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Comparison between ***short in tandem repeats*** **(str) and** ***single nucleotide variants*** (snv) **methods in forensic genetics for the identification of individuals.**

Comparison between short tandem repeat (STR) and single-nucleotide variant (SNV) methods in forensic genetics for individual identification.

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SUMMARY

Introduction: Forensic genetics plays a fundamental role in identifying individuals in criminal investigations, using genetic markers with high discriminatory power.
This study aimed to compare methods based on Short Tandem Repeats (STRs) and Single Nucleotide Variants (SNVs), evaluating their effectiveness, applicability, and limitations in the context of human identification. Methods: This is an integrative literature review, with searches conducted between August 2025 and July 2026 in the PubMed and Virtual Library databases.
Health, Scielo, and Google Scholar. Descriptors combined with Boolean operators were used, without language restriction, considering articles published between 2021 and 2026. After applying the inclusion and exclusion criteria, 10 studies were selected for analysis.
Results: The results showed that STRs remain the gold standard in forensic genetics due to their high discriminatory power and broad standardization. In contrast, SNVs demonstrated important advantages in the analysis of degraded DNA and in samples with low amounts of genetic material. It was also observed that technologies such as massive parallel sequencing increase the sensitivity and precision of the analyses. Furthermore, the analysis of flanking regions of SNPs showed potential to enhance the power of genetic discrimination.

Studies have also indicated that the combination of STRs and SNVs significantly improves results in different forensic contexts. Final considerations: It is concluded that the integration of STRs and SNVs represents the most effective strategy for human identification in forensic genetics.

Descriptors: *Human genetics, Forensic genetics, Genetic markers, Single Nucleotide Variants (SNVs), Short Tandem Repeats (STRs), Sequence analysis, DNA.*

1 INTRODUCTION

With regard to the identification of individuals — perpetrators of crimes or victims —, and

It is essential to use effective techniques to prove the participation of each individual in this context;

Therefore, genetics has proven to be an effective science for substantiating such evidence. Before

Due to the use of DNA in criminal cases, many suspects have either escaped arrest or been convicted.

erroneously, because they did not use precise techniques to solve the cases and resorted to...

However, over the years, it has become clear that this type of evidence is not sufficient to obtain witnesses or fingerprints.

It is not always reliable. However, this scenario has changed with the implementation of genetic techniques in...

forensic science (Barbosa, 2018).

Forensic genetics consists of the technical and scientific use of genetic knowledge and methods.

validated as a tool for accessing information derived from materiality, with the potential to

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relevance to the investigation that questioned it. For this, the application of genetic markers It brought greater precision in associating biological traces with individuals, contributing to criminal investigations and kinship analysis and victim identification in disasters (Dias, 2020).

Currently, two types of genetic markers dominate the forensic tool: the *Short Tandem Repeats* (STRs), widely used in human identification panels, and *Single Nucleotide Variants* (SNVs), which have gained prominence due to their abundance in the genome and the possibility of analysis in degraded samples (Weir, 2015).

These microsatellites differ in their characteristics. STRs are highly polymorphic, In other words, they exhibit variability in the number of repetitions, which means that each individual has different results. a unique profile, providing high discriminatory power and being necessary for identification. of only a few loci. SNVs, on the other hand, are more abundant in the genome and stand out for presenting... They have a lower mutation rate, and they also allow typing in short fragments of DNA, which is useful. in degraded materials (Pedroza, 2025).

The present study aims to compare methods based on STR markers. (Short Tandem Repeats) and SNV (Single Nucleotide Variants) regarding efficacy, applicability and limitations in identifying individuals in the context of forensic genetics, considering advances Recent advancements in genotyping and sequencing technologies. Furthermore, the aim is to describe the... molecular fundamentals of these markers, analyze their advantages and disadvantages in different scenarios — such as degraded samples, biological traces, and kinship tests — and assess the potential of SNVs as a complementary or alternative tool to STRs in routine forensic work.

2 METHODOLOGY

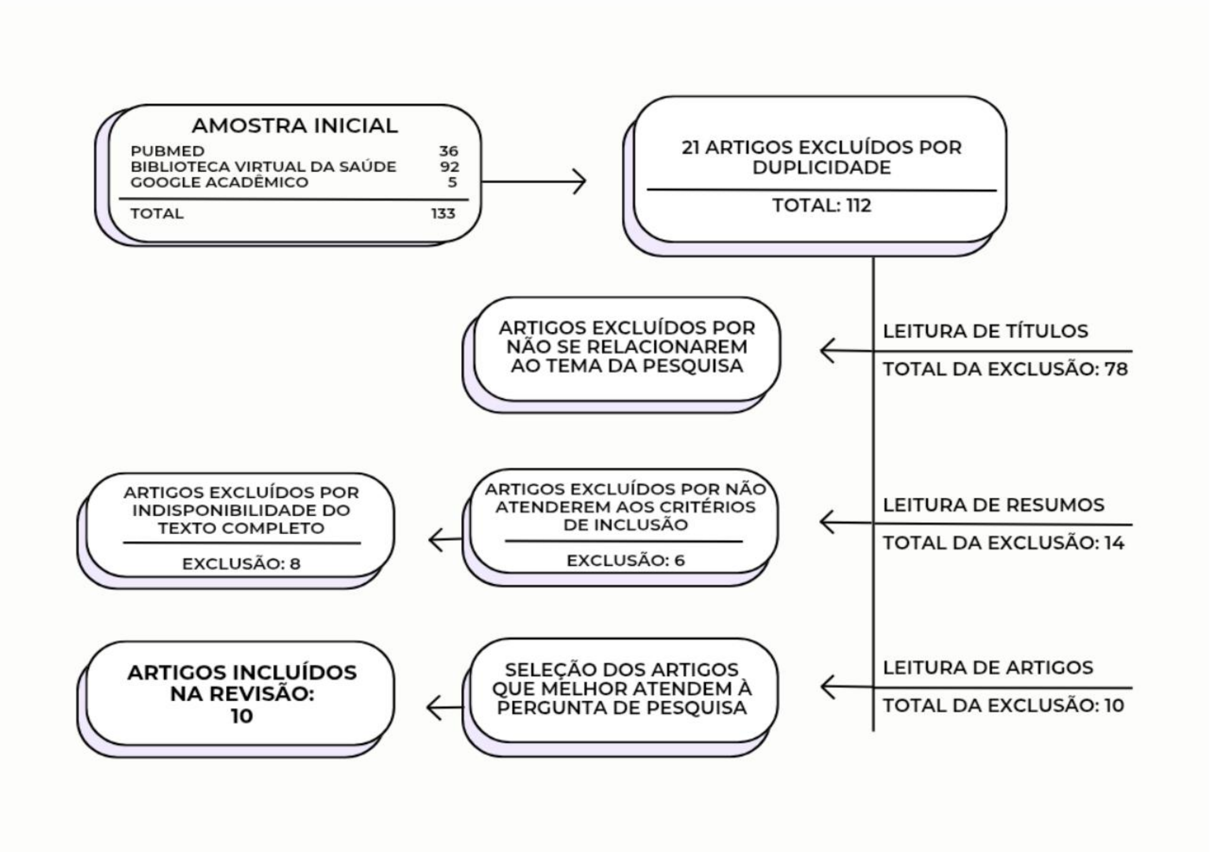
This study consists of an integrative literature review. The collection of references The survey was conducted between August 2025 and July 2026, through structured searches in PubMed, Virtual Health Library (VHL), SciELO and Google Scholar databases, as well as on official websites and scientific societies. There were no language restrictions, being Selected articles were those published between 2021 and 2026. The following criteria were used for this purpose. descriptors, obtained from searches in the Health Sciences Descriptors (DeCS) and in Medical Subject Headings (MeSH): Human genetics, Forensic genetics, Genetic markers, Single Nucleotide Variants (SNVs), Short Tandem Repeats (STRs), Sequence analysis, DNA, combined together with the Boolean connector AND. Examples of structured combinations include: *Human genetics AND Forensic genetics, SNVs AND STRs, Genetic markers AND Sequence analysis, DNA.*

The inclusion criteria considered articles available in full that address the use of genetic markers (SNVs and STRs) applied to forensic genetics, with emphasis on studies of identification of individuals, in evaluating the reliability of methods, and in comparative analyses. As exclusion criteria, duplicate articles, articles with restricted access, or articles that... were not considered. They deal with applications of genetic markers aimed exclusively at distinct areas of genetics. forensic and that do not involve human identification.

3 RESULTS

Based on a structured search conducted in the PubMed and Virtual Library databases... Using the Health and Google Scholar databases, 133 studies were identified. Of these, 21 were excluded due to... Due to duplication, 112 studies remained for analysis. After reading the titles, 78 articles were excluded. because they were not related to the proposed theme. In the abstract reading stage, 14 studies were Excluded because they did not meet the inclusion criteria or because the full text was unavailable. A total of 20 articles were submitted for full reading. After complete reading, 10 articles were selected. that best answered the research question, comprising the final corpus of the analysis (Figure 1).

Figure 1. Flowchart for article selection, 2026.



Source: Author's own work, 2026.

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Among the 10 articles selected for this review, the evidence was examined. scientific studies on forensic genetics, establishing a survey of the use of techniques of SNP and STR for the identification of individuals. The main points investigated involved the Consolidation of STR markers as the gold standard in forensic investigation with regard to Identification of individuals: the advantages of using SNVs to identify human beings. when the collected biological sample is in a degraded state or has a reduced quantity of DNA, and the complementarity between the techniques.

The main characteristics of the selected studies, as well as their objectives and outcomes, are: presented in Table 1.

Table 1. Characteristics of the selected scientific articles, according to title, authors, year of publication, objectives and results, 2026.

Title	Authors	Year	Objective	Results
Exploring Y-chromosomal STRs and SNPs for forensic and genetic insights in the Jiangsu Han population	LI *et al.*	2025	To elucidate the paternal genetic structure of a given population, expand the genetic database, and provide accurate data for the advancement of forensic research and human genetics.	Technologies such as STR and SNP They have increased the accuracy in human identification, including in samples degraded. Furthermore, it began to allow for the interference of phenotypic characteristics and ancestry.
Preparation for shotgun sequencing in forensic genetics – Evaluation of DNA extraction and library building methods	KAMPMANN *et al.*	2025	Evaluate single genome sequencing (SGS) in forensic genetics, considering its performance with DNA extracted by four methods. widely used.	The combination of extraction and library preparation methods directly influences the quality of shotgun sequencing, with the association between EZ1 and EZ2, with a double-stranded library, being the most efficient, allowing the acquisition of many high-quality forensic genetic markers.

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Analysis of Human Degraded DNA in Forensic Genetics	ZUPANIÿ PAJNIÿ	2025	Solutions for analysis of degraded DNA through massively parallel sequencing (MPS) and single nucleotide polymorphisms (SNPs) as powerful markers, complementing or replacing traditional STR analysis in samples committed.	STR, SNP, and NGS work together to improve results, especially in degraded DNA samples.
Forensic applications of compound genetic markers: trends and future directions	SHABALALA *et al.*	2025	Explore the development of standard composite markers, their applications, advantages, and limitations. and discuss the use of next-generation sequencing technologies for the integration of these markers.	Composite markers show greater potential for forensic applications. This review highlights the types of compound markers and compares their sensitivity to that of... individual genetic markers.
Dense single-nucleotide polymorphism testing revolutionizes the scope and degree of certainty for source attribution in forensic investigations	MANDAPE *et al.*	2024	Describe the SNP markers, their characteristics, and the technological advances that enable high-throughput analyses and facilitate... alternative methods of attribution of origin.	SNPs work better than traditional methods in difficult situations and expand potential. investigation.
An overview of autosomal STRs and identity SNPs in a Norwegian population using massively parallel sequencing	AGUDO *et al.*	2024	Characterize the Allelic frequencies of 27 aSTR loci to evaluate the discriminatory advantage of sequence-based alternative formats (SB) compared to traditional length-based nomenclature (LB).	Autosomal STR and SNP markers analyzed by massively parallel sequencing show high genetic variability in the studied population, conferring high discriminatory power for forensic investigation purposes.

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Forensic identity SNPs: Characterization of flanking region variation using massively parallel sequencing	DAVENPORT *et al.*	2023	Characterize variations in flanking regions of forensic identity-informational SNPs using Massive Parallel Sequencing (MPS) technology.	Analysis of the flanking regions of SNPs has increased the power of genetic discrimination by identifying new alleles, reducing the probability of coincidence. The inclusion of these variations makes some SNP loci more informative than STR markers, preserving smaller amplicons for degraded DNA samples.
Concordance study on Y-STRs typing between the SeqStudio™ genetic analyzer for HID and the MiSeq™ FGx forensic genomics system	SOLDATI *et al.*	2023	Validate the agreement between the Y-STR genotyping results obtained using capillary electrophoresis (CE) and massively parallel sequencing (MPS) systems.	High concordance in allele designation, showing that massively parallel sequencing (MPS) produces reliable profiles; however, the capillary electrophoresis (CE) system demonstrated superior allelic balance compared to MPS at multi-copy loci.
Application Progress of Massively Parallel Sequencing Technology in STR Genetic Marker Detection	TAO *et al.*	2022	Review the main massively parallel sequencing (MPS) technologies applied to STR detection in forensic genetics, including platforms, tools, performance, population studies, and international initiatives.	MPS technology applied to STR offers high sensitivity, reliability, and compatibility with traditional methods, in addition to increasing discriminatory power by identifying more genetic variations. It also improves the analysis of degraded samples, although it still faces challenges. challenges.

A novel computational strategy to predict the value of the evidence in the SNP-based forensic mixtures	PASCALI	2021	Introduce and validate a new computational methodology (NITZq) that allows the simultaneous analysis of hundreds of SNPs and STR markers in a single reaction and calculates the weight of evidence in complex DNA mixtures.	The NITZq method has proven to be more reliable than traditional methods, as it reduces false inclusions, respects forensic principles, and improves the accuracy in the quantitative interpretation of evidence.

Source: Author's own work, 2026.

4. DISCUSSION

The studies analyzed demonstrate a significant evolution in identification techniques. forensic genetics, with emphasis on the consolidation of STRs as the gold standard and the growing Valuing SNPs as a complementary tool. In this context, Mandape et al. (2024) They showed that SNPs perform better in complex situations, expanding the investigative power compared to traditional methods, while Li et al. (2025) reinforce The combination of STR and SNP increases the accuracy of identification, including in samples. degraded.

Corroborating these findings, Agudo et al. (2024) demonstrated that both STR and SNP Data analyzed by massive sequencing exhibit high discriminatory power, highlighting the The efficiency of these technologies in individual identification. In a complementary way, Zupaniÿ Pajniÿ (2025) highlights the integration between STR, SNP and next-generation sequencing technologies (NGS) enhances the results, especially in degraded samples, highlighting the The importance of a combined approach.

On the other hand, studies such as that of Soldati et al. (2023) show that, although the Although massively parallel sequencing (MPS) produces reliable results, capillary electrophoresis still does not. It presents advantages, such as a better allelic balance at certain loci, which indicates that... Traditional techniques still have relevance. In line with this, Tao et al. (2022) highlight that the MPS It increases the sensitivity and discriminatory power of STRs, but still faces challenges. especially in data analysis.

Furthermore, Davenport et al. (2023) demonstrated that the analysis of flanking regions SNP significantly increases the power of genetic discrimination, and in some cases,

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to surpass that of STRs. Shabalala et al. (2025) point out that composite markers represent a A promising trend, with greater sensitivity compared to isolated markers. Additionally, Kampmann et al. (2025) showed that the quality of the results It depends directly on the extraction and sample preparation methods, reinforcing the importance of methodological standardization.

Finally, Pascali (2021) introduced an innovative approach to the analysis of mixtures of SNP-based DNA, demonstrating greater reliability and fewer false inclusions in comparison with traditional methods. Taken together, the studies analyzed indicate that, although the While STRs remain essential in forensic practice, SNPs and new technologies are expanding significantly expands the possibilities for analysis, suggesting a scenario of complementarity between the methods.

FINAL CONSIDERATIONS

This study has shown that STR markers continue to be fundamental in forensic genetics due to their high discriminatory power and broad validation. scientific. However, it has become evident that SNPs are gaining prominence, especially in situations involving degraded DNA or samples with low amounts of genetic material, answering the research question by demonstrating that both methods are effective, but more so. Effective when used in a complementary way.

The relevance of this study to biomedicine is directly related to the advancement of genetic analysis techniques, which contribute to the improvement of identification methods. human and to strengthen the role of biomedical professionals in the forensic field. For society, these These advancements represent greater reliability in criminal investigations, a reduction in judicial errors, and... Greater accuracy in identifying individuals directly impacts the promotion of justice.

Furthermore, the analysis of the studies revealed that the incorporation of new Technologies, such as massive parallel sequencing, significantly expand the The possibilities of forensic genetics are being explored, although technical and analytical challenges remain. overcome. In this way, the initial problem was solved by demonstrating that there is no replacement. It's not about the integration between STR and SNP, but rather a strategic integration between these methodologies.

However, more research is needed on this topic so that new... perspectives should be explored, especially with regard to the standardization of techniques, to analysis of complex data and the practical application of these technologies on a large scale. The advancement The continuation of this research will be essential to consolidate the use of these tools in routine forensic practice.

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