to a more collectable state.

The first way to properly preserve the specimen is to cut out the item which is stained with blood if possible. If blood was spilled on a carpet for instance, the section of carpet could be cut out and carefully contained in a labeled paper or plastic envelope or bag. If the blood is simply on a smaller object, perhaps a pen or a hairbrush for example, the item can be packaged entirely and sent to the lab. Plastic bags can be used to maintain evidence for approximately two

hours before degradation of the sample compromises the sample (Farr, 2008). The advantage to packaging the evidence this way is that it minimizes interaction of the investigator with the stain, reducing possible chances for contamination prior to lab testing, and allows experts to decide on the best way to later collect the evidence from the item. The only disadvantage to this method is that bringing in large items requires more storage space. Unfortunately, there isn't enough space to keep everything from every single crime scene at full size in our labs and police stations. Also, when samples are collected from a large item such as a couch or carpet, investigators must decide which stains and controls to collect, possibly leading to less than ideal results (Farr, 2008).

Another method for collecting dry blood or fluid stains is tape lifting. Much like the name implies, the stain is at least partially lifted from the surface with tape and then attached to a piece of paper to be analyzed at a later date. This method is often preferred by law enforcement personnel because sample collection is relatively simple to perform. A benefit to this method is that the collected samples now require little space, dilution and contamination of the sample are minimized, and a negative control sample is easily collected. Unfortunately, this leads to again the problem of having to choose which samples to collect, as it would be extremely costly to tape all possible samples at a crime scene (Farr, 2008). Tape lifting is best suited for dried bloodstains on solid, nonabsorbent surfaces of immovable objects, or small dried blood splatters (Lee, 2008).

Another method for collecting dry blood samples is to scrape the sample. An investigator scrapes the sample to pull off dry pieces which are bagged and sent to the lab. Once again, the primary advantage here, as with all the dry techniques, is that the dilution and contamination potential is minimized. But this method suffers from the fact that scraping often breaks the sample into small flakes, which are difficult to handle and get lost easily. And some surfaces are

not easily scraped. As an example, let us think of a blood stain on a smooth countertop. Ideally, the blood would be scraped off the counter and into a bag, leaving the countertop virtually untouched. However, a countertop with crumbs or other food contaminants would make scraping difficult (Farr, 2008). As with tape lifting, scraping works well on solid, nonabsorbent surfaces.

The other methods of fluid collection are "wet methods" in that they utilize a collection medium to return the blood or other dried liquid to a fluid state. One way this is done is to absorb the sample onto ½ inch long threads. The stain is diluted with a medium, the best being a 70% ethanol solution or distilled water, and then absorbed by the threads. This method contains the sample onto a small area, and requires little storage space. Alternatively, the sample can be absorbed onto ½ x ½ inch cotton squares, which are slightly easier to handle than threads. This tactic is designed for dried bloodstains on large or immovable objects where stains cannot be scraped off and objects cannot be cut to size. This method, however, greatly increases the chance of degradation and contamination of the sample. Any sample collected with a liquid medium should be air dried and refrigerated (not frozen) as soon as possible. Sometimes dry ice is used at the crime scene to deep freeze the evidence to prevent degradation. The presence of water with a sample promotes the growth of bacteria which can degrade or even completely destroy a sample. Chilling the sample significantly reduces the potential for bacterial growth and protects the evidence from harm (Farr, 2008). Wet samples should never be sealed in plastic bags as this promotes bacterial growth and sample deterioration (Lee, 2008).

The "wet methods" described above can be used for the absorption of dried blood stains, but what if the stain is wet and fresh? The same rules discussed previously apply when choosing a collection method, but because sealing wet blood stains will cause contamination and

degradation, samples must air dry before testing is begun. Therefore, samples are generally packaged in paper and moved to a secure location where they may air dry (Schiro, 2008).

The last method of blood collection is not from a bloodstain, but from liquid blood itself. If blood can be collected and chilled as a liquid, this is another viable collection method. Generally two tubes, each approximately five milliliters, should be collected in vacutainers with EDTA as the anticoagulant (Lee, 2008). If liquid blood is available at a crime scene (not being collected from an individual), it should be collected with a clean (preferably sterile) syringe or disposable pipette and transferred to a clean (preferably sterile) test tube. Blood clots can also be used to collect blood samples, and can be transferred to a clean tube using a clean spatula (Lee, 2008). Figure-2 denotes the strategy for collecting blood evidence at a crime scene, moving from the methods most preferred, to those least preferred.

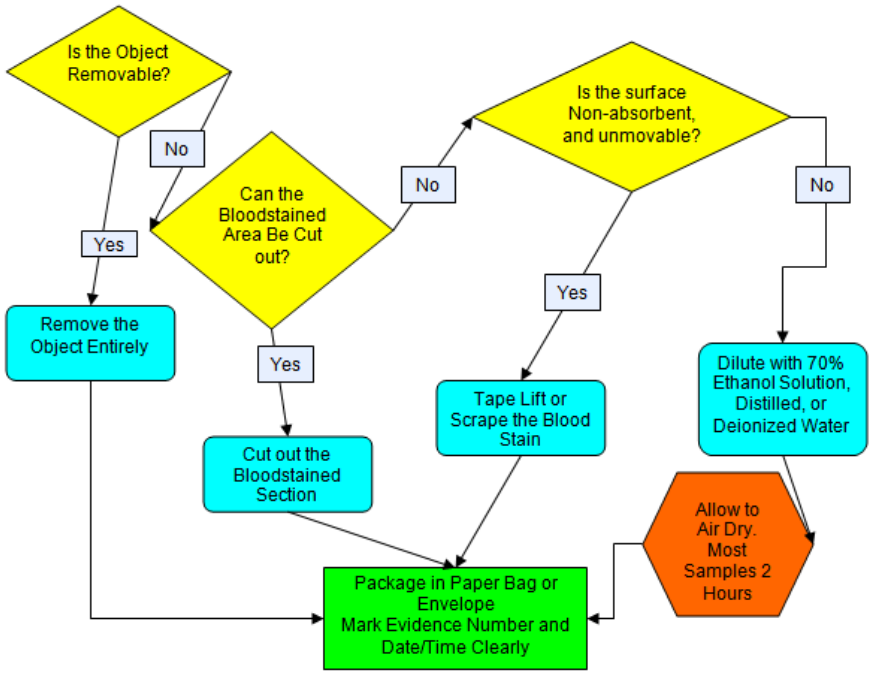

Figure 2: Blood Stain Collection Flowchart. Shown is a flowchart depicting various methods for collecting blood evidence from a crime scene. The chart moves from the most preferred method (upper left) to the least preferred method (upper right). (Drawn by IQP author).

Overall, when collecting blood evidence, preserving it in the form of dried samples is best in most every way, if a sample can be taken dry it is preferred over a wet sample, although wet samples are usually larger in volume and can be tested multiple times if needed. Dried blood stains are tested after being stained on a glass plate which can then be viewed under a microscope or other apparatus. Once this test is done, the blood cannot be reused on another slide and is hence limited to one test per slide. Keeping enough slides for sufficient testing becomes a costly and astoundingly tedious task when an investigator must accurately catalog, index, and label each and every individual slide. The main problem of dealing with wet blood is the limited time before blood cells begin to break apart. Since DNA is extracted from white blood cells within our blood, the longer blood is stored, the less chance it will be useable for any significant testing.

Collecting Evidence: Semen

Semen is generally involved in most rape cases, and can be the definitive factor in proving a suspect guilty. In the majority of cases, the presence of semen can be used as evidence if it is found on the garments of the victim, surrounding or near to their private parts, as well as in vaginal swabs collected by a doctor. In some documented cases, semen has been detected in swabs from the victim's mouth or in the anus. Semen dries rapidly on a victim's clothing, so the victim's clothing as well as the suspect's clothing need to be collected and transported to a lab for testing.

Clothing stains or swabs that have been collected are smeared on microscopic glass slides, dyed, and viewed under a microscope for the presence of sperm (Figure-3). In cases

where the male is aspermic (produces no sperm in semen) and those who are vasectomised, no sperm will be present in the semen but scientists are sometimes able to detect an abundance of an enzyme called acid phosphotase. This enzyme can be found in vaginal secretions as well, but scientists are now able to distinguish from Vaginal Acid Phosphotase (VAP) from Seminal Acid Phosphotase (SAP) by performing isoelectric focusing techniques which can separate both enzymes. This technique is a type of zone electrophoresis (similar to the gel electrophoresis mentioned in chapter one) that relies on a molecule's charge changing with the pH of its surroundings (Figure-4). This technique is especially useful for separating two proteins of equal sizes but containing different amino acid compositions (isoforms). Because sperm and vaginal acid phosphotase are of equal size, they would migrate as one band on normal electrophoresis, but they migrate differently on isoelectric gels.

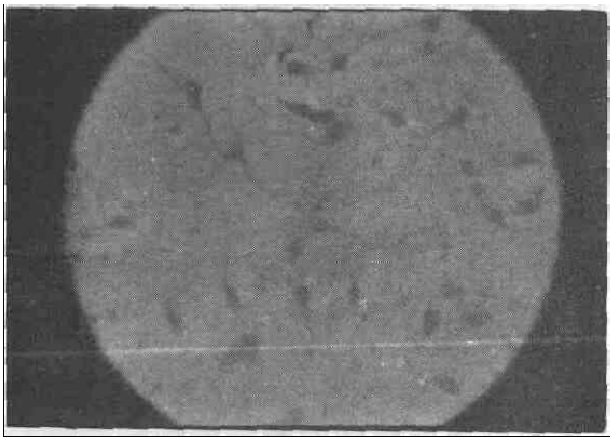

Figure-3: Photograph of Human Spermatozoa. Example of desired findings under a microscopic view for semen. (Importance of Blood…2008).

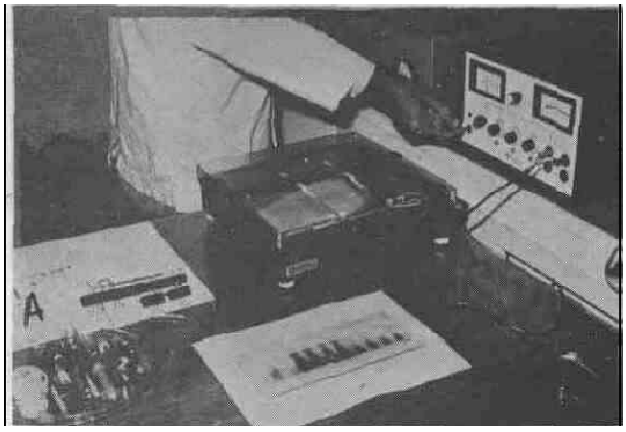

Figure-4: Photograph of Isoelectric Focusing Equipment. This technique is similar to gel electrophoresis, but in this case the process separates vaginal from sperm acid phosphotases (Importance of …2008).

Collecting Evidence: Saliva

Another common source of DNA is saliva. Saliva can also be used to prove or disprove a hypothesis based on its location. For example, a suicide by someone who hangs themselves potentially has their saliva fall onto their body and clothes, so the sample collection would contain cells from the individual's salivary glands. However, a body murdered by someone who places a dead body in a noose to make it look like a suicide would not likely contain salivary cells from the deceased.

Saliva is collected from a variety of places where other evidence is unlikely to be found. Any object which touches the mouth will most likely hold saliva useable for testing, including cigarette butts, ski masks, and even areas where the criminal may have been very close too, like a door lock. The presence of saliva is detected through the use of iodine. Because of an enzyme called amylase occurs in saliva, a light brown color will appear when a saliva sample is treated with one or two drops of iodine. Since saliva is generally deposited onto an object like other body fluids, it follows similar collection methods as blood (Importance of Blood…2008). Both chromosomal DNA and mtDNA can be analyzed from cells found in cheek swabs and other sources of saliva.

Collecting Evidence: Hair

Hair is often found at a crime scene due to the simple fact that we are likely to lose hair everywhere we go. Hair can be used to determine many different factors including what species it came from, how it was lost (Figure-5), if and how it was cut, where it is from on the body, and race. In some cases, hair may also provide clues to age and sex. Determining the nature of how the hair was lost is one of the first steps. Naturally-shed hairs appear normal and undamaged

(left photo) while forcibly removed hairs (center and right) will exhibit stretching and damage to the root area, perhaps even pulling some tissue attached (Deedrick, 2000).

Figure-5: Photographs of Human Hair Removed from the Scalp By Different Methods. Notice the difference in the root (that portion containing DNA) after each kind of removal (Deedrick, 2000).

Hairs can vary widely in size, shape, thickness, and color, making it easy to distinguish between different species. Hairs will also display characteristics as to how they have been treated. Cut hairs will appear with flat edges, split hair will appear as if broken, and hair cut with a razor will have sharp pointy edges. It will also exhibit different characteristics for where it was grown on the body. Hair from the head will look different from pubic hair and both will look different from hair grown on the chest. Race is one of the more powerful conclusions from hair examination (Figure-6). In general there are three main categories of hair, Caucasoid (European), Mongoloid (Asian), and Negroid (African). Each exhibits different combinations of coarseness, color, shape, and size.

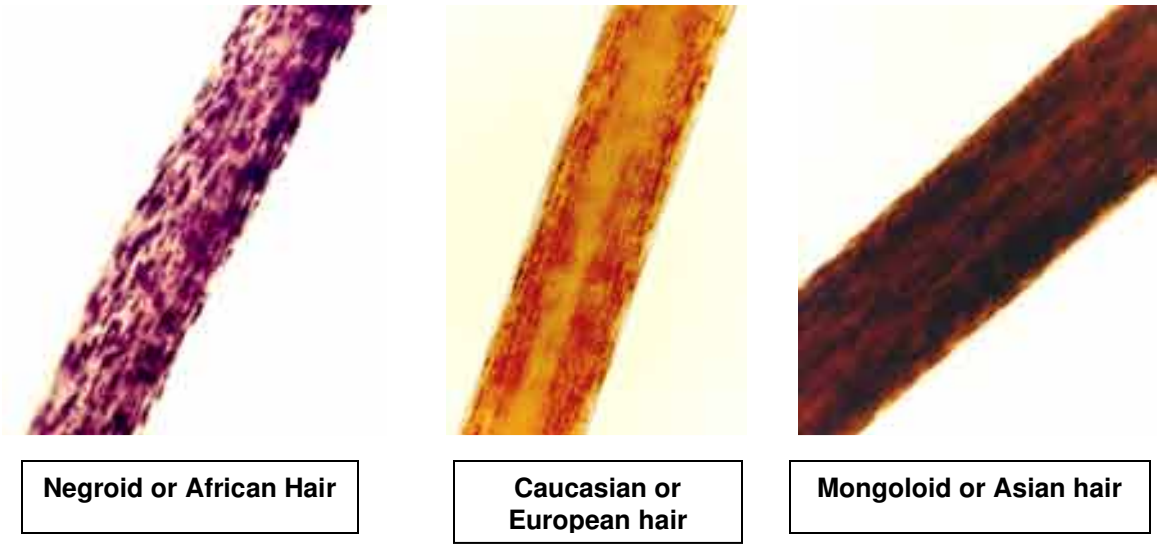

Figure-6: Race Determination From Human Hair. Hair can be used to distinguish race due to several distinct characteristics (Deedrick, 2000).

Hair is also unique in the matter which it can be tested. While body fluids contain cells which can be tested for both types of DNA, hair cannot always be tested for both. For chromosomal DNA, the root of the hair must be obtained (generally attached). Mitochondrion DNA requires that the sample be simply the hair itself, often referred to as the "shaft" of the hair. Retrieving the mtDNA from the shaft however is generally difficult and costly, usually requiring the aid of specialty labs which specialize in removing DNA samples from unusual objects (postage stamps, envelopes, ancient artifacts, etc) (Duerinck, 2008).

Chapter-2 Bibliography

Byrd, Mike (2000) *Duty Description for the Crime Scene Investigator.* http://www.crime-scene-investigator.net/dutydescription.html

Deedrick, Douglas W. (2000) *Hairs, Fibers, Crime, and Evidence. FORENSIC SCIENCE COMMUNICATIONS, JULY 2000.* *http://www.fbi.gov/hq/lab/fsc/backissu/july2000/deedric1.htm*

Duerinck, Kevin F. (2008) *Archiving Your Family's DNA*. January 2008. http://www.duerinck.com/archvdna.html

Farr, Lum (2008) *Biological Fluid Stain Evidence: Blood and Semen.* http://americancrimeschool.com/docs/blood_spatter_ppt/

Genetic Home Reference: Mitochondrial DNA. August, 2008. http://ghr.nlm.nih.gov/chromosome=MT

Importance of Blood, Semen, and Saliva in Criminal Cases. Training Manual on Forensic Science for Police Officers. http://bprd.gov.in/writereaddata/linkimages/127312420936.pdf

Lee, Dr. Henry C. (2008) *Collection and Preservation of DNA Evidence***.** http://www.promega.com/geneticidproc/ussymp7proc/0704.html

Schiro, George (2008) *Collection and Preservation of Blood Evidence from Crime Scenes.* *http://www.crime-scene-investigator.net/blood.html*

What Every Law Enforcement Officer Should Know About DNA Evidence September 1999 http://www.ncjrs.gov/nij/DNAbro/what.html

Chapter 3: Landmark DNA Court Cases

In the discussion of DNA and its admissibility in the courtroom, it is necessary to look at a brief history of how complex technology is accepted into U.S. courts even when jury members may not fully comprehend the technology. This topic involves a determination of whether the technology is generally accepted by experts, and whether it was performed properly in each case. If a technology or scientific discovery is so new that no one knows it exists, or its techniques are so complex laypersons cannot understand it, how can it be admissible in a court of law? The initial cases discussed in this Chapter may not necessarily involve DNA, but directly relate to the acceptance of technical information in general. In this chapter, we will look at a variety of landmark court cases that helped set legal precedence for the admission of DNA in the court system.

1923, Frye v United States

In Frye v United States, James Alphonso Frye (Figure-1) was convicted of murder in the second degree for allegedly killing a doctor. Frye initially admitted to the murder, but afterwards retracted his confession.

Figure-1: Photograph of James Frye and His Attorneys. In 1922 a trial judge in Washington, DC refused to let defense attorney **Marston** (seated, right) testify that his test had exonerated James Alphonso Frye (center) who had retracted a confession of murder, because the technology was not generally accepted in the scientific community. Following this precedent, lie detector evidence has been largely excluded from criminal trials to the present day, although its use has been indirectly allowed in criminal investigations and other settings.

During the trial, the defense wanted to introduce evidence that Frye had passed a recently invented test called a 'lie detector' or 'polygraph' that was then termed a "systolic blood pressure deception test". As the court records indicated:

> "It is asserted that blood pressure is influenced by change in the emotions of the witness, and that systolic blood pressure rises are brought about by nervous impulses sent to the sympathetic branch of the autonomic nervous system. Scientific experiments, it is claimed, have demonstrated that fear, rage, and pain always produce a rise of systolic blood pressure, and that conscious deception or falsehood, concealment of facts, or guilt of crime, accompanied by fear of detection when the person is under examination, raises the systolic blood pressure in a curve, which corresponds exactly to the struggle going on in the subject's mind, between fear and attempted control of that fear, as the examination touches the vital points in respect of which he is attempting to deceive the examiner (Frye v. United States, 1923)."

The defense stated that this new test had been performed on Frye, and that they could produce an expert witness as to the validity of the results obtained which would prove his innocence. However, the appellate court determined that this "deception test" had not gained a general acceptance in its field, and so did not allow the new unproven technology in court, and sustained the original guilty verdict, stating in a now famous passage:

> "Just when a scientific principal or discovery crosses the line between the experimental and demonstrable stages is difficult to define. Somewhere in this twilight zone, the evidential force of the principle must be recognized, and while courts will go a long way in admitting expert testimony deduced from a well-recognized scientific principle or discovery, the thing from which the deduction is made must be sufficiently established to have gained general acceptance in the particular field in which it belongs (Frye v. United States, 1923)."

To this date, "lie detector tests" still have not gained general acceptance in the scientific community, and the U.S. still does not allow this evidence in court. Unfortunately for the world of new technology the Frye Standard of *general acceptance* was born. Rewritten, the scientific principal or discovery must gain *general acceptance* before that evidence can be admitted before

a court. By the 1970's, forty-five states had adopted this common-law standard for the admission of novel scientific evidence (The Gale Group, 1998). But the problem with the Frye standard was that it was difficult to achieve. There was no clarification of what "general acceptance" meant, or how the "relevant scientific field" should be determined (Patton, 1990).

1975, Federal Rules of Evidence 702 (Rule 702)

In an attempt to make the Frye Standard of general acceptance less stringent, in 1975 Congress enacted the Federal Rules of Evidence (Patton, 1990). Federal Rules of Evidence, Article VII (Opinions And Expert Testimony), Rule 702 (Testimony by Experts) relaxes, a bit, the Frye Standard by allowing a little more leniency to the definition of what is termed general acceptance. The rule states:

> "If scientific, technical, or other specialized knowledge will assist the trier of fact to understand the evidence or to determine a fact in issue, a witness qualified as an expert by knowledge, skill, experience, training, or education, may testify thereto in the form of an opinion or otherwise, if (1) the testimony is based upon sufficient facts or data, (2) the testimony is the product of reliable principles and methods, and (3) the witness has applied the principles and methods reliably to the facts of the case (Federal Rules of Evidence, Article VII, Rule 702)."

In layman's terms, if the testimony would benefit the jury in understanding the technical aspects of presented evidence, it would be allowed, provided it met with the three stated conditions (described above) of Rule 702. The rules of evidence set a new definition that essentially allowed all *relevant evidence* to be admitted (Federal Rules of Evidence 402, 1975), it suggested balancing the ability of the evidence to prove a fact versus its potential to confuse a jury (Federal Rules of Evidence 403, 1975), and it set new guidelines for allowing expert testimony that must be based on sufficient facts, based on *reliable principles*, and the methods have been applied reliably to this case (Federal Rules of Evidence 702, 1975). The new standard

was considered more lenient since a method could be proved reliable without necessarily being generally acceptable.

1985, Downing v United States

Defendant, John W. Downing was indicted for mail fraud, wire fraud and transportation of stolen property. Downing was accused as being the mastermind behind a ploy to defraud vendors under the auspices of the Universal League of Clergy seeking to buy products. Downing and his co-conspirators set up factitious trade and bank references, and associated addresses. Upon request for references from a vendor, the ULC would mail out credit statements to the companies. Once the credit reports were received, the ULC would purchase product from the vendors and promptly sell them elsewhere. The ULC would then dissolve the created factitious companies as quickly as they were created, and disappear making it impossible for the vendors to recover the costs of products purchased using credit.

> "The central issue at the trial was the identification of [the] appellant as Reverend Claymore. [Co-conspirators] Silva and Piazza admitted setting up the U.L.C., but denied knowing that the suppliers were going to be defrauded. They asserted that they were innocent dupes of Reverend Claymore, who masterminded the entire scheme. They (along with the appellant) further asserted that the appellant was not Claymore, and that if the government could only find the real Claymore, their innocence would be proved.
>
> The government's case against the appellant consisted primarily of the testimony of twelve eyewitnesses who, with varying degrees of confidence, testified that the appellant was the man they knew as Reverend Claymore. These witnesses testified on the basis of their *personal observations* of Reverend Claymore for periods ranging from 5 to 45 minutes during the course of business dealings that later were discovered to be fraudulent. The appellant contended at trial that these eyewitnesses were mistaken and that their testimony was unreliable because of the short period of time in which the witnesses had to view Claymore, the innocuous circumstances of their meetings with him, and the substantial lapse of time between the meetings and the subsequent identifications (United States v Downing, 1985)".

The defense wanted to bring in an expert witness that would testify to the ability of a person to remember details in a stressful situation, and that the duration of time that the defendant was with each witness in the guise of Reverend Claymore was not significant enough to prove that the appellant and Claymore were the same person. But the court denied an expert witness on the grounds that it was the jury's task to define whether an eyewitness was credible or not. Downing was convicted on all charges leveled against him, expect for the transportation of stolen goods.

In an appeal, Downing's lawyers attempted to show that by not allowing the expert witness to testify, it was erroneous and harmful to his case. They would be able to show "(1) the "forgetting curve," i.e., the fact that memory does not diminish at a uniform rate; (2) the fact that, contrary to common understanding, stress causes inaccuracy of perception and distorts one's subsequent recall; (3) the "assimilation factor," which indicates that witnesses frequently incorporate into their identifications inaccurate information gathered after the event and confuse it with the event; (4) the "feedback factor," which indicates that where identification witnesses discuss the case with each other they can unconsciously reinforce their individual identifications; and (5) the fact that studies demonstrate the absence of a relationship between the confidence a witness has in his or her identification and the actual accuracy of that identification (United States v Downing, 1985).

> "The district court articulated two reasons for refusing to permit the appellant's expert witness to testify: (1) the witness would usurp the "function of the jury"; and (2) there was additional evidence "such as fingerprints [and] handwriting." We note at the outset, and the government concedes, that the court was in error as to the second ground: no fingerprint or handwriting evidence was offered against appellant; rather, the government's case rested almost exclusively on the eyewitness identifications (United States v Downing, 1985)".

The appeal failed since the expert witness was still denied, and the original guilty verdict was upheld. This case was deemed a landmark because it established that evidence submitted to a case must be *relevant*, and not overwhelm or confuse a jury.

1986, Colin Pitchfork

Colin Pitchfork (Figure-2) was the first person *convicted* of murder with the use of DNA. Lynda Mann and Dawn Ashworth, 1983 and 1986 respectively, were sexually assaulted and killed. Semen samples were taken from both victims.

Figure-2: Photograph of Colin Pitchfork. This person in England was the first person convicted of murder using DNA evidence. [After giving a blood sample] his [DNA] proved to be identical with that of the rapist. But by the time this was confirmed, Pitchfork had already admitted both murders. (Wilson, 2003)

Using a newly developed technique created by Dr. Alec Jeffreys of Leicester University (Figure-3), along with Dr. Peter Gill and Dr. Dave Werrett, a DNA profile was created from the DNA isolated from the semen samples. Gill commented:

> I was responsible for developing all of the DNA extraction techniques and demonstrating that it was possible after all to obtain DNA profiles from old stains. The biggest achievement was developing the preferential extraction method to separate sperm from vaginal cells – without this method it would have been difficult to use DNA in rape cases" (Forensic Science Service, 2008).

Richard Buckland, a local boy, was initially charged with the murder, and confessed to the death of Ashworth during questioning. However, it was subsequently found that Buckland's

DNA did not match either of the murder scene profiles, so in a twist of fate, Buckland was exonerated of the crime becoming the first person to have been proved innocent using DNA.

Figure-3: Photograph of Dr. Alec Jeffreys. **"**The founder of DNA fingerprinting… first made his world-changing discovery by separating strands of DNA into different sizes and showing them as bands on a photograph. What first seemed to him to be 'a complicated mess' has now become invaluable for police investigation University of Huddersfield 2008)".

Starting from scratch, general blood typing was conducted on male members between certain ages in the three surrounding towns where the bodies were found. The crime scene blood type matched 10% of the male population in the area, so those 10% (about 5000 men) were then further profiled using Dr. Jeffrey's technique. A local baker, Pitchfork had conned a coworker, Ian Kelly to take the test in his stead keeping his DNA out of the pool. He would have gotten away with the murder had his loose lipped coworker not talked about the switch in a local pub. The conversation was overheard, and the authorities were alerted. Colin Pitchfork was subsequently apprehended. Pitchfork was previously known to the authorities for having been convicted in the past for flashing. He immediately confessed. Subsequently his DNA was tested, and was found to match the evidence from both murder victims. Although his case did not actually go to trial due to his confession, he is usually credited with being the first DNA based murder conviction. Colin received a life prison sentence for both murders in 1988.

1988, Andrews v Florida

Tommie Lee Andrews was the first person to be convicted in the United States using DNA evidence (Genetic Fingerprinting, 2008). "At a pre-trial hearing, the judge agreed that the

DNA evidence was admissible (Wilson, 2003), so on October 27, 1987 Andrews stood trial on charges of burglary, aggravated burglary, and rape when his DNA was matched to the samples that were found at the original crime scene February 22, 1987.

During this first trial, the prosecutor had to convince the jury that DNA evidence technology was reliable and trustworthy. Unfortunately, when he was challenged to back up his assertion that there was a one in ten billion chance that Andrews was wrongly accused, not having the complete facts, the jury was split and the judge issued a mistrial.

When Andrews was tried on a second count of rape, the prosecution had his statistics in order, and also had two fingerprints found at the crime scene as evidence that proved to belong to him. Andrews was convicted and served a twenty-two year prison sentence for the crime. "At that time, no state had a DNA databank. However, after witnessing the power of DNA evidence, state courts and state legislatures would soon grapple one year later with the issue of whether DNA evidence should be admitted at trial as identity evidence, and whether establishing state DNA databanks would be feasible and of value to law enforcement (Wake Forest Law Review, Fall 1999)".

Andrews was retried in February 1988 for the first count of rape (originally a mistrial), and this time the jury convicted him, and he received an additional 78 year sentence for rape, 22 years for burglary, and 15 years for battery, bringing his total sentence to over 100 years (Wilson, 2003).

1989, People v. Castro

This was the "first case to seriously challenge a DNA profile's admissibility (NCJRS, 2008)". Joseph Castro was accused of two counts of second-degree murder. The people of New

York wanted to show DNA evidence in the case to prove that blood stains on the defendant's watch belonged to the victim and not to Castro which would prove his guilt.

The court, in the most critical assessment of DNA analysis performed to that date, developed a so-called three prong test for DNA evidence: 1) is there a generally accepted scientific theory arguing that DNA sequences differ between individuals and that difference can be tested, 2) is there a reliable technology that can be performed to detect these DNA differences, 3) was that DNA technology applied correctly in this particular case. Following the application of the three prong test for admissibility of DNA evidence with the Castro evidence, the court concluded it failed prong three, and the testing was not performed correctly in this case. Under prong three, "A scientist may have no trouble accepting the general proposition that DNA typing can be done reliably, yet still have doubts about the reliability of the test being performed by a particular laboratory (Thompson and Ford, 1989)". "After the Castro pretrial hearing, the DNA evidence was deemed inadmissible, as a matter of law. [The defense (Figure-4) asserted that] [t]he testing laboratory failed in several major respects to use the generally accepted scientific techniques and experiments for obtaining reliable results, within a reasonable degree of scientific certainty (People v. Castro, 1989)". Specifically the Lifecodes laboratory was criticized because:

1. The test failed "due to contamination of the probe or the control lane.
2. The testing laboratory failed to conduct further testing.
3. The testing lab's error of 6 standard deviations from the mean is "scientifically unacceptable".

Following this trial, it was determined that some sort of STANDARD needed to be in place for DNA testing, so the FBI created the now famous "Technical Working Group on DNA Analysis Methods" (TWGDAM) to establish universal procedures for testing DNA.

Figure – 4: **Photograph of Castro Defense Attorneys Scheck and Neufeld.** Scheck and Neufeld challenged the quality of Lifecodes' laboratory work, arguing that the lack of national standards for forensic DNA testing methodology made the value of such evidence dubious at best. (Forensic DNA Controversy 5, 2008)

On the defense: *Barry Scheck (left) and Peter Neufeld were concerned about the reliability of DNA typing evidence.*

1991, People v. Miles

In this landmark case, the defendant Reggie Miles had been convicted of twelve counts of criminal conduct stemming from an incident where he had broken into a house and sexually assaulted the victim. He was originally sentenced to 120 years incarceration, and the court imposed consecutive and extended prison sentences.

In his appeal, Miles challenged some of the aspects of the case. In particular, Miles challenged the admission of DNA evidence, the effectiveness of his counsel, incorrect jury instructions, and the imposition of consecutive and extended sentences. After consideration, the DNA was admitted as evidence since DNA testing met the Frye test. The second part of the DNA challenge was based on prong three as described in 1989, People v. Castro. The defense tried to discredit the company Cellmark for their testing methodology, and cited cases where data from Cellmark were not admitted due to inconstancies in testing methodology.

It was shown however, that Foreman – a scientist for Cellmark – did indeed follow the correct methodology and in particular the new TWIGDAM (Technical Working Group – Interagency Working Group of DNA Methodology) guidelines, promulgated by the FBI. Having proved that Cellmark had properly maintained, tested, transported, and documented the DNA evidence correctly, the court rejected the defendant's challenges to the admission of the DNA

evidence (The People v. Miles, 1991), so the DNA evidence was allowed, and the original guilty verdict stood. This case switched the tide back in favor of using DNA fingerprinting.

Chapter-3 Bibliography

Adler, Ken "The Lie Detectors". Retrieved July 10, 2008.
(http://www.kenalder.com/liedetectors/law.htm)

Federal Rules of Evidence (1975) **Rule 702**, Pub. L. 93-595, § 702, Jan. 2, 1975, 88 Stat. 1926.

Federal Rules of Evidence (1975a) **Rule 401**, Pub. L. 93-595, § 401, Jan. 2, 1975, 88 Stat. 1926.

Federal Rules of Evidence (1975b) **Rule 402**, Pub. L. 93-595, § 402, Jan. 2, 1975, 88 Stat. 1926.

Federal Rules of Evidence (1975c) **Rule 403**, Pub. L. 93-595, § 403, Jan. 2, 1975, 88 Stat. 1926.

Federal Rules of Evidence (1975d) **Rule 702**, Pub. L. 93-595, § 702, Jan. 2, 1975, 88 Stat. 1926.

Forensic Science Service. Retrieved July 19, 2008.
(http://www.forensic.gov.uk/forensic_t/inside/news/list_casefiles.php?case=1)

Forensic DNA Controversy 5. Retrieved August 18, 2008.
(http://www.geo.umn.edu/scitech/courses/HSci3333/AV/FDNAcontro5.htm)

Frye v. United States (1923) Supreme Court of Appeals of District of Columbia, 293 F. 1013; 1923 U.S. App. LEXIS 1712; 54 App. D.C. 46; 34. A.L.R. 145, December 3, 1923, Decided. Retrieved July 10, 2008.
(http://www.patrickcrusade.com/FRYE_V_US.html)
(http://www.law.harvard.edu/publications/evidenceiii/cases/frye.htm)

Genetic Fingerprinting. Retrieved August 12, 2008
(http://en.wikipedia.org/wiki/Genetic_fingerprinting)

Lake Forest Law Review (Fall 1999) "DNA Databanks: Law Enforcements Greatest Surveillance Tool?", Volume 34, Fall (1999)

NCJRS: National Criminal Justice Reference Service. Retrieved August 19, 2008
(http://www.ncjrs.gov/spotlight/forensic/legislation.html)

Patton, Stephen M. (1990) "DNA Fingerprinting: The Castro Case." *Harvard Journal of Law and Technology*. Volume 3. Spring Issue (1990) pp. 223-240.
(http://jolt.law.harvard.edu/articles/pdf/v03/03HarvJLTech223.pdf)

The Gale Group (1998) “DNA Evidence." *West's Encyclopedia of American Law*. (http://www.answers.com/topic/dna-evidence-1)

The People of the State of Illinois v. Reggie E. Miles, Defendant
Appellate Court of Illinois, Fourth District
217 Ill. App. 3d 393; 577 N.E.2d 477; 1991 Ill. App.

The People of the State of New York, Plaintiff, v. Joseph Castro (1989), Defendant
Supreme Court of New York, Bronx County.
545 N.Y.S.2d 985; 1989 N.Y. Retrieved August 20, 2008 from LexisNexis®

Thompson and Ford (1989) “DNA Typing: Acceptance and Weight of the New Genetic Identification Tests.” 75 Va L Rev 45, pp. 57-58.

United States v. Downing (1985) Retrieved July 17, 2008.
http://www.altlaw.org/v1/cases/542949

University of Huddersfield (April 2008). Retrieved August 19, 2008.
(http://www.hud.ak.uk/news/hudd-lines/news_stories/08_04_stories/04_alec_jeffreys.html)

Wake Forest Law Review Association, Inc. Wake Forest Law Review Database (1999) “The Use of Genetic Testing in the Courtroom” Retrieved August 15, 2008 via LexisNexis® Academic.

Wilson, Colin (2003) “Written in Blood: A History of Forensic Detection”. November 16, 2003 pp. 306 and pp 307.

Chapter 4: Sensational DNA Cases

At this point, after reading the previous chapters, you may be able to answer such questions as: What exactly is DNA? How can it be analyzed and used in forensic settings? Is DNA testing technology reliable? How does one accept complex technical information in U.S. courts? Unfortunately, much of this information is not realized by the general public, so the purpose of this chapter is to remind the lay reader of key sensational court cases they likely are already familiar with, but to remind them of the role DNA evidence played, as another way to demonstrate the power of this new technology.

With the mystery that lies behind these mysterious twisted chemical strands, we face this question: Can DNA evidence be used in a court of law? How do we punish or liberate someone of an offense by a means that we can not justify? Many people have heard of Watson and Crick, and most likely even fewer would be able to recall what the acronym "D-N-A" stands for. Very few understand anything beyond the very simplistic principles of DNA genetics, which with a little understanding could change pubic acceptance of this complex discovery from 1953. Despite controversies regarding the ethical issues of DNA fingerprinting (to be discussed in Chapter-5), it has proven to be an unbelievably helpful tool in the world of forensic science. An examination of sensational DNA cases will serve as a powerful reminder of why DNA fingerprinting is necessary and helpful in the US court of law.

The Boston Strangler

One example of a case very widely known by the public is the case of the Boston Strangler. A series of strangulations occurred in the Boston area in the early 1960's, and eventually Albert DeSalvo (Figure-1) was arrested who later admitted to being the strangler. But many in the law enforcement community were not convinced he was the true strangler, and recent DNA evidence from his latest victim did not match DeSalvo.

Figure-1: Photo of Albert DeSalvo. This man admitted to being the Boston Strangler, but not everyone in law enforcement is convinced he was the strangler (Bardsely, Crime Library).

Albert DeSalvo was previously known to police as "the measuring man." DeSalvo would pose as a talent scout looking for new models to join his agency. He would proceed by knocking on a door, introducing himself, and saying that the individual's name was given to him recommending them as a model. He would take their measurements and vital signs, sneaking a hands on touch whenever possible (Fisher, 2003). Some reports were made to police by women who felt uncomfortable.

On March 17th, 1960, Cambridge police arrested DeSalvo on suspicions of burglary. After being arrested, he confessed to being the "measuring man." He served two years in prison followed by eleven months probation. After this, DeSalvo began another phase, "Green man." The name came from the green clothes he wore. This phase consisted of brutal sexual assaults. Police estimate that he committed sexual assaults against 300 people, while DeSalvo claims the number is closer to 2,000 (Fisher, 2003).

As New England police searched for the "Green Man," Boston homicide detectives were on the hunt for a baffling killer responsible for eleven rape murders from 1962 to 1964. The chain of eleven unsolved murders preceded as follows, each with its own sickening twist but with linked details that were strangely unique. Most included sexual assault, sometimes with a foreign object and strangulation with an object of clothing from each woman.

On June 14th, 1962, Anna Slesers (age 55) was found sexually molested and strangled with a cord from her bathrobe. Strangulation with a nylon stocking killed Nina Nicols (age 68) on June 30th, 1962. The same day, Helen Blake (65) was found sexually molested and strangled with her nylons. Ida Irga (age 75) was found on August 21st, 1962, sexually assaulted and strangled, and was ornamented with a knotted pillowcase. Jane Sullivan (age 67) was found drooping over her bathroom tub with her head submerged, on August 30th, 1962, a week after being sexually assaulted and strangled with nylons.

Up until this point, known as phase one of the strangler cases, the Boston Strangler was thought to only target elderly women. It was thought that he was attacking all of these women out of hatred for his own mother. This *modus operandi* altered on December 5th 1962 with the strangulation of Sophie Clark, age 19. The murders did not stop there. Following were Patricia Bissette (age 23), sexually and strangled with nylon stockings. On March 10th, 1963, Beverly

Samans (age 23) was found with twenty-two bash marks from a knife. This was the first time a knife was used. Sexually assaulted and strangled with nylons, Evelyn Corbin (age 58) was killed on September 6th, 1963. On November 23rd, 1963, Joann Graff (age 23) was found sexually assaulted and strangled with imprints of the perpetrator's teeth left on her breast. Lastly, Mary Sullivan (age 19) was found sexually assaulted and strangled with stockings on January 4th, 1964, a year and a half after the first associated murder. These assaults and murders completed phase two of the Boston Strangler cases. A clear motive was not traced. With the huge alarm instilled in the public from the unidentified killer, extra precautions were taken by single women in the Boston area, but coincidently enough, there were no signs of forced entry in any of the thirteen murders.

On October 27th, 1964, a falsely identified detective entered a women's home and tied her to a bed, sexually assaulting her. Suddenly, the stranger proclaimed, "I'm Sorry," and left the house. The description from the assaulted woman led to the arrest of Albert DeSalvo. Despite his history of crime, rape, and abuse, he was not suspected to be involved with the cases linked to the Boston Strangler. However, this situation suddenly changed when DeSalvo was brought up on rape charges, he jumped to confess, in great detail, to these eleven unsolved mysteries as well as two additional assaults and murders. Added to the previously described eleven murders were those of Mary Sullivan and Mary Brown: Mary Mullen (age 85) was found on June 28th, 1962, dead from a heart attack, but later the murderer confessed to strangling her until death. Mary Brown (age 69) was found beaten and stabbed on March 9th, 1963.

The ironic thing was that DeSalvo was found guilty without a single piece of physical evidence. For example, the bite marks did not match DeSalvo's. In a court system founded on the principles of innocence until proven guilty, how could this be? Some claim DeSalvo was

covering up for someone else, or perhaps that he wanted to be sent to a mental institute with thoughts that he was insane, rather than spending life in prison. In the end, it turns out that despite the confession, there was more evidence to prove DeSalvo more innocent of these strangler crimes than guilty. To start off with, there were so many different trends displayed in the sting of assaults and murders, specialists argue that it could not be the work of a single person. Robert Ressler, former profiler for the FBI and criminologist stated, "*You're putting together so many different patterns here that it's inconceivable behaviorally that all these could fit one individual."* (Wuebben, 2001).

Additionally DeSalvo confessed to thirteen murders when the Boston Strangler had only been accused of eleven. He confessed to killing Mary Sullivan with his bare hands, but tests showed that she was strangled with stockings and scarves. James Starrs, forensic expert, reexamined the body of Mary Sullivan through an autopsy, and found that the hyoid bone in her neck was not broken, which most likely would have been if she was strangled. In addition, Casey Sherman, the nephew of Mary Sullivan, one of the Boston Strangler's victims, tried to piece together all of the evidence years after his aunt's death. What he found was astonishing to him:

> "*I wanted to prove that DeSalvo did do it, and at least have some kind of closure. Once I peeled back the onion, I realized this guy didn't do it. The only thing connected to DeSalvo was his confessions and not a shred of physical evidence. He was simply confessing to events that never happened*." (Burns, 2006)

When Sherman looked back at the murder, what he found conflicted with DeSalvo's confession. The prime suspect in the killing of Mary Sullivan (not DeSalvo) said at the time of her death, he was watching football on television with his grandfather, but this turned out to be a

poor alibi when records show that there was not a single football game aired on January 4th, 1964, the day of Ms. Sullivan's murder.

With respect to DNA evidence and this famous strangler case, on October 26, 2001, DeSalvo's body was exhumed from a gravesite in Massachusetts and taken to York College Pennsylvania for autopsy and DNA analysis, led by James E. Starrs, a leading forensic scientist from George Washington University (Bardsley, 2008). Two months later, on December 13, 2001, Court TV reported that the DNA evidence taken from Mary Sullivan's remains did not match Albert DeSalvo. During a news conference, James Starrs told reporters: "We have found evidence, and the evidence does not and cannot be associated with Albert DeSalvo" (Bardsley, 2008). Although this evidence shows DeSalvo likely did not sexually assault Sullivan, it does not prove DeSalvo was not in present during the assault.

Orenthal James Simpson

The famous O.J. Simpson trial lasted a lengthy nine months. The media coverage that surrounded the trial was a huge hype, both because of O.J.'s previous role as a running back in the NFL as well as his race. Despite the overwhelming evidence that would lead most people to believe that Simpson was guilty, some on the jury only believed the evidence (including DNA in blood) was planted against him in an act of racism.

O.J. Simpson was on trial for the murders of his former wife, Nicole Brown Simpson, and her friend, Ronald Goldman. On Sunday, June 12th, 1994, a passerby found a white dog pacing in front of 875 South Bundy Drive. As the dog started to follow a trail behind the neighbor, Steven Schwab, he noticed the stomach and paws of the dog were matted with blood.

Mr. Schwab asked his neighbor, Suka Boztepe, to watch the dog, but as the dog became restless, he took him for a walk. The dog dragged him back to a dim pathway by 875 South Bundy Drive where they found a body laying motionless on the path.

The first LAPD cruiser arrived on the scene at 12:13 am (Jones, 2008). The body of Nicole Brown (Figure-2) was found face down on the back stairs of the three-story condominium, and to her right was another frozen body, that of Ronald Goldman (Figure-3). Upstairs, the two children of Nicole Brown Simpson, ages nine and six, were found fast asleep.

Figure-2: Photo of the dead body of Nicole Brown Simpson (Wagner, 1999).

Figure-3: The Body of Ron Goldman (Wagner, 1999).

O.J. and Nicole met when she was eighteen and he was thirty. Their marriage lasted seven years, but Nicole filed for divorce in 1992 on claims of abuse. Two years later, she met Ron Goldman but supposedly the two were just friends.

The most intriguing part about this infamous case is the extravagant amount of DNA evidence left at the scene. Blood from O.J, Brown, and Goldman were prevalent throughout the crime scene (Nicole's home), O.J.'s home and his bronco. O.J.'s blood was found at Nicole's condo in her walkway (Figure-4), the back gate, and in a footprint left from Goldman, in his car (specifically on the instrument panel, steering wheel, and console), in his house in the foyer and driveway, and also on the legendary glove. The blood of Nicole Brown was found pooled in the steps of her condo, on a pair of socks in O.J.'s bedroom, in the bronco (on the steering wheel, console and driver's side carpet) and also on the glove. Blood from Goldman was also found on the console in O.J.'s bronco and on the glove.

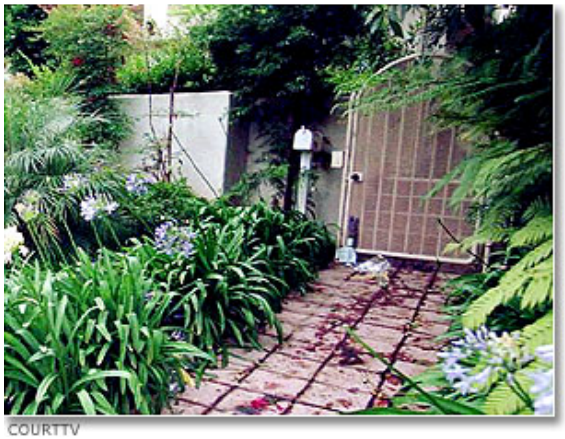

Figure-4: The Bloody Walkway of Nicole Brown's Condo. (Wagner, 1999)

Four blood drops of O.J.'s blood on the walkway to Nicole's condo, as well as one in the driveway, were the most powerful evidence against O.J. throughout the trial. DNA analysis was conducted on the blood droplets by a private lab in Maryland called Cellmark, the California Department of Justice Lab and the Los Angeles Police Department Lab. Independently, each lab concluded that blood was indeed that of O.J. Simpson. A restriction fragment length polymorphism test (discussed in Chapter-1) was conducted on one droplet that concluded that the blood in the driveway had a 1 out of 170 million match to Simpson's.

This evidence alone almost seems like enough to convict Simpson of the murders; however it was not that easy. The defense attorney tried to argue that the evidence was tampered with, or that lab procedures could have contaminated the blood samples. One criminalist testified to writing their initials on the package containing the swatches, yet no initials were found. These minor inconsistencies and general doubts about DNA testing made the DNA evidence lose its value (Wang, 2001).

The prosecution claimed that Simpson cut his hand while murdering Brown and Goldman, and left a trail of blood behind him as he proceeded to drive his bronco home. They said the blood of the victims was transferred into his car because it was on his body. They claimed he disposed of his clothing, not realizing there was blood on his socks, which he left in his bedroom. They also believe that the blood-saturated glove left behind Simpson's home was definitely his.

But the defense told a much different story. They claimed Simpson had cut his hand during the evening of the crime, and left traces of his blood as he was in his car, home, and driveway. When he later traveled to Chicago, he cut himself again by breaking a glass upon learning of the death of his ex-wife. Although the story seems unbelievable, the defense had

many other small stories that added up against the prosecution. A criminalist from the LAPD lab admitted to spilling some of Simpson's blood from a vile while working in an evidence processing room. From here it could be argued that the spilt blood could have contaminated the samples taken from the crime scene. The defense also argued that samples were mishandled because they were collected with damp swabs and then put into plastic bags and left in a hot truck for several hours. Experts agreed that DNA degrades quickly when it are contained in moist, warm environments. They agreed that this type of environment could so heavily damage the DNA that if it was contaminated with a second DNA, that of the second DNA would completely mask the original collection. With the way things were lining up, the defense's theory started to fall into place. The mix-ups did not even stop there. Blood samples were taken from Simpson the day after the crime, but the samples were never logged and were stored in an unlabeled envelope. Blood samples were missing and un-accounted for. More blood was found in some vials than marked down in log books. The mishaps went on and on. (Thompson, 2008). Overall, when the mismanagement of DNA evidence was analyzed, a clear trend of serious problems due to cross-contamination and handling procedures provided the jury with possible doubt.

In addition, LAPD detective Mark Fuhrman, the man who testified to finding blood at Simpson's home and on the gloves lost credibility due to racial remarks he had used in the past. Although denying that he ever had used the word "nigger," an audio tape was found in which Fuhrman used that word 41 times (Wikipedia, 2008). When Simpson tried on the glove everyone believed was his, it didn't fit, although the prosecution claimed the glove shrunk after being soaked with blood.

After 134 days of televised testimony, Simpson pleaded not guilty to both murders. It came to a point where the trial was the most watched program on television. It was an ongoing soap opera, and everyone awaited the verdict. The OJ case was a sprawling debate between racism, justice, and technology. Despite the prosecutions DNA laden evidence, on October 3, 1995, the jury returned a verdict of not guilty (Cable News Network, 1995). Nine months, 120 witnesses, 45,000 pages of evidence, and 1,100 exhibits later, this case came to a halt. In a subsequent 1997 civil trial, with the easier to obtain "preponderance of evidence" standard, OJ was found responsible for the two deaths.

This infamous case provided a massive warning sign to all law enforcement communities that proper training in how to handle DNA evidence to prevent degradation or contamination is critical. Samples are now clearly marked for site of retrieval and chain of custody (see Chapter-2). The case shows that even if DNA testing can be highly accurate, its mismanagement can lead to juror doubt.

Chapter-4 Bibliography

Bardsley, Marilyn. "The Boston Strangler."
Retrieved June 12, 2008.
(http://www.trutv.com/library/crime/serial_killers/notorious/boston/22.html)

Burns, Karie Sable. 1994-2006. "Albert DeSalvo - The Boston Strangler?"
Retrieved June 10, 2008 *(*http://www.karisable.com/skazdesalv.htm)

Cable News Network, 1995. "Not Guilty."
Retrieved July 1, 2008. (http://www.cnn.com/US/OJ/daily/9510/10-03/index.html)

Fisher, Mark; Fisher, Kristi, 2000. Revised 2003. "Albert DeSalvo."
Retrieved June 12, 2008. (http://carpenoctem.tv/killers/desalvo.html)

Jones, Thomas L. “O.J. Simpson.”
Retrieved June 19, 2008.
(http://www.trutv.com/library/crime/notorious_murders/famous/simpson/brentwood_2.html)

Thompson, William C. “Proving the case: The Science of DNA: DNA Evidence in the O.J. Simpson Trial. “
Retrieved on June 25, 2008.
(http://phobos.ramapo.edu/~jweiss/laws131/unit3/simpson.htm)

Wagner, Dick. 1999. “The O.J. Simpson Case.”
Retrieved July 10, 2008. (http://www.wagnerandson.com/oj/OJ.htm)

Wang, Julia. 2001. “The Blood and DNA Evidence in the O.J. Simpson Trial”
Retrieved June 25, 2008. (http://www.bxscience.edu/publications/forensics/articles/dna/r-dna02.htm)

Wikipedia, Modified 2008. “O.J. Simpson Murder Case.”
Retrieved June 30, 2008. (http://en.wikipedia.org/wiki/O.J._Simpson_murder_case)

Wuebben, Mike. 2001. “The Boston Strangler.” CBN News.
Retrieved June 13, 2008.
(http://www.cbsnews.com/stories/2001/02/14/48hours/main272108.shtml)

Chapter 5: DNA Databases

Introduction

When Dr. Alec Jeffereys created the first techniques to use DNA as a fingerprint profile for use in criminal investigations, in his wildest dreams could he have imagined how important his discovery would be to the world of forensics internationally? Would he have thought that the ground-breaking work producing DNA profiles would be indexed and store millions of profiles in databases? Would he have imagined the social and scientific impact and the ensuing debates that still rage today? In this chapter we will discuss the topic of storehouses of DNA profiles, the database. We will briefly delve into the history, current databases, the data contained in them, their uses with regards to cold hits and cross linked criminal cases, and some of the social, ethical, privacy, and security concerns brought about by their use.

Why Databases

In discussing any technology, the first question one asks is, why do we need it? A database is by definition is, *"a structured set of data held in a computer, especially one that is accessible in various ways"* (Oxford, 2008). When we discuss DNA, we have very structured data element or elements to work with. Thus we need only a computer and software package specifically designed to store that information for easy retrieval and cross reference.

Short DNA Database History

In April of 1995, in England, the Forensic Science Service (FSS) set up the world's first national intelligence DNA database (FSS,

2008). The FSS performs the day-to-day running of the National DNA Database or NDNAD. The FSS is responsible for loading the DNA profiles, and by February of 2006, over 3 million DNA profiles were entered into NDNAD (POST, 2006).

The UK utilizes a technique called SGM Plus® to create profiles for the NDNAD. These profiles contain ten STRs, plus a gender marker. Using this combination, the probability of the DNA profiles of two unrelated individuals matching is on average less than 1 in 1 billion. The discriminatory power of the analysis decreases for related individuals (POST – Box 1., 2006).

In 1997, Police Services in Australia endorsed the establishment of a national criminal DNA database. Also in 1997, Victoria Australia was the first to enact legislation to regulate the use of DNA Databases.

In 1998, the U.S. FBI set up the National DNA Index System or NDIS to enable city, county, state and federal law enforcement agencies to compare DNA profiles electronically (Crimtrac, 2008). For the purposes of this chapter, we will focus on the Combined DNA Index System or CODIS. Originally the indexes were limited to sex offender and violent criminals. Currently the FBI has indexes for Convicted Offender, Forensic, Arrestees, Missing Persons, Unidentified Human Remains and Biological Relatives of Missing Persons (FBI, 2008).

Database Profile

The information contained in a U.S. DNA fingerprint consists of 13 core STR's or Short Tandem Repeats which are generated in the laboratory. This method uses highly polymorphic regions that have short repeated sequences of DNA (the most common is 4 bases repeated, but there are other lengths in use, including 3 and 5 bases). Because different people have different

numbers of repeat units, these regions of DNA can be used to discriminate between individuals (Wikipedia, 2008).

The polymorphisms displayed at each STR region are by themselves very common, typically each polymorphism will be shared by around 5 - 20% of individuals. But when looking at multiple loci, it is the unique combination of these polymorphisms to an individual that makes this method discriminating as an identification tool. The more STR regions that are tested in an individual, the more discriminating the test becomes (Wikipedia, 2008). The information that is loaded into these systems varies from country to country. In the United States, there are 13 loci used giving the discrimination power of 1 in a quintillion.

Who, MGL Chapter 22E

Now that we know what a database is, we can now look at who contributes. By whom, we mean the data representing an individual's genetic makeup chosen by the aforementioned entities to be used for identification. Where do the samples come from that are entered into these databases? The law for who must provide samples varies from state to state. In Massachusetts, the General Laws of Massachusetts Chapter 22E spell them out plainly:

> **Section 3 Submission of DNA Sample:** Any person who is convicted of an offense that is punishable by imprisonment in the state prison and any person adjudicated a youthful offender by reason of an offense that would be punishable by imprisonment in the state prison if committed by an adult shall submit a DNA sample to the department within 1 year of such conviction or adjudication or, if incarcerated, before release from custody, whichever occurs first. The sample shall be collected by a person authorized under section 4, in accordance with regulations or procedures established by the director. The results of such sample shall become part of the state DNA database. The submission of such DNA sample shall not be stayed pending a sentence appeal, motion for new trial, appeal to an appellate court or other post conviction motion or petition.
>
> **Section 15 Expungement of Record:** Any person whose DNA record has been included in the state DNA database may apply to the superior court to have such record expunged on the grounds that the conviction or judicial determination that resulted in the inclusion of the person's DNA record in the state DNA database has been reversed and the case dismissed; provided, however, that one year shall have elapsed from the date the

> judgment reversing or dismissing the conviction became final or such person shall have obtained, in writing, authorization from the district attorney that no further prosecution is contemplated under the original offense for which such person was convicted or for which the original judicial determination was entered (MGL, 2008).

The law did get a bit of a boost when Governor Mitt Romney signed a law to expand the MA DNA database declaring "the long arm of the law just got a little longer" (Mittanica, 2003). Originally, the law only required offenders convicted of 33 sex and violent crimes to be entered. The new law mandated that all convicted felons, including those incarcerated or on parole, provide a DNA sample.

In 2003 the number of samples that were entered from Massachusetts numbered just 20,000 (Mittanica, 2003). Today there are in excess of 61,000 (as of 6/2008). In addition the law extended the time limit to submit the DNA sample from 90 days to one year. This would help in preventing a criminal to slip though legal or administrative loopholes (Mittanica, 2003).

The chart below outlines qualifying offences for each state in the union. A qualifying offence is defined as an offence that will meet the states code for obtaining that person's DNA to add to the database.

STATE DNA DATABASE LAWS
QUALIFYING OFFENSES
(As of August 2008)

	FELONY CONVICTIONS					MISDEMEANOR CONVICTIONS			ARRESTS			
STATE	All Convicted Felons	Juvenile Adjudications	Jail & Community Sentences	Retroactive Jail & Prison	Retroactive Probation & Parole	Certain Misde - meanors	Numerous Misde - Meanors	All Misde - meanors	Murder Arrestees	Sex Crimes Arressts	Burglary Arrests	All Felony Arrrests
ALABAMA	✓	✓	✓	✓	✓	✓						
ALASKA	✓	✓	✓	✓	✓	✓			✓	✓		
ARIZONA	✓	✓	✓	✓	✓	✓			✓	✓	✓	
ARKANSAS	✓		✓	✓		✓						
CALIFORNIA	✓	✓	✓	✓	✓	✓			✓	✓	✓*	✓*
COLORADO	✓	✓	✓	✓	✓	✓						
CONNECTICUT	✓		✓	✓	✓	✓						
DELAWARE	✓		✓			✓						
FLORIDA	✓	✓	✓	✓	✓	✓						
GEORGIA	✓	✓	✓			✓						
HAWAII	✓		✓	✓	✓	✓						
IDAHO			✓	✓	✓							
ILLINOIS	✓	✓	✓	✓		✓						
INDIANA	✓		✓	✓								
IOWA	✓	✓	✓	✓	✓	✓						
KANSAS	✓	✓	✓	✓	✓	✓			✓	✓	✓*	✓*
KENTUCKY	✓	✓	✓	✓	✓							
LOUISIANA	✓	✓	✓	✓		✓			✓	✓	✓	✓
MAINE		✓	✓	✓								
MARYLAND	✓		✓	✓		✓			✓	✓	✓	
MASSACHUSETTS	✓	✓	✓	✓	✓							
MICHIGAN	✓	✓	✓	✓		✓						
MINNESOTA	✓	✓	✓	✓		✓			✓	✓	✓	
MISSISSIPPI	✓		✓	✓								
MISSOURI	✓		✓	✓	✓	✓						

	FELONY CONVICTIONS					MISDEMEANOR CONVICTIONS			ARRESTS			
STATE	All Convicted Felons	Juvenile Adjudications	Jail & Community Sentences	Retroactiv e Jail & Prison	Retroactive Probation & Parole	Certain Misde - meanors	Numerous Misde - Meanors	All Misde - meanors	Murder Arrestees	Sex Crimes Arressts	Burglary Arrests	All Felony Arrrests
MONTANA	✓	✓	✓									
NEBRASKA			✓									
NEVADA	✓		✓			✓						
NEW HAMPSHIRE		✓	✓	✓	✓							
NEW JERSEY	✓	✓	✓	✓	✓	✓	✓					
NEW MEXICO	✓	✓	✓	✓	✓				✓	✓	✓	
NEW YORK	✓		✓	✓	✓	✓	✓					
NORTH CAROLINA	✓		✓	✓		✓						
NORTH DAKOTA	✓		✓	✓					✓*	✓*	✓*	✓*
OHIO	✓	✓	✓	✓	✓	✓						
OKLAHOMA	✓		✓	✓								
OREGON	✓	✓	✓	✓	✓	✓						
PENNSYLVANIA	✓	✓	✓	✓		✓						
RHODE ISLAND	✓		✓									
SOUTH CAROLINA	✓	✓	✓	✓	✓	✓						
SOUTH DAKOTA	✓	✓	✓	✓	✓	✓			✓	✓	✓	✓
TENNESSEE	✓	✓	✓						✓	✓	✓	
TEXAS	✓	✓				✓			✓	✓	✓	
UTAH	✓	✓	✓	✓	✓	✓	✓					
VERMONT	✓		✓	✓	✓	✓						
VIRGINIA	✓	✓	✓	✓	✓				✓	✓		
WASHINGTON	✓	✓	✓	✓		✓	✓					
WEST VIRGINIA	✓		✓			✓						
WISCONSIN	✓	✓	✓									
WYOMING	✓	✓	✓	✓	✓	✓						
	46	32	49	40	26	34	4	0	13	13	11	5

*States with delayed implementation dates for arrestee collection requirements.

Table 1: State DNA Database Laws for Qualifying Offences (DNAResource.com, 2008)

What is CODIS

CODIS is a searchable database software that is built in a tier architecture that began as a pilot project for the FBI in 1990 serving 14 state and local laboratories. There are now over 170 labs in the United States, plus an additional 40 labs in 25 countries around the world using CODIS software for their own databases (FBI, 2008). The DNA Identification Act of 1994 formally authorized the FBI to operate CODIS, and set national standards for forensic DNA testing (Lotter, 2008). The CODIS system supports National DNA Index System (NDIS), State DNA Index System (SDIS) and Local DNA Index System (LDIS).

At its highest level, NDIS supports national level data and is controlled by the Federal Bureau of Investigation. Each state has SDIS allowing labs within each state to exchange profiles and LDIS which equates to the local laboratory within the state (FBI, 2008).

CODIS Statistics

The National DNA Index (NDIS) contains over 6,031,000 offender profiles, and 225,400 forensic profiles as of June 2008. Ultimately, the success of the CODIS program will be measured by the crimes it helps to solve. CODIS's primary metric, the "Investigation Aided," tracks the number of criminal investigations where CODIS has added value to the investigative process. As of June 2008, CODIS has produced over 71,500 hits assisting in more than 71,800 investigations. The individual statistics for Massachusetts are (CODIS, 2008):

Massachusetts Statistical Information	Total
Offender Profiles	61,073
Forensic Samples	3,274
Number of CODIS Labs	2
NDIS Participating Labs	2
Investigations Aided	926

Table 2: Massachusetts DNA SDIS Statistical Information (CODIS, 2008)

Database Use

CODIS, as stated above, has many uses. In addition to the basic indexes contained in CODIS, its greatest power comes from its ability to cross index the individual indexes for 'cold hits'. A cold hit is when a profile is entered into the database and a lead is created linking it to a missing person or forensic evidence from a past crime scene or serial crime. In the table above, note the 'Investigations aided' row showing that CODIS to date (June 2008) has aided in 926 crime investigations that may have gone unpunished if no database existed.

Database Abuse

So we've seen the good a DNA database can do, but what are the downfalls? Who are the watchdogs for this incredibly powerful technology? After all, the DNA molecule contains information about a predisposition of some cancers and other medical problems. What is keeping companies like insurers or employers from using that information for discriminating against clients or employees? But it should be clear that the CODIS loci do not contain any medical predisposition data, thus so long as the sample is destroyed after obtaining a reliable and accurate profile, no further information can be obtained.

A second problem is how much is too much? In the UK, their database is growing by 30,000 per month which are taken from *suspects* or crime scenes. According to [their] website, 5.2% of the UK population is on the database, compared with 0.5% in the United States (Manchester, 2007). The larger the number of samples, the higher the cost to analyze them. [Home Office Spokeswoman in the UK] said there are no Government plans to introduce a *universal compulsory*, or voluntary, national DNA database, but that the Home Office is currently undertaking a review of the Police and Criminal Evidence Act (Pace) 1984, which sets the powers to take and retain biometric data (Manchester, 2007).

Although there are no physical information about a person such as eye color, hair color, predisposition for certain medical conditions, ancestry is included. This is helpful in finding a person of interest or narrowing a search but it can also lead to racial profiling.

Overall, National Association of Criminal Defense Lawyers is deeply concerned about the unnecessary expansion of the CODIS database. With the collection of an individual's DNA comes the potential for gross misuse of that data. DNA samples can reveal extremely sensitive, private information regarding physical and mental traits and the likelihood of the occurrence of genetic conditions and diseases. And as Justice Brennan wrote in his concurrence in Whalen v. Roe, "The central storage and easy accessibility of computerized data vastly increases the potential for abuse of that information." While we recognize that DNA evidence is unparalleled in its scientific ability to identify the guilty and protect the innocent, its treatment is subject to human error and thus must be thoughtfully and strictly regulated to prevent mishandling, contamination, and abuse (NACDL, 2004)

Database Ethics

The ethics and social implications of using a DNA database are highly debated. Many believe, such as the American Civil Liberties Union – ACLU, that it gives the government (Big Brother) too much information about an individual in a society that already has given up many rights in the name of 'safety and security'. The belief is that it is just too easy to go from the 13 loci that are 'junk' DNA to keeping the entire double helix on file. Since your DNA contains everything about who you are, would an innocent person that is asked to give a DNA sample effectively giving up his or her right to privacy?

But on the other end of the spectrum, are we not getting criminals off the streets faster and more effectively with the advent of Cold Hits? Does the ends justify the means?

Future of DNA Databases

Through the combination of increased Federal funding and expanded database laws, such as the DNA Fingerprint Act of 2005 [A bill to establish an opt-out system for expungement of DNA profiles from the national index and to authorize collection of DNA samples from persons arrested or detained under Federal authority (Kyl, 2005)], the number of profiles in the U.S. NDIS has and will continue to dramatically increase resulting in a need to re-architect the CODIS software. A considerable focus during this time will be to enhance kinship analysis software for use in the identification of missing persons. The next generation of CODIS will utilize STR and mtDNA information as well as the meta data (such as sex, date of last sighting, age etc.) to help in the identification of missing persons. The re-architecture will also enable CODIS to include additional DNA technologies such a Y Short Tandem Repeat (Y-STR) and mini-Short Tandem Repeat (miniSTR).

The FBI Laboratory is committed to the support of the CODIS program. With the continued cooperation and collaboration of legislative bodies and all components of the criminal justice community – law enforcement, crime laboratories, victims, prosecutors and the judiciary – the future of DNA, CODIS and NDIS holds even greater promise to solve crime and identify missing persons (FBI, 2008).

Database Conclusions

In conclusion, we've shown in this chapter that DNA Databases are here to stay, that their power is great and also expanding. That the number of profiles entered are increasing at a rate of approximately one million per year. It's also been shown that without databases like CODIS we would not have the ability of Cold Hits that are helping to solve crimes that would have otherwise gone unsolved.

The debates over DNA databases will rage for as long as they exist. Entities such as the ACLU and others will continue to bring public awareness to the privacy and abuse issues and although we will not see the databases go away, we certainly will see stricter oversight of their use relating to who can use them, what is entered into them, what happens to the 'rest' of the DNA that is not used for in entry and how the data are controlled.

Chapter-5 Bibliography

Codis Statistics, 06/2008,
(http://www.fbi.gov/hq/lab/codis/clickmap.htm)

Crimtrack, retrieved 7/15/2008
(http://www.crimtrac.gov.au/systems_projects/KeyDatesintheHistoryofDNAProfiling.html)

DNA Resource, retrieved 8/12/2008
(http://www.dnaresource.com)

Federal Bureau of Investigation - FBI, retrieved 7/22/2008
(http://www.fbi.gov/hq/lab/pdf/codisbrochure.pdf)

FSS, 2008, Retrieved 7/15/2008
(http://www.forensic.gov.uk/forensic_t/inside/news/documents/NDNAD.doc)

Kyl, Jon Bill S.1606, 7/29/2005, Library of Congress, retrieved 8/25/2008
(http://thomas.loc.gov/cgi-bin/bdquery/z?d109:SN01606:@@@D&summ2=m&)

Lotter, Karen, 1/13/2008 "CODIS – a System of Pointers: Fighting Crime Using the US Database of DNA Profiles, retrieved 8/1/2008
(http://dna-trace-analysis.suite101.com/article.cfm/codis_a_system_of_pointers)

Manchester Evening News, 5/9/2007, retrieved 8/22/2008
(http://www.manchestereveningnews.co.uk/news/s/1015525_judge_wants_full_dna_database)

Massachusetts General Laws - MGL, retrieved 7/18/2008
(http://www.mass.gov/legis/laws/mgl/gl-22e-toc.htm)

National Association of Criminal Defense Lawyers – NACDL, 4/14/2004, "Letter to Honorable Orrin Hatch and Patrick Leahy, United States Senate on the expansion of the CODIS Database"
(http://www.nacdl.org/public.nsf/legislation/ci_03_66?OpenDocument)

Oxford Reference Online, retrieved 7/18/2008
(http://ww.oxfordreference.com)

Parliamentary Office of Science and Technology: POST, February 2006, Retrieved 7/18/2008
(http://www.forensic.gov.uk/forensic_t/inside/news/docs/postpn258.pdf)

Wikipedia: Genetic Fingerprinting, 2008, retrieved 8/5/2008.
(http://en.wikipedia.org/wiki/Genetic_fingerprinting)

The Encyclopedia Mittanica 2003, retrieved 8/20/2008
(http://myclob.pbwiki.com/11-12-2003?SearchFor=dna&sp=4)

CONCLUSIONS

In the microscopic world of the double helix, we have sought to show the different methods of extracting and typing DNA, and have shown how DNA represents the most private and individual piece of information we have. In the world of forensics, it cannot be altered and is easily left at a crimescene. As more DNA profiles are collected, and as laws change in the individual states to allow more DNA to be collected and added to databases, criminologists are given a tool to "clearly distinguish a suspect from anyone else on the planet", identify the presence of an individual at a crime scene and crosslink cases to find serial offenders and bring them to justice, or to exonerate the innocent. At a crime scene, DNA is found in blood, semen, skin cells, tissue, organs, muscle, brain cells, bone, teeth, hair, saliva, mucus, perspiration, fingernails, urine, feces, etc. and from so many other sources the chance of finding traces of the perpetrator's DNA at a crime scene is very likely. But we also showed how important the collection and preservation of those samples are, because when they are mishandled the evidence may not be allowe in court. Case studies documented here showed that even if DNA testing can be highly accurate, its mismanagement can lead to juror doubt.

Through the advancement of individual state and federal laws to allow DNA samples to be entered into databases, the data are making it easier to 'finger' an individual for a crime. While this technology needs to remain part of all law enforcement procedures, it is absolutely necessary to make sure that the ability to abuse the system is kept to a minimum so it will grow and remain part of our ability to stop and even deter crime. If every member of society knew that if they perpetrated a crime, we would know it was them, this could have perhaps stopped a crime before it happened.

Ultimately, our hope is the information contained in this IQP will help laypersons understand the technology enough to not be intimitated by it in court. It is also hoped that society will embrace the technology by supporting laws allowing a greater number of samples to be entered into databases, so those on the streets who perpetrated a crime can be brought to justice simply because their DNA told us they were present at the crimescene.