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Role of Single Nucleotide Polymorphisms (SNPs) and Short Tandem Repeats (STRs) in forensic science

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Abstract: Forensic science is the application of principles of science and technology to support legal decision-making in matters of Criminal and Civil Law. It involves presenting facts during criminal and civil investigations and in uncovering the truth, ensuring that conclusions are based on objective, reliable, and scientifically verified evidence rather than speculation or bias. The different branches of forensics like toxicology and anthropology, have helped solve real-life cases like Micheal Jackson's murder case and the Nirbhaya gang-rape case. This research paper explores the different ways in which human DNA has served the world to solve various criminal cases and paternity concerns. It covers the use of Single Nucleotide Polymorphisms (SNPs) and Short Tandem Repeats (STRs) to accurately and efficiently identify individuals and create unique DNA profiles. The study explores techniques like Polymerase Chain Reaction (PCR), fluorescent probe analysis, and advanced sequencing methods such as Sanger sequencing and Next-Generation Sequencing (NGS), highlighting their critical role in modern DNA analysis and identification. While delving into the details and the processes used in solving real-life cases, this research paper also discusses the legal and ethical issues surrounding the processing and analysis of DNA, and the potential opportunities for future developments in forensic science. The crucial role played by DNA analysis data, due to its reliability and objectivity, in deducing the incidents that might have occurred prior to a criminal event, and as evidence for zeroing in on the suspected criminal, in resolving real life court cases has been highlighted in this research paper. As rightly said by Blake Edwards, American film director and producer, "Nothing matters but the facts. Without them, the science of criminal investigation is nothing more than a guessing game."

Introduction

Every cell in a human body is made up of the same genetic blueprint of life known as DNA (deoxyribose nucleic acid),but this DNA sequence shows slight variations between different individuals, which makes each individual unique. This type of genetic variation occurs due to "single-nucleotide polymorphism",(SNPs) (pronounced as "snips") or "short tandem repeats" (STRs).

Single nucleotide polymorphisms (SNPs)

Single nucleotide polymorphisms (SNPs) are a type of genetic variation where a nucleotide (A,T,C or G) in the DNA sequence is replaced by another at a specific genome location. While 99% of the human DNA is identical amongst individuals, the SNPs are part of the 1% of variation. They occur once in every 1000 nucleotides and given that human DNA is made of around 3 billion nucleotides, SNPs occur about 4 to 5 million times. Scientists make use of SNPs in ancestry tracing, drug response, forensic identification and hence are used to predict genetic disorders and gene expression. SNPs can be either synonymous or non-synonymous and either coding or non-coding; synonymous SNPs do not change the sequencing of amino acids whereas non-synonymous SNPs can change the amino acid sequence. Coding SNPs can affect the protein structure, or the function of the protein being produced whereas non-coding SNPs affect the regulation of the genes and may cause changes in the amounts, or locations of the proteins produced. Moreover, non-synonymous SNPs may promote evolution due to natural selection. SNPs can be bi-, tri-, tetra-allelic polymorphisms; however, in humans tri-allelic and tetra-allelic is extremely rare and so SNPs are generally referred to as bi-allelic.

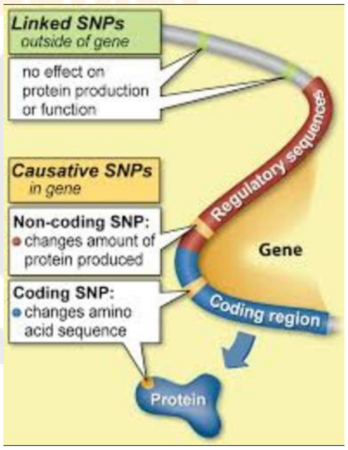
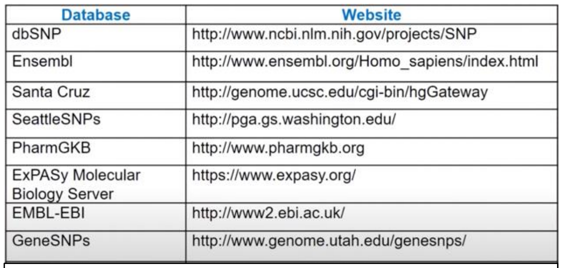


Figure 1: coding and non-coding SNPs

SNPs can be identified via the comparison of DNA sequences by randomly breaking the genome into smaller fragments, known as "shotgun". The "shotgun" method is known to be quick and highly accurate of optimized properly. In this method the genome sequence of the SNP is discovered and amplified using specific PCR primers. The amplified DNA is then sequenced to observe the nucleotide of the SNP. To observe specific SNPs, special primer is needed and if an amplification is missing, there is a variant in the SNP allele. The amplified DNA is then cut using restriction enzymes and analyzed on the agarose gel plate. Fluorescent probes have a complementary shape to the SNP variant and bind to the SNP variants. They release fluorescent signals which are then measured to determine the SNP (Tim Schedl et al, 2021). The analysis of the SNP by fluorescent probes reveals if the individual is homozygous or heterozygous at the SNP site. This is then compared with a reference database to determine the SNP frequency, potential traits or significance. This



Database	Website
dbSNP	http://www.ncbi.nlm.nih.gov/projects/SNP
Ensembl	http://www.ensembl.org/Homo_sapiens/index.html
Santa Cruz	http://genome.ucsc.edu/cgi-bin/hgGateway
SeattleSNPs	http://pga.gs.washington.edu/
PharmGKB	http://www.pharmgkb.org
ExPASy Molecular Biology Server	https://www.expasy.org/
EMBL-EBI	http://www2.ebi.ac.uk/
GeneSNPs	http://www.genome.utah.edu/genesnps/

Figure 2: Reference database of SNPs (CD genomics, 2021)

detailed analysis can identify SNPs associated with a disease and can hence allow risk assessment and early interventions.

Short Tandem Repeats (STRs)

Along with SNPs, the DNA is susceptible to other mutations such as the short tandem repeats, STRs, which are important in the forensic labs for precise analysis. STR are 2 to 6 base pairs of DNA that are repeated randomly throughout the genome. The number of repeats is variable for each individual and this is what helps in the identification of different genome samples. STRs can be used to identify genetic disorders and conditions that are mainly caused by the increase in the length of repeats of the base pairs. Examples of diseases caused by STRs include Huntington – a disease caused by a heterozygous CAG trinucleotide repeat in HTT gene - and fragile X syndrome – a disease caused by the repetition of the CGG trinucleotide in the FMR 1 gene located on the X chromosome (Dr Julia van Campen, 2022).

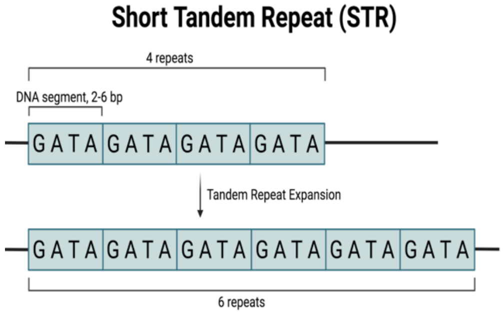


Figure 3: repetition of GATA gene to form STR

STRs are used in forensic labs to identify human remains, confirm paternity, and to study ancient humans. STR uses three processes to be analyzed, starting from being amplified. This process is done with the help of chemical reagents and heat produced by a thermal cycler. The heat causes the two strands of DNA to split and hence can synthesize new DNA molecules. The chemical reagent contains markers that can identify the synthesizing endpoints known as primers. The duplicated primers contain fluorescent labels that are identified by lasers during the testing phase. These labels help the primers to attach to single-stranded DNA and fill any empty DNA places. Using the process of electrophoresis, the DNA is separated into fragments based on their length. The capillary electrophoresis makes use of a capillary tube through which the DNA is pulled into with the help of an electric current. Finally, the DNA is interpreted and analyzed by their fragment size using various specialized softwares to create a DNA profile (Elizabeth Herkimer, 2022). This analysis of STRs and SNPs are used in paternity testing and human identification.

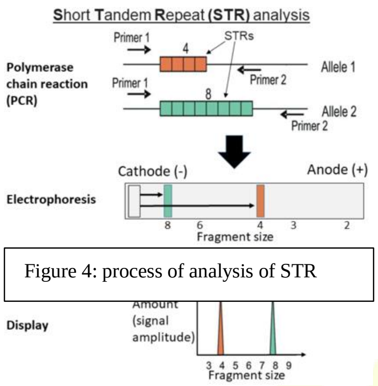


Figure 4: process of analysis of STR

Use of SNPs and STRs in paternity testing

Paternity tests use the DNA to determine a child's biological father. This test can be carried out during pregnancy (prenatal) or after birth (postpartum). This test not only help in gaining legal rights to child support and custody but also in helping children learn about their family history (Cleveland Clinic, 2017). There are two ways to acquire DNA samples for paternity tests: invasive and non-invasive ways. Invasive sampling includes chorionic villus sampling or amniocentesis whereby amniotic fluid is obtained. However, invasive methods induce a risk of miscarriage or infection, and so non-invasive methods are used to acquire DNA samples. Noninvasive sampling refers to maternal peripheral blood sampling wherein fetal DNA is present as cell-free DNA.

For a paternity test to occur, a tissue or blood sample from the probable father and the fetus/child is required. The cells are extracted from the blood via a centrifuge. The cells are then broken open by lysis buffer and proteinase K and the proteins holding the DNA together are digested. This allows the DNA to be released. A magnetic bead-based system then captures the released DNA to further analyze it. A spectrophotometer is used to identify the concentration of DNA depending on the absorption of UV radiations. The STRs or specific genetic markers in the blood sample are then identified and are compared with the father or the fetus/child using a polymerase chain reaction (PCR). The PCR amplifies the specific genetic regions containing STRs or SNPs to further analyze the DNA. In a PCR machine, the thermal cycler helps precisely control the temperature to carefully denature and extend the DNA. The primers allow short DNA sequences to the loci being analyzed and the Taq Polymerase enzyme helps synthesize new DNA molecules. The repeat numbers of the STR are then matched with the DNA samples of the father or the fetus/child, and the SNP alleles are compared between the child and the father to identify shared SNPs using a software analyzer like Genemapper. After the matching SNPs are identified, the paternity index (PI) and the combined paternity index (CPI) helps calculate the probability of paternity (POP) which is further calculated using the frequency of SNP specific alleles and the Mendelian inheritance rules. The results are either 0% or 99.99% of paternity possibility, depending on the number of matches between the two DNA samples: if there is a high number of matches between the DNA samples then paternity is highly likely (99.99%) but if there is low or no number of matches between the DNA samples then there is no chance of paternity (0%) (DNA Forensics, 2024). This procedure is accepted by the court of law in India.

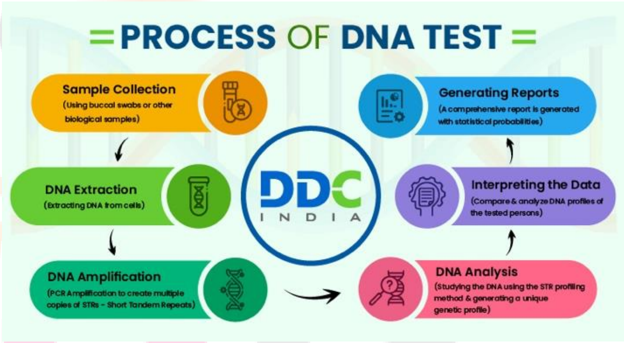


Figure 5: analysis of paternity test blood sample

Laws in India regarding paternity testing

A DNA test can only be conducted if the court makes a permit to it, and this only occurs in the case when there is a lot of evidence proving against the legitimacy of the child and evidence that the spouses have had access to each other. This is given under Section 112 of the Indian Evidence Act, 1872. A paternity test can only be conducted once consent has been given by every party part of the testing. The results of the DNA test can't be frivolously questioned as there is right to privacy. DNA tests generally are conducted in laboratories accredited by recognized bodies, such as the National Accreditation Board for Testing and Calibration Laboratories (NABL), to ensure accuracy and reliability while investigating cases that require the results to provide justice or the truth.

Figure 6: uses of paternity test

In India, a DNA test can't be carried out casually due to the concerns of the impact on the child. During a paternity test, there could be severe emotional and mental stress and impact that could affect the regular behavior of the child, especially when the child's parentage is questioned. There is a high risk that the results of the paternity test could be misused and can be used to defame an individual, further impacting their psychological well-being. Results that are not from approved labs may provide manipulated or fake results that can be devoid of credibility. India being a country that holds relationships and family honor at a high level, questioning the paternity of a child can have a lifelong consequence on the child's social standing and can cause a social stigma to arise.

Methods used for paternity testing

Regular generation sequencing (Sanger sequencing) and Next generation sequencing (NGS)

Generally, in forensic labs, without next generation sequencing (NGS) and regular generation sequencing, human identification cannot take place. The next-generation sequencing is a technique that uses technology to identify mutations and the various changes in the DNA/RNA genome of an individual while regular generation sequencing, also known as Sanger sequencing, determines the order of nucleotides in a DNA strand by using chain-terminating dideoxynucleotides (ddNTPs) during DNA synthesis.

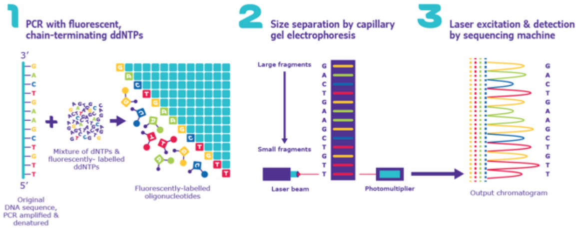


Figure 8: basic processes of Sanger sequencing

Sanger sequencing makes use of a single-stranded DNA template, a DNA primer and a DNA polymerase. For the DNA sample to be analyzed using Sanger sequencing, the DNA strand must be first purified and prepared. The required DNA needs to be denatured into a single strand and the specific primer is attached to determine the beginning point of the gene. The DNA strand should be placed in a reaction mixture that is made up of the replication enzyme (DNA polymerase), the regular deoxynucleotides (dATP, dGTP, dCTP, dTTP), the modified dideoxynucleotides (ddNTPs) that are labelled with fluorescent dyes, the specific primer and the necessary buffer conditions. Each type of dideoxynucleotide has a different fluorescent label attached to it, and once it has been added to the DNA polymerase, no more nucleotides can be attached to the DNA strand; hence, forming fragments of different lengths. The resulting fragments are then separated using a machine known as capillary electrophoresis. The smaller fragments move quickly past the capillary electrophoresis whereas the larger fragments move more slowly. As each fragment passes through a detector, the fluorescent label is excited by a laser, emitting light that identifies which base is at that position.

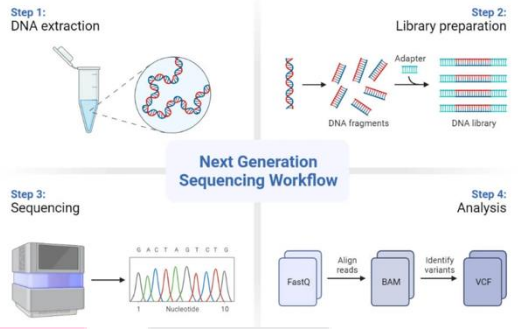


Figure 9: process of next generation sequencing

Next generation sequencing on the other hand can sequence millions of fragments simultaneously. To start the process of NGS, the DNA or RNA strands are prepared by fragmenting them into smaller lengths, generally of 150-500 base pairs long. These fragments then have specialized adapter sequences attached to their ends, creating what's called a "library." These adapters serve as identification tags and attachment points for subsequent steps. The library fragments are loaded onto a flow cell – a glass slide with lanes coated with complementary adapter sequences. Each fragment attaches to the surface and undergoes bridge amplification, where it creates thousands of identical copies in a tight physical cluster. This process is a crucial step in the process because it amplifies the signal for easier detection. Modified nucleotides labeled with different fluorescent dyes are then added one at a time to the flow cell containing the fragment. When a nucleotide is incorporated into the growing DNA strand, it releases a specific color signal which is then captured by the camera. The dye is cleaved off the DNA fragment, allowing the next nucleotide to be added and the process is then repeated for all the DNA clusters simultaneously. The NGS data is then analyzed in three stages: primary analysis, secondary analysis and tertiary analysis. In the primary analysis the fluorescent signals are first converted into a legitimate DNA sequence after which an initial quality control test filters out the low-quality reads. In the secondary analysis, a quality trimming test is done through which the adapter and low-quality reads are removed. There is a variant calling test done to identify differences from the original or reference sequence. After this is done, there is a cover analysis taken to analyze the sequencing depth of the DNA fragments. Finally, in the tertiary analysis, the biological interpretations of the variants are found and are annotated with the already known DNA fragment. There is a pathway analysis test conducted at the end which analyzes data obtained from high-throughput technologies (Campos-García et al, 2015). At the end of the three-step analysis a clinical significance assessment is done after which the report is printed.

Though Sanger's sequencing is extremely valuable in small-scale analysis and validations, it requires large amounts of purified DNA targeting a specific region. On the other hand, next generation sequencing (NGS) can work with small amounts of DNA and doesn't need prior knowledge of the target regions making it more cost-effective for whole genomes compared to Sanger sequencing. Even though Sanger sequencing can produce longer reads with extremely high accuracy, NGS can identify rare variants, analyze complex mixtures and detect novel genetic elements. Moreover, NGS does have a longer processing time that can stretch to days, but it can process billions of bases simultaneously. To further add to the benefits of NGS, it can allow access to the results midway through the process of sequencing whereas Sanger sequencing can only allow the access once the sequencing is over. Therefore, though Sanger sequencing is extremely valuable and used, next generation sequencing is more advanced to analyze genomes.

Real life examples of uses of forensic analysis in solving criminal cases

Homicide report of Michael Joseph Jackson (1958-2009)

On June 25, 2009, the American singer Michael Joseph Jackson died of acute propofol intoxication at around 6.30pm in his rented home in the 100 block of N. Carolwood in Holmby Hills, Los Angeles, California, at the age of 50. The autopsy report suggests Jackson had been administered propofol and anti-anxiety benzodiazepines lorazepam and midazolam by his doctor. Once the report was published the court concluded that Jackson's death was a homicide. Two years after which his doctor, Conrad Murray, was convicted for involuntary manslaughter and had to serve prison for 4 years but was allowed to leave in two years due to good behavior.

The autopsy report proved that no kind of foul play or trauma had occurred hence classifying Jackson's death as involuntary manslaughter in November 2011. The autopsy report revealed that Jackson was healthy for his age (age 50) and that his heart was strong; his most significant health issue was that his lungs were chronically inflamed, but this did not contribute to his death. His other major organs were normal, and he had no atherosclerosis except for some slight plaque accumulation in the arteries in his leg. The doctors had placed him to be in an acceptable weight range.

Figure 10: image of Conrad Murray

Figure 11: vials with the fingerprints of Dr. Murray

The toxicology report detected various drugs in Jackson's blood ranging from propofol to lidocaine all of which were injected into his body using an intravenous (IV) drip. At first the notion that Micheal must have committed suicide did surface the minds of the investigators, but the DNA fingerprint on the 100-milliliter vial of propofol and syringes revealed no prints of Jackson but rather prints of Dr. Murray. This confirms that the drugs were administered by him. The fingerprints were discovered by the Los Angeles Police Department (LAPD) by dusting the propofol vial with fingerprint powder. Once the prints were visible, they captured pictures of the fingerprints using high resolution forensic cameras for reference. The prints were then lifted by clear adhesive tape and the lifting tape transferred the prints on a latent lift card to preserve the prints for further analysis (Global Forensic and Justice Center, 2013).

The DNA fingerprints were then sent to a forensic laboratory for detailed analysis and identification. The fingerprint examiners analyzed the print using the various techniques such as the different bifurcations, ridge endings and dots while also comparing the overall loops, whorls and arches present. The fingerprints lifted from the crime scene were then matched to the known samples (the ones gotten during his interviews). The examiners use the minutiae points to compare them with the ones stored in the national database. The forensic labs then compared and analyzed multiple STR loci to further create a DNA profile that is extremely unique to an individual, in this case Micheal Jackson, except in the case of identical twins. If the STRs didn't provide any conclusive results, the SNPs part of the DNA in the lifted sample were analyzed by amplifying the target regions using a primer and comparing it with the known stored sample.

To create the toxicology report, the forensic experts collected an amount of blood or urine or tissue that contains the DNA of Jackson so it could be analyzed for the different drugs present in the body. The blood sample was prepared for analysis using processes such as centrifugation which helps separate chemicals from the tissue. The purified blood sample was then placed through advanced technologies such as Chromatography-Mass Spectrometry (GC-MS) and Liquid Chromatography-Mass Spectrometry (LC-MS) to quantify the toxic substances. The concentrations of substances detected were compared to known toxicological thresholds to interpret the potential effects on the body and cause of death or impairment.

The lab also had to test Jackson to confirm his identity and any hereditary health conditions that could have played a role in his untimely death. This process began with the meticulous sample collection from hair follicles, blood, and tissue, ensuring that DNA integrity was preserved through proper storage techniques. The process of DNA extraction involved breaking down cell membranes with chemical solutions to isolate high-quality DNA, which was then verified through a spectrophotometry for purity and concentration. After which, the amplification of the DNA using Polymerase Chain Reaction (PCR) allowed specific DNA segments to be multiplied, ensuring sufficient material for sequencing. The automated DNA sequencers and software analyzers provided a detailed genetic profile, confirming Jackson's identity and ruling out significant hereditary health conditions that might have contributed to his death. The entire process was accepted by the law and followed all the legal requirements.

This evidence, combined with toxicology results and witness testimonies, established that Dr. Murray had administered a lethal dose of propofol without proper monitoring or adherence to medical protocols. However, the absence of intent led the case to be classified as involuntary manslaughter rather than murder. Dr. Murray's trial highlighted his gross negligence in administering anesthetics in a non-hospital setting, leading to his conviction while giving closure to Jackson's family and friends.

Laws regarding murder case analysis in the United States of America

In the United States of America, the laws for homicide and murder are similar to those in India in many ways but differ in some ways as well. In the fourth amendment of the USA law, it is clearly stated that evidence must be obtained with proper warrants and hence protects against unlawful searches; however, in India warrants are not always required. Moreover, the fifth and sixth amendment of the USA law states that it lawfully protects the rights of suspects, including protection against self-incrimination and the right to a fair trial. The same is mentioned in Article 20 (3) of the Indian law. In the USA, the death penalty is a punishment that is only applied in some states but is abolished in others. Since, in India, the Unified Penal Code (UPC) is applicable throughout the country, death penalty is retained but will be applied under the "rarest of rare" doctrine.

In Los Angeles (LA) the punishment of the suspect depends on the degree of crime. In this case there are two degrees of murder: first degree and second degree. If the murder is committed during specific felonies like rape, kidnapping or robbery then it is considered as a first-degree murder. This has a consequence of life imprisonment without parole or death penalty if aggravating circumstances are present. A murder that is caused with an intention but without premeditation is considered as a second-degree murder and has a consequence of 15 years imprisonment with potential enhancements (e.g. use of firearms). Under the Penal Code Section 192 of the USA law, a murder that occurs during a sudden quarrel or heat of passion is considered as a voluntary manslaughter and has imprisonment of 3 to 11 years. Involuntary manslaughter is considered by the court of law if a murder is caused devoid of any intent during an unlawful act or gross negligence and has imprisonment of up to 4 years. This was the law that convicted Dr. Conrad Murray in 2011 regarding Micheal Jackson's death.

2012 Nirbhaya (Jyoti Singh) gang rape

On December 16, 2012, a 22-year-old physiotherapy intern, Jyoti Singh,was gang-raped and murdered in a private bus in Munirka, South Delhi. This case was later named as Nirbhaya which means fearless, symbolizing her struggle and death which went to become a symbol of women's resistance to rape around the world. While recounting the incident, the victims' parents informed the authorities about the gruesome details of the incident. The victim and her male friend took an auto rickshaw to Munirka bus stand and then boarded the bus at Munirka for Dwarka at about 9:30 pm (IST). There were only six other males in the bus, including the driver. One of the men, identified as a minor, had called for passengers telling them that the bus was going towards their destination. The victim's male friend became suspicious when the bus deviated from its normal route and its doors were shut.


Figure 13: image of Indian citizens fighting for Nirbhaya

When he confronted the driver, an argument erupted during which the male victim was beaten, gagged and knocked unconscious with an iron rod. The males then forced the female victim to the back of the bus where she was beaten and raped using the same iron rod while the driver continued driving though the city. A medical report later said that she suffered serious injuries to her abdomen, intestines and genitals due to the assault, and doctors said that the damage indicated that a blunt object (suspected to be the iron rod) may have been used for penetration. According to police reports, the female victim attempted to fight off her assailants, biting three of the attackers and leaving bite marks on the accused men. After the beatings and rape ended, the attackers threw both victims from the moving bus while being partially covered. One of the perpetrators later cleaned the vehicle to remove evidence. According to reports, one of the accused men admitted to having seen a rope-like object, assumed to be her intestines, being pulled out of the woman by the other assailants on the bus. The medical staff later confirmed that 95% of her small intestine was pulled out from her body using the iron rod and the attackers' hands.


Figure 14: image of the 5 perpetrators and the minor

The forensic investigators took a sample of the blood covered clothes, semen stains, vaginal swabs, hairs and other biological traces from the private bus for further analysis and investigation. The DNA from the biological fluids was then isolated using organic extraction methods for purity and a polymerase chain reaction (PCR) was performed on the same. The PCR was employed to amplify specific regions of DNA to produce enough material for analysis and to target any short tandem repeats (STRs), which are unique, repeating sequences in human DNA used for identification. The DNA profiles for possible victims were created from the STR markers at specific loci on the chromosomes and these matched the suspects arrested by the police within 24 hours of the incident. To ensure 100% confirmation of the suspects the police also analyzed the other biological fluids like semen and blood typing. The bloodstains and semen stains on the accused suspect's clothing matched the victim's blood type and DNA, hence providing more evidence. The bite marks on the victim's body were also analyzed to identify and confirm the dental patterns of the accused, corroborating their involvement. Finally, the hair samples collected from the bus were matched to the victim and the accused, strengthening the case and adding confirmability.

The forensic evidence, combined with eyewitness testimonies and the victim's statement before her death, led to the conviction of all six accused. Four of them were sentenced to death, one was a minor and sentenced to three years in a juvenile facility, and another died during the trial. The forensic analysis ensured the case was resolved with clarity and precision.

Laws regarding rape case analysis in India

Before the Nirbhaya case, the Section 376(2)(g) IPC (Gang-Rape) of India stated that when a woman was raped by two or more persons acting in furtherance of a common intention, it was considered gang-rape and the punishment for the assaulters was minimum 10 years extendable to life imprisonment. However, after the Nirbhaya case, the Indian law became stricter with gang-rape laws (Enhanced Punishment for Gang-Rape (Section 376D)) and consisted of a punishment of minimum of 20 years of imprisonment which could be extended to life imprisonment or death penalty. Moreover, if a juvenile aging between 16-18 years committed such a heinous crime like gang-rape, the Juvenile Justice (Care and Protection of Children) Act, 2015 allowed them to be tried as adults. Finally, the Indian government set up special courts to ensure speedy trials in rape and sexual assault cases.

Future Applications of Forensics


Figure 15: image of AI taking over human forensic jobs

The future in the field of forensics is currently very broad. Technological advancements in the process of DNA identification like AI can make the entire process not only faster but more accurate and efficient. Algorithms that are generated using artificial intelligence can help assist in fingerprint examination, facial recognition and reconstruction, handwriting examination, etc. Moreover, with the increase in the number of users of the digital world, the threat of cybercrimes has also increased and thus this concern needs to be addressed by the law enforcement agencies. Digital forensics plays an important and integral part of investigation of cases including cybercrime, digital evidence collection and crime scene reconstruction. The field will help in enhancing the capabilities of examination of encrypted data, recovering information from devices, along with identifying the cyber criminals. Along with all the advancements in the forensics field, another important advancement can be traced in imaging and visualization techniques. The advancement in imaging technologies enhance the ability of forensic experts to recreate the crime scene, visualize the evidence in a 3D format, along with creating the precise models to present in the courtroom as authentic evidence.

In addition to technology, developments in nanoscience are an emerging field of forensics. Nanotechnology is considered to revolutionize crime investigation science by enabling experts to detect and analyze the traces of evidence at the nanoscale level, increasing the sensitivity of forensic assays. Nanotechnology can be used in fingerprint detection using fluorescent nanoparticles, in toxicology using nanosensors, in detection of explosives and gun residues etc. Accompanied by advancements in scanning electron microscopy and transmission electron microscopy, it will enable experts to visualize the evidence with high-resolution details thus helping in the identification of criminals.

To conclude, this study describes how tools like SNPs and STRs in genetics have revolutionized methods of working with crimes, relationship identification, and knowledge of genetic heritage and disease. SNPs help us to trace the tiniest and the rarest genetic mutations or varieties, whereas STRs are used in creating unique DNA profiles that help in revealing the identity of people. These tools, combined with research methods like Sanger sequencing and NGS, have changed the face of genetic analysis. From revealing parentage to solving crime cases with real-life application, these technologies have been of utmost importance and are extremely crucial in closing criminal cases.

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