

When the Body Is Rewritten: Gene Editing, Forensic Identity and the Future of Criminal Investigation in India

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Abstract: For a long time, the human genome has been considered the ultimate identifier for a criminal investigation. It was widely accepted that nobody could change it. However, the recent developments demonstrate otherwise. The Indian criminal jurisprudence hasn't kept pace with a molecular disruption that is CRISPR-Cas9 technology, meaning clustered regularly interspaced short palindromic repeats and associated protein 9 that enables rapid and precise alteration of genetic sequences. The principle of genetic constancy, the foundational assumption underpinning DNA-based identification, is destroyed by somatic gene therapy, iatrogenic chimerism after hematopoietic stem cell transplantation and the theoretical possibility of targeted forensic evasion. Cases like Chris Long's demonstrate that chimaeras can deposit biological material with a DNA profile that diverges from their ID documents or reference sample. Chris Long, a UK citizen, had his blood DNA wholly replaced by donor DNA once he received a bone marrow transplant. India has enacted the Bharatiya Sakshya Adhiniyam, 2023 and the Bharatiya Nagarik Suraksha Sanhita, 2023, which make the forensic examination of serious crime scenes mandatory. This assumes forensic reliability that gene editing technologies render untenable. The DPDP Rules, 2025, which came into effect in November 2025, impose data protection obligations that do not apply to genetic data or to profile updates post-medical intervention.

Index Terms - CRISPR-Cas9, forensic DNA profiling, chimerism, Digital Personal Data Protection, Bharatiya Sakshya Adhiniyam, epigenetic forensics, gene editing, criminal investigation, India.

INTRODUCTION

The human genome, long viewed as a fixed biological baseline and the ultimate indicator of personal identity in criminal law, is now demonstrably mutable. The new customisation of a CRISPR-based genetic engineering drug was designed to disrupt coronavirus, with the promise of reliable manufacture through CRISPR-Cas9 protocols amid rapid developments in the clinical alteration of DNA sequences via CRISPR-based platforms [1]. Although bioethical literature systematically interrogates the clinical safety, germline implications and therapeutic modalities of gene editing, a critical forensic gap remains under-explored: what happens to the status of criminal investigations when the human body is not genetically stable? The issue has gained importance in present-day criminal justice systems, where DNA profiling, specifically Short Tandem Repeat (STR) analysis, is regarded as almost infallible evidence by trial courts worldwide, including in India. The combination of somatic gene therapies, bone marrow or stem cell transplantations, and naturally occurring or artificial human chimerism creates a new population of "genetically modified subjects". The forensic analysis of these people may no longer align with their historical or multi-tissue biological markers, posing a direct challenge to the epistemic grounds of crime adjudication.

Conventional forensic DNA profiling relies on two core assumptions that gene-editing technology undermines systematically. Initially, it presupposes that one has a single, homogeneous, and fixed genotype throughout all bodily tissues. According to this assumption, a reference buccal swab, a bloodstain at the crime scene, or a dropped hair follicle will yield completely concordant STR profiles [2]. Moreover, DNA phenotyping is the analytical inference of *Externally Visible Characteristics* (EVCs), such as eye colour, hair morphology, skin pigmentation, and biogeographical ancestry, from specific genetic markers [3]. In particular, FDP presumes that the phenotypic expression of such genetic markers exclusively depends on one's static and native genetic code. The destruction of both assumptions is taking place through modern biomedical interventions. Somatic gene editing refers to the alteration within specialised non-reproductive cells in a specific organ or tissue [4]. Therefore, somatic gene editing leads to "tissue-specific" genetic mosaicism.

Cell populations within the same individual host have distinctly different DNA sequences. Likewise, in the case of an allogeneic hematopoietic stem cell transplantation, the recipient's peripheral blood DNA profile completely changes to that of the donor's, while the other solid tissues retain the native genotype of the recipient [5]. Doctors are the cause of chimerism, which creates forensic complications. As an example, empirical research has documented individuals exhibiting donor-derived DNA profiles in both their blood and semen years after a transplant, demonstrating that unverified tissue sources can directly mislead investigative teams and produce false exclusions [6]. The uncontrolled introduction of these genetic variations poses a significant systemic risk within the Indian ecosystem, where forensic infrastructure is constantly backlogged and unevenly standardised [7].

At the same time, India's statutory regime governing forensic collection and adjudication has been overhauled more significantly than at any time in a century by virtue of the *Bharatiya Sakshya Adhiniyam, 2023* (BSA), the *Bharatiya Nagarik Suraksha Sanhita, 2023* (BNSS) and the *Bharatiya Nyaya Sanhita, 2023* (BNS). The BSA, which repealed the colonial-era Indian Evidence Act, 1872, has made DNA evidence a specific mode of expert opinion under Section 39(1) [8]. It will be subject to a higher level of judicial scrutiny about relevancy and structural integrity. The BSA does not have a formal statutory standard based on validity, like the Western Daubert doctrine, so there is no standard for assessing complex scientific phenomena, such as mosaic or edited DNA, as trial judges see fit [9]. As per Section 176(3) of the BNSS, all offences punishable by seven years or more of imprisonment must invariably be subjected to forensic examination and complete videography of the scene of the crime. The forensic biology audit, in tandem with Sections 349 and 351 of the BNSS (which establish the mandatory medical and biological examination of accused persons), elevates forensic biology from an optional investigative adjunct to a mandatory minimum requirement in criminal procedure [10]. Nevertheless, the entire statutory framework operates on an implicit assumption that biological evidence is stable and unambiguous. A premise that CRISPR-driven interventions are rapidly overturning.

The judicial approach in these areas is regulated by procedural rules. The Supreme Court, in *Kattavellai @ Devakar v. State of Tamil Nadu*, 2025 [11], inter alia, stipulated elaborate rules for the collection, chain-of-custody tracking, sealing, and speedy transport of DNA samples to prevent contamination and tampering. The court ordered the delivery of samples to Forensic Science Laboratories (FSLs) within 48 hours and prohibited the unsealing of evidence without the trial court's permission. Notwithstanding, these judicial rules were expressly created to prevent external environmental contamination and do not contemplate the one-off case in which the DNA sample is subjected to biological or therapeutic changes within the living subject. Furthermore, the provisions of the Criminal Procedure (Identification) Act, 2022 allow law-enforcing agencies to store biological and biometric information obtained from convicts, arrestees, and preventive detainees for up to 75 years [12]. The law has no way to update or reconcile these features if one is genetically altered through somatic gene therapy. This is a structural fault in India's biometrics architecture in the long view.

From the Constitution's perspective, the new development tests the protections under Articles 21 and 20(3). The judgment of *Puttaswamy (Retd.) v. Union of India* [13] brought in informational privacy under Article 21, which pertains to the right to life and personal liberty. Further, it gave a strict three-pronged test for all state surveillance and data processing. The test consists of legality, legitimate state aim and structural proportionality. At the same time, Article 20(3) prohibits a person from being forced to incriminate himself. This protection is found in the *case of Selvi v. State of Karnataka* [14]. In 2010, the state of Karnataka passed a law prohibiting involuntary neurobiological testing on the grounds of mental and bodily privacy. Although normal, non-invasive physical samples (such as fingerprints) are generally acceptable, compelling a genetically mosaic or chimeric suspect to undergo deep multi-tissue biopsies or turn over historical pre-therapy medical records raises unresolved constitutional problems about bodily integrity and informational self-determination [15].

Forensic science is now using higher-level molecular techniques to overcome these systemic disruptions. Systems like SHERLOCK and DETECTR detect target nucleic acid sequences affordably and fast using the collateral cleavage activities of CRISPR-Cas12/13 enzymes. Molecular precision that powers pathology can be exploited for identity evasion [16]. Although whole-genome editing is not practically possible, selected editing in blood lineages or buccal cells is feasible and can lead to false exclusions in normal database searches. As forensic laboratories shift from capillary electrophoresis of STR fragments to *Next-Generation Sequencing* (NGS) and genome-wide *Single-Nucleotide Polymorphism* (SNP) profiling, the data demands increase tremendously [17]. This transition is accompanied by the evolution of forensics-oriented epigenetics, in which evaluating DNA methylation at specific CpG dinucleotides allows analysts to pinpoint the tissue from which a sample is derived, assign an approximate age to the contributor, and reveal the molecular "scars" left by CRISPR endonucleases [18].

This article reviews these problems via an article. Section 2 provides insight into the methodology resulting from interdisciplinary scientific-legal collaboration. Section 3 presents the main results and discussion, including the molecular mechanics of genetic disruption, the constitutional realities and regulatory gaps in Indian bio-governance, and the technical feasibility of NGS and epigenetic countermeasures. In Section 4, an eight-part institutional blueprint for Indian law enforcement, forensic laboratories, and the judiciary is provided, followed by a final synthesis of the study's conclusions.

NEED OF THE STUDY

The lack of regulation is compounded by the formal withdrawal of the *DNA Technology (Use and Application) Regulation Bill, 2019*, from the Lok Sabha. The purpose of the Bill is to create a national and regional DNA data bank, establish a DNA regulatory board for laboratory accreditation, and determine consent regulations. The withdrawal leaves India without a dedicated legislative instrument for DNA governance, at a time when gene-editing technologies are scaling up worldwide [19]. The noted risks by Parliamentary Standing Committee on Science and Technology on privacy violation and caste-based profiling have not been addressed and are further complicated by the operationalization of the *Digital Personal Data Protection Act, 2023* (DPDP) and the DPDP Rules, 2025 notified by the *Ministry of Electronics and Information Technology* (MeitY), which impose itemized consent forms, clear purpose limitation, and a mandatory data breach notification within 72 hours to the *Data Protection Board of India* (DPBI) [20]. However, the DPDP framework treats all personal data as the same. It has removed the designation of "sensitive personal data" that was expressly afforded to biometrics under the Information Technology Rules, 2011. In doing so, it flattens the

regulatory framework and reduces the protections that are necessary for genetic data, which is highly intimate, predictive, and uniquely permanent.

RESEARCH METHODOLOGY

This paper will employ a qualitative, interdisciplinary legal-scientific research methodology to demonstrate the applicability of scientific knowledge to the investigation of new gene-editing technology within the new legal framework of Indian criminal procedure. As the problem may evolve until 2026 and is relevant, it is not possible to conduct a traditional empirical analysis of case law to this effect, as trials involving gene-edited forensic evidence are yet to pick up speed in Indian trial courts. Accordingly, this research adopts a doctrinal and conceptual framework with three stages of operation.

First, to construct a molecular model of CRISPR-Cas9 somatic therapies, iatrogenic chimerism and genetic mosaicism were reviewed in the literature on molecular biology and forensic genetics. This technical foundational work was used for identifying specific vulnerabilities in the conventional *Short Tandem Repeat* (STR) profiling and *Forensic DNA Phenotyping* (FDP) protocols.

Second, a comparative statutory and constitutional analysis was undertaken on the newly enacted criminal laws of India - namely, the BSA and BNSS, coupled with the DPDP and the DPDP Rules, 2025. This layer strengthened the assessment regarding the adequacy of evidential standards, data accuracy mandates and procedural rules in light of mutable biological identifiers.

Third, a constitutional jurisprudential analysis was conducted, focusing on the balancing tests in Justice K.S. Puttaswamy and Selvi to determine the legal boundaries of the state's power to compel multi-tissue sampling and the retention of biometrics. The legal-scientific conclusions were synthesised to create an institutional design for the police, forensic laboratories, and the justice system.

RESULTS AND DISCUSSION

3.1 Population and Sample

The premise of DNA profiling's forensic utility rests on the concept of total biological invariability: an individual's genetic sequence remains constant across all somatic tissues throughout life. The entire framework of STR analysis, built on the aforementioned assumption, examines a set of highly polymorphic loci to produce a numerical profile for database matching and kinship verification. Gene-editing technologies, especially CRISPR-Cas9, fundamentally alter this paradigm by enabling precise genome editing to modify STR alleles, SNPs, and regulatory regions in a tissue-specific manner [2].

Somatic gene editing only makes changes to non-reproductive cells in the specified organs and results in genetic mosaicism, with different cell lineages within an individual having different DNA sequences. Most importantly, these therapies target those tissues, human blood and buccal epithelial cells that are less commonly collected for forensic reference and crime-scene analysis [21]. For instance, CRISPR-based therapies for blood disorders modify hematopoietic stem cells so that the genetic profile of the patient's blood appears altered, while his skin, hair follicles, and internal organs remain largely unmodified.

This biological divergence creates severe complications for forensics. An edited person committing an offence will leave a bloodstain at the crime scene that, when analysed, will yield a standard STR profile. If this profile completely mismatches the reference buccal swab or hair sample from that person taken during detention [22]. This biological phenomenon may lead to a misleading exclusion, unintentionally exonerating a culpable suspect. Clinical scenarios of allogeneic bone marrow and stem cell transplantation substantiate the operational realities of iatrogenic chimerism. A recipient's peripheral blood DNA switches to the donor, post-transplant monitoring reveals. However, the hair roots and buccal cells show variable degrees of mixed or native genotypes. The documented forensic anomalies reveal that recipients present pure donor DNA profiles in their blood and semen several years post-treatment. This means that automated database searches can incriminate an innocent organ donor thousands of miles away while completely exonerating the true perpetrator.

Furthermore, molecular interventions similarly contaminate Forensic DNA Phenotyping (FDP). Predictive SNP models used by FDP platforms enable investigators to narrow down potential leads for addressing externally visible characteristics (EVCs) such as pigmentation, hair morphology, and facial structure [23]. Nevertheless, it is possible to modify phenotypic expression through somatic or epigenetic editing. This can refer to global changes in a subject's epigenome without direct changes to the specific genomic loci sampled by conventional FDP multiplexes. For example, targeted editing of pigmentation genes or their regulatory sequences can alter a subject's appearance while leaving their regular forensically informative genotyping markers unchanged. An analyst relying on traditional, static genotype-phenotype correlations will produce a physical profile that is inconsistent with the suspect's actual appearance. This will misdirect investigators' resources and jeopardise the evidentiary value of DNA intelligence.

3.2 Constitutional Realities and Regulatory Lacunae in Indian Bio-Governance

The entry of genetically manipulated identities enters a complex web of constitutional and procedural reforms operative in India. As per the maximum penalty prescribed for seven years or more of imprisonment, a forensic audit and videography of all relevant activities set forth in section 176(3) of the BNSS. This procedural reform may standardise the collection of scientific evidence, but it rests on an outdated assumption: that biological samples yield a definitive, single-source profile. Law enforcement officials who encounter mosaic or chimeric subjects may trigger a mandatory forensic mechanism, but the legislative framework

does not supply expert guidance to unpick multi-tissue genetic differences in forensic interpretation. Therefore, the trial record may be potentially contaminated [24].

According to section 39(1) of the BSA, DNA evidence is ‘once again’ not treated as an expert opinion, leaving its admissibility and evidential value to the court. Indian courts lack a statutory reliability check for assessing sophisticated biotechnological anomalies, unlike Western jurisdictions, where structured admissibility standards, such as the Daubert standard, may be applied. The Supreme Court ruled that forensic samples should be delivered within 48 hours and that there should be a strict chain of custody in *Kattavellai* [11]. However, these prohibitions are intended to block outside polluters and do not account for biological changes that occur internally through medical gene editing.

The Criminal Procedure (Identification) Act, 2022 requires that biometric and biological profile data be retained for up to 75 years in law enforcement files [13]. As a result, this regulatory gap gets wider. Even if a citizen undergoes somatic gene therapy, the law lacks the means to modify or revoke the citizen’s genetic profile, leaving outdated biometric data behind. This structural flaw poses a direct challenge to the fundamental right to informational privacy recognised by the nine-judge bench in the Justice K.S. Puttaswamy case [13]. According to the Puttaswamy doctrine, none of the State intrusions into personal data can be justified unless it passes the three-pronged tests: legality, legitimate state aim and strict proportionality.

Outdated genetic databases that do not reflect an individual’s biological truth fail the proportionality test and lead to errors in identification and illegal surveillance. Moreover, compelling an individual to undertake multi-tissue biopsies, namely a draw of blood, buccal cells, hair roots and skin tissue at the same time to solve a case suspected of genetic mosaicism, strongly clashes with Article 20(3) of the Constitution of India, which protects against self-incrimination. The Supreme Court in *Selvi* [14] distinguished between the collection of physical traits that do not breach bodily or mental integrity and bodily or mental tests that do, including invasive tests performed without consent. Techniques that violate bodily integrity also violate the privilege against self-incrimination.

The act of subjecting the detained suspect to repeated extractions of deep tissues, against their will, to resolve the mosaic profile resulting from CRISPR techniques, violates the bodily autonomy and physical privacy under the provisions of Articles 20(3) and 21. Asking a suspect to provide their medical history regarding past gene therapy would also raise a right-to-privacy claim. Most likely, there will be no clear law for the courts to weigh public safety against individual autonomy. Similarly, if the police mandate compliance with the DPDP and the DPDP Rules, 2025, there will be no clear law in place to assess the different rights that are engaged. The DPDP framework requires data fiduciaries to ensure data accuracy, rely on itemised consent, and issue a 72-hour notice to the DPBI in the event of a data breach [25].

While the DPDP Act does classify certain personal data, such as financial and health data, it removes the previous distinction given to biometrics, which were considered sensitive personal data, and brings highly predictive genetic data under the same regulatory regime as basic digital identifiers. Even though Section 7(2) provides broad exemptions for State law enforcement in crime prevention and investigation, the absence of specific protections for genetic data, such as encryption, sealed keys, and automatic erasure upon acquittal, puts State Biometrics Banks at risk from a security and compliance perspective [26].

3.3 Next-Generation Sequencing and Epigenetic Countermeasures

DNA evidence, aimed to ensure reliability against gene-editing threats, requires forensic science to move from conventional capillary electrophoresis fragment analysis towards sophisticated molecular countermeasures, mainly NGS and forensic epigenetics. NGS platforms, or massively parallel sequencing systems, work by sequencing target regions down to the single-nucleotide level, thereby avoiding the size-restriction limitations of STR analysis. Forensic scientists can simultaneously analyse multiple markers using this technology, including autosomal STRs, Y-chromosome markers, mitochondrial DNA (mtDNA), and phenotypic SNPs.

TABLE 1: Comparative Forensic Analysis: CE vs. NGS Technologies

Forensic Parameter	Traditional Capillary Electrophoresis	Next-Generation Sequencing
Analytical Scope	Limited to analysing short STR (Short Tandem Repeat) fragment lengths.	Enables simultaneous sequencing of STRs, SNPs (Single Nucleotide Polymorphisms), and full mitochondrial DNA (mtDNA) in a single run.
Mosaicism Detection	Insufficient for detecting low-level mosaicism; typically fails to identify variants present below 20–30% allelic frequency.	Highly sensitive; reliably detects somatic and heteroblastic variants down to 1–5% variant allele frequency.
CRISPR Detection	Fails to detect off-target mutagenesis events induced by CRISPR-Cas9 editing.	Effectively maps precise endonuclease cleavage sites and identifies larger structural variations caused by CRISPR activity.
Epigenetic Context	Completely blind to DNA methylation patterns; provides no epigenetic information.	Quantifies tissue-specific CpG methylation status across the genome, enabling age estimation and body-fluid identification.

In gene-editing scenarios, NGS provides the sensitivity to detect low-level genetic mosaicism and minor cell populations at variant allele frequencies of 1–5% [27]. This ability allows labs to verify concealed chimerism arising from a single-source

sample, as expected under conventional capillary systems. Furthermore, NGS reveals the exact genomic alterations caused by CRISPR-Cas9, including characteristic off-target insertions or deletions (indels) and the limits of guide RNA integration, which differentiate synthetic changes from natural mutations. Since mitochondrial DNA does not change substantially following nuclear somatic gene-editing therapies, NGS-based whole-mitochondrial sequencing serves as a comprehensive maternal lineage marker for confirming the identity of a mosaic tissue sample. At the same time, forensic epigenetics also provides an additional layer of analysis at specific CpG dinucleotides [28].

The epigenome is dynamic and responds to various developmental, environmental, and clinical stimuli; however, it does not change the fundamental primary sequence, leaving behind molecular scars. By studying DNA methylation states, a forensic investigator is able to pinpoint the nature, that is, the human tissue origin, of a crime-scene sample. In fact, a forensic scientist can distinguish among peripheral blood, saliva, vaginal secretions, and menstrual blood with great accuracy. This tissue analysis is essential for identifying chimerism, enabling the analyst to verify whether an unexpected profile is mosaicism specific to the tissue or contamination from an external sample [29].

Most importantly, epigenetic analysis can reveal the CRISPR 'epigenetic' footprint. NHEJ and HDR, the cellular repair pathways activated by endonucleases, induce different epigenetic changes at the cut site on the chromosome [30]. These alterations serve as molecular signatures indicating that the sample has already been modified by artificial genes. It alerts the forensic analyst to an engineered sample. Also, epigenetic methylation clocks offer a reliable age-estimation model within the range of +3–5 years [31]. This ability allows investigators to determine whether the chronological age of the donor of an unknown sample matches the biometric profile records stored in databases, thereby helping to circumvent identity evasion through bio-selection.

RECOMMENDATIONS

4.1 Actionable Institutional Recommendations

The systemic vulnerabilities arising from the interaction between gene-editing technologies and India's modified procedural architecture warrant the following eight structural reforms.

4.1.1 Mandating Multi-Tissue Forensic Sampling Protocols

The Ministry of Home Affairs must immediately coordinate with the Directorate of Forensic Science Services (DFSS) and the Indian Council of Medical Research (ICMR) to modify standard operating procedures for crime scene collection. Officials investigating a suspect or victim with a medical history of somatic gene transfer, bone marrow grafting, or allogeneic stem cell transplantation must be required by law to perform multi-tissue extractions, including blood, buccal swabs, hair, and skin.

4.1.2 Revising NABL Laboratory Accreditation Standards

The National Accreditation Board for Testing and Calibration Laboratories (NABL) must update the ISO/IEC 17025 validation frameworks for all public and private forensic laboratories. Accreditation renewals must be strictly contingent upon technical proficiency in identifying genetic chimerism, managing tissue-specific mosaicism, and deploying probabilistic genotyping systems that handle non-standard allelic distributions across multiple loci.

4.1.3 Phased Budgetary Upgrading of Forensic Infrastructure

The Ministry of Finance must dedicate targeted financial allocations to modernize Central and State Forensic Science Laboratories (CFSLS/SFSLs). This funding must be prioritised to phase out obsolete capillary electrophoresis platforms and systematically install high-throughput Next-Generation Sequencing (NGS) machinery and methylation-specific bioinformatics pipelines.

4.1.4 Institutionalising Continuing Judicial Education Frameworks

The National Judicial Academy and State Judicial Academies must institute mandatory technical modules for trial judges, prosecutors, and defence counsel. These educational programs must demystify the mechanics of CRISPR-induced genetic mutations, epigenetic ageing clocks, and the statistical complexities of massively parallel sequencing to prepare the judiciary for advanced evidentiary assessments under Section 39(1) of the BSA.

4.1.5 Reintroducing Comprehensive DNA-Specific Governance Legislation

Parliament must urgently reintroduce a modernised version of the withdrawn DNA Technology Regulation Bill. This new legislative instrument must establish a National DNA Data Bank equipped with separate, dynamic indexes for mosaic profiles, implement independent oversight boards, and create a statutory "right to genetic erasure" allowing medically altered individuals to update or delete obsolete data.

4.1.6 Enforcing Specialised DPBI Genetic Privacy Guidelines

The DPBI, exercising its statutory authority under the DPDP Act, 2023, must publish strict compliance rules for law enforcement agencies responsible for managing biological data. These guidelines must mandate high-level encryption, multi-factor biometric authentication, siloed access channels, and rigorous Data Protection Impact Assessments (DPIAs) to neutralize the risks caused by the removal of the "sensitive personal data" classification.

4.1.7 Integrating Forensic Disclosure Clauses into Clinical Trials

The Central Drugs Standard Control Organisation (CDSCO) must amend the New Drugs and Clinical Trials Rules to require clinical protocols to include explicit forensic impact disclosures. Patients volunteering for experimental CRISPR somatic modifications must be informed of potential changes to their legal forensic identities, and secure verification mechanisms must be built to allow legitimate law enforcement access during active criminal investigations.

4.1.8 Establishing Interdisciplinary Academic Research Hubs

The Central Drugs Standard Control Organisation (CDSCO) must amend the New Drugs and Clinical Trials Rules to require clinical protocols to include explicit forensic impact disclosures. Patients volunteering for experimental CRISPR somatic modifications must be informed of potential changes to their legal forensic identities, and secure verification mechanisms must be built to allow legitimate law enforcement access during active criminal investigations.

CONCLUSION

There is a monumental shift underway in the biological foundation of criminal justice. For many years, it was believed that the human genome serves as a biological constant. However, with clinical gene editing, this notion is changing. Somatic gene therapies, iatrogenic chimerism, and genetic mosaicism have transformed the human body into a dynamic and rewritable platform. The biological mutability poses a direct threat to the basic operational architectures of classic forensic identification. It poses a real risk of false exclusions or incorrect database matches in the Indian criminal justice system. As India rolls out its modernised penal laws, or the BSA and the BNSS, along with the compliance structures of the DPDP Rules, 2025, India must aggressively plug the regulatory and technological lacunae at present, which otherwise render the Indian legal system prone to scientific exploitation. The forensic scene audit, as mandated by Section 176 (3) of the BNSS, will not serve the ends of justice unless there is an immediate shift to Next-Generation Sequencing and epigenetic methylation mapping. The state must strike a careful balance between its investigative functions and the fundamental protections enshrined in Articles 21 and 20(3) of the Constitution. Law enforcement must not exploit technological advancements to rationalise undue invasions of the body or unfettered surveillance. In order to safeguard its legal system, India needs a combination of systemic statutory regulation and molecular diagnostics. India can ensure that its legal structures evolve in parallel with biotechnology and turn a potential scientific threat into a dependable mechanism for truth and justice by developing genetically literate judges, upgraded forensic laboratories, and robust privacy frameworks.

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