Importância do DNA Forense para a Biologia Moderna: uma Revisão

Importance of Forensic DNA for Modern Biology: a Review

Rosilda Paes[a]; Iraquitan Ribeiro[ab]*

[a]Pernambuco University, PE, Brazil
[b]Union Institutions for Educational Development Religious and Cultural, Graduate *Stricto Sensu* Program in Psychoanalysis of Education, PE, Brazil
*E-mail: iraquitan.j@hotmail.com

Resumo

A genética forense é bastante significativa para a biologia, polícia e justiça não só brasileira, mas de qualquer país, pois auxilia na solução de casos criminais e de família, portanto, torna-se indispensável para a biologia uma vez que estuda o DNA encontrado no núcleo de nossas células e presente em toda forma de vida. Este projeto tratou de trazer uma revisão da importância do DNA forense para a biologia moderna a fim de expor as ferramentas atuais mais utilizadas que corroboram e facilitam respostas para a polícia e justiça em casos criminais e de família.

Palavras-chave: Biologia. Chave da Vida. Criminalística. Evidências Biológicas. Genética.

Abstract

Forensic genetics is very significant for Biology, police and justice not only in Brazil, but also in any country as it assists in solving criminal cases and family, so it is essential to Biology since that studying the DNA found in our cells´ nuclei and present in all lives. This project tried to bring a review on the importance of forensic DNA for modern Biology in order to expose the most commonly used current tools that support and facilitate answers for police and justice in criminal cases and family.

Keywords: *Biology. Biological Evidence. Criminalistics. Genetics. Key of Life.*

1 Introduction

The DNA (deoxyribonucleic acid) contains the key to the nature of living things. It stores the hereditary information that is passed from one generation to the next. DNA molecules consist of multiple copies of a single basic unit and nucleotide call occurs in four forms: adenine (A), thymine (T), guanine (G) and cytosine (C). They fit into a simple pairing, where the fits perfectly with T, and G with C. The pairing idea implies a double-helix structure, with two molecular chains moving in opposite directions. The way the molecule was organized immediately suggested solutions for two of the oldest mysteries of Biology: how hereditary information is stored, and how it is replicated. Life would be another chemical reaction carried out in a laboratory, the product of normal chemical and physical processes? The double helix brought the answer and with it the revolution of the materialistic thought of the Enlightenment to the scope of the cell. And there is nothing special in it. The double helix is a fascinating structure, but its message is predictable: life is simply a matter of chemistry (WATSON, 2005; STRACHAN; READ, 2013).

The key to molecular Biology, contained in the molecule becomes a new science whose progress over the last sixty years has been impressive. Not only did it net an impressive range of new conceptions of fundamental biological processes, as it has also had an increasingly profound impact on medicine, agriculture, and the law (WATSON, 2005).

DNA is no longer a matter of interest only to scientists; it is part and affects us all. In the mid-sixties (1960), the basic mechanics of the cell had already been deciphered, and it is known as, through the "genetic code", the alphabet four DNA sequence of letters is translated into twenty alphabet letters proteins. The next burst came in 1970 with the introduction of DNA manipulation techniques and reading a sequence of base pairs. Now we can really mess with the DNA of living organisms and read the basic life story. New and extraordinary scientific perspectives have been opened: unraveling genetic diseases for cystic fibrosis cancer; revolutionizing criminal justice with new genetic identification methods, determining the closest fingerprint of each being; thorough review ideas about human origins, about who we are and where we come from; and improving agronomically important species with an efficacy previously undreamed (STRACHAN; READ, 2013).

It's our DNA that distinguishes us from all other species, and that makes us creative beings, conscious, dominant, destructive creatures we are and becomes the instruction manual of the human species.

Clearly, the science of DNA molecular Biology, what it can do for us, it still has a long way to go. But all these things will come true. The first sixty years of the DNA revolution witnessed a major scientific progress as well as the first applications of this progress to human problems. The future will see many other scientific advances, but, increasingly, the

focus is on the growing impact of the DNA in our way of life chemistry (WATSON, 2005; STRACHAN; READ, 2013).

In this review, the question of the importance of forensic DNA for Biology has been addressed in order to prove the effectiveness of this investigative tool not only for health professionals and society itself.

2 Development

2.1 Biology theoretical foundations

Biology is the branch of science that studies living beings. It focuses on the organisms´ characteristics and behavior, the species and individuals´ origin, and how they interact with each other and with their environment (STRACHAN; READ, 2013).

All bodies transmit their inheritance through genetic material based on nucleic acids may be either DNA (deoxyribonucleic acid) or RNA (ribonucleic acid), using a universal genetic code. A nuclear and structuring concept in Biology is that all life has descended from a common ancestor by a evolution process. Although the underlying unit, life exhibits a surprising diversity in morphology, behavior and life cycles and therefore has a vast field of research that is not usually studied as a single subject, but divided into several subordinate (STRACHAN; READ, 2013).

2.2 Classical biology to molecular

In 1865, Gregor Mendel first established the inheritance patterns of some existing characteristics in pea plants, showing that obeyed simple statistical rules. Although not all features show these Mendelian inheritance patterns, Mendel's work proved that the application of statistics to genetics could be of great use. Since then, more complex patterns of inheritance have been demonstrated (BRUCE, 2004).

From his statistical analysis Mendel defined the concept of allele as the fundamental unit of heredity. The term "allele" as used by Mendel, the idea expressed "gene," while nowadays it is used to specify a variant of a gene (BRUCE, 2004).

Only after Mendel's death was that his work was rediscovered, understood (early twentieth century) and was given due weight by scientists who then worked on similar problems. Mendel was unaware of the physical genes nature .We now know that genetic information is contained in the DNA (some viruses have the genetic information contained in RNA). The DNA manipulation can change the inheritance characteristics and the bodies (BRUCE, 2004).

It is the study of the molecular Biology level, overlapping in large part to other fields of Biology, genetics and particularly biochemistry. In it, studying the interactions among the various cellular systems, including the interrelationship of DNA, RNA and protein synthesis, and how these interactions are regulated in addition to the physiological properties of cells, as well as their behavior, interactions and environment, both the microscopic level as molecular (BRUCE, 2004).

Through genetics, that studies the genes, heredity, and the variation of organisms that are allowed to study how the biological characteristics are transmitted from generation to generation. The genetic term was first used to describe the study of variation and heredity, by the scientist William Batesson. Humans, as the time prehistory used genetic knowledge through domestication and selective breeding of animals and plants. Currently, gene provides valuable tools for the investigation of gene functions, i.e., the analysis of genetic interactions (BRUCE, 2004).

Within the organisms, genetic information is usually contained in the chromosomes, where it is represented in the chemical structure of the DNA molecule. The genes encoding the information necessary for protein synthesis, in turn influence the proteins in large part, the final phenotype of an organism (BRUCE, 2004).

2.3 Genetics applications

As important to humanity as the medical genetics are the applications of this science to the animal and plant breeding. We know that genetics practically began with the animals domestication (pre-scientific phase) and with Mendel´s plant genetics studies, but we live a halt not well dimensioned by the scientific community that is the production of genetically modified organisms or OMG, the impact on the environment and even on DNA stability is still not entirely known (GRIFFITHS, 1998).

The above applications are part of medical genetics. Other uses of human genetics are related to forensic medicine and criminology, namely: fabrics recognition, identity recognition through genetic characteristics especially fingerprint (fingerprinting) and the DNA test is for paternity identification of accident victims or potential murderers, in which we will stop us forward more (GRIFFITHS, 1998).

2.4 Understanding DNA

Proteins are made up of amino acids organized around the four carbon atom linkages. Although there are varieties of only twenty amino acids long sequences allow multiple repetitions of tens of thousands of combinations of amino acids to form a variety of proteins. In fact, there are about 50,000 different types of proteins in our body. The same twenty amino acids 50 thousand different combinations are connected to the other in long chains folded on themselves (BRUCE, 2004; GRIFFITHS, 1998).

The gene is a DNA region that controls a hereditary characteristic specifying how hair color, height, shape of nose and thousands of other traits. The specific sequence of bases which make up the gene generally corresponds to a single protein or complementary RNA (BRUCE, 2004; GRIFFITHS, 1998).

In DNA, the length of each filament is 600,000 times greater than the width. When cell nuclei chromosomes are divided, each of the strand serves as a template for the

formation of a new corresponding filament for each of the new cells due to the structure and base pairing. This explains the second fundamental characteristic of DNA, usually one that associates with double helix: the ability to replicate (BRUCE, 2004; GRIFFITHS, 1998).

In other words, when DNA is duplicated within each cell which is undergoing cell division, their ability to control the cells and body functions directing the proteins production also doubles. This brings us back to the main DNA function: to produce proteins. As nucleic acids direct the production of proteins and the protein sequence is unique to each person, it is the DNA that in the final analysis, controls all hereditary characteristics (BRUCE, 2004; GRIFFITHS, 1998).

The discovery of Crick and Watson was the culmination eighty years of research by many scientists. Knowledge of the structure leads to the code reading work and Watson Crick allowed to immediately realize the possibility to read and interpret the genetic background of any organism including humans. When Fredrick Sanger biochemical surveys allowed us to start the sequencing of RNA, in the 1960s, it became theoretically possible to understand all the enormous amount of information on DNA, not just isolated examples. This led to a interosseous really know the relationship between each gene and all physical characteristics, including genetic diseases (BRUCE, 2004; GRIFFITHS, 1998).

In 1975, Walter Gilbert was the first to apply a specific chemical treatment to DNA to break it into fragments and recognize the usefulness it might have on reading the text. Through new method, Sanger became theoretically possible to determine all the "text" that governs heredity of any living organism, including human (BRUCE, 2004; GRIFFITHS, 1998).

DNA molecules do two important things. Firstly, they replicate, which means that they make copies for themselves. It can be said that the replicating function DNA is like the function of a model factory, quality hundred percent where the DNA is copied faithfully plans, virtually error-free, according to Dawkins. Thus, DNA is an indirect supervision of the manufacture of a different type of molecule which is the protein (BRUCE, 2004; GRIFFITHS, 1998).

In the composition, the biochemical Erwin Chargaff determined the proportions of the four compounds: adenine (A), cytosine (C), guanine (G) and thymine (T). In 1950, he determined the exact proportionate amounts of the DNA bases in each molecule: = cytosine guanine adenine thymine =. Alfred D. Hershey, corroborated Avery group that DNA and not the genetic material is protein. The nucleic acids are provided in two types: DNA (deoxyribonucleic acid) and RNA (ribonucleic acid). The bases are the same in both molecules, except for uracil, which replaces thymine in RNA (BRUCE, 2004; GRIFFITHS, 1998).

It was discovered double stranded DNA by Watson and Crick. Due to the angles at which the chemicals of DNA bind to each other, all DNA molecules consist of two parallel spiral tracks, such as a railing spiral staircase - hence the name immediately became famous with the Watson-Crick discovery: the double helix and certainly contributed to the development of a new area of research which arose molecular Biology (BRUCE, 2004; GRIFFITHS, 1998).

This feat gained the science knowledge of how life forms are organized from generation to generation. Before that, with Mendel, it was already known that human characteristics heredity was due to genes. But it was the double helix structure discovery which allowed the clarification of how to give genetic transmissions. "Before Watson and Crick, Linus Pauling had described the structure of DNA in the form of simple helix" (BRUCE, 2004; GRIFFITHS, 1998).

The DNA molecule, which in Portuguese is called deoxyribonucleic acid, contains the heredity of every code. For the model proposed by Watson and Crick, it is constituted by two parallel chains together in nucleotide sequence arranged on the helically space, or turn on its own axis (BRUCE, 2004; GRIFFITHS, 1998).

2.5 Gene Cloning

Is the isolation and amplification of DNA PCR, but very useful in certain situations. It involves the use of restriction endonucleases, the restriction map creation and use of vectors for the recombination and cloning of the gene under study (WATSON, 2005; STRACHAN; READ, 2013).

The using together of the probes and restriction enzymes allowed the development of very accurate DNA detection techniques. Variations of this method today enable the RNA and protein fragments identification, the latter using an antibody probe. They are huge and promising applications of this technology:

- ✓ The identification and treatment of diseases genetically conditioned;
- ✓ In very sensitive diagnosis of infectious diseases;
- ✓ In prenatal diagnosis;
- ✓ In genes´ therapeutic manipulation;
- ✓ The creation of hybrid and transgenic organisms in medicine, agriculture and livestock;
- ✓ In the pharmaceutical industry;
- ✓ In evolutionary descent and studies;
- ✓ In forensic medicine, etc. (WATSON, 2005; STRACHAN; READ, 2013).

2.6 Uses and discoveries on DNA

From the research on DNA and their functions, scientists can now manipulate the genes directly under increasingly sophisticated ways. It is possible, for example, to extract DNA from a cell, this DNA fragment, separates the parts containing a number of specific genes and introducing these genes into other living organism. This is what makes the Genetic Engineering, identifying a gene by isolating it and multiplying it from various living organisms. DNA can be extracted from a drop of blood, a hair or piece of bone (WATSON, 2005;

KREUZER; ADRIANNE, 2002).

It is expected it that by decoding the DNA codes, all possible diseases that the man may have and how to change the orientation of that body can be detected, eliminating them. Another use of DNA, widespreadly, is on various issues of Legal Medicine (ALMEIDA, 2001).

2.7 The DNA in forensic medicine

Court decisions today are not only merely based intuition anymore, but also in laboratory tests that must be, as appropriate, funded by the state. There are several uses combined of DNA on issues involving paternity, crime, sexual violence, for example. The paternity test is one of the most used resources for Justice today, from techniques which employ the examination of DNA. To confirm the innocence or guilt of an accused of crime or sexual violence since having comparison means between the material found on the victim and the material found in a suspect DNA tests are performed rightly margin of 100% or close to it (IWAMURA; PARADELA; FIGUEIREDO, 2006).

2.8 Forensic study

The DNA study area involving crimes either by the need to identify the perpetrator or relate it to the crime scene is called forensic DNA to differentiate non-criminal identification from situations, such as paternity cases, which are civil, and even the identification of people killed and could not be identified by traditional methods (SMARRA; PARADELA; FIGUEIREDO, 2006; PARADELA; FIGUEIREDO, 2008).

The DNA as human identification tool can be used in various situations such as: Identifying and linking suspects to the crime; Distinguishing isolated serial crimes; Acquitting people falsely accused; Identifying remains (SMARRA; PARADELA; FIGUEIREDO, 2006 PARADELA; FIGUEIREDO, 2009).

2.9 Crime solution through DNA

Genetic DNA typing is the most important tool produced by modern science and placed at the disposal of justice to combat crime and impunity. DNA has been used to solve all kinds of crimes using biological samples such as blood, semen, hair, saliva and urine, collected in various types of substrates such as clothes, bottles, cutlery, cigarette butts, stamps and condoms. In addition to incriminate, the DNA has been used to acquit people falsely accused of crimes, including correcting mistakes made by the judicial system (SMARRA; PARADELA; FIGUEIREDO, 2006 PARADELA; FIGUEIREDO, 2009).

In order for the DNA study in forensic cases succeed, it is essential that biological samples at the scene be correctly identified, collected, packaged, stored and sent to the lab for study. The collection of the biological sample at the scene is specific assignment of the coroner, and the most important step to success in identification studies. In this sense the forensic DNA laboratory has provided an important service in the area of public safety through the publication of a manual of biological sample collection at the crime scene and forensic experts training civil police (SMARRA; PARADELA; FIGUEIREDO, 2006 PARADELA; FIGUEIREDO, 20009).

The suffering of the families who had lost relatives has devastating consequences. Failure to resolve these cases is violence committed against them and blatant disregard for human rights, and as such, must be struggled (SMARRA; PARADELA; FIGUEIREDO, 2006 PARADELA; FIGUEIREDO, 20009).

The Database aims at gathering genetic information about children, adolescents and adults missing who may still be alive and people who were killed and could not be identified by traditional methods, victims of all kinds of violence (LAYTON, 2007).

Two types of data are stored: the genetic information from the DNA donated by relatives of missing persons and the genetic information from the DNA extracted from the remains (bones, teeth, tissue, etc.). The crossing of the genetic information stored in the database allows for contact both ends of the problem: the person (or mortal rest unidentified) and family (LAYTON, 2007).

In order for the database to function efficiently, it is important the participation of the IML (Legal Medical Institute), government agencies related to human rights and non-governmental organizations (ONG). Government agencies and ONG are tracking work and screening of the alleged victims' families, for the subsequent obtaining biological sample to study the DNA. The Laboratory is responsible for the final step, which is the study, storage and comparison of genetic data from the two ends of the problem: the person (or unidentified mortal rest) and family (LAYTON, 2007).

2.10 Genetic and forensic DNA

Physical evidence that are not collected, documented and preserved appropriately has no scientific value in criminal investigations. For the correct criminals´ identification from DNA analysis and the maintenance of chain of custody, must follow strict parameters for all process steps. It is common to meet a very high number of biological samples in locations where developed violent crimes and sometimes you can get yourself hundreds of biological evidence in a single environment (PARADELA; FIGUEIREDO; SMARRA, 2001).

Throughout criminal investigations, the main materials subjected to DNA analysis include blood and blood spots; semen and semen stains; hairs (with root); tissues, bones and organs. Other sources such as urine, saliva and feces may also be analyzed, but it should be noted that only nucleated cells serve to nuclear DNA genotyping (LEE; LADD, 2001).

Information obtained from biological evidence can call these people and the objects and locations (PARADELA;

FIGUEIREDO; SMARRA, 2001). Therefore, one must consider the cell transfer possibilities involving different people, objects and environments. The transfer of biological evidence may be direct or secondary, also indirect call. In cases of secondary transfer, the biological material is carried by an intermediate medium. In this case there is no direct contact between the source of biological material and the deposit surface. It is very important that professionals involved in the investigation are careful not to put their own cells in places and objects associated with the crime and not to transfer cells present in the materials analyzed from one point to another (LEE; LADD, 2001).

Evidence located at crime scenes must be shot before touched or moved. Their relative location on environment and conditions of the material must be documented through photos, film or, in the absence of such resources, through schemes and detailed reports. On receipt of the samples, the forensic laboratory should investigate and record the presence and packaging state of the seals and labels. Data on the evidence must be checked. If you perform some preliminary test on the material, this procedure must be registered (LAYTON, 2007).

2.11 Sample collection

The biological material in liquid form is typically collected by absorption. They can be removed with the aid of a disposable syringe or an automatic pipette, always sterile and transferred to a laboratory tube also sterile. When already coagulated, samples should be transferred to the pipe using a spatula free from contaminants (LEE; LADD, 2001).

We need to set strict standards for all steps of the DNA analysis, including the collection, chain of custody maintenance, laboratory analysis and interpretation of results. To prevent any and all biological evidence, it must be subjected to forensic lab as fast as possible in order to avoid degradation, contamination and mixing of the material. It is essential that the items be packaged separately, each sample identified and sealed. The state in which biological samples are found to be documented and the relative position of each item must be documented (SMARRA, PARADELA; FIGUEIREDO, 2006).

Some recommendations as the use of gloves and free from contaminants instruments are often forgotten by the fact that the professional responsible for collection of biological material works without prior training, without the proper material, under great mental load and speed for pressure conditions due to the fact that there is a small number of police in some regions of the country, and therefore they can not ensure the isolating of all the crime scenes (SMARRA, PARADELA; FIGUEIREDO, 2006).

2.12 The DNA and the Brazilian family

In terms of social impact, it is very difficult to establish a parallel between the forensic genetics and other scientific tools used for justice, since none of them are compared to this in terms of their high discrimination power. However, law operators and the scientific community should be alert to the fact that DNA tests are not absolutely infallible, like any other human activity. We need to program in Brazil, as already occurs in other countries, strict quality standards to ensure the credibility of this important investigative tool (LEITE, 2000).

2.13 The human DNA identification: applications and limits

The gene recombination process provides a high variability degree among living organisms. Every human being has a unique genetic profile, with the exception of monozygotic twins who share the same set of genes. As the DNA molecule has specific regions with considerable genetic variability can be compared to a DNA barcode able to identify and compare individuals, including determining whether or not a link between these genetic (SMARRA, PARADELA; FIGUEIREDO, 2006; OLIVEIRA-COSTA, 2003).

The typing by DNA analysis is an important tool for the distribution of justice and can make it more agile due to time and resource savings. Notably, many clinical laboratories are switching to the execution of such genetic tests, since these services are a lucrative activity. However, in several cases, the offering of the service is not accompanied by the necessary quality guarantees (SMARRA, PARADELA; FIGUEIREDO, 2006; OLIVEIRA-COSTA, 2003).

A key issue concerning the DNA use as evidence is the scientific validation of analytical methods. For DNA analysis, several questions can be postulated for the interpretation of data, including at this point the choice and the proper use of techniques; the aforementioned population frequencies used for the calculations and the type of statistical analysis employed; the adopted quality controls; the procedures documentation; the quality of used equipment and reagents and technical training of the professionals involved (SMARRA, PARADELA; FIGUEIREDO, 2006; OLIVEIRA-COSTA, 2003).

All steps taken for the typing of DNA, from collection to the interpretation of statistical significance of the data obtained will be embodied in an expert report written that will serve the interests of its readers. In the final instance, the report may also serve as conviction element for judges, prosecutors and lawyers from criminal prosecution (SMARRA, PARADELA; FIGUEIREDO, 2006; OLIVEIRA-COSTA, 2003).

It is up to lawyers, judges and the scientific community be aware of the fact that the tests are not absolutely infallible, like any other human activity. It must be programmed in Brazil, as already occurs in other countries, strict quality standards to ensure the credibility of such an important tool (SMARRA, PARADELA; FIGUEIREDO, 2006).

2.14 Techniques used to genotyping of genetic markers

The DNA quantification after its extraction is important for improving the quality of the resulting DNA product PCR16.

Excess DNA in a PCR sample can saturate the reaction, causing them to appear technical artifacts and nonspecific amplification which may hinder their analysis. Since its lack may result into the loss of one allele, when the individual is heterozygous, or even in its non amplification (BUTLER, 2004).

The DNA quality and quantity must be examined after extraction, and checked the degradation possibility. When referring to samples used in criminal or liable to degradation and contamination investigation, it is recommended to use the quantification of human DNA. Such quantification can be accomplished by hybridization of a probe using a given locus in a DNA sample immobilized on a nylon membrane - dot blot and by commercial kits. Although these techniques are more complex and expensive than spectrophotometry, they quantify the human DNA only, as they have the same specific probes. This feature may be essential in forensic cases there is a possibility of external DNA contamination. However, it is often not used because there is a need of 5 to 10μL DNA product, which frequently is not obtained (MANDREKAR *et al.,* 2001).

A method which is replacing other techniques for quantification using a small amount of DNA, being specific for DNA, and also allowing for the presence of the polymerase enzyme inhibitors and DNA quantification by real time PCR. Especially in forensic cases there tiny amount of DNA is being highly recommended. It consists of using fluorescence markers that are used for the amplification of regions of human genome (ANDERSON, 2002).

Real time PCR is a technique that should be reported, due to the fact of being utilized in forensic science to determine the amount of viable human DNA for amplification. This technique differs from traditional PCR by having probes labeled with fluorophores providing real-time detection of the amplified fragments is simultaneously quantified. Thus, there is no need of using gels and analysis by Sourthern blotting (ANDERSEN, 2003).

However, to perform the real-time PCR, specific equipment and appropriate probes are required. The human DNA can be specifically quantified for further analysis of the genetic profile by STRs, as well as to verify the presence or absence of enzyme inhibitors polymerase (ANDERSEN, 2003).

It simply consists of the selective PCR amplification of a specific DNA target sequence from a heterogeneous collection of DNA, using a pair of primers that are complementary to a certain extent in both DNA strands to be amplified. The target DNA sequence, whose continuation is originally known, is called the template DNA. The DNA polymerase enzyme directs the positioning of DNA precursors - dNTPs - starting the synthesis of new DNA strands. With increasing temperature, the DNA polymerase enzyme catalyzes the reaction, incorporating the nucleotide at the terminal position to the initiator, adding the bases of the template DNA, promoting extension of fita (SAIKI; SCHARF; FALOONA, 2001).

The PCR reaction is prepared using various reagents that must have specific concentrations for all kinds of analysis. Currently, there are several PCR kits containing all pre-standardized reagents that facilitate use of PCR in forensic laboratories. The reagent that will direct the optimization of each reaction will be the primer or primer, which flank DNA region to be copied, and an oligonucleotide synthesized chemically and added to the reaction at high concentrations (BUTLER, 2004).

PCR involves three steps: denaturation, annealing and polymerization. Denaturation occurs when the DNA molecule is heated above the temperature of 90 ° C, wherein the double helix hydrogen bonds are broken, affecting the separation of the complementary strands. The next step is the primers´ hybridization, attached to two regions: forward and reverse, at a temperature which may vary from 45 to 72 °C and must first be optimized. The last step is the polymerization where the DNA polymerase catalyzes extension of the tape in the direction 5'→ 3`, examining the starting primer by incorporating the appropriate nucleotide (A - T C - G) (BUTLER, 2004).

The Single Sequence Length Polymorphism - SSLP or single sequence length polymorphism encompass or VNTR variable number tandem repeats, or minisatellites, also the STR and microsatellite or short tandem repeats and function as fingerprint markers in the genome of each individual. The difference between them is the length of sequence repeats, and microsatellites in this structure are shorter, since they have formed repetitions from 2 to 9 base pairs, and minisatellite, 10-64 base pairs. This satellite DNA in most cases is not transcribed (NELEMANN; MOLLER; MORLING, 2004).

The Single Nucleotide Polymorphism - SNP or single nucleotide polymorphism is a DNA sequence variation occurring when a nucleotide is modified in other DNA sequences that may or may not encode genes. Currently, STRs and SNPs are widely employed for human identification and have significant differences. The analysis of SNPs may also be associated with individual phenotypes, with a further possibility of identifying physical characteristics such as the iris color (BUTLER, 2004; GILL, 2005).

Electrophoresis is a widely used methodology for the separation, isolation, analysis and handling of nucleic acids. The nucleic acids have an overall negative net charge, due to its phosphate groups of the scaffold, therefore, when applied to an agarose or polyacrylamide gel they will migrate towards the anode in an electrical field. Under appropriate buffer conditions, voltage and milliamperes, small fragments migrate more easily than larger ones. Currently, capillary electrophoresis is widely used and has the same principle as the electrophoresis gel analyzed by laser, with the difference that has to capillary electrophoretic separation of the fragments

DNA (BUTLER, 2004; MANDREKAR *et al*., 2001).

The DNA fragments amplified by PCR are identified after polyacrylamide gel electrophoresis followed by staining with silver or by fluorescent signal detection, wherein the primers used in PCR are labeled with fluorochromes, allowing analysis by automated sequencer. The type variation type and gel concentration provides different separation characteristics, allowing different resolutions and analysis. In characterizing genetic link polyacrylamide gel electrophoresis or capillary electrophoresis is used for analyzing images. In addition or paternity exclusion, compares the alleles present in the child with the alleged father, and one would be required maternal allele and the other parent. The same goes for inclusion suspected of a crime, which compares the DNA found on the victim, as with bite marks or semen presence, or the crime scene. There may be a mixture of biological samples containing the victim DNA and the aggressor. In this way, the victim's DNA is faced with the suspicious and successively with the DNA of the samples present in the crime scene (SULLIVAN *et al*., 2002).

Agarose or polyacrylamide gels may be made of a variety of shapes, sizes, and porosities and can be run in a number of different configurations. These parameters choices depend primarily on the size of fragments to be separated. **Polyacrylamide** gels are more effective at separation of small DNA fragments (5-500pb), which is the case in forensic DNA analysis, as its resolving power is extremely high. But, despite of being run rapidly and accommodating comparatively large amounts of DNA, polyacrylamide gels have the disadvantage of being more difficult to prepare and handle than capillary electrophoresis (SAMBOOK *et al*., 2001; FORNEY, 2001).

Agarose gels have lower resolving power than polyacrylamide gels, but have a greater range separation. DNAs of 50bp to several megabases in size can be separated on agarose gels of various concentrations and configurations. Small DNA fragments (50-20000pb) are best resolved in agaroses gels run in conformation horizontal electric field strength and direction constant. The DNA fragments are compared with size markers or ladders or standards (SULLIVAN *et al*., 2002).

It should be noted that capillary electrophoresis is widely used in forensic DNA analysis by enabling large numbers of samples to be analyzed in an automated manner, and require few sample quantities for the injection process and can be easily reinjected if necessary. Capillary electrophoretic separation is performed in less than one hour, compared to the many hours required to the one performed in polyacrylamide gels for human identification. Besides time, the number of steps to prepare the acrylamide gel causes may be a greater chance of error in handling. The disadvantage is the initial cost for the purchase of equipment, much higher than those being used in gel electrophoresis polyacrylamide (BUTLER. 2004).

2.15 The judicial expertise in forensic genetics in Brazil

There is no perfect crime. This sentence is a truth that became even more evident with the investigative genetics use. In all metropolises throughout the world for crimes difficult to be solved, however, the forensic genetics laboratories can now see the invisible, the DNA molecule (deoxyribonucleic acid), cell component responsible for loading and transmit genetic information in all people (IWAMURA; PARADELA; FIGUEIREDO, 2003; SMARRA; PARADELA; FIGUEIREDO, 2006).

Scientific evidence is an important component of many processes in civil and criminal areas. Usually, the technical nature of information is not fully understood by all law enforcement professionals. In terms of social impact, it is very difficult to establish a parallel with other scientific tools used for justice, since none of them are compared to genetics in relation to their high discrimination power. However, lawyers, judges and the scientific community should be alert to the fact that the tests are not absolutely infallible, like any other human activity (SMARRA; PARADELA; FIGUEIREDO, 2006).

By using DNA evidence, it is known that DNA profiles are used by criminal investigators to prove the guilt or to save an innocent. Besides, it has other purposes as paternity testing and other cases where the authorities need to prove whether individuals are relatives or not, to identify corpses to study the evolution of human populations and hereditary diseases (SMARRA; PARADELA; FIGUEIREDO, 2006; FONSECA, 2005).

3 Conclusion

We saw that Biology has numerous branches and among these gene is located. In turn, the gene has a very important tool that is DNA. It is the key to all human beings, where we leave traces that can be used by forensic your favor. It is necessary a greater approach to the subject, and its goals contribute to the elucidation of criminal and social cases, as an indispensable tool is easily found in all lives´ forms.

References

ALMEIDA, M.C. A prova do DNA: uma evidência absoluta? Âmbito Jurídico, 2001. Disponível em http://www.ambito-juridico.com.br/site/index.php?n_link=revista_artigos_leitura&artigo_id=5534. Acesso em: 30 jun. 2014.

ANDERSON, S. Sequence and organization of the human mitochondrial genome. *Nature*, v.290, p.457-465, 2002. doi: 10.1038/290457a0.

ANDERSEN, J. Quantification of DNA by slot-blot analysis. *Methods Mol. Biol*., v, 98, p.19-26, 2003.

BRUCE, A. *Biologia molecular da célula*. Porto Alegre: Artmed, 2004.

BUTLER. J.M. Short tandem repeat analysis for human identity testing. *Current Protocols in Juman Genetic.*, v.14, n.8, 2004;14(8). doi: 10.1002/0471142905.hg1408s41.

FONSECA C. Paternidade brasileira na era do DNA: a certeza que pariu a dúvida. *Cad. Antropol. Soc.*, v.22, p.27-51, 2005.

FORNEY LJ. Structure of microbial communities in activated sludge: potential implications for assessing the biodegradability of chemicals. *Ecotoxicol. Environ. Safety*, v.49, n.1, p.40-53, 2001.

GILL, P. Automated short tandem repeat (STR) analysis in forensic casework. *Eletrophoresis*, v. 1543-1552, 2005.

GRIFFITHS, A.J.F. *Introdução à genética*. Rio de Janeiro: Guanabara Koogan, 1998.

ISFH - Internacional Society For Forensic Haemogenetics. Recommendations of the DNA commission of the internacional society for forensic haemogenetics relating to the use of PCR-based polymorphism. *Forensic Sci. Int*., v.55, n.1, p.1-3, 2002.

IWAMURA, E.S.M.; MUÑOZ, D.R. Analise de DNA em Medicina Legal, banco de dados e controle de qualidade. *Saúde Ética Justiça*, v. 8, n.1/2, p.13-17, 2003.

KREUZER, H.; ADRIANNE, M. *Engenharia genética e biotecnologia*. Porto Alegre: Artmed, 2002.

LAYTON, J. *Genética forense*: como funciona o banco de dados de DNA nos Estados Unidos. São Paulo: How Stuff Works Brasil, 2007.

LEE, H.C.; LADD, C. Preservation and Collection of Biological Evidence. *Croatian Med. J.,* v.42, n.3, p.225-228, 2001.

LEITE, E.O. *DNA como meio de prova de filiação*. Rio de janeiro: Forense; 2000.

MANDREKAR, M.N. *et al.* Development of a human DNA quantitation system. *Croat Med. J*., v.42, n.3, p.336-342, 2001.

NELEMANN, L.J.; MOLLER, A.; MORLING, N. PCR typing of DNA fragments of the short tandem repeat (STR) system in Danes and Greenland Eskimos. *Forensic Sci. Int*., p.6-51, 2004.

OLIVEIRA-COSTA, J. *Entomologia forense*. Campinas: Millennium; 2003.

PARADELA, E.R.; FIGUEIREDO, A.L.S. Uso das tipagens por DNA nos tribunais. Jus Navigandi 2008. Disponível em http://jus.com.br/artigos/10808/uso-das-tipagens-por-dna-nos-tribunais. Acesso em 18 mar. 2014.

PARADELA, E.R.; FIGUEIREDO, A.L.S. *A perícia judicial em genética forense no Brasil*. São Paulo: LTC, 2009.

PARADELA, E.R.; FIGUEIREDO, A.L.S.; SMARRA, A. A identificação humana por DNA: aplicações e limites. Âmbito Jurídico, v.30, n.9, 2001.

SAIKI, R.K.; SCHARF, S.; FALOONA, F. Enzymatic amplification of beta-globin genomic sequences and restriction site analysis for diagnosis of sickle cell anemia. *Science*, v.20, p.1350-1354, 2001.

SAMBROOK, J. *Molecular cloning*. New York: Cold Spring Harbor Laboratory, 2001.

SMARRA, A.; PARADELA, E.; FIGUEIREDO, A. *Genética forense no Brasil*. São Paulo: Scientific American Brasil, 2006.

SULLIVAN, K.M. *et al*. Automated DNA profiling by fluorescent labeling of PCR products. Genome Resarch, 2002. Disponível em: http://genome.cshlp.org/content/2/1/34.short 1-40. Acesso em: 15 jun. 2014.

STRACHAN, T.; READ AP. *Genética molecular humana*. Porto Alegre: Artmed, 2013.

WATSON, J.D. DNA. *O segredo da vida*. São Paulo: Companhia das Letras, 2005.