.Advancement In DNA As Source Of Biometric Authentication

Mohammed Sanaullah Qaseem, Syed Abdul Wahab Asif, Zeeshan Fatima Armeen, Israr Ahmed Qureshi

Associate Professor, Nizam Institute of Engineering and Technology.
Associate Professor, Nizam Institute of Engineering and Technology.
Assistant Professor, Nizam Institute of Engineering and Technology.
Assistant Professor, Nizam Institute of Engineering and Technology.

Abstract

DNA differs from standard biometrics in several ways. DNA requires a tangible physical sample as opposed to an impression, image, or recording. DNA matching is not done in real-time, and currently not all stages of comparison are automated. DNA matching does not employ templates or feature extraction, but rather represents the comparison of actual samples.

Keywords

Deoxyribonucleic acid Biometrics, DNA Sources, DNA Amplification Polymerase Chain Reaction, Electrophoresis, Miniature Analytical Thermal Cycling Instrument, Timeline with New Technology.

1. DNA Identification technology

Deoxyribonucleic acid (DNA) Biometrics could be the most exact form of identifying any given individual. Every human being has its own individual map for every cell made, and this map, or 'blueprint' as it more often is called, can be found in everybody cell. Because DNA is the structure that defines who we are physically and intellectually, unless an individual is an identical twin, it is not likely that any other person will have the same exact set of genes.

Figure 1: DNA Technology

DNA can be collected from any number of sources: blood, hair, finger nails, mouth swabs, blood stains, saliva, straws, and any number of other sources that has been attached to the body at some time. DNA matching has become a popular use in criminal trials, especially in proving rape cases. The main problems surrounding DNA biometrics is that it is not a quick process to identify someone by their DNA. The process is also a very costly one.

DNA Biometrics is not a fool proof method of identification. If forensic scientists to not conduct a DNA test properly, a person's identification code can be skewed. Another problem is matching prior DNA samples to new samples; this is a bigger problem in DNA fingerprinting.

Deoxyribonucleic acid (DNA) provides the most reliable personal identification. It is intrinsically digital, and does not change during a person's life or after his/her death.

This chapter addresses three questions: First, how can personally identifying information are obtained from DNA sequences in the human genome? Second, how can a personal ID be generated from DNA-based information? And finally, what are the advantages, deficiencies, and future potential for personal IDs generated from DNA data (DNA-ID)?

2. DNA as a Source of Biometric

- DNA is unique to every individual on the planet
- •Only identical twins share the same DNA
- •It can be easily obtained from a variety of sources
- •It is readily used in forensics to match crime scene evidence to individuals
- •It does not change during the life

3. DNA Sources

- Paper or plastic cup
- Glass
- Ear wax
- Fingernail clippings
- Socks

- Urine
- Licked stamps
- Cheek swabs
- Sweaty t-shirts
- Hair with roots
- Hair without roots
- Dried blood
- Whole blood
- Chewed gum
- Dental floss
- Cigarette butts
- Used tissue
- Dried skin
- Used razor
- Other biological specimens

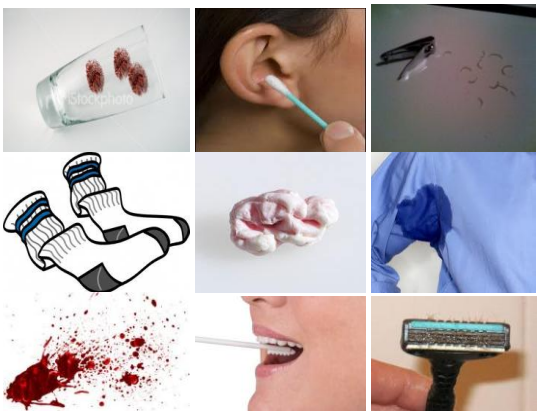

Figure 2: Sources of DNA

4. Human DNA

Humans have 23 homologous ("pairs of") chromosomes resulting in 46 total.

- One set of 23 from each parent is passed on to offspring.
- 99.7% of human DNA is shared.
- 0.3% (~ 1 million nucleotides) is variable!
- This variability is inherited and is therefore unique to each individual.
- These variable regions, called Short Tandem Repeats (or STRs), can be examined to distinguish one person from another.

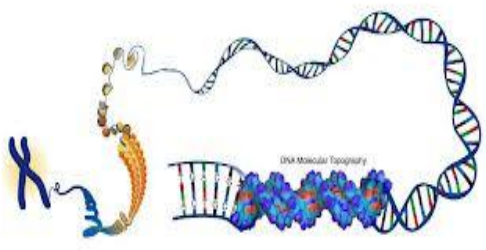

Figure 3: Human DNA Structure

5. Cracking the DNA Code

Three Important Steps:

•Extract (obtain and isolate DNA from sample)

•Amplify (create multiple copies of the "target sequences")

•Sequence (obtain unique code of nucleic acid bases from the DNA sample

6. Human identification based on DNA polymorphism

A human body is composed of approximately of 60 trillion cells. DNA, which can be thought of as the blueprint for the design of the human body, is folded inside the nucleus of each cell. DNA is a polymer, and is composed of nucleotide units that each has three parts: a base, a sugar, and a phosphate. The bases are adenine, guanine, cytosine and thymine, abbreviated A, G, C and T, respectively. These four letters represent the informational content in each nucleotide unit; variations in the nucleotide sequence bring about biological diversity, not only among human beings but among all living creatures. Meanwhile, the phosphate and sugar portions form the backbone structure of the DNA molecule. Within a cell, DNA exists in the double-stranded form, in which two antiparallel strands spiral around each other in a double helix. The bases of each strand project into the core of the helix, where they pair with the bases of the complementary strand. A pairs strictly with T, and C with G.

Within human cells, DNA found in the nucleus of the cell (nuclear DNA) is divided into chromosomes. The human genome consists of 22 matched pairs of autosomal chromosomes and two sex-determining chromosomes, X and Y. In other words, human cells contain 46 different chromosomes. Males are described as XY since they possess a single copy of the X chromosome and a single copy of the Y chromosome, while females possess two copies of the X chromosome and are described as XX.

The regions of DNA that encode and regulate the synthesis of proteins are called genes; these regions consist of exons (protein-coding portions) and introns (the intervening sequences) and constitute approximately 25% of the genome. The human genome contains only 20,000−25,000 genes. Therefore, most of the genome, approximately 75%, is extragenic. These regions are sometimes referred to as 'junk' DNA; however, recent research suggests that they may have other essential functions. Markers commonly used to identify individual human beings are usually found in the noncoding regions, either between genes or within genes (i.e., introns).

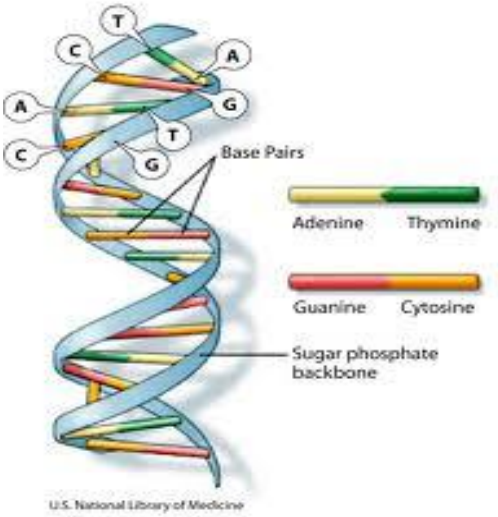

Figure 4: DNA molecule schematic

6.1 DNA Sample Collection

DNA can be easily obtained from a variety of biological sources, not only body fluid but also nail, hair and used razors. For biometric applications, a buccal swab is
the most simple, convenient and painless sample collection method. Buccal cell collection involves wiping a small piece of filter paper or a cotton swab against the inside of the subject's cheek, in order to collect shed epithelial cells. The swab is then air dried, or can be pressed against a treated collection card in order to transfer epithelial cells for storage purposes.

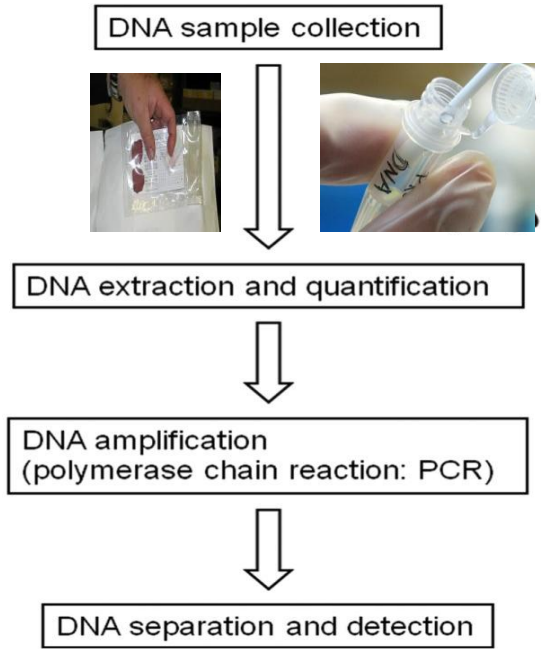

Figure 5: DNA sample collection

6.2 DNA Extraction And Quantification

There are many methods available for extracting DNA. The choice of which method to use depends on several factors, especially the number of samples, cost, and speed. Extraction time is the critical factor for biometric applications. The author has already reported the "5-minute DNA extraction" using an automated procedure. The use of large quantities of fresh buccal cells made it possible to extract DNA in a short time.

In forensic cases, DNA quantitation is an important step. However, this step can be omitted in biometrics because a relatively large quantity of DNA can be recovered from fresh buccal swab samples.

6.3 DNA Amplification (Polymerase Chain Reaction: PCR)

The field of molecular biology has greatly benefited from the discovery of a technique known as the polymerase chain reaction, or PCR. First described in 1985 by Kary Mullis, who received the Novel Prize in Chemistry in 1993, PCR has made it possible to make hundreds of millions of copies of a specific sequence of DNA in a few hours. PCR is an enzymatic process in which a specific region of DNA is replicated over and over again to yield many copies of a particular sequence.

This molecular process involves heating and cooling samples in a precise thermal cycling pattern for approximately 30 cycles. During each cycle, a copy of the target DNA sequence is generated for every molecule containing the target sequence.

In recent years, it has become possible to PCR amplify 16 STRs, including the gender assignment locus called 'amelogenin,' in one tube.

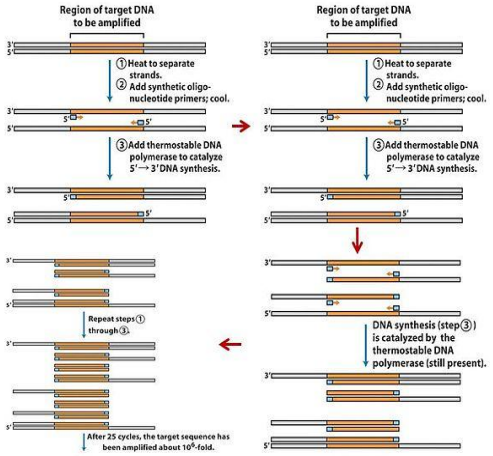

Figure 6: DNA amplification with polymerase chain reaction (PCR).

6.4 DNA Separation and Detection

After STR polymorphisms have been amplified using PCR, the length of products must be measured precisely; some STR alleles differ by only 1 base-pair. Electrophoresis of the PCR products through denaturing polyacrylamide gels can be used to separate DNA molecules from 20−500 nucleotides in length with single base pair resolution. Recently, the fluorescence labelling of PCR products followed by multicolour detection has been adopted by the forensic science field.

Up to five different dyes can be used in a single analysis. Electrophoresis platforms have evolved from slab-gels to capillary electrophoresis (CE), which use a narrow glass filled with an cross-linked polymer solution to separate the DNA molecules. After data collection by the CE, the alleles (i.e., the type or the number of STR repeat units), are analyzed by the software that accompanies the CE machine.

It takes around four hours, starting with DNA extraction, to obtain data from 16 STRs including the sex determination locus.

7. Principles of DNA Biometrics

Humans have 23 pairs of chromosomes containing their DNA blueprint. One member of each chromosomal pair comes from their mother; the other comes from their father. Every cell in a human body contains a copy of this DNA. The large majority of DNA does not differ from person to person, but 0.10 percent of a person's entire genome would be unique to each individual. This represents 3 million base pairs of DNA.

Genes make up 5 percent of the human genome. The other 95 percent are non-coding sequences, (which used to be called junk DNA). In non-coding regions there are identical repeat sequences of DNA, which can be repeated anywhere from one to 30 times in a row. These regions are called variable number tandem repeats (VNTRs). The number of tandem repeats at specific places (called loci) on chromosomes varies between individuals.

For any given VNTR loci in an individual's DNA, there will be a certain number of repeats. The higher number of loci is Analysed, the smaller the probability to find two unrelated individuals with the same DNA profile.

DNA profiling determines the number of VNTR repeats at a number of distinctive loci, and use it to create an individual's DNA profile. The main steps to create a DNA profile are: isolate the DNA (from a sample such as blood, saliva, hair, semen, or tissue), cut the DNA up into shorter fragments containing known VNTR areas, sort the DNA fragments by size, and compare the DNA fragments in different samples.

8. Benefits of DNA Biometric Systems

- Accurate: the chance of 2 individuals sharing the same DNA profile is less than one in a hundred billion with 26 different bands studied.

9. Weaknesses of DNA Biometric

- DNA matching is not done in real-time
- Intrusive: a physical sample must be taken, while other biometric systems only use an image or a recording

10. Applications of DNA Biometrics

DNA evidence has been used in courts of law since 1985 to prove guilt or innocence. It is also used for paternity testing, identification of missing or dead people.

11. Advances in DNA Technology

11.1 Extracting DNA

- New commercial products are available that allow for the rapid collection and extraction of DNA
- The Bode Technologies Buccal DNA Collector functions similarly to FTA™paper

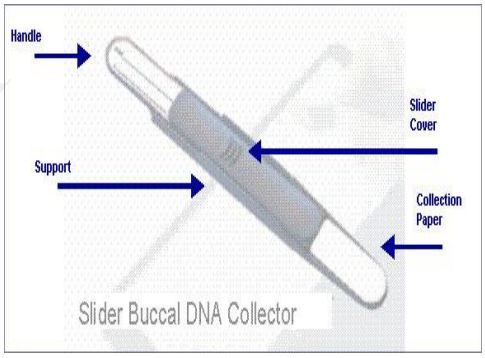

Figure 7: Slider Buccal DNA Collector

- A scraping of cheek cells can be collected and transferred directly to the PCR reaction tube for amplification, greatly reducing extraction time

TIME: less than 30 seconds

11.2 Amplifying DNA

- Products in the research stage can amplify DNA in minutes rather than hours!
- The new devices rapidly change temperature, allowing DNA to be copied at a much quicker rate
- MATCI(Miniature Analytical Thermal Cycling Instrument) is a portable PCR unit that can perform 32 cycles in about 21 minutes.

Figure 8: Miniature Analyical Thermal Cyclic Instrument

- On-chip PCR utilizes glass microchips with sample chambers to perform PCR
  TIME: approximately 20 minutes

11.3 Sequencing DNA

- High-throughput DNA analysis is commercially available with products like the ABI 3730xl.
- Microchip sequencers in the research phase have small channels etched in them that perform the DNA separation and laser detection.
- The small distance (~2cm) the DNA travels (opposed to 35cm in standard machines) allows results in as little as 30 seconds
- High-throughput microchips have also been shown to provide results up to 5 times faster than current machines.
- New research in microchip technology is aiming to combine DNA amplification and sequencing.
- Adding DNA extraction to the continuous flow microchip is also in the works.
- Combining all three steps to obtain a DNA profile is the DNA profiling method of the future, and the one that is most applicable to biometrics.

12. Timeline with New Technology

- Obtaining a sample such as a swab of cheek cells (buccal swab): 10 seconds
- Extracting DNA: ~10 seconds
- Amplifying DNA: ~20 minutes
- Sequencing DNA: 30 seconds –5 minutes
- Total: Less than 30 minutes

13. Conclusion

DNA is highly individualizing and has great potential as a biometric identifier.

The nature of DNA and the state of current technology prevents DNA from being an efficient biometric

Development of biometric authentication technologies has progressed rapidly in the last few years. Personal identification devices based on unique patterns of fingerprints, iris, or subcutaneous veins in the finger have all been commercialized.

All of these methods of verification are based on matching analog patterns or feature-point comparisons. Because they lack absolute accuracy, they have not yet achieved a universal standard.

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