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SATELLITE DNA- THE KEY TO SOLVING CRIME

Ipsita Kukreja[1] and Prakhar Kapoor[2]*

[1]M.D.S, Dept.of Oral & Maxillofacial Pathology, Bharati Vidyapeeth Dental College & Hospital, Pune (Mah.), India.
[2]Asst. Prof. Dept.of Oral & Maxillofacial Pathology, Sri Aurobindo College of Dentistry & PG Institute, Indore (M.P), India.

ABSTRACT

Forensic odontology is a very important indispensible part of forensic medicine today. The tooth as a consequence of its elemental structure has withstood the sands of time. It is a very useful source of genetic material, many a times the only source. This review focuses on the collection of DNA at crime scenes, DNA analysis techniques and the role of satellite DNA in identifying a unique match of a crime suspect. It throws light on the various advances in forensic dentistry using the principles of DNA analysis. In addition to the above aspects it is extremely important for a forensic pathologist to be well versed with various aspects of time of death. Different parameters pertaining to time of death have also been discussed.

KEY WORDS: Forensic, Satellite DNA, Microsatellites, DNA technology, Time of death.

INTRODUCTION

Sherlock Holmes said “it has long been an axiom of mine that the little things are infinitely the most important”, but never imagined that such a little thing, the DNA molecule, could become perhaps the most powerful single tool in the multifaceted fight against crime.

Twenty years after the development of DNA fingerprinting, forensic DNA analysis is the key to the conviction or exoneration of suspects and the identification of victims of crimes, accidents and disasters, driving the development of innovative methods in molecular genetics, statistics and the use of massive intelligence databases [1].

Forensic Dentistry has been defined by Keiser – Nielsen as that branch of odontology which in the interest of justice deals with the proper handling and examination of dental evidence and with the proper evaluation and presentation of dental findings [2].

Over the years various conventional methods have been used in forensic dentistry like oral autopsy, obtaining dental records of the dead, comparison of ante mortem and post mortem data, followed by creating a dental profile. It also involves visual examination of bite marks and lip prints etc. However these conventional methods of identification involve one very basic element that may not always be readily available and that is dental records. Conventional methods may also be difficult to reach a positive identification in cases where the bodies are mutilated, where the facial skeleton (and as a result the jaws) may not be intact, in cases of mass disasters, plane crashes, terrorist attacks like the attack on the World Trade Centre in NYC and natural disasters. Since teeth are most resistant to damage, few fragments of dentition or bone may be extracted from the debris in the above mentioned events and in these cases it is only possible to make a positive identification using DNA technology [3].

Human identification is one of the major aspects of forensic science. The revolution caused by Watson and Crick in 1953, who discovered the double helix model of DNA, which is responsible for the genetic inheritance of human beings, has led to important changes in nearly all fields of science including forensic medicine and odontology. Three decades later, Jeffrey’s et al created radioactive molecular probes that could recognize highly variable regions of DNA and thus determine specific patterns in an individual which were named as DNA fingerprints [3].

Various biological samples can be employed for isolation of DNA such as bone tissue, hair bulb, biopsy samples, saliva, blood, skin, finger or toe nails, and / or a

Corresponding Author:- **Prakhar Kapoor** Email:- doctor.prakhar@gmail.com

tooth with root material as well as other body tissues. It is possible to obtain DNA from virtually all human body tissues with variations in the quantity and quality of DNA extracted from each tissue.[3] Investigators gather samples from the crime scene and from suspects and then analyze it for a set of specific DNA regions or markers. A match of one marker is not usually unique, but if a sample matches four or five markers, there is a very good chance it is a match.

Collection of DNA at the crime scene

Smear slides, scalpels, tweezers, scissors, sterile cloth squares, UV light, luminol and/or blood collection kits (for sample collection of suspects or living victims). Luminol ($C_8H_7N_3O_2$) is a versatile chemical that exhibits chemiluminescence, with a striking blue glow, when mixed with an appropriate oxidizing agent. It is a white to slightly yellow crystalline solid that is soluble in most polar organic solvents, but insoluble in water. Luminol is used by forensic investigators to detect trace amounts of blood left at crime scenes as it reacts with iron found in hemoglobin. It is used by biologists in cellular assays for the detection of copper, iron, and cyanides, in addition to the detection of specific proteins by Western Blot [4].

The Phadebas Forensic Press test is used for detecting and identifying hidden saliva stains. Locating saliva stains is a challenging task to perform with light sources as these stains don't fluoresce very well. Phadebas Forensic Press test is selective, the reason being that alpha-amylase activity in saliva is typically several orders of magnitude higher than in other body fluids.

The Phadebas Forensic paper is a new, commercially available product that detects saliva stains by reacting with amylase. When the paper is pressed against a positive saliva stain a blue spot occurs. Hedman et al performed an experiment to test the sensitivity of the Phadebas paper. They prepared a set of dilutions (1:1, 1:5, 1:50, 1:100, 1:200, 1:500) on cotton fabric. Blue spots could be seen for dilutions of 1:100 when incubated at room temperature, and 1:200 in 37°C. However, incubation at room temperature provided a better reproducibility between runs compared to 37°C. The Phadebas Forensic paper was compared to four different fluorescent light sources, Quaser 2000/30, Crimescope CS-16, Polilight and Labino UV Spotlight, with respect to the ability of finding known saliva stains (1:1, 1:5, 1:25, 1:100) on different materials. The materials tested were cotton fabric (T-shirt), denim, suede, leather, painted wood and untreated wood. On denim, no stains could be seen with the light sources, but with the Phadebas Forencic paper stains were visible for both pure saliva and a 1:5 dilution. DNA analysis (AmpFlSTR SGM Plus) was performed on both the detected stains on the different materials and on the corresponding spots on the Phadebas Forensic paper [5].

DNA Collection & Comparison

Collection of evidence in forensic investigation is of utmost importance and must be performed diligently and carefully with as little contamination as possible.

1. Blood on Clothing

Investigators submit whole pieces of clothing or they may use a sterile cloth square and a small amount of distilled water to collect a small sample of blood.

2. Dried blood on furniture?

Investigators send the whole object to the lab

3. Dried blood on a wall, tub or some other object too big or difficult to move to the lab?

Investigators scrape the blood sample into a sterile container for further analysis

What happens after the samples are collected?

A DNA profile is created….how??

Markers are found by designing small pieces of DNA (probes) that will seek out and bind to complementary DNA sequences. This creates a distinct pattern. Again, one marker is not usually unique, but with four or five regions the match is likely. The DNA profiles are compared with samples from suspects to find possible matches. If there are no suspects, a national database called CODIS may be used to find potential suspects.

Sources of DNA at Crime Scenes

Examples of sources from real cases:

1. Saliva on the stamp of a stalker's threatening letter
2. Skin cells shed on a ligature of a strangled victim
3. Perspiration on a baseball cap discarded by a rapist was compared with the DNA in the saliva swabbed from a bite mark on a different rape victim
4. DNA analysis of a single hair (without the root) found deep in a victim's throat
5. Maggots can contain DNA of a perpetrator

However sometimes evidence can be planted falsely or even tampered with.

DNA evidence can be falsely planted in many ways

1. Sneezing or coughing over evidence
2. Person touches their mouth, nose or other part of the face and then touches the area that may contain the DNA to be tested.
3. Scene personnel can deposit hairs, fibers, or trace material from their clothing
4. Wind can carry in contaminants

DNA Isolation from a tooth

DNA can be isolated from a tooth using the process of cryogenic grinding. Cryogenic grinding is used to extract DNA from calcified tissues such as teeth. In a freezer mill a ferromagnetic plunger is oscillated back and forth in an alternating electric current. Liquid nitrogen is used to cool the sample, which results in making it extremely brittle and also protects the DNA from heat degradation. The tooth is reduced to powder to increase the

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surface area and expose trapped cells to biochemical agents that release DNA into the solution [6].

Another technique used for extraction of DNA from anthropological specimens is the orthograde entrance technique. Earlier to recover DNA from ancient teeth, retrograde entrance technique was used. An alternative "ortho-grade entrance technique" is now used in which the DNA is extracted by perforating the tooth from the coronal aspect from the enamel instead of from the apical end [7].

DNA isolation from a lip print

It has recently been determined that lysochromes (Sudan Black) are quite effective in developing recent latent lip prints, as well as older ones, on porous surfaces. Once the print has been detected, a trace is available from which to procure cell remains that can supply enough DNA to be analyzed by the polymerase chain reaction technique.

STRUCTURE OF DNA TECHNOLOGY AND FINGERPRINTING

The forensic scientist obtains a genetic profile of an individual from nuclear DNA recovered from a biological stain deposited at the crime scene. Potential contributors of the stain must either be known to investigators and compared to a known profile or searched against a database of DNA profiles, such as those maintained in the Combined DNA Index System (CODIS).

WHAT IS THE HUMAN GENOME? (Fig.1)

The number of repeating units of genetic information that are sufficient to encode the blue print of a human being is three million. However most of these units are functionless junk. Functional DNA comprises only about a sixth of the total human DNA. But is the remaining really functional junk?

P Bennet says that 3 % of the human genome encodes expressed protein sequences and the inclusion of non-expressed regions with known functions as well as pseudogenes, recognized gene fragments and all intronic sequences brings the total to 30 %. Of the remaining 70 %, 55 % is unique and 15 % is repetitive. Depending on whether the units are dispersed singularly or clustered it is referred to as interspersed repetitive DNA or satellite (tandemly repeated) DNA respectively.

Interspersed DNA has short and long inter-nuclear elements referred to as SINE and LINE respectively. Alu is primate specific and belongs to the SINE family. It is imperfectly repeated around three quarter of a million times within the human genome. This makes it the single most abundant human DNA sequence [8].

Tandemly repeated DNA also called as satellite DNA is a genomic sequence, which is found widely distributed throughout the genome. However it differs from interspersed DNA in that a basic repeat unit is duplicated a number of times at one locus. The repeat units are clustered together and are not singularly present. Also the number of clusters or tandem repeats as they are referred to vary from one individual to the next. This along with their polymorphism makes them very helpful in forensic genetics.

Based upon both the size of the individual repeating unit and the overall repeat length, tandemly repeated DNA has been split into three subgroups, known as satellites, minisatellites, and microsatellites [8].

Satellite DNA

1. First of the tandemly repeating DNA sequences to be discovered
2. So named by its appearance as minor or "satellite" bands that separated from the "bulk" DNA upon density gradient centrifugation
3. The basic repeat can vary from as little as 5 to as many as several 100 base pairs;

However, the overall repeat size at any one locus is enormous, and may cover anywhere from around 100 kb (kilo base pairs to several Mb (mega base pairs).

Disadvantages

1. Because of its enormous size and restricted localization, satellite DNA is of no real use for either individual DNA profiling or genetic linkage studies.
2. Also it is not transcribed and it is found on heterochromatin, which lacks actively expressed genes.[8]

Mini-satellite DNA-single locus probes

These are moderate arrays of tandem repeats spanning approximately 100 bp (base pairs) to 20 kb in length.

It can be subdivided into two types:

1. Telomeric
2. Hyper-variable

Telomeric DNA consists of 10–15 kb of hexa-nucleotide repeats (mainly TTAGGG), added to the telomeres of all chromosomes by the enzyme telomerase

1. It protects the ends of chromosomes from degradation
2. Provides a means for the complete replication of telomeric sequences
3. Plays a role in the pairing and orientation of chromosomes during cell division

Hyper-variable mini-satellite DNA: first discovered in 1985 by Alec Jeffreys and colleagues at Leicester University. Initially the technique developed by Jeffrey's team was known as DNA fingerprinting.

The basic repeat unit may vary in length from six to > 50 nucleotides, with the overall number of repeats at any one locus usually being highly polymorphic between individuals Commonly known as variable number tandem repeats or VNTRs

It is their highly polymorphic nature that makes minisatellites so useful in the field of DNA profiling.

SOUTHERN BLOTTING TECHNIQUE uses the principle on mini satellites

1. Involves hybridizing short synthetic probes containing common core sequences, such as GGGCAGGANG to an individual's genomic DNA.
2. The probes would "stick" to dozens of DNA fragments, the sizes of which were determined by the number of repeats they contained. Consequently a complex banding pattern or "fingerprint" would be produced, which was essentially unique to that individual
3. Offspring would display a pattern made up of equal combinations of the bands present in their parents' fingerprints

DISADVANTAGES

1. There is no practical way of knowing which pairs of bands in the fingerprint represented alleles at a particular mini satellite locus
2. Not possible to calculate allele frequencies
3. Could be a chance matching
4. Potential technical difficulties and a considerable opportunity for human error
5. Uneven distribution throughout the genome made them relatively poor genetic markers. Unlike satellites, which as mentioned previously, tend to cluster centromerically, mini satellites appear to prefer telomeric regions.

Most of the potential for human error lay within a process known as "binning". This was where a decision had to be made as to which allele (or repeat number) corresponded to which band on the Southern blot autoradiograph. Although this was usually easy enough for any one autoradiograph, comparing data from one autoradiograph to the next, or worse still between different laboratories could be considerably more difficult. Today, the replacement of mini-satellite with microsatellite sequences has overcome the problem of binning [8].

Micro-satellites-short tandem repeats

1. Simple mononucleotide to pentanucleotide repeats, varying from a few tens of bases up to typically one hundred
2. They are spread more or less evenly throughout the entire human genome i.e. the eucharyotic part
3. Microsatellites are thought to arise by a process that has been referred to as "DNA slippage", "polymerase slippage", or "slipped strand mis-pairing"
4. These MICROSATELLITES FORM THE PRINCIPLE OF DNA FINGER-PRINTING AND PROFILING
5. Microsatellite DNA forms the marker of choice for various genetic applications

Microsatellites arise by a process called as strand slippage (Fig.2). Slippage is caused within the complex of proteins that is responsible for DNA replication. There is a mis-pairing between the original template strand and newly synthesized DNA strand. Resulting region of unpaired DNA is then forced to loop out. If this loop is on the new strand it results in the addition of a repeat unit.

Bennett says that DNA profiling is the universally accepted system for marking and cataloguing micro-satellite markers [8].

As a result, human microsatellite markers are now named in standard formats—for example, D12S324, where 12 is the chromosome on which the marker is located and 324 comprises a unique identifier. Cytogenetic location, heterozygosity, allele frequencies, and assay conditions, can be obtained via the internet from standard databases. The work is collaborative and information is exchanged regularly to ensure that the relevant globally accessible databases are kept up to date. Large mini-satellite containing DNA fragments are separated in low-resolution media such as agarose.

Microsatellite containing DNA fragments are usually small enough to be amplified using the polymerase chain reaction (PCR) and separated in high-resolution media like polyacrylamide. Because of this, alleles differing in size by only a single repeat unit can be resolved unambiguously. This fact alone has contributed to mini-satellites being replaced by microsatellites [8].

Using only a single probe, the match probability was estimated to be $<3 \times 10^{11}$ and two probes together gave a value of $<5 \times 10^{19}$ (so low that the only individuals sharing DNA fingerprints are monozygotic twins.

Differential lysis

DIFFERENTIAL LYSIS was developed that selectively enriched the sperm concentration in vaginal fluid/semen mixtures, thereby avoiding the problem of the victim's DNA (which is in great excess) masking the rapist. A method to enrich for sperm DNA in a mixture of sperm and epithelial cells is by preferentially lysing the latter using detergent and protease [8].

In addition to genomic DNA, there is another DNA that also plays an important role in genetics i.e. mitochondrial DNA.

Mitochondrial DNA

Mitochondrial (Mt) DNA is inherited from the maternal line and is used to test relatedness if there are several generations between ancestor and descendent. In contrast to genomic DNA, which codes for 1,00,000 genes Mt DNA codes for 13 different genes. It is located in the cytoplasm of every cell. The advantage of mt DNA lies in its copy number, which is between ~200 and 1,700 per cell. This means that it has a greater probability of survival than nuclear DNA does. Forensic applications include analysis of samples that are old or severely damaged, or low in DNA (such as hair shafts) [9]

There are various methods that have been used to analyze DNA and protein namely Southern blotting, Western Blotting, Northern Blotting, Restricted fragment length polymerization and polymerase chain reaction. In

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addition to these there are certain other techniques which have been described below.

Laser capture micro-dissection. (Fig.3)

Laser capture micro-dissection (LCM) is a unique process that does not alter or damage the morphology and chemistry of the sample collected, nor the surrounding cells. LCM can be performed on a variety of tissue samples including blood smears, cytologic preparations, cell cultures and aliquots of solid tissue. Frozen and paraffin embedded archival tissue may also be used. On formalin or alcohol fixed paraffin embedded tissues, DNA and RNA retrieval has been successful, but protein analysis is not possible (requires frozen section). The schematic diagram shown above illustrates the procedure [10].

USE IN FORENSICS:

1. To assess parentage
2. To analyze mixed samples of hair follicles and cells
3. Genomic molecular profiling

Chemiluminiscence

Chemiluminiscence simply means the emission of light as a result of a chemical reaction. Sometimes forensic samples are contaminated with non-human DNA as well. Primate specific alpha satellite DNA sequence on chromosome 17 (D17Z1) is estimated to be present in 500 to 1,000 copies per chromosome.

Hybridization of a biotinylated oligonucleotide probe to sample DNA immobilized on nylon membrane is done. The oxidation of luminol by the horseradish peroxidase enzyme results in the emission of photons, which is detected on standard autoradiography film. The intensity of the signal on film is a function of DNA quantity. This is the principle of chemiluminiscence.

The specificity of this quantitation method for human DNA will be useful for the analysis of samples that may also contain bacterial or other non-human DNA, for example forensic evidence samples, ancient DNA samples, or clinical samples. Less than 150 pg of human DNA can easily be detected with a fifteen minute exposure. The entire procedure can be performed in one and a half hours hours [11].

Flow Cytometry

Flow cytometry is a technique for counting and examining microscopic particles, such as cells and chromosomes, by suspending them in a stream of fluid and passing them by an electronic detection apparatus. It allows simultaneous multi-parametric analysis of the physical and/or chemical characteristics of up to thousands of particles per second

USES

1. Total DNA content (cell cycle analysis, cell kinetics, proliferation, ploidy, aneuploidy, endo-reduplication, etc.)
2. Total RNA content
3. Chromosome analysis
4. Protein expression and localization protein modifications, phospho-proteins

Microarrays

A DNA microarray (also commonly known as gene chip, DNA chip, or biochip) is a collection of microscopic DNA spots attached to a solid surface. Scientists use DNA microarrays to measure the expression levels of large numbers of genes simultaneously or to genotype multiple regions of a genome. Each DNA spot contains picomoles (10^{-12} moles) of a specific DNA sequence, known as probes (or reporters). These can be a short section of a gene or other DNA element that are used to hybridize a cDNA or cRNA sample (called target) under high-stringency conditions. Probe-target hybridization is usually detected and quantified by detection of fluorophore-, silver-, or chemiluminescence-labeled targets to determine relative abundance of nucleic acid sequences in the target.

The core principle behind microarrays is hybridization between two DNA strands, the property of complementary nucleic acid sequences to specifically pair with each other by forming hydrogen bonds between complementary nucleotide base pairs. A high number of complementary base pairs in a nucleotide sequence mean tighter non-covalent bonding between the two strands. After washing off of non-specific bonding sequences, only strongly paired strands will remain hybridized. So fluorescently labeled target sequences that bind to a probe sequence generate a signal that depends on the strength of the hybridization determined by the number of paired bases, the hybridization conditions (such as temperature), and washing after hybridization. Total strength of the signal, from a spot (feature), depends upon the amount of target sample binding to the probes present on that spot. Microarrays use relative quantization in which the intensity of a feature is compared to the intensity of the same feature under a different condition, and the identity of the feature is known by its position.

In addition to the basic knowledge of genetics and various techniques listed above, it is also important for a forensic odontologist to be well versed with a rough estimation of the time of death. Many parameters play a role. A brief discussion of the same follows.

Rigor Mortis: Muscle relaxation immediately after death is followed by a gradual onset of rigidity without shortening of the muscle. This is caused by conversion of glycogen into lactic acid. It is manifested 1-6 hours after death with onset being immediate. It reaches a maximum within 6-24 hours and disappears within 12-36 hours [12].

Livor Mortis: is the settling of blood to the dependent parts of the body. The area where the blood settles will be dark blue or purple in color. It will not usually develop where there is pressure from clothing or objects. Therefore, important information regarding whether

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a victim was clothed for a period of time after death or if body position was changed can be gained from a careful inspection of the livor's distribution. Small spots or hemorrhages, which may be present within the sclera of the eyes, may be suggestive of asphyxia.

Algor Mortis: refers to cooling of the body. Postmortem body temperature declines progressively until it reaches the ambient temperature. The metabolism of the body generates heat which is regulated to a narrow range. If the body cools at a uniform rate, then the rate of temperature decrease could be used to accurately determine the time of death. However, the body temperature is a narrow range, not a fixed temperature. Activity, illness, decomposition, infection and absorption of heat can maintain or raise body temperature after death. The body cools by radiation (transfer of heat to the surrounding air by infrared rays), convection (transfer of heat through moving air currents) and conduction (transfer of heat by direct contact with another object). Therefore, many factors may influence the rate of heat loss. Careful consideration of the scene, clothing, victim size, activity and physical factors must be considered in interpreting cooling rate.

The Glaister equation is one formula used for determining the approximate time period since death based on body temperature.

$$\frac{98.4\% - \text{measured rectal temperature}}{1.5} = \text{approximate hours since death}$$

Temperature has to be considered in light of all the scene data. For example, a deceased person who has been in a closed car all day with the sun shining on the car who is observed at night could not be expected to cool in a regular manner. In fact, an individual in this situation may well have a body temperature above "normal". Several individuals who have studied the effects of body cooling suggest that the rate is not constant, but rather more heat is lost during the first few hours, then as the body begins to reach ambient temperature, the rate of heat loss slows [13].

FOOD IN STOMACH: (This information can be gained at autopsy)

SIZE OF MEAL TIME IN STOMACH (starts to empty within 10 minutes)
Light 1 - 2 hours
Medium 3 - 4 hours
Heavy 4 - 6 hours
Variations:

Liquid is digested faster than semi-solid food, which is digested faster than solid food.

Emotional state may also influence the rate of stomach emptying.

Postmortem Tissue Changes: [13]

Decomposition: Involves two major components. These components are:

Autolysis: The process by which digestive enzymes within the body cells break down carbohydrates and proteins. Autolysis usually starts in the pancreas.

Putrefaction: The major component of decomposition which is due to bacterial activity.

Characteristics of putrefaction include:
1) Gas formation and bloating
2) Green discoloration of abdomen
3) Marbling along blood vessels-a brown black discoloration in blood vessels caused by hydrogen sulfide gas
4) Blisters and skin slippage
5) Loss of hair and nails

Mummification: Drying of the body or its parts with "leather-like" changes. Mummification is characteristically seen on the tips of the fingers and nose. It can occur in as little as 1 - 2 days.

Skeletonization: Characterized by removal of soft tissue. Occurs largely as a result of insects and animals.
Adipocere: Formation of a waxy substance due to the hydrogenation of body fat. A moist, anaerobic environment is required for the formation of adipocere. Methods for the estimation of time of death can be summarized as the rate method and concurrence method.
Rate Method: Estimation by evaluating the presence/absence of an indicator in a deceased in conjunction with the known behavior of such indicators.
Concurrence Method: Estimation by evaluating events which happen at or near the time of death, or offer information suggesting a time period for the death event.

METHOD TYPE INDICATOR [14]

Method Type	Indicator
Rate Method	Rate of drying or discoloration of blood pools
Rate Method	Rigor Mortis
Rate Method	Livor Mortis
Rate Method	Algor Mortis
Rate Method	Decomposition
Rate Method	Flora (plants) around body
Rate Method	Fauna (insects) around body
Concurrence Method	Time of last known meal
Concurrence Method	Stopping of watch (due to trauma/damage)

In addition to analysis of human DNA, analysis of non-human DNA is equally important and finds application in forensics.

Non-human DNA analysis finds application in various fields such as:
1. Illegal trade of endangered species
2. Murder
3. Tiger born DNA in traditional medicines, Rhinoceros horns
4. PCR-based fingerprinting methods such as RANDOM AMPLIFIED POLYMORPHIC DNA (RAPD) can allow identification of plant strains and have been used in the analysis of masses in a murder case.

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5. Bioterrorism-Bacillus Anthracis.

Future of genetic forensics

A ‘sci-fi’ vision of a hand-held device (the ‘lab on a chip’) that would allow rapid DNA profiling at the crime scene is close to realization, with developments in microfabrication of capillary electrophoretic arrays and single integrated platforms that extract, amplify and sequence DNA have already been developed, but it will be some time before such devices are validated for forensic use

DNA DATABASES-ETHICAL ISSUES

As futuristic as it may seem, DNA databases have their own problem. DNA databases raise various ethical issues, as governments often for their selfish interests collect evidence without the consent of the individual under suspicion. This raises serious issues as listed below. It is important for us to take prior consent for use of any information or evidence, which will be used, in court and to ensure that profiles of acquitted individuals are not misused.

The use of any database involves a balance between the rights of the individual and the interests of the state

1. Many samples are taken without consent
2. Retention of profiles of people at a mass screening
3. Retention of profiles of people who have been acquitted
4. In some jurisdictions only when there is a very serious offence is the DNA sample taken
5. Obstacles to overcome
6. Samples may not be pure, may be contaminated and limited in quantity
7. Must pass the test of admissibility in court (admissibility criteria and legislation differ between different countries)
8. External accreditation of forensic laboratories to internationally recognized standards (such as ISO17025) is a prerequisite
9. Adoption of new advances across boundaries is slow

Thus DNA profiling has various uses such as:

1. To identify criminals in forensic science for solving cases such as murders
2. To identify the true biological father to determine paternity
3. To identify racial groups to rewrite biological evolution
4. To verify claims of being relatives to established residents in case of immigrants

However, as powerful as DNA analysis is, it is far from being the sine qua non of forensic casework. DNA evidence must always be considered within the framework of other evidence of many types, and the role of the forensic geneticist is not to make presumptions of guilt or innocence, but to provide unbiased information to judge and jury. Microsatellite DNA has tried to solve this problem because of its specificity and uniqueness. It thus forms the principle of DNA fingerprinting and profiling.

Figure 1. The Human Genome.

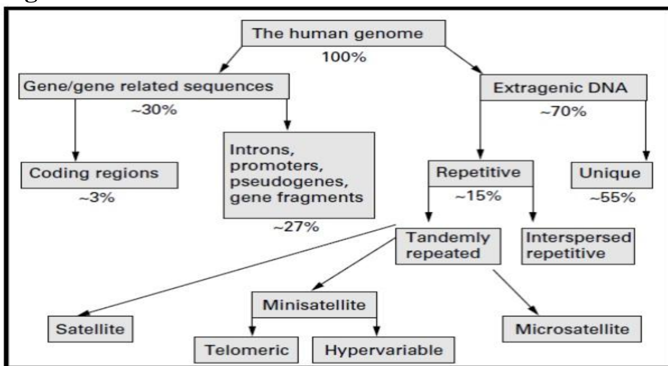


Figure 2. Strand Slippage

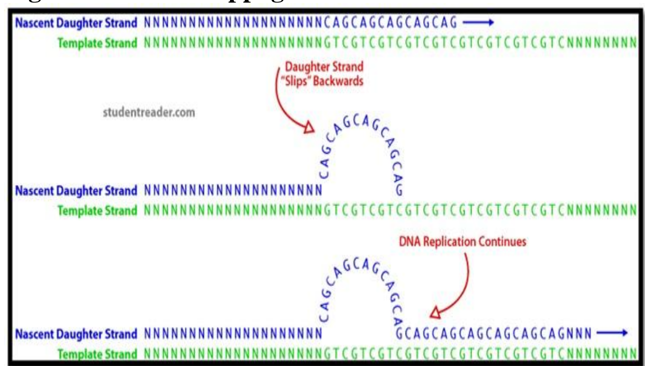


Figure 3. Laser Capture Microdissection

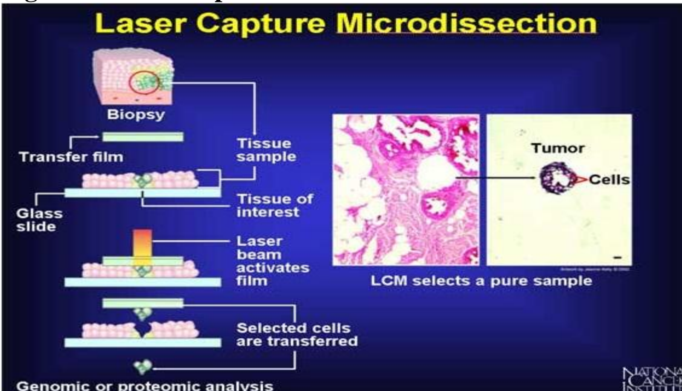
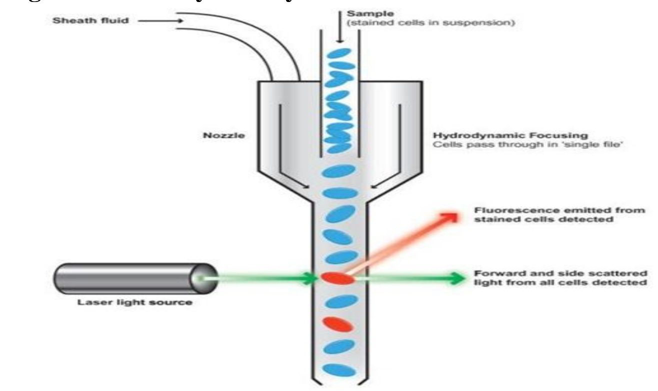


Figure 4. Flow Cytometry



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