

Short Notes on DNA Profiling

Sanika Swapna*

Department of Biotechnology, Osmania University, Hyderabad, Telangana, India

Commentary

The process of obtaining a specific DNA pattern, referred to as a profile, from a person or a sample of body tissue is known as DNA profiling. Even though we are all unique, the majority of our DNA is identical to that of other people. Specific locations, on the other hand, differ greatly from person to person. These areas are referred to as polymorphic. Polymorphisms are differences between people in these variable locations. From our parents, we each inherit a unique set of polymorphisms. A DNA profile can be created by analysing DNA polymorphisms. Human DNA profiles can be used to determine the source of a DNA sample found at a crime scene or to determine parentage. Short tandem repeats are a type of polymorphism used in one of the current DNA profiling approaches. Short tandem repeats (or STRs) are non-coding DNA segments that include nucleotide sequence repetitions. Scientists can create a DNA profile by looking at STRs at 10 or more genetic loci. These genetic loci are generally spread over multiple chromosomes.

A DNA profile can inform a scientist if the DNA belongs to a male or a woman, and whether the sample being examined is from a specific person. Most cells in the body, including white blood cells, sperm, hair roots, and bodily tissue, contain DNA. Because epithelial cells are present in body fluids like saliva and perspiration, DNA traces can be discovered. DNA samples are collected from crime sites by forensic experts and police officers. A mouth swab can also be used to capture DNA straight from a person (which collects inner cheek cells). More information can be found in the articles Forensics and DNA, as well as Crime Scene Evidence.

The nucleus of a cell is where DNA is stored. To split open the cells, remove the DNA, and isolate it from other cell components, chemicals are used. Because forensic analysis sometimes requires just a little amount of DNA, the STRs at each genetic locus are copied several times using the Polymerase Chain Reaction (PCR) to obtain enough DNA to create a profile. During PCR, certain primers are utilised to affix a fluorescent tag to the copied STRs.

A genetic analyser is used to assess the size of the STRs at each genetic locus. The genetic analyser uses gel electrophoresis to separate the replicated DNA and can detect the fluorescent dye on each STR. This is the identical piece of DNA sequencing equipment used in the lab. The size of the STRs can be used to calculate the number of times a nucleotide sequence is repeated. This information can be used by a forensic scientist to identify if a body fluid sample belongs to a specific person. When two DNA profiles from distinct samples match, it's unlikely that the samples came from the same person. This is solid indication that the samples came from the same place.

DNA profiling can be used to identify human remains or to solve old or unsolved crimes. When conventional methods (physical appearances, dermatoglyphic fingerprints, dental charts) have failed, the availability of parental DNA samples may allow identification of a body. A relationship will be ruled out if the DNA profiles are dissimilar. Teeth are valuable evidence in forensic cases because they are resistant to postmortem degradation and extreme environmental conditions. Teeth are also easily transportable and a good source of DNA. Comparisons of antemortem dental records with skeletal remains have long been used to identify individuals, even in mass graves. Dental records may be crucial in determining the identity of individual victims in affluent societies. However, dental records are unlikely to be available in less affluent communities, which are more likely to be involved in human rights violations associated with mass murder. In this case, DNA analysis may be the only option for identification.

There are numerous examples in the media of crimes being solved decades after they occurred because evidentiary material was re-examined for the first time using DNA profiling, or more sensitive DNA techniques became available. To solve cold cases, law enforcement agencies, forensic laboratories, and a centralised DNA database must work together. Statutes of limitation imposed with the knowledge that witness accounts may no longer be accurate with time may need to be reconsidered because DNA testing can still provide answers after many decades [1-5].

References

1. Butler, John M, Yin Shen and Bruce R McCord. "The development of reduced size STR amplicons as tools for analysis of degraded DNA." *J Forensic Sci* 48 (2003): 1054-1064.
2. Edson, Suni M, JP Ross and M D Coble, et al. "Naming the dead-confronting the realities of the rapid identification of degraded skeletal remains." *Forensic Sci Rev* 16 (2004): 63-88.
3. Presciuttini, Silvano, Chiara Toni and Elena Tempestini, et al. "Inferring relationships between pairs of individuals from locus heterozygosities." *BMC Genet* 3 (2002): 1-11.
4. Clayton TM, JP Whitaker and CN Maguire. "Identification of bodies from the scene of a mass disaster using DNA amplification of short tandem repeat (STR) loci." *Forensic Sci Int* 76(1995): 7-15.
5. Ludes, Bertrand, A Tracqui and H Pfitzinger, et al. "Medico-legal investigations of the Airbus A320 crash upon Mount Ste Odile, France." *J Forensic Sci* 39 (1994): 1147-1152.

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*Address for Correspondence: Sanika Swapna, Department of Biotechnology, Osmania University, Hyderabad, Telangana, India, E-mail: sanika.swapna5@gmail.com

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