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DNA Forensic and Forensic Investigative Leads

Johannes Hendrik Smith[1]* and M. Singh[2]

[1]*Department of Forensic and Criminal Investigation Science, College of Law: School of Criminal Justice, University of South Africa (UNISA), Pretoria, Gauteng, South Africa*

[2]*Department of Genetics, University of the Free State, Free State, South Africa*

Abstract

The chapter explores the fundamental principles of Deoxyribonucleic acid (DNA) in the context of forensic DNA profiling. Moreover, it explores the use of forensic DNA databases and the comparative searches carried out within them. The outcomes of these comparative searches produce Forensic Investigative Leads (FILs), which require communication with detectives for more investigation and follow-up. To successfully investigate these FILs, it is crucial to have efficient communication and engage in multidisciplinary detective work. This entails examining further corroborating evidence that could either absolve an innocent person from blame or contribute to the apprehension and compelling conviction of the perpetrator.

Keywords: Deoxyribonucleic acid • Forensic DNA database • Familial searching • Forensic investigative leads • Forensic investigative genetic geology • Criminal casework investigations

Introduction

Criminal investigations extensively depend on Deoxyribonucleic Acid (DNA) forensic investigation leads, transforming forensic science by offering crucial information for identifying suspects, connecting individuals to crime scenes and verifying or disproving criminal testimonies [1,2]. Although the act of discarding a cigarette butt in a public area may appear harmless, justifying the presence of DNA discovered in a recently burglarised residence presents a substantial difficulty for individuals who are being investigated [3].

Deoxyribonucleic Acid (DNA)

DNA, the hereditary code of all living beings, is crucial in distinguishing individuals based on biological material by examining genetic variations [4-6]. DNA, which encodes biological properties such as protein expression and physical attributes, shows significant similarities among individuals, with just a 0.3% variation in genetics [7]. Genetic information plays a fundamental role in forensic science in confirming identity and conducting criminal investigations [4,8,9].

Different patterns of repeating sequences found in DNA, such as VNTR and STR, allow for the unique identification of individuals using tandem repeat analysis [10,11]. Despite having the same genetic material, monozygotic twins have separate genetic profiles due to mutations that occur after the division of the zygote, which sets them apart [12]. Despite their widespread use, conventional length-based STR approaches cannot distinguish between monozygotic twins [4,13-15]. Ultra-deep Multiple Parallel Sequencing (MPS) has emerged as a solution for finding genomic variations, such as copy number differences and single nucleotide polymorphisms) [16-18].

In creatures such as humans, DNA is found in nuclear DNA in cell nuclei and mitochondrial DNA (mtDNA) in mitochondria. In the double helix structure of DNA, the nucleotides are coupled together - adenine with thymine and guanine with cytosine - to create base pairs [19,20]. The process of DNA replication and recombination, essential for genetic inheritance, is made possible by the complementary base pairing. During fertilisation, chromosomal pairs are separated, where each parent contributes half of the DNA to the offspring [21,22]. This separation leads to the creation of genetic variety. DNA replication, which is susceptible to mutations, results in the emergence of genetic variants as time progresses, which occur due to errors in DNA replication or repair, resulting in alterations in DNA sequences [23,24]. These changes contribute to the distinctiveness of individuals [25,26]. Forensic DNA profiles employ fragments from locations in the genome to detect alleles and heterozygosity by analysing repetitive nucleotide sequences [2,27,28]. Different alleles at each locus are distinguished by motif repetition and sequence type variations [29].

Forensic DNA profiling

Forensic DNA profiling was first introduced in the early 1980s [30]. Since then, it has been developed and established as a powerful tool. The advancements in DNA analysis have significantly improved the criminal justice system by enabling the investigation of small biological traces such as blood, saliva and skin cells to link perpetrators [31,32]. Forensic Identification Leads (FILs) play a crucial role in connecting persons to crime scenes and verifying or disproving reports of incidents [2]. In addition, a perpetrator's DNA on objects such as balaclavas can indicate an effort to hide one's identity while engaging in illegal actions [32].

Forensic DNA profiling became possible due to identifying notable discrepancies in minisatellite repeats among people [4, 33]. Southern Blotting techniques were initially used to generate distinct DNA patterns by exploiting minisatellite dispersion. This technique used restriction enzymes to generate DNA pieces of different sizes [33]. The approach, introduced by Sir Alec Jefferys in 1984, resulted in the initial successful DNA profiling in the U.K. This technology has been essential in criminal investigations and in proving innocence [34,35].

The Polymerase Chain Reaction (PCR) significantly impacted DNA analysis by enabling the amplification of small quantities of DNA [36]. The Polymerase Chain Reaction (PCR) is a DNA analysis technique that amplifies Short Tandem Repeat (STR) loci. This process produces amplicons labelled with fluorescent markers, allowing for the determination of their size. The amplicons are separated based on size using either gel or capillary electrophoresis, resulting in the generation of a STR genotype that can be compared. The PCR technique and improvements such as qualitative PCR

***Address for correspondence:** Johannes Hendrik Smith, Department of Forensic and Criminal Investigation Science, College of Law: School of Criminal Justice, University of South Africa (UNISA), Pretoria, Gauteng, South Africa; E-mail: thejhsmith@gmail.com*

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(qPCR) have dramatically enhanced the sensitivity and specificity of DNA analysis [37,38].

Furthermore, the utilisation of Short Tandem Repeats (STRs) in a Polymerase Chain Reaction (PCR)- based methodologies has improved the precision and resilience to deterioration of forensic DNA profiling [25]. Implementing automation and optimisation techniques in PCR operations has decreased analysis time, accelerating forensic casework [39]. Although there have been significant developments, the importance of DNA collecting procedures persists due to their direct influence on the reliability of profiling. The quality and amount of DNA samples play a critical role [40].

DNA analysis technologies have substantially improved in the last thirty years, improving discrimination ability, speed and sensitivity [41,42]. Forensic DNA profiling has evolved from time-consuming RFLP procedures to quick PCR-based techniques, making it an essential tool in criminal investigations. It provides reliable identification and evidence evaluation capabilities [43,44]. Due to ongoing research and technical progress, forensic DNA analysis is anticipated to enhance its accuracy and effectiveness [4,35].

Short Tandem Repeats (STRS)

Short Tandem Repeats (STRs) are the main instrument utilised in forensic DNA analysis because of their polymorphism characteristics and the fact that they vary throughout the genome [45-47]. The DNA motifs, which are repeated sequences of DNA ranging from two to six base pairs, exhibit variation in the amount of repeats among individuals. This variation enables the creation of highly discriminating DNA profiles [47]. Forensic scientists utilise the process of tallying the occurrences of repeated sequences at multiple STR sites to create distinct DNA profiles, which assist in identifying individuals [48].

Autosomal STRs are utilised to distinguish individuals, whereas Y-chromosomal STRs (Y-STRs) are employed to establish male ancestry and identify male contributors in mixtures [49,50], STR analysis, along with other DNA techniques, is a fundamental component of forensic DNA profiling, assisting in identifying individuals and determining kinship Contemporary Short Tandem Repeat (STR) chemistry enables the analysis of small amounts of DNA, with specific kits amplifying more than 24 loci to improve differentiation Forensic scientists utilise STR profiles to compare them with reference samples to establish matches, hence assisting in excluding or implicating individuals based on DNA evidence [51].

STR typing is valuable for generating forensic investigative leads in criminal casework. A match between a suspect's DNA and evidence found at the crime site greatly assists criminal investigations. Although STR analysis has certain limitations, such as the requirement for reference samples for comparison and the possible difficulties in interpreting mixture samples, it remains a fundamental technique in forensic DNA analysis. It provides essential information for individual identification and the criminal justice system [52,53] (Table 1).

The forensic practitioner uses statistical analysis to assess the probability of random coincidence or the existence of additional individuals sharing the same DNA profile. Match probability calculation involves using haplotype frequencies from reference databases encompassing various populations [54,55].

The principal technique in forensic DNA analysis is length-based STR analysis, often performed using capillary electrophoresis [54,56]. Although Next-Generation Sequencing (NGS) has many drawbacks, such as a low marker multiplexing capacity and difficulties with complex mixes, it has advantages, such as enhanced throughput and accuracy [57]. Next-Generation Sequencing (NGS) offers comprehensive data on the nucleotide sequence, which improves the ability to distinguish and accurately analyse forensic evidence. Second-generation sequencing technology enhances the ability to detect and achieve higher success rates, especially when dealing with intricate or deteriorated materials. This technology makes it well-suited for assessing mixed STR patterns [58]. The technique can differentiate between primary and secondary alleles and detect stutter peaks, improving forensic analysis accuracy [59].

Single Nucleotide Polymorphisms (SNPS)

Single Nucleotide Polymorphisms (SNPs) are base substitutions, insertions, or deletions that occur at single positions in the genome of any organism [60]. Point variations in the DNA sequence known as SNPs are found in the human genome's coding and non-coding sections, including the mitochondrial, sex-linked and autosomal DNA [61]. Their forensic applications include individual identification, ancestry determination, lineage tracing and phenotypic prediction. Single Nucleotide Polymorphisms (SNPs), more prevalent than Short Tandem Repeats (STRs) in the human genome, provide benefits such as smaller amplification sizes, lower mutation rates and the ability for high-throughput genotyping. Multiplexed sequencing allows combining Single Nucleotide Polymorphisms (SNPs) with other genetic markers to improve resolution in intricate DNA samples. Phenotyping predictions derived from SNPs offer vital insights into an individual's physical characteristics, assisting investigations in cases when there is no suspect or DNA database match. This method enhances forensic DNA analysis and has potential use in investigative situations.

Forensic DNA analysis process

Forensic DNA profiling is essential for identifying persons by examining and analysing distinct genetic variants exclusive to each person [3,62]. Length-based Short Tandem Repeat (STR) genotyping has been widely used in forensic investigations for almost thirty years and is the principal method forensic practitioners use. This approach examines the diversity in the length or number of repetitions of specific DNA sequences, referred to as Short Tandem Repeats (STRs). Forensic laboratories commonly depend on commercially available Short Tandem Repeat (STR) kits with several genetic markers. These kits enable exact DNA profiling techniques that can differentiate between persons. Length-based STR analysis involves subjecting DNA samples to Polymerase Chain Reaction (PCR) to amplify specific target sequences. Subsequently, capillary electrophoresis separates and identifies the amplicons of varying sizes. Each amplicon corresponds to a distinct STR locus and is distinguished by length. The electropherogram obtained serves as a visual depiction of the DNA profile, facilitating the comparison with reference samples [3].

Although length-based STR typing is commonly employed, it has certain drawbacks, such as limited multiplexing capability, dependence on size-based genotyping and difficulties in analysing complicated mixes. NGS technologies have advanced capabilities that enable simultaneous analysis of many markers and deliver detailed information on nucleotide sequences. This technological progress allows for more effective examination of deteriorated samples and intricate combinations, enhancing forensic DNA analysis [3].

Table 1. The description and interpretation of the possible outcomes of the STR profile.

Outcome of Match Report	Description	Interpretation
Match (suspect included/unidentified body or human remains identified)	The forensic DNA profiles of the exhibit material and reference DNA samples are the same (no differences).	Several loci in the forensic DNA profiles are genetically similar, and the likelihood ratio, RMP, or population occurrence of statistics will indicate the degree of individuality as to the source thereof.
Non- Match (the suspect excluded/identity of the body or human remains could not be established)	The forensic DNA profiles of the exhibit material and reference DNA samples are different.	Due to the profiles being different, the source origin is different.
Inconclusive	No comparison could be conducted.	Insufficient data or technical issues or not able to make any finding to a match or non-match.

Y-chromosomal Short Tandem Repeats (Y-STRs) are used to identify the biological sex of male donors and track their paternal ancestry. Y-STR haplotypes are highly valuable in sexual assault instances that involve mixed DNA samples. Y-STR analysis enhances autosomal DNA testing by identifying male contributors and excluding unjustly accused individuals [3].

In addition to Short Tandem Repeats (STRs), Single Nucleotide Polymorphisms (SNPs) provide supplementary information in forensic DNA analysis. Single Nucleotide Polymorphisms (SNPs) are genetic differences that occur at individual nucleotide sites and are present throughout the entire genome. They offer individual identity, ancestry, lineage and phenotypic estimation data. In contrast to Short Tandem Repeats (STRs), Single Nucleotide Polymorphisms (SNPs) have several advantages, including a greater prevalence in the genome, a smaller size of the amplified DNA fragment and the potential for higher-throughput genotyping.

Single Nucleotide Polymorphisms (SNPs) have emerged as practical choices for forensic DNA analysis, mainly due to the introduction of Next-Generation Sequencing (NGS) technologies. These markers can be integrated with other markers, such as STRs, Y-STRs and X-STRs, in a unified process, improving accuracy and offering significant insights into intricate DNA data. Phenotyping predictions derived from SNPs provide valuable information about physical characteristics, assisting in investigations where conventional DNA profiling techniques fail to identify any potential suspects or matches in the database [3].

Thus, whereas length-based STR analysis continues to be a fundamental technique in forensic DNA profiling, using NGS technology and SNPs provides improved capabilities and insights. These technological improvements enhance the efficiency and precision of DNA sample analysis, facilitating the identification of persons and assisting in criminal investigations.

Evaluating the statistical weight of matching DNA

Forensic DNA analysis's reliability depends on its findings' statistical significance [62-64]. Forensic practitioners analyse the statistical data to compare DNA profiles obtained from physical evidence with those under suspicion. Typically, this comparison can result in three possible scenarios: the person being investigated is the origin, another person has an exact match, or the match is due to contamination or error. Regarding judicial processes, DNA evidence should not be relied upon only but should be evaluated in conjunction with other corroborating evidence [64,65]. Forensic practitioners in different jurisdictions use various approaches to determine the relevance of DNA matches, frequently relying on statistical techniques. Some individuals express the anticipated frequency of an event in the least risky group, whereas others utilise probability of similarity. However, failing to include genetic isolation can distort the evaluation, perhaps resulting in inaccurate positive or negative outcomes [66].

Match probability quantifies the possibility of encountering a DNA profile unrelated to the accused individual. The determination is made using Random Match Probability (RMP), which allows for calculating a likelihood ratio. RMP, or Random Match Probability, quantifies the likelihood of a random person having a DNA profile matching a crime scene sample. It is determined by analysing the frequencies of alleles in the population [54,55,62].

Forensic laboratories commonly express evidence regarding Combined Probability of Inclusion (CPI), which estimates the frequency of detected DNA profiles in the population. CPI aids in evaluating the importance of any correlations between exhibit material and suspects' DNA profiles, assisting in determining culpability or innocence. The Likelihood Ratio (L.R.) approach, becoming more prevalent in forensic laboratories, involves comparing the probability of evidence under multiple hypotheses. Nevertheless, many laboratories in Southern Africa continue to depend on the CPI approach [54,62]. While being computed, L.R. figures are frequently communicated in court to facilitate understanding. DNA evidence aids in assessing the probability of a suspect's culpability, facilitating judicial decision-making [67].

Deciphering DNA profiles from a single source is relatively simple. Still, it becomes more complicated when dealing with mixtures that involve numerous contributors, especially when the DNA levels are low. Probabilistic genotyping techniques and software are employed to analyse mixtures and offer statistical evidence. Although there are standardised parameters, subjective decisions can still influence the interpretation of DNA mixtures [68].

Reliability of DNA test methods

The progress in DNA testing techniques and the enhanced comprehension of legal professionals have substantially impacted its development, making it a fundamental component of the legal system. Judge Van Zyl's recent Tom v S case summary clearly explains the features and influence of forensic DNA evidence in trial courts [64,69]. DNA evidence is categorised as expert testimony, necessitating a dependable scientific foundation and compliance with criteria that govern the admissibility of expert evidence. The reliability of the evidence depends on various elements that impact the integrity of scientific analysis. These criteria include the skill of forensic practitioners, the integrity of the crime scene, the control of DNA samples, the reliability of testing procedures, the credibility of statistical data and the soundness of deductions.

Initially adopted in the 1980s, forensic DNA evidence encountered legal hurdles that raised doubts about its reliability and presentation. During legal proceedings, defence attorneys frequently challenge DNA evidence based on multiple factors, such as quality control, interpretation, verification, accreditation and the documentation of the evidence's handling. Judicial scrutiny, as demonstrated in cases such as S v S.B. and others, prioritises rigorous adherence to protocols, precision of instruments, proficiency of examiners, quality control and other criteria that influence the reliability of evidence [70,71]. The dependability of forensic DNA evidence relies on strict adherence to a quality management system based on ISO 17025 standardised protocols, precision of laboratory techniques and compliance with international and national standards [70,71]. It is an internationally good practice and mandatory in some countries that the DNA laboratory's quality management system and test methods be subjected to peer review. DNA analysis remains reliable for criminal investigations when carried out according to established guidelines despite possible errors.

Impact of DNA backlogs

The ongoing problem of DNA delays and backlogs, where cases surpass the designated timeframe for reporting DNA findings, is a significant challenge in forensic science in several nations, including Southern Africa. This persistent issue generates substantial public apprehension and impedes the endeavour for legal fairness. Casework delays have far-reaching repercussions, affecting various elements of the legal process. For instance, postponing forensic cases owing to backlogs can interrupt ongoing judicial proceedings and extend the detention of innocent individuals awaiting exoneration. Furthermore, police frequently rely on DNA evidence to advance investigations before cases are considered ready for court. The processing of DNA samples from crime scenes and buccal samples from various categories of individuals is causing delays in loading forensic DNA profiles into the database for comparison searches. Consequently, serial rapists and offenders who could have been promptly recognised in the forensic DNA database are allowed to persist in abusing innocent victims.

Investigation of Forensic Investigative Leads (FILs)

FILs are a valuable investigative tool that aids in investigating certain crimes and positively impacts the reduction of crime and conviction rates. Forensic Investigative Leads assist and improve the investigative processes in apprehending repeat offenders and resolving unsolved cases. FILs gives the victims and their families closure [71]. In South Africa, the forensic practitioner communicates Forensic Investigative Leads (FILs) to the detective using electronic communication to the information management system used by the detectives. Detectives, also known as investigating officers, are responsible for following up and investigating the following four different types of FILs:

1. DNA Person-to-crime FILs (known person of the forensic DNA database is linked to the crime scene(s).
2. DNA Crime-to-crime FILs (DNA linking different crime scenes and no known person on the forensic DNA Database).

3. Fingerprint FILs.
4. Integrated Ballistic Identification System FILs.

The criminal case at the station is automatically opened for investigation on the information management system if it is closed. The detective is responsible for investigating all FILs following a Standard Operating Procedure (SOP). Detectives are required to investigate and follow up on forensic investigative leads. The SOP offers additional details and emphasises the requirement to complete the investigation diary in the case docket at each step of the FIL processing and investigation. Additionally, the content within the case docket must be electronically scanned and saved in the information management system. This measure ensures that the content, including witness statements, can be printed when a docket must be reconstructed in case of misfiled dockets [54].

Efficient forensic support is contingent upon the seamless collaboration of multiple parties, including law enforcement, forensic experts, prosecutors and pertinent agencies. Inadequate collaboration and correspondence between these entities may hinder the procedure and result in deficiencies. Face-to-face, phone, or email encounters are the most effective ways for investigators to communicate with diverse stakeholders, such as victims, complainants, expert witnesses and other investigators. The primary communication between forensic practitioners and detectives is system-based, or email, with phone conversations or in-person meetings held sometimes as needed. The interaction between different specific parties, such as detectives, forensic practitioners, investigators and legal professionals (e.g., SPPs), affects how evidence is interpreted during an investigation.

If the complainant attests that the suspect had a legitimate purpose for being on the property, the suspect may be removed from the investigation. The investigation moves along as new information becomes available or if the evidence is strong enough to substantiate the charges. There are several possible outcomes from a state of reasonable suspicion to have enough evidence of the offence's components to support charging the person of interest. The complainant will be approached and requested to provide a statement to confirm whether they know the person of interest identified in the FIL. This step will be taken before approaching the person of interest for a statement or making an arrest, depending on other supporting circumstantial evidence in the case. Detectives must additionally [54]:

1. Investigate the modus operandi of suspects in their cases and identify patterns in which the same methods were used to link suspects.
2. Seek assistance from the Crime Intelligence Analysis Centre to conduct modus operandi and intelligence screening to confirm the person of interest linked or identify potential suspects.
3. Request assistance from the Section: Investigative Psychology to confirm behavioural connections between cases where serial murderers and rapists are involved.

In addition, the detective must notify the State Public Prosecutor (SPP) from the National Prosecution Authority if a trial-ready case contains FILs or information linking the suspect to other cases. It is important to liaise with the SPP involved as early as possible to assess the strength of the evidence and receive advice on any additional investigations that may be necessary.

For a more complete picture, forensic evidence must be integrated with additional details about the suspect's history and behaviours, as it is just a partial collection of observations and evidence. Interpreting the evidence while accounting for its location and portability helps investigators develop logical interpretations or hypotheses. Once it was established that the suspect lacked a legitimate reason or excuse for being at or inside the premises, the interview plan aimed to afford the suspect every opportunity to provide an independent account of their activities. Forensic Identification and Location (FIL) evidence could then be utilised to verify the accuracy and truthfulness of the suspect's statements. The detective would follow the investigative process, incorporating corroborative and similar act evidence to construct a case and enhance the investigation. Corroborative evidence is crucial in connecting the suspect and the crime. In property crime investigations, corroborative evidence may include a witness observing the suspect's vehicle in the vicinity of the crime, CCTV footage showing the suspect nearby, search or call data on the suspect's phone originating from the crime scene and photos of the suspect in the vicinity. Additional supporting evidence bolsters the reasonable suspicion that the suspect was involved [54].

Recognising the value of using behavioural data and multifaceted approaches in investigating FIL casework is essential. Behavioural data can be helpful in cases where witness accounts and tangible proof are missing. Case docket analysis identifying patterns, similarities and distinctive behaviours can be instrumental in investigating the possibility of a single offender committing serial or multiple offences, such as in FIL casework, aiding law enforcement in addressing ongoing. Thus, following the procedure mentioned earlier helps create a plausible suspicion about a suspect's possible involvement. When there is no relationship between the victim and the perpetrator and no witnesses, it is far more challenging to solve FIL cases. Examining the offender's method of operation and identifying a pattern-often indicated by a signature-can be very helpful when examining serial and multiple offenders in forensic investigative casework [54].

Avoiding erroneous interpretations in which evidence is wrongfully interpreted as contradicting a valid hypothesis is crucial. FIL cases that were categorised as unreliable due to validity concerns that entailed identifications based on potentially biased information and because of the presentation of interdependent evidence as if it independently supported a hypothesis compromises the integrity and the casework investigation. Moreover, misunderstanding of FILs can be resolved by elucidating sub-hypotheses regarding the source and activity levels and expanding the knowledge base on factors such as the rarity of observed characteristics within a population and the dynamics of evidence. Many overturned rulings in appeals did not involve new evidence, suggesting that these issues could have been avoided if better interpretations had been made during the trial [54].

Information from victims, witnesses and people with knowledge of the crime or the suspect, physical evidence at the scene of the crime, psychological profiling, police and other agency files, informants, personal identification numbers, vehicle registration numbers and physical descriptions like photographs are some of the ways suspects can be traced. Thus, Investigators need detailed information from various sources, including victims and witnesses, to find a suspected person. Finding suspects will be much easier if victims or witnesses can describe or identify the people who committed the crime. This information includes motivations, skills and possible non-suspects. Obtaining personal descriptions by speaking with people who can characterise the alleged offender is frequently done through interviews. Informers can also be used as a source of information and prove useful. When a complainant's cell phone was stolen during the crime and used by the perpetrator, cell phone surveillance can be used. The information in witness and victim accounts is frequently helpful in the dockets that have been analysed to help find the suspect.

In some cases, finding a suspect remains difficult despite extensive investigation efforts and the attentiveness of investigators. Similarly, there are instances where a lack of evidence makes it difficult for the police to locate a suspect or make an arrest. Even if the technology and instruments used by detectives have greatly improved over the past few decades, there are still some situations where specific individuals are impossible to apprehend.

Traditionally, the percentage of assigned crimes that law enforcement officers have been able to resolve has been relatively low. Instead of actively seeking solutions, detectives frequently adopt a counterproductive "quick fix" mentality and wait for things to happen-such as witness appearance, informers' tips, or forensic results. Furthermore, depending on the investigation techniques adopted, so-called "quick fix" approaches could unintentionally support the notion that a particular strategy is adequate for successfully investigating most cases. If these "quick fix" approaches do not work, detectives can mistakenly think there is nothing else they can do. It is critical to understand that resolving crimes involves human labour and technology. An experienced investigator should use every accessible resource to investigate a case. Time is of the essence and squandering it could result in significant evidence being lost or destroyed [54].

Several reasons may impact the effective utilisation and investigation of FILs by detectives. The following are some of the reasons that may impact the utilisation and the investigation of FILs [54]:

1. The non-adherence of the SOP for the management of FILs is indicative that there is poor command and control in mentoring and ensuring the management of investigating FILs.
2. Lack of enforcement of 24-hour docket inspections.
3. Detectives not complying with the docket inspection instructions.
4. The resource limitations that detectives experience makes their workload much more challenging.

Moreover, several operational factors are more important than one in resolving homicide cases. These include allocating cases to three or four investigators, using computer system searches and interviewing neighbours, friends, acquaintances and witnesses. Inexperienced detectives require three to eight times more time than seasoned detectives when investigating similar offences. Moreover, when inexperienced detectives are appointed as commanders, case dockets are managed ineffectively due to inadequate inspections, a lack of investigator guidance and substandard investigations. Detectives frequently encounter difficulties connecting suspects to other crimes through FILs. Detectives are sometimes concerned about insufficient command and control, a burdensome caseload and insufficient resources, such as inexperienced detectives, vehicles, computers and photocopiers. By adhering to proper norms and standards, detective commanders can efficiently manage case dockets and guarantee the quality of FIL investigations from beginning to end, thereby enhancing crime detection. Concerns have been raised regarding the proficiency of detective skills and the need for ongoing development [54].

When FIL notifications are handled without clear procedures, law enforcement organisations frequently need help figuring out what must be done and by whom. Stressing the value of FIL investigations can aid in the settlement of previous crimes and act as a deterrent to similar ones. Law enforcement agencies should implement an accountability system to guarantee prompt action in response to FILs, in particular with sexual assault.

Within the San Francisco, California-based Combined DNA Index System (CODIS), sexual assault offenders were linked to two or more sexual assault offences (Davis & Wells: 44-48). As mentioned earlier, a third of the instances in the cases ended in convictions; this percentage may have been impacted by ongoing court issues and the victim's and prosecutor's hesitation to press charges (Davis & Wells: 44-48). Forty-four per cent of DNA samples had expired because of the statute of limitations, according to the results of another study. Due to a lack of proof, less than half of the submitted criminal allegations were dismissed. However, in somewhat fewer than half of the cases of sexual assault, the defendant was taken into custody.

Although the approaches are helpful for detectives to apply in new FILs in unsolved cases, these approaches, while potentially very helpful, are only sometimes successful since there is little and reliable information available:

1. Use cutting-edge technology to test historical evidence and, when practical, gather new evidence.
2. Use resources such as the media, other law enforcement and the relatives of those affected by the case to pay fresh attention.
3. Follow-up witnesses and suspects should offer fresh details contributing to the case's resolution.

Investigators must take a thorough and systematic approach to ensure that FIL cases are sufficiently investigated. It is crucial to adhere to appropriate investigation standards, including compliance with investigation procedures. Frequent case docket inspections by commanders (case reviews) provide an opportunity for new insights and can assist in finding details that have been missed. The cornerstones for ensuring the sufficiency of FIL investigations include stressing attention to detail and keeping channels of communication open with the stakeholders.

Conclusion

Society expects publicly supported organisations, such as forensic services, to provide accurate and meaningful analyses and services at a reasonable cost. Forensic DNA profiling has benefitted criminal investigations, although it is not entirely free from potential problems. Until 1975, a novel forensic test method in the U.S. had to be demonstrated to be generally accepted by the relevant scientific community. However, it excluded FILs such as fingerprints and firearms. The 1993 Daubert admissibility ruling requires that forensic methods be proven reliable (Daubert v. Merrell Dow Pharm), which impacted the courts after accepting forensic results. Suppose ISO17025 is correctly applied and adhered to in a laboratory. In that case, the quality and reliability of the scientific outputs from a forensic science laboratory, including the reporting of FILs, will be supported.

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Conflict of Interest

None.

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