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Keywords: Forensic Science; Short Tandem Repeat (STR) Analysis; DNA Profiling; Capillary Electrophoresis; Forensic DNA Testing; NGS; Biological Evidence Short tandem repeat (STR) analysis is a crucial technique in forensic science, providing high-resolution DNA profiling for criminal investigations, paternity tests, and identification of missing persons. This document outlines the key stages of STR analysis, including sample collection and preservation, DNA extraction and quantification, PCR amplification of STR loci, capillary electrophoresis, and data interpretation. Proper handling and storage of forensic samples are essential to prevent DNA degradation and contamination. PCR amplification, using Taq polymerase, enables the replication of STR loci for analysis. Capillary electrophoresis then separates these fragments, generating an electropherogram that is interpreted using specialized software. STR profiling is widely used due to its sensitivity, accuracy, and ability to analyze degraded DNA samples. Despite its advantages, challenges such as DNA mixture interpretation and environmental degradation persist. The continuous advancement of forensic DNA technology, including nextgeneration sequencing (NGS), aims to enhance STR analysis efficiency and accuracy. This document also discusses various STR kits used in forensic science, their applications, and standard protocols ensuring reliable results. STR analysis remains a cornerstone of forensic DNA testing, playing a significant role in legal and investigative processes worldwide.

Abstract

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Introduction

Short tandem repeats (STR) profiling is an invaluable tool in forensic science, offering high levels of discrimination and requiring just trace quantities of DNA in order to produce full or partial profiles^{1,2}. Short tandem repeats are repeats of units of 3-7 base pairs of DNA, with the average number of repeats for various STR loci among any given population forming a DNA profile, commonly bi-allelic. DNA profiling is an essential methodology in the field of forensic investigations³. Over thirty years ago, the first official usage of DNA profiling resulted in the conviction of a convicted murderer. the forensic science Nonetheless. analytical techniques have evolved so much so that DNA profiling developed before the confession was capable of exonerating $him^{4,5}$. As a result of the ever-growing list of applications for DNA profiling in regulatory processes for pharmaceuticals, plants, and organically manufactured agricultural the accuracy, effectiveness, products, and sensitivity have improved significantly⁶.

In the context of forensic science, STR kits aid in the expeditious determination of a suspect's DNA profile in addition to identifying potential matches from donations detected at the crime scene^{7,8}. From transnational organized crime to theft, homicide, and missing persons, forensic investigations and DNA databases play an important role in solving crime9. In recent cross-country investigations, STR profiling has been widely used, as the temporary storage of manufactured goods in bolt hole lock-ups between theft and resale usually happens in another country^{10,11}. Such STR data can be obtained from production lines of DNA analysis, objects recovered from crime and scenes. clothing¹².Simultaneously, STR can inform postbombing recovery teams about unidentified remains in the context of mass disasters and terrorist attacks^{13,14}.

Background of Forensic Science

Forensic science is instrumental in the detection and investigation of crime. Based on the exchange principle, it is an amalgamation of physical, medical, and biological sciences that are used in law and justice^{15,16}. It allows for the determination of physical facts from legal evidence through the application of principles and procedures in the field of science¹⁷. Precise methods and techniques were developed to conform to the requirements of any court of law for the purpose of scientific investigation and crime detection^{18,19}. Forensic study has grown largely since its early applications, but there is an issue with forensic specialists, including law enforcement, legal

advisors, and court personnel regarding the validity, reliability, and admissibility of their procedures and techniques²⁰. As technology flourishes, the need for a foundation becomes inevitable, in terms of utilizing more practical tools and applications on one hand to enhance one's work as a legal professional and on the other hand to secure one's innocence^{21,22}.

Forensic science began with the evolution of two fundamental principles. The first principle is the gradual acceptance of the fact that violent crime occurs. The second principle behind the formation of scientific crime detection is the realization and acceptance that an association exists between the suspect and the crime scene^{23,24}.Forensic science began to formalize and gain recognition during the 1800s, when a deep understanding of analytical chemistry, microscopy, serology, toxicology, and pathology was developed²⁵. The first applications of DNA were through the use of cells. The forensic use of DNA evidence is no longer just a tool in serious crimes, but has also revolutionized the involvement, liability, and overall success of justice in desired crime policies^{26,27}.DNA is not deemed to be the complete answer to solving crimes, particularly in cases involving serious pattern crimes, reported crimes, and new offenses. The application of forensic science is not limited to criminal investigations and therefore can be applied to the matters of civil nature mentioned below²⁸. With the acquisition of greater resources, skills, and a larger customer base, forensic science has expanded. Now, this technique is no longer restricted to the domain of criminal law. It has additional applications in civil disputes. To assist a country's criminal and civil judicial systems, extensive scientific and technical laboratories are set up^{29,30}.

Overview of STR Kits

Short tandem repeats (STRs) were first discovered in forensic science and then explored in genetic studies on evolutionary biology, population genetics, family studies, and paternity testing³¹. STR analysis has been playing a vital role in personal identification, identity disputes, criminal investigations, and the identification of missing individuals. The highly polymorphic nature, reproducibility, sensitivity, specificity, consilience, and strong signal-to-noise ratios make STRs ideal for most forensic applications³². The availability of multiple STR loci and sequence-based sizing information has made it possible for modern forensic kits to be multiplexed to analyze, interpret, and establish consensus profiles in degraded, limited, or mixed forensic biological evidence.

Although STRs explore abundant features inside the human genome, commercial STR kits are limited, covering less than 1% of the genome^{33,34}. Furthermore, future genomic studies should target these potentially informative loci for data mining and application in forensic, genealogical, and anthropological studies. STR is a repetitive sequence that partly, but mostly, obeys the forensic casework laws as X/Y-chromosomal gene markers. STR kits amplify specific DNA regions to identify genetic characteristics³⁵. STR kits are specifically manufactured to amplify particular DNA regions. They consist of mixtures of primers that create many copies of a DNA region, resulting in an ameliorating product that can be easily visualized and analyzed. The kit amplifies specific regions of interest for forensic science because these loci are highly polymorphic and display genetic diversity in world populations. Providing a maximum of 24 STR loci, the kit facilitates the amplification of the target loci more quickly and robustly with minimal chances of contamination³⁶. Other kits are also being used. Standardization of protocols for STR genotyping is important for accurate scientific research and crime solving³⁷. Standard protocols allow the results produced by different groups to be reproducible and reliable. Standardized reagents and consumables provide method reliability, decrease contamination, and allow standardization among authorities. STR profiling data from DNA experts should be standardized. STR kits have importance in forensic science for crucial individualization. STR kits are equally important in genetic diversity studies^{38,39}.

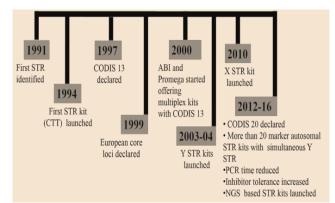


Figure 1; Timeline of key milestones in STR kit development for forensic DNA analysis. It highlights major advancements from the first STR identification (1991) to the launch of the first STR kit (1994), the establishment of CODIS 13 markers (1997), and the introduction of Y-STR (2003) and X-STR kits (2010). Recent innovations (2012–2016) include the CODIS 20 system, improved PCR efficiency, and NGS-based STR kits, enhancing forensic accuracy and speed⁴⁰.

Comprehensive Definition and Purpose of STR Kits in Forensic Analysis

Short tandem repeat (STR) kits are specialized tools that are specifically designed for the extraction and amplification of short tandem repeat sequences found within DNA samples^{32,40}. The significance of STR lies in its ability to assist analysts in making accurate judgments or conducting in-depth investigations and analyses related to the identification of individuals ³³. The primary purpose of employing STR detection within forensic analysis is to significantly enhance the accuracy and reliability of DNA profiling results³⁴. Moreover, STR kits have shown substantial promise not only in legal matters but also in various other domains, including paternity tests, kinship analysis, ancestry determination, genetic diversity assessments, and even in fields such as molecular anthropology and archaeology^{14,24}.The remarkable advantage of utilizing STR is that it enables the rapid differentiation of individuals even within extensive datasets, making it indispensable for disaster victim identification scenarios⁴⁴.Furthermore, the comprehensive analysis of systems and perpetrator data has played an immense role in advancing forensic science and improving overall investigative outcomes⁴⁵.

STR, which stands for Short Tandem Repeats, is a specific type of repetitive DNA. Due to its unique specificity and the automatic inheritance of its patterns, STR facilitates the distinct identification of individuals through easily recognizable and consistent patterns⁴⁶. This type of genetic marker possesses several notable characteristics, including a high degree of polymorphism, a low mutation rate, and a comparatively short genetic distance among individuals⁴³. Research studies have demonstrated that a large number of the various STR loci can be isolated, often resulting in perfect repeated triplets with numerous repeats¹⁴.STRs are distributed throughout the human genome, often with an average interval separating them. Before STRs and other molecular markers can be effectively utilized in practical applications, they must be detected through a process called PCR (Polymerase Chain Reaction), as their resulting output can be extraordinarily complex and intricate. In contrast to standard DNA analysis techniques, analyzing mitochondrial DNA regions or Y-chromosome markers tends to be relatively straightforward when conducted on male and female individuals^{48,49,50}.

Table 1; Advantages of STRs (Short Tandem Repeats) for Forensic DNA Typing^{48,49,50}

Advantage	Description
Abundance of known	Many STR markers are well-
STRs	documented.
Small size suits for	STRs are effective for
degraded samples	degraded DNA.
Ease in multiplexing	Multiple STR loci can be
	analyzed together.
Frequent occurrence	STRs are distributed widely
throughout the genome	across DNA.
Useful for small	PCR amplification allows
quantity of DNA	analysis of minimal DNA.
Similarity in allele size	Allele sizes are consistent for
	efficient comparison.
Highly variable	STR markers are highly
	polymorphic.

Types of STR Kits

STR kits are classified into two major categories: multiplex and single-plex. Multiplex kits are designed to amplify, detect, and report on multiple STR loci in a single reaction tube⁵¹. There are several multiplexes with different combinations of STR loci, and at different times certain combinations may be more useful for the forensic practitioner than others⁵². Multiplex kits used for forensic examiner casework testing are generally optimized to efficiently analyze forensic samples that may be damaged, contain inhibitors, be of limited quantity, and/or be of mixed origin^{53,54}. Essentially, the method combines the amplification of known STR loci with a detection and reporter system. A microfluidic system may be used to assist in the separation of the STR amplicons since their size differences allow them to be resolved by system55.

In contrast, single plex kits typically focus on only one STR locus in the amplification, detection, and reporting systems^{56,3}. Historically, single plex investigation of each locus was more prevalent; however, this application is much less feasible for forensic case analysis than a multiplex format⁵⁷. In general, it is believed that multiplex kits are more desirable for the investigative casework conducted by law enforcement agencies and private forensic laboratories, but single plex systems may be used, for example, in academic institutions carrying out research in forensic science or as a confirmation of a frequency in casework should an atypical result seen when troubleshooting investigations. he Essentially, the selection of kit(s) is decided based on the requirements of an investigation^{33,34}. Numerous STR kits are commercially available, designed to suit the needs of any crime laboratory interested in adopting STRs for forensic purposes. There are a variety of STR kits, many of which are approved for use in qualifying laboratories. New

kits and STR locus combinations continue to evolve and are added as technology matures 41,58 .

Table 2; Comparison of Multiplex and Single-Plex STR Kits:	
Features, Applications, and Limitations	

Features, Applications, and Limitations Types of STR Kits			
Category	Description	Applications	
Multiplex Kits	Designed to amplify, detect, and report on multiple STR loci in a single reaction tube.	Efficient analysis of forensic samples, including damaged, limited quantity, mixed- origin, or samples with inhibitors.	
Single-Plex Kits	Focus on only one STR locus for amplification, detection, and reporting.	Academic research in forensic science or confirmation of frequency during atypical results in forensic casework investigations.	
Key Featu	res of Multiplex and Si	ngle-Plex Kits	
Feature	Multiplex Kits	Single-Plex Kits	
Locus Coverage	Multiple loci in one reaction tube.	Focuses on a single locus.	
Efficiency	Highly efficient for forensic casework.	Less efficient for casework, but valuable for specific research or validation.	
Forensic Suitability	Optimized for analyzing degraded, inhibited, or mixed-origin samples.	Limited suitability for forensic casework.	
Applications	Law enforcement casework, crime labs.	Research institutions, troubleshooting atypical results in casework.	
Separation Method	May use microfluidic systems for resolving amplicons by size differences.	Not typically reliant on advanced separation systems.	
A	dvantages and Limitat	tions	
Category	Advantages	Limitations	
Multiplex Kits	High throughput; multiple loci in a single reaction; faster and more comprehensive.	More complex design and potential for cross- reactivity.	
Single-Plex Kits	Simplicity; focus on individual loci; useful for confirmation and research.	Time-consuming and less practical for large-scale forensic casework.	

Commercially Available STR Kits

Forensics is a relatively small area of the world's market, and there are only a few companies are developing and selling that forensic instruments and reagents, including STR kits^{51,52}. All instruments and reagents have several advantages, such as ease of use, speed, reliability, throughput, the possibility efficiency, of automation, and compatibility with various sample types. Although created by different manufacturers, all STR kits have the same chemistry and rely on the same science, and thus are capable of yielding similar results⁵³. There are many versions of STR kits on the market, from research kits to commercial human identification kits with different capabilities, including options that are specific for casework laboratories, user experience, and applications^{54,55}.

Several commercially available STR kits on the market provide information about their user experience and applications and the country of the company that made the STR kits⁵⁶. The market generally offers new kits for empowering STR typing for demanding casework applications. STR kits have operational protocols and serve particular forensic applications with case validation and guidelines certified⁵⁷. Some STR kits also display DNA quality and yield faster protocol estimates to help users determine if the DNA sample is suitable for STR profiling, even when the mass is limited, which is very important for dealing with DNA mixtures. Commercially available STR kits already have standards and certifications to guarantee their reliability, performance, and guality^{58,59}. The regulations and certifications of several commercially available STR kits are compiled. To overcome the problem of competition between companies that offer various polymorphic DNA analysis systems and forensic science tools, manufacturers must develop their products along with the technology⁶⁰. A summary of several commercially available STR kits and their forensic applications, accuracy, user-friendliness, and distributor regions is provided. Displays of other options and alternatives to kits are possible, depending on the distributor or manufacturer offering the alternatives⁶¹. User experiences and feedback are discussed, and reviews of the quality and speed of the results, along with some case examples, are used to evaluate the quality and availability of the kits. Case studies with the commercially available STR kits, as well as the applications, benefits, and drawbacks provided by the kits, are also discussed⁶². This discussion is important to help examine and evaluate the STR

kits and thus make the right decision in acquiring the appropriate STR kit that can meet users' cases and forensic applications' needs ⁶³.

Table 3; Key Features and Benefits of STR Kits

Feature	Description	
Ease of Use	Designed for user-friendly	
Lase of Use	operation.	
Speed	Provides faster results for	
opeeu	forensic analysis.	
Reliability	Ensures consistent and	
Reliability	reproducible outcomes.	
	Optimized for analyzing	
Efficiency	forensic samples, even with	
	limited DNA mass.	
Throughput	Capable of handling multiple	
Throughput	samples simultaneously.	
	Many kits are compatible	
Automation Possibility	with automated systems for	
	streamlined processes.	
Sample Compatibility	Suitable for various sample	
	types, including degraded and	
	mixed-origin DNA.	

Table 4; Types of STR Kits and Their Applications

Туре	Applications	Examples
Research Kits	Used in academic and research settings for experimental purposes.	DNA quality analysis, validation studies.
Commercial Identification Kits	Designed for human identification in forensic casework.	Crime scene analysis, victim identification.
Casework- Specific Kits	Tailored for casework laboratories to handle specific challenges like DNA mixtures or degraded samples.	High-profile criminal investigations.

|--|

Feature	Commercial STR Kits	Research STR Kits
Focus	Forensic applications and casework validation.	Experimental and exploratory studies.
Certification and Standards	Certified with operational protocols and guidelines.	May lack certifications for forensic validation.
Speed	Offers faster protocols for time- sensitive applications.	Speed may vary depending on the research purpose.
User-Friendliness	Optimized for non-specialist use in forensic labs.	Requires technical expertise.

Table 6	Market and	Distribution	of STR Kits

Aspect	Description
Manufacturers	Few companies dominate the market, each offering unique STR kits.
Geographic Distribution	Kits available globally, with country-specific distributors and regulations.
Alternatives	Custom kits or alternatives are available depending on the distributor or manufacturer.
Competition	Encourages innovation and improvement in technology and kit performance.

Table 7; Casework Benefits of Commercial STR Kits

Benefit	Description
	Allows users to determine
	DNA sample suitability for
DNA Quality Assessment	STR profiling, even in
	limited quantities.
	Certified protocols ensure
Validation	reliability and performance
	in forensic applications.
Versatility	Useful for both standard and
	complex forensic cases
	involving degraded or mixed
	DNA samples.
User Feedback	Includes reviews on quality,
	speed, and usability for
	forensic practitioners.

Key Components of STR Kits

DNA analysis in the fields of civil and forensic genomics relies on STR markers' ability to segregate alleles from samples containing allelic ladders⁶⁴. Each of the STR kits contains a standard laboratory aliquot setting and quality performance tool⁶⁵.One of the most important parts of a kit is the reagents needed for amplification of the STR sequences from the extracted DNA solution. These reagents contain the primers, MgCl, and buffer needed for amplification. Another important part of the kit is the Klenow fragment and Tag polymerase needed for amplification of PCR products. Moreover, reverse sample DNA is needed for the amplification of the allelic ladders^{66,67}. Internal Lane standards will provide guidance for capillary analysis while size standards provide guidance for allele calling. Each of the parts listed is important for the amplification of STR sequences. In the laboratory manuals, a kit lists the protocols used in the laboratory for the most effective and efficient analysis of the DNA samples. There are quality control components that are listed in the protocols that are used to validate the results, show the laboratory is running up-to-date standards, and that the results found are accurate. The investigator must follow the validation policies as

set forth by the government. Some kits are PowerPlex and Quantifiers. When an individual is looking for the kit, they would need to look to see the parts for each of the kits. The laboratory protocols are described in the user manual for validation and analysis of results to assist in human identification. New protocols look at more complex samples and may have fewer parts or they are already combined. Each of these kits plays a crucial role in the forensic identification process with the need to use a combination of kits. Each lab must work within their own guidelines and run the appropriate protocols for their case^{68,69,70,71}.

Table 8; Compo	onents of STR	Kits
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Component	Description	Purpose
Reagents	Includes primers, MgCl, and buffer needed for DNA amplification.	Essential for amplifying STR sequences from the extracted DNA solution.
Klenow Fragment	A DNA polymerase fragment used in the amplification process.	Facilitates the synthesis of DNA during PCR.
Taq Polymerase	A thermostable DNA polymerase.	Catalyzes the synthesis of DNA strands during PCR at high temperatures.
Reverse Sample DNA	Reverse DNA strands used in amplification.	Necessary for generating allelic ladders for analysis.
Internal Lane Standards	Guides capillary analysis during electrophoresis.	Ensures proper alignment and measurement of STR fragment sizes.
Size Standards	Provides reference points for allele calling.	Assists in accurately determining allele sizes.

Applications of STR Kits

Several applications of STR include forensic science, covering criminal case resolution, missing persons, and mass disaster victim recovery; civil law cases; anthropological studies; and genetic research for gene association and basic genomic problem solving^{8,72}. DNA cases have been solved not only in individual case identifications that have resolved unknowns in mass disasters and human rights issues for missing persons' identifications, but the bodies and remains exhumed during the genocide against Tutsis in Rwanda demonstrate the significance of the original application in forensic sciences^{73,74}. Paternity examinations account for the majority of the identification work conducted using DNA tests⁷⁵. Gene mapping markers such as STR

are used in genetic research to assist in gene association testing for human conditions. Research on the Y chromosome STR markers is of anthropological interest because they primarily segregate with surnames. STR testing on the X chromosome can help to resolve unclear mother and maternal child DNA mixtures and to estimate the maternal contribution from complicated samples with multiple contributors⁷⁶. The forensic STR technology was initially developed in the late 1980s, after being released from a Naval Crime Laboratory⁷⁷.

The STR technology has universal applicability, especially in forensic science and law enforcement and judicial systems, and it has implications for resolving and preserving law and justice.[3] This technology has applications, though limited to some extent in the undersigned forensic fields, such as medical examiners, in other forensic and nonscenarios outside crime forensic scene investigations^{78,33}. The use of STR technology is considered a significant tool in forensic biological associations such as family military and mass disaster victim identifications, missing persons, anti-doping specifications, and wildlife species whenever biological evidence is discovered and stored in forensic files^{11,7}.STRs are being globally used and appreciated by the global police community⁷⁹. In general, the DNA database initiative is increasingly gaining ground, and technological advancements are evermore on the increase⁸⁰. The problems of forensic exclusions, cross-border procedures, data sharing and security, and privacy policy issues are being resolved to best practice standards worldwide⁸¹.

STR kits are used during criminal investigations, both at the scene of a crime and at crime labs when processing biological evidence. There are numerous high-profile cases where law enforcement officials solved crimes by using STR analysis. Currently, numerous arrestees have been connected to their biological evidence left at cold case crime scenes once that evidence has been processed through an STR kit. STR analysis has been used to clear suspects through the elimination of those who are not the source of crime scene DNA or to link arrestees to numerous other crime scenes, giving law enforcement officials additional forensic evidence to solve their cases. The use of STR kits can potentially reopen cold cases by identifying new suspects, evewitnesses, and developing new leads in those unsolved cases. It is imperative that crime labs and law enforcement in general follow the evidentiary standards set out in their states in addition to following the rules regarding Chain of Custody. The COC guidelines lay out the minimum evidentiary standards that must be maintained in order for the evidence to be introduced in court. At a minimum, basic training for collection, processing, and storage of DNA evidence must be completed by the individual or individuals involved in the processing of evidence. STR profiles are routinely used in courts to help a jury find an individual offender guilty of a crime. STR technology has also been a huge part of the national conversation involving wrongful convictions and has been integral in exonerating people who have been wrongly imprisoned for crimes that they did not commit. STR profiles obtained from crime scenes can help to validate or confirm a confession of an innocent person. The more evidence that directly implicates someone in a crime, the more difficult it becomes for them to challenge their conviction. Police officer access to STR kits can become a hotbutton issue because their improper use can lead to lawsuits and wrongful conviction. In order to become familiar with using their STR kit, officers should be trained on it in a classroom setting and become familiar with it before using it for their first forensic submission.

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conversation involving wrongful national convictions and has been integral in exonerating people who have been wrongly imprisoned for crimes that they did not commit. STR profiles obtained from crime scenes can help to validate or confirm a confession of an innocent person⁸⁸. The more evidence that directly implicates an individual in a crime, the more challenging it becomes for them to challenge their conviction^{89,90}. Police officer access to STR kits can become a sensitive issue due to the potential for lawsuits and wrongful convictions resulting from their improper use. In order to become familiar with using their STR kit, officers should be trained on it in a classroom setting and become familiar with it before using it for their first forensic submission⁹¹.

Advantages and Limitations

STR profiling techniques have several advantages when compared to other molecular genetic methods⁹².As these profile a much greater number of genetic markers on multiple loci throughout the human genome, they are much more discriminating than older genetic marker systems^{93,94}. Consequently, this enables the individual potential for much more precise identification⁹⁵. The STR markers are also relatively short in length, thereby conferring additional advantages for forensic analysis in that they are not only extremely stable, but they are also much more easily further amplified using PCR methodology, an essential characteristic given that forensic analyses often involve the analysis of highly degraded DNA⁹⁶. Moreover, the CNVs in some STRs further add to their discriminating potential⁹⁷.

However, several important limitations still exist that affect the utility of STR profiling. The major limitation is the requirement for high-quality DNA samples as a reliable source of template DNA98. This requirement limits the successful amplification and therefore profiling of DNA samples that are highly degraded, such as those present in skeletal tissue or soil-exposed remains, or DNA that is present in very low amounts⁹⁹. Even smaller amounts of DNA present as a mixture of DNA from multiple contributors can reduce the reliability of DNA profiles from one sample readily isolating DNA¹⁰⁰. Indeed, the requirements for integrity and specificity of DNA samples are also the basis of potential contamination concerns, where low-level mixed DNA is inadvertently amplified and interpreted ¹⁰¹. It is consequently well recognized that the potential sources of contaminating DNA are varied and complex, and include sample

collection and storage, as well as technical contamination within the state of the art in forensic science today¹⁰². This issue is critically relevant for forensic samples and has instigated considerable research in the development of the relatively new field of forensic DNA sampling, contributing to the investigation of its handling to interpret the potential challenges of DNA contamination¹⁰³.

Table 9; summarizing the advantages and limitations of STR profiling

profiling			
No	Advantages of STR Profiling	Limitations of STR Profiling	
1	Highly discriminating due to multiple	Requires high-quality DNA samples fo	
	loci across the human genome.	reliable results.	
2	Short STR markers make them stable	Degraded DNA or low-quantity	
	and easier to amplify using PCR.	samples may fail to amplify properly.	
3	STRs are effective for forensic analysis	DNA mixtures from multiple	
	even with degraded samples.	contributors can reduce reliability.	
4	Copy Number Variations (CNVs) in	Contamination risks due to improper	
	STRs enhance discrimination potential.	sample handling and storage.	
5	Widely used in forensic science, law	Technical contamination can impact	
	enforcement, and genetic studies.	DNA interpretation and profiling.	

Recent Developments and Future Directions

In recent years, remarkable new developments in STR technology have improved the sensitivity, accuracy, and effectiveness of forensics⁶⁵. Some of these advancements include kits capable of analyzing up to 27 loci, an increasing number of kits validated for forensic use, and kits capable of improving sensitivity for low template DNA^{104,105,16}.Next-generation sequencing has been heralded as the third wave of forensic DNA testing and is of great importance to countries and academics¹⁰⁷.STRs can be identified from sequencing data produced using NGS, and this will greatly assist in the detection of inter-kit incompatibilities, the analysis of complex samples, identifying pathogen characteristics, and genetic information^{3,108}. Unlike STRs, DNA methylation profiles can be used to identify gender, age, body tissue, cell nature, and may be helpful in determining the potential identity profile. In order to improve the reliability of the interpretation of data and increase the use of DNA methylation, more targeted and less than 5 ng of DNA is required for forensic and more freely available prediction software^{109,110}.International technological societies are developing functional groups to support the discussion of STR and forensic scientists and the resulting outcomes bv maximizing their technological strategy^{3,111}. The group plans to undertake international harmonization initiatives to guide future forensic techniques in this space. Although STR development in this field is increasing, much further work needs to be undertaken. STR analysis has been used to provide essential evidence for solving crimes, disasters, and issues of parentage^{11,111}. Blood and semen-derived samples are routinely used for forensic DNA

casework analysis. Autosomal STR profiling has been used in a majority of forensic laboratories worldwide, although Y-chromosome STR analysis and mitochondrial DNA typing are also performed as necessary for parentage and missing person investigations^{112,113}. An immediate application of the resulting scientific knowledge was the development of mini autosomal STR kits and PCR inhibitors removal kits. The current trend is to develop a multiplex reaction capable of amplifying the radically increased number of STR loci in a fast and easy-to-use format^{6,114}. Lab-on-chip technology has been combined with a PCR-CE microfluidic device for STR analysis, and this would further enable multiplexing capabilities¹¹⁵.Non-autosomal STR markers have been introduced, and another kit designed for actively decaying DNA has been released¹⁰.

Procedure of STR analysis

Standard protocols are employed by most forensic laboratories, and while new methods are being tested, they have yet to be widely adopted. First, an evidence sample is collected and preserved with a proper method in order to maintain its integrity. Then, DNA is extracted, and the quantity and quality are assessed. Next, the DNA is amplified using PCR for STR loci. Capillary electrophoresis is used to separate the STR fragments. The electropherograms are read by software and interpreted by experts to generate a DNA profile for future comparison. The steps below summarize the main procedure of STR analysis:

1. Sample Collection and Preservation

The first step in forensic STR analysis is collecting biological samples from crime scenes, ensuring proper reference samples from victims and suspects. Traditional samples include blood, sperm, saliva, and hair, which must be properly stored to prevent degradation. Environmental factors like temperature and moisture can affect DNA quality, so laboratories follow strict guidelines for preservation. STR systems are optimized for longterm storage and forensic casework. Different regions may have varying forensic practices, so laboratories should follow standardized collection guides^{115,116,117,118}.

2. DNA Extraction and Quantification

The second stage of forensic STR analysis is DNA extraction, with various methods offering different advantages and limitations. DNA quantification follows, assessing the quality and quantity of extracted DNA for further testing. Several kits, both manual and automated, use silica-based technology for DNA isolation. The choice of extraction method depends on the sample type, laboratory equipment, and expertise. While organic extractions yield purified DNA, they may remove inhibitors like humic acid from bone samples^{115,116,119}.

3. PCR Amplification of STR Loci

Forensic DNA analysis relies on generating detectable STR profiles using polymerase chain reaction (PCR). PCR amplifies specific STR loci from millions to billions of copies, with Taq polymerase being the gold standard due to its high-temperature stability and efficiency. Various PCR instruments and reagents enable high-throughput sequencing with small reaction volumes. Primer design software ensures optimal sequence selection, checking for SNPs, secondary structures, and primer-dimers. Ideal primers are 22-29 nucleotides long, with a melting temperature of 60-63°C and 45-55% GC content^{120,121,122}.

4. Capillary Electrophoresis

Capillary electrophoresis is widely employed in forensic labs to separate amplified STR products by size. Emerging in the late 1980s and early 1990s, it serves \mathbf{as} а high-resolution alternative to traditional electrophoresis, enabling gel simultaneous analysis of multiple loci from STR amplification. While sharing principles with gel electrophoresis, capillary electrophoresis is more objective, provides higher resolution for smaller fragments, and delivers results faster. The primary buffer used is a pH-controlled TBE solution comprising 89 mM Tris, 89 mM Borate, 2 mM EDTA, and 10% glycerol. The separation process utilizes long, narrow capillaries where high voltage is applied at the injection end, allowing negatively charged DNA to migrate towards the positively charged electrode based on size. The injection process attracts DNA molecules into a focused sample band. Forensic samples, such as human blood or semen, require a DNA detection system to visualize fluorescently labeled DNA fragment sizes. The characteristics of the electrophoresis system and sample purification influence peak shapes and resolution, enabling accurate allele scoring. A pooled polymer solution facilitates the simultaneous analysis of STR fragments produced during amplification, resolving best in a 4-7%linear polyacrylamide polymer. DNA electrophoresis runs at high constant voltages, typically ranging from 3.0 to 15.0 kV, with capillaries varying between 50 to 150 microns. Both side and end injection methods offer distinct advantages and limitations, while the electrical power needed for STR fragment separation must be considered in capillary design. Common issues

during runs include sample pull-up, plateaus, peak splitting, and long run times. The resulting data is presented as a computer-generated electropherogram, detailing size determinations and signal strength values in a panel format. Accurate sizing often relies on the allelic ladder technique, where "bin" sizes stem from a calculator influenced by allele size range panels and sample length. Key parameters such as electrical length, color channel, injection time, sample current, and ejection time are critical for effective capillary electrophoresis in STR analysis^{123,124,125,126}.

5. Data Analysis and Interpretation

STR chemistries create DNA fragment complexes analyzed using various software tools. These applications generate raw data, perform initial STR delineation, and assess data quality for complete STR profiles. Multiple CPUs validate results individually against standards or through consensus from individual call lists. Typically, inter-study consensus of allele calling software is employed. although multiple programs may validate variant calls to enhance accuracy. Common call algorithms utilize (1) a binning algorithm for peak assignment, (2) a peak height threshold for allele calling, and (3) a quality score indicating call confidence. They also incorporate signal intensity balance and reference dye ratio algorithms to assess DNA quality and detect mixed sample contributions. Quality scores may vary by DNA event category, with stutter position data recorded due to software calling tendencies. The call algorithm database confirms unusual peaks and validates small alleles or haplotypes not in the database^{127,128,129}. reference Differentiating mixtures from artifacts is essential, evaluated through peak height ratios, peak area ratios, and minor contributor percentages, to robustly interpret STR profiles. Recommendations emphasize assessing allelic peak height and area balance. Low template DNA is particularly challenging, increasing allele drop-out risk and stutter proportions. Evaluating CSF variation in replicates to assess stutter percentages in low templates is advised, alongside peak height and area ratio analysis. The protocols for data analysis and interpretation considerably affect final STR profile conclusions in violent crimes and disaster victim identifications. Standard practices and quality assurance ensure reliable results across laboratories, with specific recommendations for interpreting mechanical mixtures and low template DNA. Strict quality control and validation processes for software and interpretation guidelines have

been underscored since their introduction, preceding the development of allele balancing software^{130,131}.

Conclusion

The primary objective was to present information to national and international audiences about the range of STR kits used in forensic science today. It explored the advantages and disadvantages of a range of STR kits used for various legal agencies and forensic DNA laboratories to help answer various types of casework. It also documented the different software packages used in testing and issues of terminology; the ongoing challenges were discussed, such as mixture analysis and the complexity of stutters. The limitations of the interpretation of certain loci in some populations, issues of privacy and ethical considerations, and the potential strengths and pitfalls of family searching were also presented. The purpose of this summary is to provide an overview of the major points discussed. In conclusion, STR analysis has been used for over 30 years, and today it forms a cornerstone of DNA profiling for forensic as it is efficient, robust, and identification accurate. It has been responsible for both supporting convictions and freeing the innocent and aiding the identification and repatriation of victims of mass disasters or conflict. However, the core technology has not substantially changed, and STR testing is more efficient than nearly all other available. Further technologies currently exploitation of direct sequencing, massively parallel sequencing, rapid, and low-template testing is anticipated; however, challenges over analytical specificity, interpretational thresholds, and mixture analysis still exist. These and the issues of using STR GIS for building stronger cases currently remain a focal point for research and operational development, as does a fresh attempt to understand the rates at which mutations occur in STR loci in different populations. Regular professional development of forensic science practitioners will ensure optimal use of these increased capabilities and a faster initial interpretation of cases where the evidence is found to be abundant, of good quality, and without evidence of acceleration or elevated stutter production. Many other capitalizing uses of STR kits are documented, and these have applications far beyond their original use in criminal investigations. It is therefore crucial that the forensic community begins a process of embracing these new uses and applies them in a responsible, accountable, and transparent manner.

References

- Keerti A, Ninave S. DNA fingerprinting: Use of autosomal short tandem repeats in forensic DNA typing. Cureus. 2022. nih.gov
- [2]. Kulthammanit N, Sathirapatya T, Sukawutthiya P, Noh H, Vongpaisarnsin K, Wichadakul D. STRategy: A support system for collecting and analyzing next-generation sequencing data of short tandem repeats for forensic science. Plos one. 2023 Jul 17;18(7):e0282551. plos.org
- [3]. Alketbi SK. The role of DNA in forensic science: A comprehensive review. International Journal of Science and Research Archive. 2023. <u>uclan.ac.uk</u>
- [4]. Kulthammanit N, Sukawutthiya P, Noh H, Vongpaisarnsin K, Wichadakul D. STRategy: A support system for collecting and analyzing short tandem repeats for forensic science. bioRxiv. 2023 Feb 21:2023-02. biorxiv.org
- [5]. Tanudisastro HA, Deveson IW, Dashnow H, MacArthur DG. Sequencing and characterizing short tandem repeats in the human genome. Nature Reviews Genetics. 2024 Feb 16:1-6. [HTML]
- [6]. Smith JH, Singh M. DNA forensic and forensic investigative leads. J Forensic Med. 2024. <u>researchgate.net</u>
- [7]. Carratto TM, Moraes VM, Recalde TS, Oliveira ML, Teixeira C. Applications of massively parallel sequencing in forensic genetics. Genetics and Molecular Biology. 2022 Sep 19;45(3 Suppl 1):e20220077. <u>scielo.br</u>
- [8]. Soldati A. Characterisation of apparent mismatches detected during routine short tandem repeat analysis in parentage investigations. 2023. ufs.ac.za
- [9]. Jia J, Liu X, Fan Q, Fang C, Wang M, Zhang J, Li W, Shi L, Zhang X, Chen C, Yu Z. Development and validation of a multiplex 19 X-chromosomal short tandem repeats typing system for forensic purposes. Scientific reports. 2021 Jan 12;11(1):609. <u>nature.com</u>
- [10]. Kaur L, Sharma SG. Forensic DNA analysis: a powerful investigative tool. InCrime Scene Management within Forensic Science: Forensic Techniques for Criminal Investigations 2022 Mar 24 (pp. 1-40). Singapore: Springer Singapore. [HTML]
- [11]. Zema T, Sulich A, Grzesiak S. Charging stations and electromobility development: a cross-country comparative analysis. Energies. 2022. <u>mdpi.com</u>
- [12]. Kuzmenko OV, Smiianov VA, Rudenko LA, Kashcha MO, Vasilyeva TA, Kolomiiets SV,

Antoniuk NA. Impact of vaccination on the COVID-19 pandemic: bibliometric analysis and cross country forecasting by fourier series. Wiad. Lek. 2021 Jan 1;74(10 pt 1):2359-67. researchgate.net

- [13]. Alfano V, Guarino M. The effect of selfesteem on the spread of a pandemic. A crosscountry analysis of the role played by selfesteem in the spread of the COVID-19 pandemic. Social Science & Medicine. 2023. <u>nih.gov</u>
- [14]. Jin S, Yang G, Hilaire J, Ojo M, Tindale S, Areal F, Jones G, Frewer LJ. Consumer responses to plant viruses in the context of an emerging agri-food risk: a cross-country comparison. Journal of Risk Research. 2024 Oct 24:1-31. tandfonline.com
- [15]. Zhang M. Forensic imaging: a powerful tool in modern forensic investigation. Forensic Sciences Research. 2022. <u>oup.com</u>
- [16]. Weber A, Hoplight B, Ogilvie R, Muro C, Khandasammy SR, Pérez-Almodóvar L, Sears S, Lednev IK. Innovative vibrational spectroscopy research for forensic application. Analytical Chemistry. 2023 Jan 10;95(1):167-205. [HTML]
- [17]. Haddrill PR. Developments in forensic DNA analysis. Emerging topics in life sciences. 2021. portlandpress.com
- [18]. 18. Primorac D, Schanfield M. Forensic DNA applications: An interdisciplinary perspective. 2023. [HTML]
- [19]. Shepitko VY, Shepitko MV. The role of forensic science and forensic examination in international cooperation in the investigation of crimes. Journal of the National Academy of Legal Sciences of Ukraine. 2021;28(1):179-86. library.kr.ua
- [20]. Yadav S, Yadav S, Verma P, Ojha S, Mishra S. Artificial Intelligence: An Advanced Evolution In Forensic and Criminal Investigation. Current Forensic Science. 2023;1(1):e190822207706. <u>researchgate.net</u>
- [21]. Galante N, Cotroneo R, Furci D, Lodetti G, Casali MB. Applications of artificial intelligence in forensic sciences: C urrent potential benefits, limitations and perspectives. International journal of legal medicine. 2023 Mar;137(2):445-58. [HTML]
- [22]. Casino F, Dasaklis TK, Spathoulas GP, Anagnostopoulos M, Ghosal A, Borocz I, Solanas A, Conti M, Patsakis C. Research trends, challenges, and emerging topics in digital forensics: A review of reviews. IEEE Access. 2022 Feb 24;10:25464-93. <u>ieee.org</u>

- 2025, VOL. 6, NO.1 , 1-17, e-ISSN: 2706-9915, p-ISSN: 2706-9907
- [23]. 23. Gardner EA, DellaRocco R, Bever R. Forensic Science in the United States. I: Historical Development and the Forensic Science Laboratory System. Forensic Science Review. 2022 Jul 1;34(2):72-82. [HTML]
- [24]. 24. Houghton AB. Forensic Pathology: Medicolegal Death Investigation and Management of Fatalities in Mass Disasters and Terrorist Events. InThe Distributed Functions of Emergency Management and Homeland Security 2023 Jul 19 (pp. 337-353). CRC Press. [HTML]
- [25]. 25. Roger K. Visual Data in Education and Health Research: Historical Reflections and Current Prognostications. Journal of Medical Education and Curricular Development. 2023 Apr;10:23821205231171469. <u>sagepub.com</u>
- [26]. 26. Gordetsky JB, Stump JA, Craig JC, Valencia A. HF01-12 A HISTORY OF RENAL TUMORS THROUGH THE PAGES OF ROBBINS PATHOLOGY AND CAMPBELL'S UROLOGY. Journal of Urology. 2024 May 1;211(5S):e282. auajournals.org
- [27]. 27. Little and MA, Buikstra JE. Foundation and History of Biological Anthropology. A Companion to Biological Anthropology. 2023 Mar 8:14-38. [HTML]
- [28]. 28. Sumner DR, Hildebrandt S, Nesbitt A, Carroll MA, Smocovitis VB, Laitman JT, Beresheim AC, Ramnanan CJ, Blakey ML. Racism, structural racism, and the American Association for Anatomy: initial report from a task force. The Anatomical Record. 2022 Apr;305(4):772-87. <u>wiley.com</u>
- [29]. 29. Kim J, Elgerud L, Tuller H. Gaining community entry with survivors for forensic human rights and humanitarian intervention. Forensic Sciences Research. 2022. <u>oup.com</u>
- [30]. 30. Robinson AT. Pathology–The Beginnings of Laboratory Medicine. Labmedicine. 2023. [HTML]
- [31]. 31. Hoogenboom J, Sijen T, van der Gaag KJ. STRNaming: Generating simple, informative names for sequenced STR alleles in a standardised and automated manner. Forensic Science International: Genetics. 2021 May 1;52:102473. [HTML]
- [32]. 32. Shrivastava P, Jain T, Kumawat RK. Direct PCR amplification from saliva sample using non-direct multiplex STR kits for forensic DNA typing. Scientific Reports. 2021. <u>nature.com</u>
- [33]. 33. Jäger R. New perspectives for whole genome amplification in forensic STR analysis.

International Journal of Molecular Sciences. 2022. <u>mdpi.com</u>

- [34]. 34. Fan H, Wang L, Liu C, Lu X, Xu X, Ru K, Qiu P, Liu C, Wen SQ. Development and validation of a novel 133-plex forensic STR panel (52 STRs and 81 Y-STRs) using single-end 400 bp massive parallel sequencing. International Journal of Legal Medicine. 2022 Mar;136(2):447-64. [HTML]
- [35]. 35. Almeida JL, Korch CT. Authentication of human and mouse cell lines by short tandem repeat (STR) DNA genotype analysis. Assay Guidance Manual [Internet]. 2023. nih.gov
- [36]. 36. Fan H, Zeng Y, Wu W, Liu H, Xu Q, Du W, Hao H, Liu C, Ren W, Wu W, Chen L. The Y-STR landscape of coastal southeastern Han: Forensic characteristics, haplotype analyses, mutation rates, and population genetics. Electrophoresis. 2021 Aug;42(16):1578-93. researchgate.net
- [37]. 37. Li R, Shen X, Chen H, Peng D, Wu R, Sun H. Developmental validation of the MGIEasy Signature Identification Library Prep Kit, an all-in-one multiplex system for forensic applications. International Journal of Legal Medicine. 2021 May;135:739-53. researchgate.net
- [38]. 38. Smajlović-Skenderagić L, Idrizbegović S, Brkanić L, Bilić A, Huel R, Parsons TJ. Challenges with co-amplification of microbial DNA in interpretation of STR profiles obtained from human skeletal remains. Forensic Science International: Genetics. 2021 Mar 1;51:102452. [HTML]
- [39]. 39. Jordan D, Mills DE. Past, present, and future of DNA typing for analyzing human and non-human forensic samples. Frontiers in Ecology and Evolution. 2021. <u>frontiersin.org</u>
- [40]. Shrivastava P, Dash HR, Kumawat RK, Srivastava A, Imam J. STR Typing and Available Kits. In: Dash H, Shrivastava P, Mohapatra B, Das S, editors. DNA Fingerprinting: Advancements and Future Endeavors. Singapore: Springer; 2018. p. 4. https://doi.org/10.1007/978-981-13-1583-1_4.
- [41]. Pedroza Matute S, Iyavoo S. Applications and Performance of Precision ID GlobalFiler NGS STR, Identity, and Ancestry Panels in Forensic Genetics. Genes. 2024. <u>mdpi.com</u>
- [42]. Dash HR, Elkins KM, Al-Snan NR. Fast, High-Sensitive, and High-Resolution DNA Techniques. InAdvancements in Forensic DNA Analysis 2023 Dec 7 (pp. 61-78). Singapore: Springer Nature Singapore. [HTML]

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- [43]. Poethe SS, Holtel J, Biermann JP, Riemer T, Grabmüller M, Madea B, Thiele R, Jäger R. Cost-Effective Next Generation Sequencing-Based STR Typing with Improved Analysis of Minor, Degraded and Inhibitor-Containing DNA Samples. International Journal of Molecular Sciences. 2023 Feb 8;24(4):3382. <u>mdpi.com</u>
- [44]. Chatterjee A. Development and Validation of a Multiplex STR Amplification Reaction for Academic and Research Purposes. 2023. <u>uab.edu</u>
- [45]. Forouzesh M, Irani S, Soleimani A, Monabati SJ. Application of Y-STR, DIP-STR and SNP-STR markers in interpretation of forensic genetic profiling: A narrative review. Iranian Journal of Public Health. 2022 Jul;51(7):1538. <u>nih.gov</u>
- [46]. Fan H, Xie Q, Wang L, Ru K, Tan X, Ding J, Wang X, Huang J, Wang Z, Li Y, Wang X. Microhaplotype and Y-SNP/STR (MY): A novel MPS-based system for genotype pattern recognition in two-person DNA mixtures. Forensic Science International: Genetics. 2022 Jul 1;59:102705. <u>sciencedirect.com</u>
- [47]. Yazdanian M, Karami S, Tahmasebi E, Alam M, Abbasi K, Rahbar M, Tebyaniyan H, Ranjbar R, Seifalian A, Yazdanian A. Dental radiographic/digital radiography technology along with biological agents in human identification. Scanning. 2022;2022(1):5265912. wiley.com
- [48]. Bhattacharjee R, Kar AK. Cheiloscopy: A crucial technique in forensics for personal identification and its admissibility in the Court of Justice. Morphologie. 2024. [HTML]
- [49]. Rajan-Babu IS, Dolzhenko E, Eberle MA, Friedman JM. Sequence composition changes in short tandem repeats: heterogeneity, detection, mechanisms and clinical implications. Nature Reviews Genetics. 2024 Mar 11:1-24. [HTML]
- [50]. Rębała K, Nedzvetskaya DE, Kotova SA, Zabavskaya TV, Rybakova VI, Kholodova MV, Tsybovsky IS. STR typing of European elk (moose) and European roe deer with novel forensic assays reveals contrasting patterns of genetic structure of the two cervids in Belarus. Russian Journal of Genetics. 2022 Dec;58(12):1493-503. researchgate.net
- [51]. Schwaller P, Vaucher AC, Laplaza R, Bunne C, Krause A, Corminboeuf C, Laino T. Machine intelligence for chemical reaction space. Wiley Interdisciplinary Reviews:

Computational Molecular Science. 2022 Sep;12(5):e1604. <u>wiley.com</u>

- [52]. Teale AM, Helgaker T, Savin A, Adamo C, Aradi B, Arbuznikov AV, Ayers PW, Baerends EJ, Barone V, Calaminici P, Cances E. DFT exchange: sharing perspectives on the workhorse of quantum chemistry and materials science. Physical chemistry chemical physics. 2022;24(47):28700-81. rsc.org
- [53]. Anstine DM, Isayev O. Generative models as an emerging paradigm in the chemical sciences. Journal of the American Chemical Society. 2023. acs.org
- [54]. Seifrid M, Pollice R, Aguilar-Granda A, Morgan Chan Z, Hotta K, Ser CT, Vestfrid J, Wu TC, Aspuru-Guzik A. Autonomous chemical experiments: Challenges and perspectives on establishing a self-driving lab. Accounts of Chemical Research. 2022 Aug 10;55(17):2454-66. <u>acs.org</u>
- [55]. Chu AE, Kim J, Cheng L, El Nesr G, Xu M, Shuai RW, Huang PS. An all-atom protein generative model. Proceedings of the National Academy of Sciences. 2024 Jul 2;121(27):e2311500121. pnas.org
- [56]. Hall CL, Kesharwani RK, Phillips NR, Planz JV, Sedlazeck FJ, Zascavage RR. Accurate profiling of forensic autosomal STRs using the Oxford Nanopore Technologies MinION device. Forensic Science International: Genetics. 2022 Jan 1;56:102629. <u>fsigenetics.com</u>
- [57]. Abedini J, Cook B, Bell S, Chang X, Choksi N, Daniel AB, Hines D, Karmaus AL, Mansouri K, McAfee E, Phillips J. Application of new approach methodologies: ICE tools to support chemical evaluations. Computational Toxicology. 2021 Nov 1;20:100184. sciencedirect.com
- [58]. Vadisetty R. Multi Layered Cloud Technologies to achieve Interoperability in AI. In2024 International Conference on Intelligent Computing and Emerging Communication Technologies (ICEC) 2024 Nov 23 (pp. 1-5). IEEE. [HTML]
- [59]. Dilsiz N. A comprehensive review on recent advances in exosome isolation and characterization: Toward clinical applications. Translational Oncology. 2024. <u>sciencedirect.com</u>
- [60]. Ni Z, Wölk M, Jukes G, Mendivelso Espinosa K, Ahrends R, Aimo L, Alvarez-Jarreta J, Andrews S, Andrews R, Bridge A, Clair GC. Guiding the choice of informatics software and tools for lipidomics research

applications. Nature methods. 2023 Feb;20(2):193-204. nature.com

- [61]. Parmar P, Ryu J, Pandya S, Sedoc J et al. Health-focused conversational agents in person-centered care: a review of apps. NPJ digital medicine. 2022. <u>nature.com</u>
- [62]. Erten Uyumaz B, Feijs L, Hu J. A review of digital cognitive behavioral therapy for insomnia (CBT-I apps): are they designed for engagement?. International journal of environmental research and public health. 2021 Mar 12;18(6):2929. <u>mdpi.com</u>
- [63]. King JL, Woerner AE, Mandape SN, Kapema KB, Moura-Neto RS, Silva R, Budowle B. STRait Razor Online: An enhanced user interface to facilitate interpretation of MPS data. Forensic Science International: Genetics. 2021 May 1;52:102463. [HTML]
- [64]. Al-Shuhaib MB, Hashim HO. Mastering DNA chromatogram analysis in Sanger sequencing for reliable clinical analysis. Journal of Genetic Engineering and Biotechnology. 2023 Nov 13;21(1):115. <u>springer.com</u>
- [65]. Moura-Neto R, King JL, Mello I, Dias V, Crysup B, Woerner AE, Budowle B, Silva R. Evaluation of Promega PowerSeq[™] Auto/Y systems prototype on an admixed sample of Rio de Janeiro, Brazil: Population data, sensitivity, stutter and mixture studies. Forensic Science International: Genetics. 2021 Jul 1;53:102516. [HTML]
- [66]. Garcia FM, Bessa BG, Dos Santos EV, Pereira JD, Alves LN, Vianna LA, Casotti MC, Trabach RS, Stange VS, Meira DD, Louro ID. Forensic applications of markers present on the X chromosome. Genes. 2022 Sep 7;13(9):1597. <u>mdpi.com</u>
- [67]. Behl A, Mishra A, Mishra IK. Tools and techniques used in forensic DNA typing. Handbook of DNA profiling. 2021. <u>researchgate.net</u>
- [68]. Kanthaswamy S, Brendel T, Cancela L, Andrade de Oliveira DA, Brenig B, Cons C, Crespi JA, Dajbychová M, Feldl A, Itoh T, Landi V. An inter-laboratory study of DNAbased identity, parentage and species testing in animal forensic genetics. Forensic Sciences Research. 2022 Dec;7(4):708-13. <u>oup.com</u>
- [69]. Huffman K, Ballantyne J. Single cell genomics applications in forensic science: Current state and future directions. Iscience. 2023. <u>cell.com</u>
- [70]. Devesse L. Characterisation and differentiation of five UK populations using

massively parallel sequencing of forensic STRs. 2022. <u>core.ac.uk</u>

- [71]. Luttman AM, Komine M, Thaiwong T, Carpenter T, Ewart SL, Kiupel M, Langohr IM, Venta PJ. Development of a 17-plex of penta-and tetra-nucleotide microsatellites for DNA profiling and paternity testing in horses. Frontiers in Veterinary Science. 2022 Apr 7;9:861623. <u>frontiersin.org</u>
- [72]. Song F, Wei X, Zhou C, Wang S, Deng C, Liao M, Luo H. Resolving the recombination pattern of 38 X-STRs from Chinese Han threegeneration pedigrees. Legal Medicine. 2022 Nov 1;59:102135. [HTML]
- [73]. Damour G, Baumer K, Legardeur H, Hall
 D. Early noninvasive prenatal paternity
 testing by targeted fetal DNA analysis.
 Scientific Reports. 2023. <u>nature.com</u>
- [74]. Millogo M, Soubeiga ST, Bazie BV, Zohoncon TM, Ouattara AK, Yonli AT, Simpore J. Disputed paternity presumption in Burkina Faso: determination of the biological fathers of children using ABOrhesus/hemoglobin electrophoresis and STR assays. Journal of Genetic Engineering and Biotechnology. 2021 Dec 1;19(1):130. sciencedirect.com
- [75]. Pilli E, Berti A. Forensic DNA analysis: technological development and innovative applications. 2021. [HTML]
- [76]. Zedda N, Meheux K, Blöcher J, Diekmann Y, Gorelik AV, Kalle M, Klein K, Titze AL, Winkelbach L, Naish E, Brou L. Biological and substitute parents in Beaker period adult– child graves. Scientific reports. 2023 Oct 31;13(1):18765. nature.com
- [77]. Lynch V. The impact of forensic DNA profiling on gender privacy. 2022. <u>sun.ac.za</u>
- [78]. Butler JM. Recent advances in forensic biology and forensic DNA typing: INTERPOL review 2019–2022. Forensic Science International: Synergy. 2023. <u>sciencedirect.com</u>
- [79]. Alketbi SK. Emerging Technologies in Forensic DNA Analysis. Perspectives in Legal and Forensic Sciences. 2024. <u>uclan.ac.uk</u>
- [80]. Padmanabhan AS, Sapna S. Forensic Investigation Approaches of DNA Analysis and Criminal Investigation. International Journal of Safety & Security Engineering. 2023 Feb 1;13(1). <u>researchgate.net</u>
- [81]. Wang M, Chen H, Luo L, Huang Y, Duan S, Yuan H, Tang R, Liu C, He G. Forensic investigative genetic genealogy: expanding pedigree tracing and genetic inquiry in the

genomic era. Journal of Genetics and Genomics. 2024 Jul 3. sciencedirect.com

- [82]. Dowdeswell TL. Forensic genetic genealogy: A profile of cases solved. Forensic Science International: Genetics. 2022. [HTML]
- [83]. Levine C. Anyone You Are Related to Can Be Used against You: Criminal Discovery Statutes and Investigative Genetic Genealogy. Cardozo L. Rev., 2024. <u>ssrn.com</u>
- [84]. Moletsane RK. The role of DNA evidence in criminal proceedings. 2022. [HTML]
- [85]. Oosthuizen T, Howes LM. The development of forensic DNA analysis: New debates on the issue of fundamental human rights. Forensic Science International: Genetics. 2022. <u>fsigenetics.com</u>
- [86]. PALMBACH T, SHUTLER G. Legal Considerations for Acceptance of New Forensic. Forensic Botany: Principles and Applications to Criminal Casework. 2024 Aug 26:265. [HTML]
- [87]. Xu X, Vinci G. Forensic Science and How Statistics Can Help It: Evidence, Hypothesis Testing, and Graphical Models. arXiv preprint arXiv:2312.17735. 2023. [PDF]
- [88]. Presser JR, Robertson K. AI Case Study: Probabilistic Genotyping DNA Tools in Canadian Criminal Courts. Law Commission of Ontario: Toronto, ON, Canada. 2021. <u>lcocdo.org</u>
- [89]. Hamid HBBA. Understanding the Impact of DNA Evidence in the Criminal Justice System. JMCL. 2022. <u>um.edu.my</u>
- [90]. Cronin A. Interpretation and presentation of statistical methods: Understanding statistical evidence in the Australian criminal justice system. 2023. <u>gut.edu.au</u>
- [91]. Xu X, Vinci G. Forensic Science and How Statistics Can Help It: Evidence, Likelihood Ratios, and Graphical Models. Wiley Interdisciplinary Reviews: Computational Statistics. 2024 Sep;16(5):e70006. [HTML]
- [92]. Marwaha S, Knowles JW, Ashley EA. A guide for the diagnosis of rare and undiagnosed disease: beyond the exome. Genome medicine. 2022. <u>springer.com</u>
- [93]. Tedersoo L, Albertsen M, Anslan S, Callahan B. Perspectives and benefits of highthroughput long-read sequencing in microbial ecology. Applied and environmental microbiology. 2021 Aug 11;87(17):e00626-21. <u>asm.org</u>
- [94]. Moffitt JR, Lundberg E, Heyn H. The emerging landscape of spatial profiling

technologies. Nature Reviews Genetics. 2022. [HTML]

- [95]. Vandereyken K, Sifrim A, Thienpont B, Voet T. Methods and applications for singlecell and spatial multi-omics. Nature Reviews Genetics. 2023 Aug;24(8):494-515. <u>nature.com</u>
- [96]. Liu B, Zhou H, Tan L, Siu KT, Guan XY. Exploring treatment options in cancer: tumor treatment strategies. Signal transduction and targeted therapy. 2024 Jul 17;9(1):175. nature.com
- [97]. Saini DK, Chopra Y, Singh J, Sandhu KS, Kumar A, Bazzer S, Srivastava P. Comprehensive evaluation of mapping complex traits in wheat using genome-wide association studies. Molecular Breeding. 2022 Jan;42:1-52. nih.gov
- [98]. Li S, Tollefsbol TO. DNA methylation methods: Global DNA methylation and methylomic analyses. Methods. 2021. nih.gov
- [99]. Jarvis ED, Formenti G, Rhie A, Guarracino A, Yang C, Wood J, Tracey A, Thibaud-Nissen F, Vollger MR, Porubsky D, Cheng H. Semiautomated assembly of high-quality diploid human reference genomes. Nature. 2022 Nov 17;611(7936):519-31. <u>nature.com</u>
- [100]. Pervez MT, Hasnain MJ, Abbas SH, Moustafa MF, Aslam N, Shah SS. [Retracted] A Comprehensive Review of Performance of Next-Generation Sequencing Platforms. BioMed Research International. 2022;2022(1):3457806. wiley.com
- [101]. Tao J, Bauer DE, Chiarle R. Assessing and advancing the safety of CRISPR-Cas tools: from DNA to RNA editing. Nature Communications. 2023. <u>nature.com</u>
- [102]. Lai JJ, Chau ZL, Chen SY, Hill JJ, Korpany KV, Liang NW, Lin LH, Lin YH, Liu JK, Liu YC, Lunde R. Exosome processing and characterization approaches for research and technology development. Advanced Science. 2022 May;9(15):2103222. <u>wiley.com</u>
- [103]. Amiteye S. Basic concepts and methodologies of DNA marker systems in plant molecular breeding. Heliyon. 2021. <u>cell.com</u>
- [104]. Uguen K, Michaud JL, Génin E. Short Tandem Repeats in the era of next-generation sequencing: from historical loci to population databases. European Journal of Human Genetics. 2024. [HTML]
- [105]. Wu F, Cai G, Xi P, Guo Y, Xu M, Li A. Genetic diversity analysis and fingerprint construction for 87 passionfruit (Passiflora spp.) germplasm accessions on the basis of SSR fluorescence markers. International Journal of

Molecular Sciences. 2024 Oct 8;25(19):10815. nih.gov

- [106]. DeForest N, Wang Y, Zhu Z, Dron JS, Koesterer R, Natarajan P, Flannick J, Amariuta T, Peloso GM, Majithia AR. Genomewide discovery and integrative genomic characterization of insulin resistance loci using serum triglycerides to HDL-cholesterol ratio as a proxy. Nature Communications. 2024 Sep 14;15(1):8068. <u>nature.com</u>
- [107]. Hu X, Liu J, Xu T, Qin K et al. Research progress and application of the thirdgeneration sequencing technologies in forensic medicine. Legal Medicine. 2024. [HTML]
- [108]. Mekhfi L, El Khalfi B, Saile R, Yahia H, Soukri A. The interest of informative ancestry markers (AIM) and their fields of application. InBIO Web of Conferences 2024 (Vol. 115, p. 07003). EDP Sciences. <u>bio-conferences.org</u>
- [109]. Gudapati S, Chaudhari K, Shrivastava D, Yelne S. Advancements and Applications of Preimplantation Genetic Testing in In Vitro Fertilization: A Comprehensive Review. Cureus. 2024. <u>nih.gov</u>
- [110]. Chiswell K, Zaininger L, Semsarian C. Evolution of genetic testing and gene therapy in hypertrophic cardiomyopathy. Progress in Cardiovascular Diseases. 2023 Sep 1;80:38-45. [HTML]
- [111]. Sijen T, Harbison SA. On the identification of body fluids and tissues: a crucial link in the investigation and solution of crime. Genes. 2021. <u>mdpi.com</u>
- [112]. Amankwaa AO, McCartney C. The effectiveness of the current use of forensic DNA in criminal investigations in England and Wales. Wiley Interdisciplinary Reviews: Forensic Science. 2021 Nov;3(6):e1414. wiley.com
- [113]. Odah M. The Double Helix of Justice: The Crucial Role of DNA in Advancing Criminal Investigations. 2024. preprints.org
- [114]. Ge J, Budowle B. Forensic investigation approaches of searching relatives in DNA databases. Journal of Forensic Sciences. 2021. [HTML]

[115]. Ye X. STR Profiling's Contribution to Forensic Science. In2021 International Conference on Culture, Design and Social Development (CDSD 2021) 2022 Jan 24 (pp. 141-144). Atlantis Press. <u>atlantis-press.com</u>

[116]. Benecke M. Forensic DNA samples: collection and handling. Molecular Analyses. 2022. <u>oapen.org</u>

- [117]. Kulthammanit N, Sathirapatya T, Sukawutthiya P, Noh H, Vongpaisarnsin K, Wichadakul D. STRategy: A support system for collecting and analyzing next-generation sequencing data of short tandem repeats for forensic science. Plos one. 2023 Jul 17;18(7):e0282551. plos.org
- [118]. Schulte J, Rittiner N, Seiberle I, Kron S, Schulz I. Collecting touch DNA from glass surfaces using different sampling solutions and volumes: Immediate and storage effects on genetic STR analysis. Journal of Forensic Sciences. 2023 Jul;68(4):1133-47. <u>wiley.com</u>
- [119]. Wan TY, Hwa HL, Lee TT, Lu YW. High efficiency sperm enrichment from forensic mock samples in bubble-based acoustic filtration devices for short tandem repeat (STR) analysis. Lab on a Chip. 2024. <u>rbcbioscience.com</u>
- [120]. Khehra N, Padda I, Swift C. Polymerase chain reaction (PCR). StatPearls. 2023. <u>statpearls.com</u>
- [121]. Sathyanarayana SH, Wainman LM. Laboratory approaches in molecular pathology: the polymerase chain reaction. Diagnostic Molecular Pathology. 2024. [HTML]
- [122]. Uduwawala H, Manamperi A, Gunaratna GP, Karunanayake L, Ceruti A, Abd El Wahed A, Fernando L, Premaratna R, Hapugoda M. Detection of pathogenic Leptospira with rapid extraction followed by recombinase polymerase amplification (RPA) and quantitative polymerase chain reaction (qPCR) assay-A comprehensive study from Sri Lanka. Plos one. 2024 Mar 15;19(3):e0295287. plos.org
- [123]. Xu R, Chang Z, Wen D, Liu Y, Wang C, Qu W, Tang X, Jia H, Li J, Cai J, Li G. A preliminary exploration for co-detecting RNA virus and STR type on capillary electrophoresis in forensic practice. Electrophoresis. 2023 Oct;44(19-20):1579-87. [HTML]
- [124]. Connon CC. ... STR Amplification Options: Coupling with Standard or Fast PCR, Traditional or Normalized DNA Extraction, and/or Traditional or Alternative Capillary Electrophoresis. Forensic DNA Analysis: Methods and Protocols. 2023. [HTML]
- [125]. Al-Snan NR. Transition of capillary electrophoresis to next generation sequencing for forensic DNA analysis: Need of the hour. InNext Generation Sequencing (NGS) Technology in DNA Analysis 2024 Jan 1 (pp. 3-20). Academic Press. [HTML]

- [126]. Geldenhuys A. Evaluating the use of capillary electrophoresis in the forensic DNA profiling of burnt teeth. 2023. <u>uct.ac.za</u>
- [127]. Holland MM, Tiedge TM, Bender AJ, Gaston-Sanchez SA, McElhoe JA. MaSTR[™]: an effective probabilistic genotyping tool for interpretation of STR mixtures associated with differentially degraded DNA. International Journal of Legal Medicine. 2022 Mar;136(2):433-46. [HTML]
- [128]. Fan H, Wang L, Liu C, Lu X, Xu X, Ru K, Qiu P, Liu C, Wen SQ. Development and validation of a novel 133-plex forensic STR panel (52 STRs and 81 Y-STRs) using singleend 400 bp massive parallel sequencing. International Journal of Legal Medicine. 2022 Mar;136(2):447-64. [HTML]
- [129]. Lee LY, Tan J, Lee YS, Syn CK. Shedder status—an analysis over time and assessment of various contributing factors. Journal of Forensic Sciences. 2023 Jul;68(4):1292-301. wiley.com
- [130]. Gettings KB, Tillmar A, Sturk-Andreaggi K, Marshall C. Review of SNP assays for disaster victim identification: Cost, time, and performance information for decision-makers. Journal of Forensic Sciences. 2024 Sep;69(5):1546-57. <u>wiley.com</u>
- [131]. Deans ZC, Biricik A, De Rycke M, Harton GL, Hornak M, Khawaja F, Moutou C, Traeger-Synodinos J, Renwick P. Twelve years of assessing the quality of preimplantation genetic testing for monogenic disorders. Prenatal Diagnosis. 2023 Apr;43(4):506-15. wiley.com