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FORENSIC DNA ANALYSIS: TECHNOLOGY AND APPLICATION

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FORENSIC DNA ANALYSIS: TECHNOLOGY AND APPLICATION

> It will be long before a British jury will consent to convict a man upon the evidence of his finger prints; and however perfect in theory the identification may be, it will not be easy to submit it in a form that will amount to a legal evidence.
>
> - From an 1892 review in *The Athenaeum of Finger Prints*, by Sir Francis Galton.(1)

INTRODUCTION

The proposal that human fingerprints could be used as a tool for identification, and as evidence in criminal proceedings, was revolutionary in its day. Francis Galton's century-old caution notwithstanding, however, the use of fingerprints as evidence has been long established as an invaluable tool in the prosecution of criminals, as well as in the identification of missing persons and human remains.

Over the past decade, a forensic technology even more revolutionary in concept than fingerprints has entered into common use. Forensic-DNA typing, or profiling, was first used in 1986 in England in the case of Colin Pitchfork, who was eventually convicted of the sexual assault and murder of two teenage girls. It is significant to note, in light of recent developments in Canada, that the technology was used in this initial case to exonerate a young man who had falsely confessed to the murders.

In an attempt to identify the murderer of the teenage girls in the Pitchfork case, the police authorities took the extraordinary step of requesting the entire male population of the area to

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(1) Quoted in: National Research Council (U.S.), The Evaluation of DNA Evidence, National Academy Press, Washington, D.C., 1996, p. 1-1.

give DNA samples voluntarily for testing. Colin Pitchfork at first avoided being tested by the new technique by persuading an acquaintance to give a blood sample on his behalf. Later, after Pitchfork had been arrested for the murders (without the involvement of forensic-DNA profiling), the DNA-typing procedure proved that he had, indeed, committed both crimes. He is now in prison serving a number of concurrent sentences, including two life sentences for murder.(2)

The value of forensic-DNA profiling in exonerating innocent persons has recently been much in the news in Canada, in connection with two murder cases. In 1985, Guy Paul Morin was arrested for the murder of nine-year old Christine Jessop, a crime that also involved sexual assault. Morin was acquitted in his first trial (in 1986) but was re-tried, and convicted, in 1992. In 1995, after 15 months in prison, Morin was exonerated on the basis of DNA testing, a technology not available when the crime had originally been committed. In fact, the DNA sample obtained from Christine Jessop's clothing was so degraded by 1995 that an advanced form of the technology, only recently perfected, was needed to perform the analysis. The Morin case, and the manner in which it was originally investigated and prosecuted, is currently under intense review by the Ontario government.

More recently, forensic-DNA analysis was used to exonerate David Milgaard, who had been convicted in 1969 of the rape and murder of Gail Miller in Saskatoon. Milgaard spent almost 23 years in prison.(3) The Milgaard case differs from the Morin case in several important ways. First, there was a large amount of DNA (from semen) available for analysis from the clothing of Gail Miller. A U.S. forensic serologist, Edward Blake, who is also an expert on forensic-DNA, has suggested that this material, properly analysed, would almost certainly have exonerated Milgaard in 1992 when new tests were carried out.(4)

The second major way in which the Milgaard case differs from that of Guy Paul Morin is that police have since arrested a suspect on the basis of the forensic-DNA evidence developed in 1997. Larry Fisher, a convicted serial rapist, who had long been suspected of being

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(2) Marie Lussier, "Tailoring the Rules of Admissibility: Genes and Canadian Criminal Law," *The Canadian Bar Review*, Vol. 71, p. 325, June 1992.

(3) David Roberts and Kirk Makin, "*DNA Test Exonerates Milgaard*," *The Globe and Mail* (Toronto), 19 July 1997, p. A1.

(4) Stephen Strauss, "Canadian Testing Incompetent, U.S. Expert Says," *The Globe and Mail* (Toronto), 22 July 1997, p. A4.

involved in the rape and murder of Gail Miller, has been arrested by the RCMP; Fisher's DNA profile matches that obtained from the semen taken from Gail Miller's clothing.[5]

Forensic-DNA profiling has now been used in many criminal and civil cases around the world, and has become an established technology. The first time DNA-typing evidence was used in Canada was in 1988. By October 1989, the central RCMP laboratory in Ottawa was able "to offer a national casework service in forensic DNA typing."[6] In addition to the Morin and Milgaard/Fisher cases described above, one of the most notorious cases in which the prosecution has used DNA-typing evidence in this country was the 1991 murder trial of Allan Legere in New Brunswick. Legere was eventually found guilty of murder, partly on the basis of the DNA evidence.

In this paper, the technology of forensic-DNA analysis and profiling will be described and the idea of establishing a national forensic-DNA data bank will be discussed. First, however, is a short summary of the scientific background that has led to the development of the DNA-profiling procedure.

CHROMOSOMES, DNA AND MOLECULAR GENETICS

All living organisms are composed of cells, the basic integrated units of biological activity. In humans, as in other higher organisms, the hereditary material **deoxyribonucleic acid**, or **DNA**, is contained in the cell nucleus in microscopic assemblages known as **chromosomes**. Human cells have 23 pairs of chromosomes for a total of 46. A typical human cell has one pair of sex chromosomes, and 22 pairs of non-sex chromosomes, known as **autosomes**. The units of inheritance are known as **genes**: human beings are thought to have 50,000 - 100,000 genes which are contained in the chromosomal DNA in the cell nucleus.

The history of forensic-DNA analysis, also called forensic-DNA typing, (or popularly, "DNA fingerprinting"), is little more than a decade old. The basic science goes back at least to 1953, however, when two young Cambridge University researchers, James Watson and Francis Crick, discovered the molecular structure of DNA.[7] Their landmark paper in molecular

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(5) Alanna Mitchell and David Roberts, "Fisher Charged in 1969 Sex Slaying," *The Globe and Mail* (Toronto), 26 July 1997, p. A1.

(6) Lussier (1992), p. 327.

(7) J.D. Watson and F.H.C. Crick, "*Molecular Structure of Nucleic Acids,*" *Nature*, Vol. 171, 1953, p. 737-738.

genetics opened the way for the dramatic advances in recent years in our understanding of inheritance, development and metabolism. Any discussion of DNA typing and its important contribution to forensic science therefore requires some understanding of the molecular basis of inheritance.

DNA is a complex double-chained molecule twisted into a helical form: the "double helix" structure that has become familiar through popular science articles. The structure of DNA resembles a spiral ladder in which the "sides" are made of sugar-phosphate molecules and the "rungs" are formed from pairs of chemicals known as **bases** or **nucleotides**. In DNA from all sources there are only four bases: adenine, thymine, guanine and cytosine. The pairing of the bases is specific: adenine is always paired with thymine, and cytosine is always paired with guanine. In biochemical shorthand, as shown in Figure 1, the base-pairs are represented as A-T (adenine-thymine) and G-C (guanine-cytosine). It is estimated that there are about 3 billion base-pairs in the human **genome**, the term used to describe the total hereditary material in the 46 chromosomes.

These four nucleotide bases represent the "genetic alphabet" and the sequences of base-pairs along the length of the DNA molecule comprise a biochemical vocabulary which encodes the genetic information essential to life processes. The absolute specificity of base-pairing also provides a mechanism through which "parent" DNA molecules can be copied to form identical "daughter" DNA molecules in the process of reproduction. The mechanism, known as **replication** (as opposed to duplication), is possible because the two sides of the parent DNA molecule are **complementary** rather than identical. In the replication process, the parent DNA molecule "splits" along its length, each side serving as a **template** for one of the new (and identical) daughter molecules.

Although genes are composed of DNA and contained in the chromosomes in the nucleus of the cell, only a small fraction of that DNA is actually used to form genes. Put another way, most of the DNA in our chromosomes has no known function; the portion of such DNA may be more than 95% of the total complement in humans.(8) Another source suggests that only 2.5-3.3% of DNA can be expected to be found in the genes.(9)

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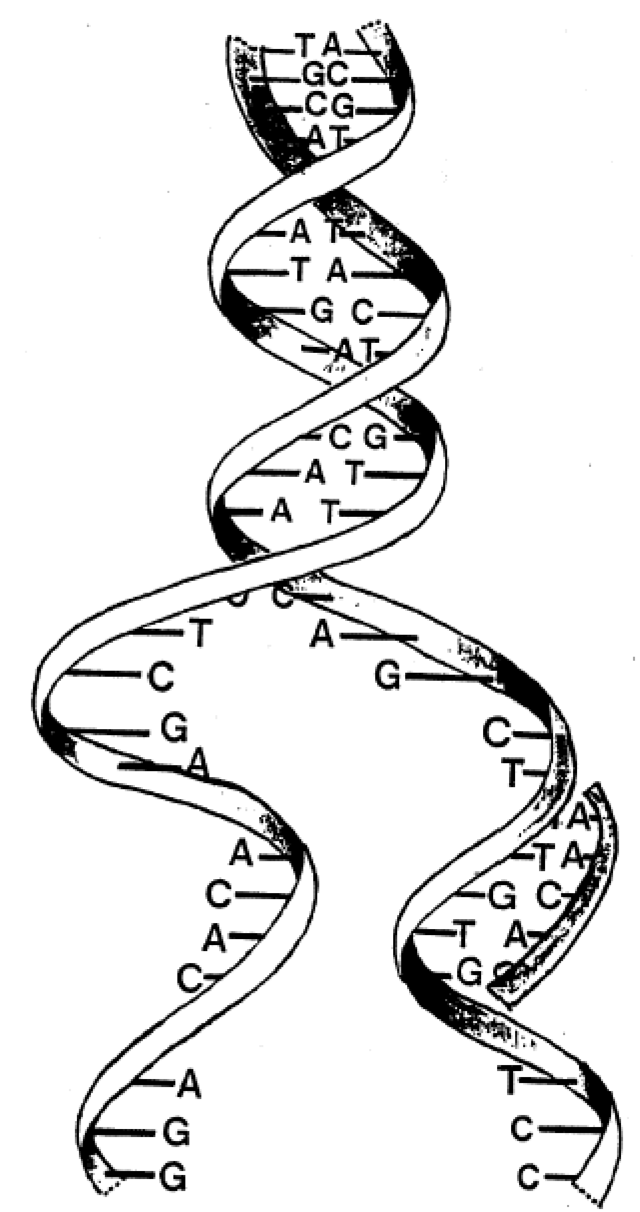
(8) J. Robertson, A.M. Ross, and L.A. Burgoyne, Editors, *DNA in Forensic Science*, Ellis Horwood Publisher, 1990, p.24. (The actual percentage of non-coding DNA is not known with accuracy. The estimate provided in this source is 98.5%.)

(9) Paul Berg and Maxine Singer, *Dealing with Genes - The Language of Heredity*, University Science Books, 1992, p. 138.

Figure 1

THE DNA MOLECULE



Source: RCMP Central Forensic Laboratory.

These observations seem to fly in the face of traditional (or evolutionary) logic which dictates that any cellular component, particularly one as important as DNA, must have an essential function. The presence of so much DNA with no known genetic role in chromosomes is a mystery. Ironically, however, it is this chromosomal "flotsam and jetsam" or "junk DNA" that is of special interest to the forensic scientist.

In the next several paragraphs, a number of terms essential to an understanding of forensic DNA analysis will be introduced and discussed.

A. Variable Number Tandem Repeats (VNTR)

The specific base-pair sequences in the genes are known to define the function a certain gene will perform in the organism. It is also known that the non-coding DNA contains repeated base-pair sequences arranged in tandem which, while having no known function, are inherited by the individual from his/her parents just as functional genes are inherited. (Coding DNA also contains such repeats, but less commonly than non-coding DNA.) These **tandem repeats**, in total, make up a molecular-DNA "fingerprint" that is believed to be unique for each individual (with the possible exception of identical twins) because the number of repeated sequences can vary from person to person. These non-coding base-pair repeated sequences bear the complicated name **variable number tandem repeats**, abbreviated to **VNTR**.

When DNA is extracted for use in forensic analysis, the DNA is cut into fragments by **enzymes**, special chemicals which break down large molecules (such as DNA) into smaller sub-units. An enzyme which is used to cut the DNA molecule into fragments is called a **restriction enzyme**, **restriction nuclease**, or **restriction endonuclease**, the first and last being abbreviated to **RE**. Many different REs are known and they are differentiated on the basis of the point at which they will cut the DNA molecule. That point is known as a **recognition sequence**, a specific sequence of four, five or six nucleotides.

The resulting fragments of DNA produced by the enzyme's action will differ in length from person to person. There are two reasons for this. One reason is that the cutting sites of different individuals' DNA may appear at different places along the molecule. The second reason is that the region of DNA between cutting sites may contain more or fewer tandem repeats of nucleotide sequences, hence the name "variable number tandem repeats."

B. Restriction Fragment Length Polymorphisms (RFLP)

The DNA fragments of interest in forensic-DNA analysis and typing are called **restriction fragment length polymorphisms**, abbreviated to **RFLP** (pronounced "riflip"). The term "polymorphism" refers to the fact that genes, and non-coding DNA sequences, can exist in more than one form on separate chromosomes. The reader will recall that chromosomes exist in pairs, one pair inherited from each parent. Where a specific gene, or non-coding DNA sequence, is identical on each of the pair of chromosomes, the condition is said to be **homozygous**, in contrast to a **heterozygous** condition, where the two genes, or sequences, differ in some way.(10)

The physical basis of the differences lies in the nucleotide sequences in the DNA molecule. The sequences will differ in one or more nucleotide pairs, which is an actual physical difference; hence the term "polymorphism," which means, literally, more than one form. RFLPs occur both in the coding regions of DNA (that portion of the DNA which codes for genes), and in non-coding DNA, which does not have a genetic function. RFLPs are quite common in the human genome, and at least several thousand have been identified. RFLPs have been extremely useful in the diagnosis of genetic disease; for example, the malfunctioning gene that causes cystic fibrosis was located precisely on human chromosome 7 through the use of a series of RFLP markers.(11)

The methods by which RFLPs are detected, identified and utilised in forensic-DNA typing, are described in the next section.

C. Short Tandem Repeats (STR)

Short tandem repeats, as the name implies, are similar to VNTRs described above, except that the repeated units are much shorter. Those fragments chosen for forensic use generally have a tandem repeat unit of only three to four base-pairs, which may be repeated in the DNA molecule from a few to dozens of times. Clearly, units of only three to four base pairs are extremely small; this presents both an advantage and a problem in forensic-DNA work. The advantage is that only small amounts of even badly degraded DNA may be sufficient for forensic use. The problem is that a very small sample of very short DNA segments - the short tandem repeats - needs to be

(10) Where a specific gene occurs in two or more forms, the different forms are known as alleles. A person may be homozygous or heterozygous for a particular allele.

(11) Berg and Singer (1992), p. 153.

increased in size for analytical convenience and efficiency. This is done through the use of a relatively new technology known as the **polymerase chain reaction**.

D. Polymerase Chain Reaction

The polymerase chain reaction, or **PCR**, is an innovative technique for increasing the amount of a specific sequence of DNA in a sample. The technique has proven to be invaluable in forensic-DNA work, and is also used widely in genetic research generally.

The term "polymer" - which literally means "many parts"- refers to a chemical molecule made of a very large number of repeated units of one or more small molecules. A "polymerase" is an enzyme that produces multiple copies of (in the context of this discussion) a specific segment of DNA; the "chain reaction" aspect means that the process will continue for as long as desired to produce the required amount of DNA. Literally, PCR can make millions or billions of copies of a selected, or target, DNA sequence, in a test tube, and accomplish this feat within a matter of a few hours.(12) This is technically called "DNA amplification"; in popular parlance, it is sometimes referred to as "molecular Xeroxing."

The PCR process is similar to the mechanism by which DNA duplicates itself in the cell. There are three steps in the process, as carried out in the laboratory: first, the double-stranded DNA segment, or sequence, is separated into two strands by heating; next, the single-stranded segments are prepared through being hybridized with "primers" - short DNA segments - that define the target sequence to be amplified; and, third, the enzyme **DNA polymerase** is added to the mixture, along with a quantity of the four nucleotide bases, and the replication process begins.(13) The three-step cycle is repeated, usually 25-30 times.

Dr. Ron Fourney, who is with the RCMP's Central Forensic Laboratory in Ottawa, is a recognized expert on forensic-DNA typing, particularly in the use of PCR:

> The PCR method uses basic cellular chemistry and enzymes in a controlled "molecular copying process" to synthesize (amplify) exponential numbers of "target sequence" from the original DNA extracted from forensic samples. PCR technologies selectively amplify

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(12) *Ibid.*, p. 156. (The discoverer of the polymerase chain reaction, Dr. Karry Mullis, was awarded the Nobel Prize in 1993.)

(13) National Research Council (U.S.) (1996), p. 2-11.

> DNA fragments of interest to the forensic scientist and capitalize on fragments that have common differences between individuals.[14]

As noted, the PCR technology is particularly useful where forensic-DNA typing is carried out using short tandem repeats (STR). This technology will be discussed below.

E. Mitochondrial DNA (mDNA)

Not all of the DNA in human and other organisms is located in the chromosomes in the nucleus of the cell. Some DNA is found in organelles called **mitochondria**, which are within the cells but outside the nucleus of the cell. The mitochondria carry out essential metabolic functions, notably with respect to cellular energy production and respiration. Although mitochondrial DNA is not often used for forensic purposes, it can be - and has been - used in certain situations to establish family relationships.

The most celebrated use of such DNA for identification purposes took place in September of 1992 when scientists with the Forensic Science Service in the United Kingdom were asked to analyse mDNA from the bones of five bodies exhumed from a grave in Ekaterinburg in the Ural Mountains in Russia. Ekaterinburg is the location where Czar Nicholas II and his family were murdered in 1918.

Mitochondrial DNA is passed from one generation to the next, essentially unchanged, solely through the maternal line of a family. (Unlike the eggs from the female, the male sperm does not typically contribute mitochondria to the offspring.) By comparing the mitochondrial DNA from the five exhumed bodies with that from a blood sample donated by Prince Philip (whose maternal grandmother was Czarina Alexandra's sister), and also with that in blood from two surviving maternal relatives of the Czar, scientists were able to demonstrate, with approximately 99% certainty, that the bodies found in Ekaterinburg were in fact those of the Russian Royal Family.[15]

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(14) Ron N. Fourney, "Forensic Reality and the Practical Experience of DNA Typing," *Canadian Police Chief Magazine*, 1996, p. 48.

(15) Dermot O'Sullivan, "Romanov Riddle: DNA Tests Identify Bones of Czar and Family," *Chemical & Engineering News*, 19 July 1993, p. 6-7. (The mystery of the Princess Anastasia remains unresolved. However, most accounts of the execution say that the bodies of Anastasia and her brother, Prince Alexei, were burned and buried separately.)

Using the same technology, scientists have also been able to demonstrate that Anna Anderson, who claimed to be the Princess Anastasia, was a fraud.(16)

METHODS OF FORENSIC-DNA PROFILING

The current level of sophistication and expertise in the science and technology of molecular genetics has provided the basis for the "genome project," an international program to determine the sequence of all the base-pairs in the 23 pairs of human chromosomes. The approximately 3 billion base-pairs in the human genome incorporate both the specific sequences which constitute functional genes, and the 95% (or more) of human DNA which is non-coding; that is, which has no known genetic function. It is important to understand that the genome project is separate, and different, from forensic-DNA profiling, although some of the same technologies are used in both activities.

Another essential point is that the DNA profile, or "DNA fingerprint," of an individual as used in forensic-DNA profiling does not represent the genetic make-up of that person. It represents only a number of fragments of the person's DNA; these have been extracted, processed and utilised to form an individualised molecular-DNA "snapshot" that can be used for identification purposes. The forensic-DNA profile does not give any information on the individual's genetic make-up.

Forensic-DNA profiling can make use of any specimen that contains DNA. As shown in Figure 2, the list can include hair (with the root attached), blood stains, semen, bone marrow, or any other tissue or bodily fluid that has nucleated cells. In the use of blood stains, it is the DNA from the white blood cells that is used: mature human red blood cells do not have nuclei and so contain no DNA. Semen normally contains large amounts of DNA in the sperm cells, which makes it very useful for DNA typing, especially in cases of sexual assault. (If the rapist had been vasectomized, however, there would be no sperm cells and the specimen would not be useful with current RFLP technology.)

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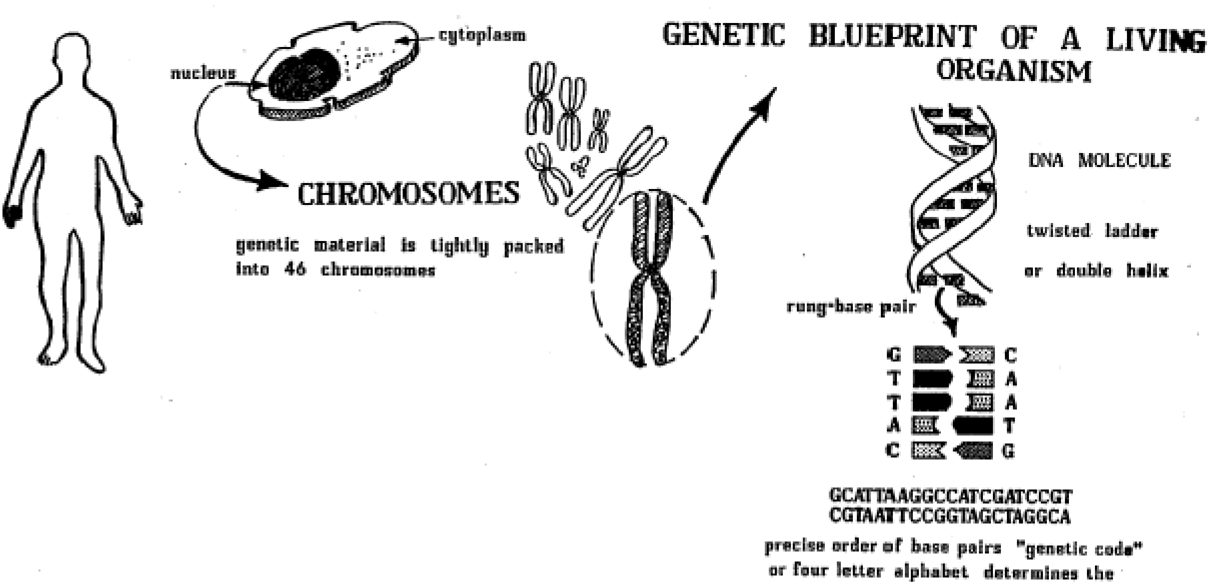
(16) Strauss (1997), p. A6.

Figure 2

Sources of DNA for Forensic DNA Typing

HAIR (roots)
BLOOD (white blood cells)
SEMEN
BONE MARROW, SPLEEN, MUSCLE etc.



Source: RCMP Central Forensic Laboratory.

The standard forensic-DNA typing technology initially used in Canada was the RFLP technology; this is now being replaced by the newer PCR/STR (polymerase chain reaction/short tandem repeat) technology. As of May 1997, the RCMP's Central Forensic Laboratory in Ottawa, as well as the laboratories in Regina and Vancouver, had converted to PCR/STR from RFLP; the RCMP laboratories in Halifax and Edmonton were still using the RFLP technology; and the Winnipeg laboratory was using both technologies. Full conversion of the RCMP forensic laboratory system to PCR/STR analysis is expected to be completed in early 1998.[17] The Centre for Forensic Sciences in Toronto also uses the PCR/STR technology.

A. RFLP (Restriction Fragment Length Polymorphism) Analysis

The following description of RFLP analysis is illustrated in Figure 3.

First, the DNA is extracted from the specimens, using established procedures. In the next step, the extracted DNA is broken into fragments, using restriction enzymes. Although there are several hundred such enzymes, or REs, available today, the laboratories of most North American law enforcement agencies and governments (Canada included) selected one specific RE (called "*Hae*III") in order to achieve uniform results and to facilitate "networking" of DNA-typing information.

After the extracted DNA has been digested by the enzyme, the various fragments are sorted according to size, using a technique called **agarose gel electrophoresis**, initially used in genetics research and adapted to forensic use. Agarose gel is a jelly-like material containing pores through which the DNA molecules can pass. The digested DNA samples are loaded into slots at one end of a flat slab of the gel. An electric current is applied across the gel causing the DNA fragments to migrate through the material. The smaller fragments migrate farther than the larger ones, to give the end result of an orderly array of fragments separated by size.

In the next step, the DNA fragments are **denatured** by soaking the gel in an alkali solution. In denaturing, the hydrogen bonds holding the two sides of the double helix of the DNA together are broken, with the result that there are now **single-stranded** DNA fragments arrayed on the gel in place of the original double-stranded fragments.

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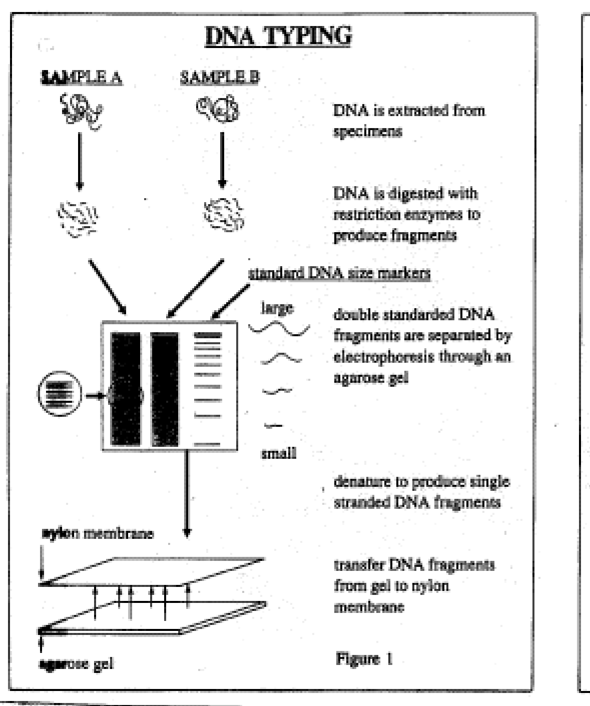
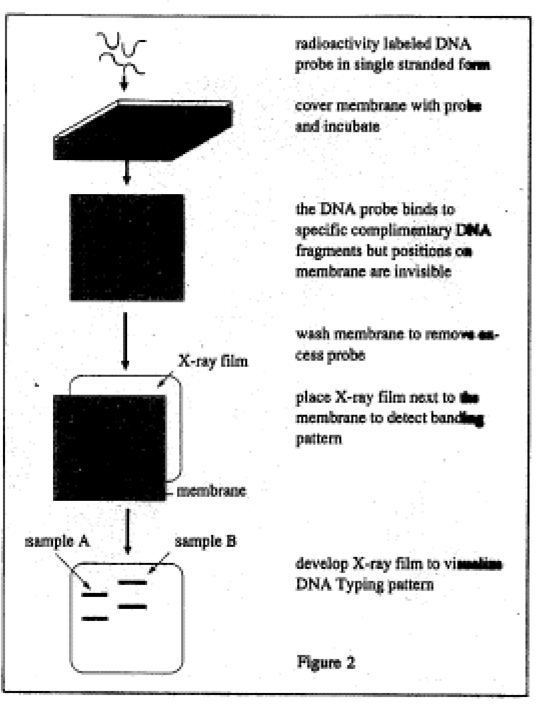
(17) RCMP, personal communication, May 1997.

Figure 3





Because the agarose gel is not sufficiently stable to be used in the rest of the RFLP-typing procedure, the DNA fragments are transferred to the surface of a thin nylon membrane. This technique, called "Southern blotting" or "Southern transfer," is named for Edwin Southern, the scientist who developed it. When the DNA is fixed to the nylon membrane, the fragments are ready to be analysed.

The subsequent analytical technique is called **nucleic acid hybridisation**. The term is explained as follows. Hybridisation is a process that involves pairing the single-stranded DNA (nucleic acid) fragments on the nylon membrane with specific complementary DNA strands; the reader will recall from the earlier discussion that the double-stranded DNA molecule comprises two complementary, rather than identical, strands.

The hybridisation is carried out with strands of DNA which have been labelled with a radioactive isotope, usually an isotope of phosphorus. These strands are known as **DNA probes**, so-called because their base sequences are known and they are used specifically to bind only to those DNA strands containing complementary sequences. Because the probes carry a radioactive label, the newly hybridised strands can be visualised as images on an x-ray film. The visual result is often compared to a supermarket “bar code.”

The specimen in question can then be compared with known specimens through their x-ray images. If there is a difference in the patterns between the DNA from the suspect individual and the DNA from the specimen taken from the crime scene, the suspect will be exonerated. If the patterns match, the prosecution can use this fact as evidence linking the suspect to the crime scene.

B. PCR/STR (Polymerase Chain Reaction/Short Tandem Repeat) Analysis

As noted above, the RFLP technology is being replaced in Canada by the newer PCR/STR technology.

In some basic respects, PCR/STR technology is similar to the RFLP technology described above. The selection and extraction of the DNA is the same, and in both technologies the selected fragments of DNA are placed in a special gel and sorted by size through the use of an electric current. However, with PCR/STR, a much smaller amount of DNA in a sample is adequate to carry out the profiling; even badly degraded DNA, such as might be obtained from decayed or severely burned bodies, can be used. In fact, enough DNA can be extracted from a single hair follicle, or from a saliva trace on a cigarette butt or envelope, to carry out the profiling using this

technology.[18] Additional advantages of PCR/STR are that the technology is less susceptible than earlier PCR-based methods to being compromised by contaminants, and there is a "significant advantage in deciphering the origin of specific DNA profiles from complex sample mixtures...i.e., mixed blood stains, commingled remains and sexual assault samples."[19]

The principal difference between the two technologies is the use of polymerase chain reaction (PCR) to amplify the amount of DNA in the sample. A second important difference is that the PCR/STR technology lends itself well to the use of fluorescent labels for detecting the DNA bands visually, and several such systems have been developed. Also, fluorescence is amenable to automated detection, which greatly facilitates subsequent analysis of the forensic-DNA profiles and the storage and retrieval of data.[20]

Dr. Fourney describes the use of automated fluorescent detection, as follows:

> A major tool employed by both clinical diagnostic laboratories and numerous larger forensic laboratories has been automated fluorescent detection of DNA fragments using DNA sequencers...Essentially, several DNA fragments can be labelled simultaneously with a different fluorescent tag in a single reaction tube (multiplex analysis) during the (PCR) amplification process. Automated detection incorporates the technique of "real time analysis" of DNA fragments as they migrate through a polyacrylamide gel past a laser window which excites the fluorescent tag (fluorochrome) of the fragment and detects the specific enhanced light using an array of CCDs (charge coupled devices). DNA fragments are precisely sized ... calibrated and entered into a digital computer base ...
>
> ... a major characteristic of this detection method is the precision and accuracy afforded through the use of an internal sizing standard run in the same lane (of the gel) as each STR sample. The internal lane standard is recognized by the computer and used to generate a fragment size calibration curve, thereby providing an accurate quantitation of the amount of a fluorescent signal (from the tagged fragment) and a precision standard for evaluating any potential aberrant electrophoretic migration patterns. With the aid of the computer and precise digital sizing data, the forensic scientist evaluates each fragment with regards to match or nonmatch.[21]

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(18) National Research Council (U.S.) (1996), p. 2-11.

(19) Fourney (1996), p. 48.

(20) Keith Inman and Norah Rudin, *An Introduction to Forensic DNA Analysis*, CRC Press, 1997, p. 48.

(21) Fourney (1996), p. 50.

PCR/STR profiling systems are extremely sensitive and capable of analyzing a DNA sample as small as 1 ng (1 nanogram = one- billionth of a gram); however, DNA samples of 2-8 ng are considered optimal for the processing of numerous forensic samples in the multiplex format described above.(22)

A simplified illustration of the PCR/STR technology is shown in Figure 4.

POPULATIONS AND PROBABILITIES

An important point regarding the admissibility of DNA-typing evidence in court can be noted at this point. Admissibility of evidence can be **general** or **specific**:

> (**General admissibility**) ... refers to whether *any* evidence derived from the technique in question should be introduced in court. Once a technique has gained general admissibility, its results can still be ruled inadmissible if they were obtained in an unreliable manner. General admissibility focuses on reliability of the technique while **specific admissibility** focuses on that of its results. (Emphasis in the original)(23)

The basic science and technology behind forensic-DNA typing is not under serious question in Canada, or elsewhere. The theory is scientifically sound and the technology used to obtain DNA profiles is both well-established and evolving in accuracy and efficiency.

One of the most important issues associated with forensic-DNA typing is the individuality of a so-called “DNA fingerprint.”(24) It was noted above that a forensic-DNA profile does not represent the complete genetic make-up of an individual; rather, it is a selection of DNA fragments which can be used as identification markers. The key to the usefulness of the DNA-typing procedure is the fact that the use of "an appropriate number and combination of probes demonstrates that, with the exception of identical twins, each individual (person) has a unique pattern."(25)

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(22) *Ibid*.

(23) Lussier (1992), p. 340.

(24) Although the term "DNA fingerprint" is not officially used, it continues to be a convenient shorthand term for journalists and writers both inside and outside the scientific community. The RCMP originally used this term but stopped doing so, partly because of confusion with conventional fingerprinting, which resulted in mis-routing of mail and inquiries within the organization.

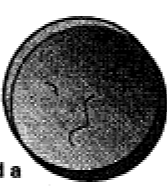
(25) Barry D. Gaudette, "DNA TYPING - A New Service to Canadian Police," *RCMP Gazette*, Vol. 52, No. 4, p. 2, 1990.

Figure 4

How DNA fingerprinting works

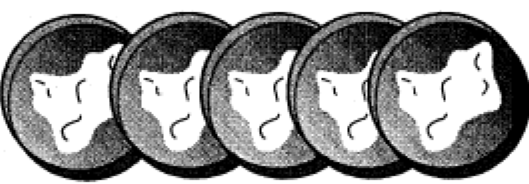
The process for analyzing DNA – deoxyribonucleic acid, the genetic blueprint found in every cell of the human body – to determine whether two samples "match" is enormously complicated. It involves intricate laboratory work and sophisticated application of mathematical formulas:

1. Forensic experts begin by taking blood, saliva, semen, skin or hair from the crime scene and a suspect.



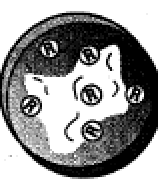
2. The genetic material is extracted and mixed with enzymes, which cut the material into fragments.

3. Sometimes fragments are replicated by a technique known as polymerase chain reaction (PCR).

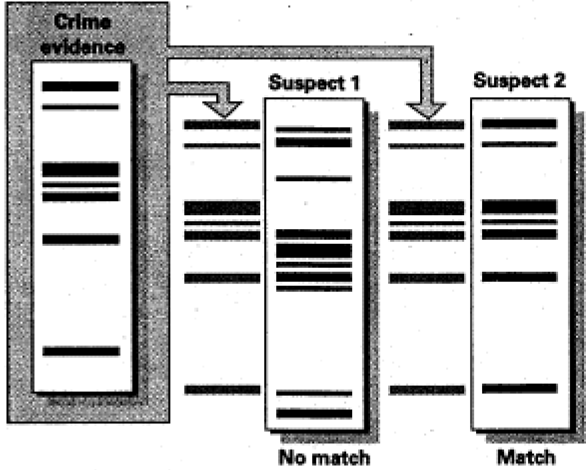


4. After being placed in a special gel, an electrical current is applied to sort the fragments by size.

5. Lasers light up fluorescent tags and the fragment lengths are measured.



6. The resulting patterns, which resemble a supermarket bar code, can be photographed and examined.



Sources: Chicago Tribune, Cellmark Diagnostics, Lifecodes Corp., Cetus Corp.

(Dallas Morning News, Knight-Ridder Tribune)

Source: The Globe and Mail, 19 July 1997, p. A6

This assertion is not made as a consequence of an inclusive analysis of the forensic-DNA profiles of the entire human population, or even of a small fraction of the human population. The claim for uniqueness of a forensic-DNA profile rests on statistical probabilities developed by population geneticists:

> Finding that two samples have the same DNA patterns does not necessarily mean they come from the same individual, just as finding two specimens with the same blood type does not mean they come from the same person. RFLP patterns represent only a snapshot of the unique DNA sequence of each individual ... population genetics is an essential element in forensic uses of all genetic techniques, including DNA technologies.
>
> *The validity of forensic DNA tests does not hinge on population genetics*. Interpreting test results, however, depends on population frequencies of the various DNA markers ... In other words, population genetics provides meaning - numerical weight - to DNA patterns obtained by molecular genetics techniques. (Emphasis in the original)(26)

If a set of patterns produced through forensic-DNA typing indicates a match between evidence from, say, a bloodstain and a known DNA sample from a suspect or a victim, established population frequencies of the RFLP or STR patterns are used to determine the probability of the match's having arisen randomly. Once the forensic laboratory has matched RFLP or STR patterns from two samples of DNA an analyst may estimate how frequently such a match might be expected to arise by chance in a given population.

Two steps are involved in this process. First, the frequency of the individual bands are ascertained by examining random population samples. This step may be described as a fundamentally empirical exercise, involving comparisons with established data bases for various sub-populations. Such data bases (which do not identify the individual sources of the DNA specimens) exist in Canada, the United States, and elsewhere in the world.

The second step calls for an estimate of the population frequency of the overall DNA pattern. In contrast to the basic empiricism of the first step, the second step is a fundamentally theoretical exercise which draws upon information and procedures developed by population

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(26) United States Congress, *Genetic Witness: Forensic Uses of DNA Tests*, Office of Technology Assessment, Washington, D.C., 1990, p. 66.

geneticists. The statistical significance of forensic-DNA profiles, or fingerprints, in terms of their usefulness in criminal and civil proceedings is an important subject.

A heated debate on this issue has taken place in scientific journals, and in the news media, particularly in the first half of the present decade. An extensive literature is now available on the matter. In particular, two reports have been generated by the United States National Research Council. The first - *DNA Technology in Forensic Science* - was published in 1992.[27] The second US-NRC report, *The Evaluation of Forensic-DNA Evidence*, was published in 1996.[28]

The major controversy that erupted over forensic-DNA typing - and which led to the two reports noted above - concerned the statistical methods used, principally by population geneticists, to interpret the significance of matching forensic-DNA profiles. The probability that two forensic-DNA patterns could match entirely by chance has been, and is, considered unlikely in the extreme.

An important issue in this debate is the possible influence of population substructures on the significance of individual profiles obtained with forensic-DNA technology. If human matings were entirely random - that is, if individuals always wed, and mated with, persons who were totally unrelated - there would have been much less concern about the individuality of forensic-DNA profiles. However, humans often do not mate randomly in most population subgroups.

In an extreme example, individuals in an isolated community (for example on an island) would mate with persons who were related in some way, perhaps as distant, or not-so-distant, cousins. Similarly, marriages within the ethnic and racial communities in cities and regions in both Canada and the United States are common, and often lead to the mating of persons with a shared ancestry. The question inevitably arises as to whether identical forensic-DNA profiles might be more likely to be obtained from different individuals in such communities than in the general population.

Most authorities now seem to agree that this question has been adequately answered, and that forensic-DNA profiles, even from a theoretical point of view, are acceptably specific in identifying individuals when the technology is rigorously applied. (It is even possible to identify

(27) National Research Council (U.S.), *DNA Technology in Forensic Science*, Victor A. McKusick, Chairman, National Academy of Sciences, Washington, D.C., April 1992.

(28) National Research Council (U.S.), *The Evaluation of DNA Evidence*, National Academy Press, Washington, D.C., (1996).

siblings of the same sex using the current technology.) The reliability of a profile increases with the number of markers that are used: in RFLP analysis, for example, the use of five markers (rather than three or four) greatly decreases - virtually to nil - the likelihood that similar forensic-DNA profiles could be obtained from different individuals.[29]

In Canada, the PCR/STR system is seen as producing profiles that are highly individual and random matches are judged to be very unlikely. The likelihood of a random match in the system used by the RCMP is described by Dr. Fourney as follows:

> A multi-DNA fragment match in the (RCMP's) DNA analysis procedure is considered exceedingly rare and extremely probative evidence. Currently the Royal Canadian Mounted Police use three multiplex systems which have excellent discrimination potential and (which are also) capable of gender determination. The estimated frequency of the average genetic profile in the Canadian population across (the) 10 STR loci (used in the system) is one in 94 billion.[30]

In most cases, it should also be noted, a suspect will be associated with a crime scene by evidence other than his/her forensic-DNA profile. The profile then becomes corroborating evidence, and usually will not have to stand alone in the prosecution's case. However, where the suspect is identified and apprehended entirely on the basis of a forensic-DNA profile - as could happen through the use of a forensic-DNA data base - concerns about the individuality of the identifying profile rise accordingly.

With respect to the **specific admissibility** of forensic-DNA evidence, the question is whether a forensic-DNA profile has been developed using the appropriate technology, and whether that technology has been rigorously applied. It is possible that, as this technology becomes more widely used, the quality of individual tests on samples might decline as demand rises to meet the evidentiary needs of both the prosecution and the defence.

In Canada, most forensic-DNA typing is done in government laboratories. In addition to the forensic laboratories operated by the RCMP, which handle most such analyses in Canada, DNA typing is also done by the Centre of Forensic Sciences in Toronto and the Laboratoire

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(29) *Ibid*., p. 4-23.

(30) Fourney (1996), p. 50.

de Police Scientifique in Montreal.(31) There are several private laboratories operating in Canada and, in addition, work is sometimes done by private United States laboratories under contract. According to the RCMP, most private-laboratory work is done for civil cases, particularly paternity cases, and for use by defence counsel. Arguably, quality control is more readily achieved in Canada, because of the relatively large government involvement, than in the United States, where private companies are more widely operating.

The quality control, or quality assurance of one organization will be described. TWGDAM, the Technical Working Group on DNA Analytical Methods, first met in November 1988; the meeting was hosted by the United States Federal Bureau of Investigation (FBI) Laboratory and Academy. At that time, TWGDAM consisted of 31 scientists representing 16 forensic laboratories in the United States and Canada - including that of the RCMP - and two research institutions.(32)

The purpose of TWGDAM is described by Inman and Rudin as follows:

1. to pull together a select number of individuals from the forensic science community who are actively pursuing the various DNA analysis methods;

2. to discuss the methods now being used;

3. to compare the work that has been done;

4. to share protocols; and

5. to establish guidelines where appropriate.(33)

TWGDAM has produced detailed guidelines for forensic-DNA profiling: *Guidelines for Quality Assurance Program for DNA Analysis*. The guidelines were first published in 1991; they were updated in 1996.(34)

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(31) The RCMP has a formal link on DNA typing to its American counterpart, the FBI, through participation in The Technical Working Group on DNA Analytical Methods (TWGDAM), a North American organization which meets three times a year at the FBI Academy in Quantico, Virginia.

(32) Inman and Rudin (1997), p. 188. The comparable European Technical Working body is EDNAP, the European DNA profiling group.

(33) *Ibid*.

(34) *Ibid*, p. 188-189.

Finally, it can be noted that, in addition to its use in human forensic work, forensic-DNA profiling has found a place in wildlife research and casework, in Canada and elsewhere. The technology can be used in a variety of applications, from species identification based on bloodstains or meat samples, to estimating the health of a population by determining the amount of inbreeding that might have occurred. Poaching has placed the survival of many wildlife species at risk. DNA typing based on small evidentiary specimens can be used in cases involving poachers just as it can in cases involving murderers and sex offenders.

NATIONAL DNA DATA BANKS

A. Use of DNA Data Banks in Other Countries

During this century, thousands of crimes have been solved through the use of automated systems that search data banks for a match with unidentified latent fingerprints taken from crime scenes. In Canada (and the United States) an Automated Fingerprint Identification System (AFIS) conducts comparison searches against the national repository of the fingerprint collection and a parallel repository of latent fingerprint impressions from crime scenes. Criminal records are generated from the fingerprint forms and entered on the Canadian Police Information Centre (CPIC) computer to which Canadian police forces and other accredited law enforcement agencies have direct access.(35)

Forensic DNA profiles are, in terms of their use in identification, similar to fingerprints; as witness the popular use of the term "DNA fingerprint." The ability of forensic-DNA typing to link scene-of-the-crime evidence to a suspect is well established and, as noted, has enabled authorities to obtain convictions in a significant number of cases. The Solicitor General of Canada has referred to the use of forensic-DNA typing to obtain "convictions in hundreds of violent crimes."(36) In the United States since 1986, forensic-DNA typing has been used in more than 24,000 cases.(37)

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(35) Royal Canadian Mounted Police, Information and Identification Services Directorate, see web site - http://www.rcmp-grc.gc.ca.

(36) Government of Canada, "Herb Gray and Allan Rock Introduce Bill to Establish a National DNA Data Bank," Press Release, April 10, 1997.

(37) Inman and Rudin (1997), p.21.

The potential of DNA technology to assist in solving crimes, particularly violent crimes where DNA evidence is left at the scene, would be significantly enhanced by the creation of forensic-DNA data banks, similar to those already in existence for fingerprints. The possibility of establishing DNA data banks has been widely discussed in Canada and elsewhere. In some jurisdictions, notably the United States and the United Kingdom, forensic-DNA data banks already have been established.

The United Kingdom's computerized DNA data base is operated by the Forensic Science Service (FSS) at Birmingham; it became operational in April 1995. The U.K. *Criminal Justice and Public Order Act 1994* empowers the police in the UK to take DNA samples from anyone charged with a "recordable offence" - which includes a wide variety of offences, including non-violent crimes - whether or not the DNA was immediately relevant to the offence with which the person was being charged.(38) The DNA profiles used in the UK data base are being produced using the PCR/STR technology, which, as noted earlier, is the technique that the RCMP is adopting in Canada. In 1995, the UK data base was expected to contain 4 million DNA profiles by the year 2000.(39)

The UK's forensic-DNA data bank has been used extensively:

> ...more than 50,000 STR (short tandem repeat) samples have been added to their National Offender Database and helped to solve more than 1500 crimes that previously had no prime suspect.(40)

Most, if not all, states in the United States now have legislation in place mandating the collection and analysis of samples for DNA data banks. Generally, DNA samples in that counry are collected from convicted felons, particularly rapists, upon their release from prison. The rationale for this approach is that a relatively small number of people are responsible for a disproportionately large number of violent crimes; some studies have suggested that the recidivism rates for some crimes, after imprisonment, may be as high as 50%. DNA samples are typically sent to the state forensic-DNA laboratory for typing and storage. The FBI is leading

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(38) Patsy Hughes, "DNA Fingerprinting," Research Paper 96/44, Science and Environment Section, House of Commons Library (UK), 27 March 1996, p.24.

(39) Charles Arthur, "Suspects' DNA goes on file," *New Scientist*, 25 March 1995, p.7.

(40) Fourney (1996), p.44.

the effort in the United States to create a national data bank, and pilot programs have been implemented.[41]

B. A Proposed Canadian DNA Bank

The first phase of the federal government's legislative strategy involving forensic-DNA typing was implemented on 13 July 1995, when Bill C-104, An Act to amend the Criminal Code and the Young Offenders Act (forensic-DNA analysis), came into force. That legislation permitted authorities, under warrant, to take DNA samples from suspects in certain crimes.

On 10 April 1997, the Canadian federal government introduced in the House of Commons Bill C-94, the *DNA Identification Act*, to create a national data bank containing DNA profiles from convicted offenders:

> The new law will require persons convicted of designated offences to provide samples of bodily substances for forensic-DNA analysis, with the resulting profiles maintained in a national DNA bank.
>
> The data bank will consist of a **convicted offenders index** that will contain DNA profiles of adult and young offenders convicted of designated *Criminal Code* offences, and a **crime scene index** that will contain DNA profiles obtained from unsolved crime scenes.[42]

When introducing Bill C-94, the Solicitor General, Mr. Gray, said:

> Canada will be one of only a handful of countries in the world to have a national DNA data bank. This will give us a powerful investigative tool that will protect Canadians from violent criminals. It will help ensure that those guilty of serious crimes, such as repeat sex offenders and violent offenders, are identified and apprehended more quickly while excluding innocent suspects.[43]

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(41) Inman and Rudin (1997), p.133-134. (The US armed forces have also instituted a DNA collection program from military personnel, through the Armed Forces DNA Identification Laboratory, AFDIL. This data bank is directed toward the identification of victims of war, and military exercises.)

(42) Government of Canada, "Herb Gray and Allan Rock Introduce Bill to Establish a National DNA Data Bank," Press Release, 10 April 1997.

(43) *Ibid*.

The designated *Criminal Code* offences under the bill would have been divided into primary and secondary lists. The primary list would have included the most serious violent offences, including sexual offences. Upon conviction of an accused, the court would have ordered his or her bodily substances to be obtained for the purpose of data banking. The list of primary offences was as follows:

- sexual interference (s. 151)
- invitation to sexual touching (s. 152)
- sexual exploitation (s. 152)
- incest (s. 155)
- offence in relation to juvenile prostitution (s. 212(4))
- murder (s. 235)
- manslaughter (s. 236)
- causing bodily harm with intent (s. 244)
- assault causing bodily harm or with a weapon (s. 267)
- aggravated assault (s. 268)
- unlawfully causing bodily harm (s. 269)
- sexual assault (s. 271)
- sexual assault causing bodily harm or with a weapon (s. 272)
- aggravated sexual assault (s. 273)
- kidnapping and forcible confinement (s. 279), and

- any offence under any of the following provisions of the *Criminal Code*, chapter c-34 of the Revised Statutes of Canada, 1970 as they read from time to time before 4 January 1983, namely:

  rape (s. 144)
  sexual intercourse with a female under fourteen, between fourteen and sixteen (s. 146)
  sexual intercourse with feeble-minded (s. 148); and

- as they read before 1 January 1998; namely,

  sexual intercourse with step-daughter (paragraph 153(1)(a)).

The secondary list of designated offences would have required samples for data bank purposes, upon court order, following conviction of secondary offences where the judge was satisfied that such an order was in the interests of public safety;

- piratical acts (s. 75)
- highjacking (s. 76)
- endangering safety of aircraft or airport (s. 77)
- seizing control of ship or fixed platform (s. 78.1)

- using explosives (s. 81(1)(a))
- causing death by criminal negligence (s. 220)
- causing bodily harm by criminal negligence (s. 221)
- failure to stop at the scene of an accident (s. 252)
- assault (s. 266)
- torture (s. 269.1)
- assaulting a police officer (s. 270(1)(a))
- hostage taking (s. 279.1)
- robbery (s. 344)
- breaking and entering with intent, committing offence or breaking out (s. 348(1))
- mischief - that causes actual danger to life (s. 430(2))
- arson (s. 433 & s. 434.1) and

- an offence under any of the following provisions of the *Criminal Code* as it read from the time before 1 July 1990; namely:

    s. 433 – arson
    s. 434 - setting fire to other substance, and

- attempt or conspiracy to commit any of the above.

Under Bill C-94, young offenders would have been treated in the same way as adults for the purposes of inclusion in the DNA data bank; and their DNA profiles while in the bank would have been governed by the same rules of access. Unlike the situation for adults, however, the periods of retention for the DNA profiles of young offenders would have paralleled provisions for police records set out in the *Young Offenders Act*. For adults, profiles would have been retained indefinitely, unless the conviction were reversed or the offender were granted a pardon.

The proposed data bank legislation had a number of other features. DNA samples could have been collected retroactively from currently sentenced offenders under two circumstances: first, where an offender had been declared a “dangerous offender” under Part XXIV of the *Criminal Code*; or, second, where an offender had been convicted of more than one sexual offence, and was currently serving a term of two years of more, even if on parole. There was also a provision for “retrospective application,” where a judge, in the interests of public safety, could have ordered that a DNA sample be taken from persons charged with a designated offence prior to the legislation coming into effect and convicted afterwards.

Bill C-94 would also have provided for restrictions on access to DNA samples and on data collected under the legislation:

> Stringent rules will govern the collection, use and retention of DNA profiles and biological samples. Access to DNA profiles contained in the convicted offenders index and to samples will be strictly limited to those directly involved in the operation of the data bank. Only the name attached to the profile will be communicated to the appropriate law enforcement authorities for the purpose of investigating criminal offences. Criminal penalties will also be created to guard against any misuse or abuse of DNA profiles or biological samples.(44)

Although Bill C-94 died when the Prime Minister called the federal election on 27 April 1997, Solicitor General Andy Scott said that similar legislation would be introduced in the new session of Parliament beginning in September 1997.(45) The various points of view on the legislation, including those noted below, will be debated at that time.

It should be noted that the costs associated with a proposed national forensic-DNA data bank would be substantial. The technology is at the cutting edge, and is expensive. Forensic DNA profiles can be computerized, however, which would produce operational efficiencies. Also, the PCR/STR technology that is being adopted in Canada by the RCMP will cost less than the older RFLP (restriction fragment length polymorphism) technology, although the precise amount of savings is not yet known. The start-up costs for the data bank are estimated at $2.9 million, and it is anticipated that annual operating costs would about $3.0 million.(46)

C. Contrasting Views

Predictably, there is a divergence of opinion in Canada on how the DNA data bank should be organized and run. In the following paragraphs, a sense of the contrasting views will be presented, through the positions of the Privacy Commissioner of Canada, the Canadian Bar Association, and the Canadian Police Association.

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(44) *Ibid*.

(45) Keith McArthur, "Proposal to Set up a DNA Bank Will Be Retabled," *The Globe and Mail* (Toronto), 12 September 1997.

(46) RCMP, Personal Communication, 9 May 1997.

1. Privacy Commissioner

The Privacy Commissioner of Canada (PCC), while supporting the use of forensic-DNA analysis to aid police in apprehending violent criminals, has expressed reservations about the creation of a forensic-DNA data bank and about how such a data bank might be used. An individual's right to privacy, "privacy" being interpreted as including the individual's unique DNA characteristics and genetic make-up, lies at the heart of the PCC's concerns:

> We acknowledge the value of RFLP (restriction fragment length polymorphism) analysis in solving crimes of violence. We accept its potential utility when authorized by statute and when sufficient care is taken to ensure the accuracy of the information generated by the analysis. But we strongly oppose a government cataloguing the identifying genetic characteristics of the overwhelmingly non-criminal male population (as has been considered in the United Kingdom).(47)

The PCC has expressed concern about the creation and use of a forensic-DNA data bank by the police to apprehend criminals. As an example, the Commissioner has cited the Pitchfork case in the UK (noted earlier in this paper). In an attempt to solve the sex murders of two teenage girls, the UK police had amassed, through a voluntary program, more than 3,600 forensic DNA profiles of males from the local area where the crimes occurred; later, the police used this *ad hoc* "data bank" to apprehend the perpetrator of a different crime:

> ...the (DNA) samples were not used for (the Pitchfork) investigation alone. Police officers later matched a DNA print from one of the volunteers to a semen sample from a previous unsolved rape. For the police, this was merely clever sleuthing. For civil libertarians, it raised the spectre of future population databases of genetic characteristics, not merely identification features, being used as another instrument of control in society.(48)

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(47) The Privacy Commissioner of Canada, Genetic Testing and Privacy, Ottawa, 1995, p.48. (At the time of writing, RFLP analysis was the principal forensic DNA technology being used in Canada.)

(48) *Ibid*.

An observer might well agree, however, that the apprehending of a rapist through this use of forensic-DNA technology was indeed "clever sleuthing." Furthermore, because an individual's forensic-DNA profile gives no information on that person's "genetic characteristics" – a possible exception being that the PCR/STR technology being phased in by the RCMP will determine the individual's gender – the same observer might also ask whether the "spectre of future population databases of genetic characteristics" is a realistic fear.

Nonetheless, the PCC made a recommendation (in his 1995 report), the first part of which states:

> Governments should not establish banks of genetic samples of convicted persons or the general population for criminal justice purposes. Governments should not establish genetic databases of the general population for criminal justice purposes.[(49)]

However, in the second part of this recommendation, the Commissioner appears to soften this viewpoint:

> If genetic databases are found to be acceptable, they should only be used for identification. The information contained in a genetic database and any genetic samples related to the crime should not be used to try to identify other characteristics that may have a genetic link, such as personality.[(50)]

In fact a forensic-DNA data bank, such as was proposed by the federal government in Bill C-94, would not use the genetic material for anything other than identification purposes in the apprehending of criminals. The PCC's point is well taken, however; a data bank established for purposes of identification should not be used for other, greatly expanded, purposes, particularly those with a rationale as fragile as attempting to link an individual's genetic complement with personality traits that might be judged, rightly or wrongly, as indicating criminal potential.

In its 1995 response to the Department of Justice consultation paper *Obtaining and Banking DNA Forensic Evidence*, the Office of the PCC appears to have accepted the federal government's proposal to establish a forensic-DNA data bank, although with some restrictions

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(49) *Ibid*, p. 50, Recommendation No. 11.

(50) *Ibid*.

on sampling, use of the DNA profile, and disposition of the DNA sample after use. Some of the suggested restrictions by the PCC are listed below.

The DNA sample should be collected by a health-care professional.

- The least intrusive collection method should be used, and the suspect/convicted offender should be permitted to specify the sampling method, consistent with good forensic practice.

- DNA evidence should not be collected unless the information is relevant to the crime in question, the crime must involve violence or the likelihood of violence, and the collection must be authorized by a judge.

- DNA samples should not be taken routinely from all convicted persons, but only from convicted offenders guilty of a violent offence.

- The preference of the Office of the PCC is that the DNA sample or the analysis of the sample should not be retained, because of concerns about their possible future use in the search for genetic traits linked to criminal behaviour.

- The database should contain only information on certain *convicted* offenders; where the individual is acquitted, for example, both the sample and the analysis should be discarded.

The PCC also discussed whether the DNA data bank should be used to solve crimes other than the crime for which the DNA sample was originally obtained:

> After conviction (of the individual), DNA information could be used, without a court order, to seek a connection with any unsolved crime of a similar nature. For example, genetic information from the DNA of someone convicted of a sexual assault could be used to look for a match with unsolved sexual assaults. Use of the DNA to resolve crimes that are not of the same nature as the one for which the person was convicted, should require a judge's approval. This would prevent a fishing expedition.

It is not clear from the PCC's brief, however, why a "fishing expedition" would be an unacceptable use of the DNA data bank. That is, what are the specific objections to linking the banked forensic-DNA profile of a person convicted of robbery with the DNA profile obtained from the scene of a more serious crime, such as rape or murder, especially if that link led to the individual's arrest and conviction for the more serious offence?

2. Canadian Bar Association

The National Criminal Justice Section of the Canadian Bar Association (hereafter, the Section) supports the creation of a national DNA data bank "provided it is established with appropriate respect for the liberty and privacy interests of individuals."[51] The Section proposes a number of limitations and safeguards on collection, retention and use of DNA samples, and these are summarized below.

- The Section recommends that a forensic-DNA data bank be used for the limited purpose of "providing police with reasonable grounds to obtain a search warrant for another bodily fluids sample, where a match is found between the DNA of an unknown sample and a DNA sample held in the data bank." The rationale for this recommendation is that the data bank match in and of itself may not be reliable as evidence in court.

- The Section recommends, as a balance between privacy interests and the need to protect society, that the data bank should only contain DNA profiles only for crimes such as "homicide and serious sexual and violent offences, including breaking and entering and committing a sexual offence."

- In the cases of young offenders, the Section recommends that DNA profiles should be maintained only for a limited period of time, if there has been no further related offence. However, exceptions to this rule may be made for serious violent crimes committed by young offenders, and the DNA retained for an indefinite period.

- The Section "strongly opposes the seizing of (DNA) samples upon arrest," unless a warrant has been obtained. The Section's opposition is based on the view that a seizure of a DNA sample before conviction is constitutionally unsound. (Under current legislation, fingerprints and photographs of the accused may be taken at the time charges are laid.)

- The Section believes that police officers can be trained to take samples for DNA analysis, after conviction of an accused. The Section cites examples of some police agencies (for example, the Vancouver City Police) who have a training program and a standard kit for blood sample collection. However, if the sample is taken in prison, the Section believes that "prison health professionals" should be responsible for taking the sample.

- The Section shares the belief of the Privacy Commissioner of Canada that DNA samples should not be retained in a national data bank; only the results of the analysis, the forensic-DNA profile, should be retained. The concern of the two organizations is the same; namely, that the existence of a collection of DNA samples might constitute an "invitation" for inappropriate research into the possible linkages between genes and criminal behaviour.

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(51) National Criminal Justice Section, the Canadian Bar Association, *DNA Data Banking*, April, 1996, p.12.

1. Canadian Police Association

The value of forensic-DNA typing to the police, and by extension to the criminal justice system, has been proven in many criminal investigations. Not only has the technology linked criminals to particular crimes, it has also been used successfully to exonerate individuals who have been wrongly convicted, the cases of Guy Paul Morin and David Milgaard being the best known in this country. It is not surprising, therefore, that police agencies want the collection of DNA samples, and the operation of a national data bank, to be as efficient and as comprehensive as possible.

The Canadian Police Association believes that the same preconditions and restrictions should apply to the collection and retention of forensic DNA profiles as currently apply to fingerprints under the *Identification of Criminals Act*:

> ...like fingerprints before them, DNA samples have a dual investigative relevance. First, they are a method by which a person suspected of a specific crime can be either linked or eliminated through comparison with a trace or crime scene sample such as semen, hair or blood. Second, and far more importantly where there is no evidence suggesting a particular individual, crime scene evidence could be matched to previously held DNA evidence contained in a DNA Data Bank. In this sense, DNA evidence is exactly analogous to fingerprints in that they are in existence because of a statutorily authorized threshold of prior activity which has led to the retention of the record in the first place. ... their forensic investigative value is profound. Failure to make full use of both the gathering of such material and retention is nothing short of irresponsible given the undeniable alternative of non-prosecution of most serious crimes.(52)

The concern expressed by the Office of the Privacy Commissioner of Canada that DNA samples might be used for research into the genetic basis of criminal behaviour are summarily dismissed by the Police Association as “unjustifiable.” The Association’s brief does not suggest, however, that DNA samples should be used for purposes other than the identification of suspects in crimes.

A major point of disagreement between the Canadian Police Association and both the Privacy Commissioner of Canada and the Canadian Bar Association is on the question of

when the DNA sample should be collected. As noted above, both the PCC and the National Criminal Justice Section of the CBA have argued that DNA samples should not be seized at the time of arrest, but only after conviction. The Police Association argues that the sample should be taken at the time of the arrest, as is done with fingerprints. Moreover, the Police Association would support, and even expand, the list of designated offences for which DNA samples could be collected. The Association has suggested a possible scenario which, in its view, supports the taking of a DNA sample at the time of arrest, even for a relatively "minor" offence.

> In essence, we advocated that the current law, pursuant to the *Identification of Criminals Act*, which permits taking of offender information (fingerprints) at time of arrest for indictable offences, was exactly the process which must be followed with the technological upgrade which DNA samples represent. This process of taking information prior to conviction ensures that the material will be obtained, unlike a process which allows taking of samples following conviction...
>
> Our criminal justice system grants bail to over 95% of persons charged with criminal offences. If, to use a common example, a person is charged with a break and enter but is actually, unknown to police, responsible for a string of unsolved rapes in which trace evidence exists, he will be released without DNA samples being taken. The offender will know that the only way his DNA will be obtained, and (he will) be captured for rapes, is if he returns and is convicted on the original charge. Does anyone really believe that such persons will not fail to appear for court?(53)

The Association cites a statistic to the effect that, in 1995, more than 66,000 people in Canada either broke bail or failed to appear as required. Also, the Association says that in Canada,

> ...warrants issued for people who fail to appear on such charges as break and enter are not generally returnable throughout Canada. What this means is that if the same undetected rapist for whom a break and enter warrant is outstanding in Ottawa, is picked up in

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(52) The Canadian Police Association, *DNA Data Bank Amendments - A Response to the Solicitor General's Consultation Document* (undated), p.1-2.

(53) Neal Jessop, President, The Canadian Police Association, "An Open Letter to all Members of Parliament," *The Hill Times*, 14 April 1997.

> Alberta, current practice is that he would not be returned to face the "minor" break and enter charge.(54)

Overall, the Canadian Police Association is of the opinion that the proposed legislation would not have gone far enough in creating an optimally effective DNA data bank. In the "open letter" to Members of Parliament cited above, the Association's president urged rejection of Bill C-94 as drafted, and the introduction of more comprehensive and effective legislation.

CONCLUSION

As was the case with fingerprints, forensic-DNA profiling has become an accepted, and now probably indispensable, technology in forensic science. The rapidity of its acceptance - it is only eleven years since the Pitchfork murder case was resolved - reflects the technology's solid foundation in molecular genetics. This foundation accounts for the technology's formidable, and rarely challenged, reputation for accurate identification based on objective observations. As noted earlier, forensic-DNA profiling can reach back over the decades - and even centuries - to answer important questions of identity and lineage through the use of the genetic code.

Equally impressive has been the rapid evolution of the technology. In 1986, the forensic-DNA profiles that ultimately resolved the Pitchfork murders (first by exonerating the innocent self-confessed suspect, and second by confirming the guilt of Pitchfork himself) were complicated, time-consuming, and labour-intensive. Today, using the leading-edge type of automated PCR/STR technology being adopted by Canada's RCMP, profiles can be developed in much less time, and with much improved discrimination capability.

The technology undoubtedly will continue to evolve, with expectations of increased efficiency, wider applicability, and – it is hoped - lower costs for each forensic-DNA profile developed. Dr. Fourney has suggested that future developments will see the "the automation of the entire process from the extraction of DNA to the generation and detection of discrete markers eventually leading to a final digital entry into a database that is searchable."(55)

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(54) *Ibid*.

(55) Fourney (1996), p.50.

At the same time, he notes, there is a major challenge facing forensic laboratories world-wide: the adoption of a common set of standards for human identification.

On the other hand, as the technology finds a greater degree of application, within forensic science and beyond, total costs to society for the use of the technology may well increase, even as unit costs decline. The question of the benefits versus the costs of using the technology will no doubt arise and come under close examination, particularly by governments.

A great advantage of forensic-DNA technology is, as noted, that it is based on objective science; the more it becomes automated and removed from the possibility of human error, the greater will be its objectivity. In recent months, police forces and forensic laboratories in both Canada and the United States have come under pronounced criticism for their mishandling of criminal investigations. The Milgaard, Morin and Bernardo cases are the most notorious in this country.[(56)]

The Morin case, in particular, witnessed a failure in the application of forensic science, particularly in the analysis of fibre evidence, which involves a degree of subjective interpretation. Forensic-DNA analysis, as noted, led to the exoneration of Guy Paul Morin and others, in situations where traditional technologies and methods had failed, for whatever reason.

There will very likely be more examples in this vein. While a positive forensic-DNA match is persuasive evidence of a suspect's association with a crime, it is not absolute proof. There is always a chance, however slight, that the match might be a random one: it is impossible to prove a negative, and statistical probability cannot be ignored. Additional evidence and information is usually required to obtain a conviction. However, a negative forensic-DNA match, referred to as an **exclusion**, is absolute. In this context, it is significant that the FBI in the United States has reported that "fully 1/3 of all suspects in rape cases are released before trial because DNA evidence exonerates them."[(57)] Even if this figure may be slightly exaggerated, as Inman and Rudin suggest, the power of the technology to prove innocence cannot be denied. In all cases where forensic-DNA technology is used, however the possibility of human error - particularly sample mix-ups – has to be guarded against. Any technology is only as reliable as the persons using it.

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(56) Editorial, "On Guard for Thee?" *The Globe and Mail* (Toronto), 22 July 1997.

(57) Inman and Rudin (1997), p. 21.

Finally, there are a number of projects under way in the United States, Canada, and elsewhere that are making use of forensic-DNA technology to free the innocent from incarceration. The original initiative here has been the Innocence Project at the Benjamin N. Cordozo School of Law at Yeshiva University in New York City. In Canada, the Osgoode Hall Law School at York University in Toronto will launch a similar project. In this effort, the York University group will work with the Association in Defence of the Wrongly Convicted (AIDWYC) in Scarborough, Ontario.[58]

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(58) Kirk Makin, "Police 'Tunnel Vision' Gives No Justice, Critics Say," *The Globe and Mail* (Toronto), 22 July 1997, p. A1, A5.

GLOSSARY

Adenine: one of the four building blocks of DNA, indicated by the letter **A**.

AFIS: Automated Fingerprint Identification System.

Agarose: gel medium used for separating DNA fragments.

Allele: one of two or more alternative forms of a gene or a genetic marker.

Amplification: applied to DNA, it is the process of making multiple copies of a DNA sequence using the polymerase chain reaction (**PCR**).

Autoradiogram: also called **autoradiograph** or **autorad**; an x-ray film on which radioactive or chemiluminescent probes have left an image determining the position of specific DNA fragments. Sometimes described as a "genetic bar code."

Autosome: any chromosome other than the X and Y sex chromosomes.

Band: the visual image of a specific DNA fragment on an autorad. (The "bar" in the bar code.)

Base: in this context, a subunit of nucleic acid. The four bases are **adenine**, **thymine**, **cytosine** and **guanine**, indicated by the letters A, T, C and G.

Base Pair: the "rungs" of the DNA "ladder" are composed in part of base pairs. Adenine always pairs with thymine; cytosine with guanine.

Chromosome: the nuclear structure, visible under a microscope, that contains the genes which are transmitted from one generation to the next.

Coding: that region of the DNA that carries genetic information that has the capability of producing a protein. (Opposite - **Noncoding**.)

Cytosine: one of the four building blocks of DNA, indicated by the letter **C**.

Denaturation: the separation of double-stranded DNA into two complementary single strands by heat or chemical means; an essential step in forensic-DNA profiling.

Deoxyribonucleic Acid, DNA: the genetic material of most organisms, including humans.

Diploid: the state of having two sets of chromosomes, in pairs; humans have 23 chromosomes in pairs, for a total of 46, in all adult cells, except for germ cells. (See **haploid**.)

DNA: deoxyribonucleic acid.

DNA Polymerase: an enzyme that synthesizes DNA from an existing template. (See **polymerase chain reaction** or **PCR**.)

DNA Probe: a short segment of DNA labeled with a radioactive or chemical tag that is used to detect the presence of a particular DNA sequence or fragment.

Electrophoresis: A technique, used in forensic-DNA profiling, in which the DNA fragments are separated according to size by their rate of movement in an electric field through a gel.

Enzyme: a protein catalyst of a specific biochemical reaction; in forensic-DNA work, some of the enzymes used are restriction nucleases and DNA polymerase.

Eukaryote: a type of cell, including most human cells, that contains a nucleus, which in turn contains the chromosomes.

Gel: a semi-solid matrix, usually agarose or acrylamide, used in electrophoresis to separate molecules by size. (**gel electrophoresis**)

Genetic Marker, Marker: a defined location on a chromosome having known genetic characteristics.

Genome: the total genetic makeup of an organism.

Guanine: one of the four building blocks of DNA, indicated by the letter **G**.

HaeIII: a restriction enzyme, or restriction endonuclease, used in RFLP analysis; the standard enzyme used in Canada and the United States.

Haploid: having one set of chromosomes. (See **diploid**.) Sperm and egg cells are haploid.

Heterozygous: having a different allele (or version) of a gene at a particular locus on each chromosome in a pair, in a diploid organism. (The opposite is **homozygous**.)

Homozygous: having the same allele (or version) of a gene at a particular locus on both chromosomes in a pair, in a diploid organism. (The opposite is **heterozygous**.)

Hypervariable: a DNA locus that shows extreme variation between people. Forensic-DNA analysis is based on such variability in the DNA.

Locus: the specific physical location of a gene, or specific DNA sequence, on a chromosome.

Noncoding: a region of DNA which does not code, meaning that it lacks the capacity to produce a protein.

Nucleus: an organelle found in eukaryotic cells, including human cells, in which are found the chromosomes.

PCR: polymerase chain reaction.

Polyacrylamide: a polymer which, formulated as a gel, is used to separate small DNA fragments in an electrophoretic field.

Polymerase Chain Reaction (PCR): a process mediated by a DNA polymerase, yielding millions of copies of a desired DNA sequence.

Polymorphism: the presence of multiple alleles of a gene in a population.

Probe: a short segment of synthetic tagged DNA, used to detect a specific DNA fragment or sequence.

Prokaryote: a cell lacking a nucleus; all prokaryotes are bacteria. (See **eukaryote**.)

Restriction Enzyme, Restriction Endonuclease: an enzyme that cuts DNA at specific locations determined by the particular DNA sequence.

Restriction Fragment Length Polymorphism (RFLP): variation in the length of DNA fragments produced by a restriction enzyme that cuts the DNA at a polymorphic locus. The polymorphism may be in the restriction enzyme site or in the number of tandem repeats between the cut points. Variable Number Tandem Repeats (VNTR) loci are used in forensic-DNA analysis.

STR: short tandem repeat.

Tandem Repeats: repeating units of an identical DNA sequence arranged in succession in a particular region of a chromosome.

Thymine: one of the four building blocks of DNA, indicated by the letter **T**.

Variable Number Tandem Repeats (**VNTR**): repeating units of an identical DNA sequence, arranged in succession in a particular region of a chromosome; the number of repeats varies between individuals, which makes forensic-DNA identification possible.