



Journal of Medical & Health Sciences Review



MODERN INSIGHTS OF DNA FUNCTION AND HEREDITY: A REVIEW OF MOLECULAR GENETICS AND CRISPR GENE

Mariam Fatima^{1*}, Muhammad Haseeb Anwar Tarar¹, Arooba Maryam²,
Muhammad Azhar Ud Din^{3,4}, Ifra Muzaffar¹, Hafiz Muhammad Saif UR Rahman⁵,
Rida Sattar⁶

¹ Department of Biochemistry, University of Agriculture Faisalabad, Pakistan

² Institute of Molecular Biology and Biotechnology, University of Lahore, Pakistan

³ WHO Regional Reference Laboratory (RRL) for Polio Eradication Initiative, Public Health Laboratories Division (PHLD), National Institute of Health (NIH), Islamabad, Pakistan

⁴ Abasyn University, Islamabad, Pakistan

⁵ Department of Biosciences, University of Veterinary and Animal Sciences, Lahore, Pakistan

⁶ Department of Pathobiology, Faculty of Veterinary Sciences, Bahauddin Zakariya University, Multan, Pakistan

ARTICLE INFO:

Keywords:

DNA structure, heredity, genetic code, CRISPR gene editing, molecular biotechnology.

Corresponding Author: Mariam Fatima

Department of Biochemistry,
University of Agriculture
Faisalabad, Pakistan

mariamfatimas165@gmail.com

Article History:

Published on 21 August 2025

ABSTRACT

Deoxyribonucleic acid (DNA) serves as the fundamental blueprint for life, governing both the structural development and functional regulation of living organisms. The technology explores the modern understanding of DNA role in heredity and molecular genetics that highlighted key discoveries that have shaped the field. The discovery of intricate molecular mechanisms such as epigenetic modifications, non-coding RNA and the gene environment interactions has evolved beyond Mendelian genetics. The mechanism of genetic inheritance, replication and expression illustrates how traits are passed from one generation to the next generation. This review article highlights how mutation and variations in DNA sequences influence health, evolution and disease susceptibility. A significant focus is placed on revolutionary CRISPR-Cas9 gene editing technology which has transformed genetic research and holds immense promise for future therapeutic applications. After enabling precise modifications in the genome, CRISPR opens new avenues for the treatment of genetic disorders and advancement in biotechnology. This review emphasizes how the integration of classical molecular genetics with cutting edge gene editing techniques offers a comprehensive understanding of DNA function for addressing agricultural and global health challenges.

INTRODUCTION

The molecule DNA carries the genes and other important hereditary information in all living beings. Almost every cell carries DNA as its main source of guidelines for living. To do their jobs in growth, repair, and metabolism, all cells depend on DNA, which is used to produce proteins they use [1, 2]. Every DNA molecule is formed by two long, chain-like parts of nucleotides that are spirally twisted into a double helix shape. Altogether, the nucleotides include adenine (A), thymine (T), cytosine (C), and guanine (G) [3]. The arrangement of these bases makes the genetic code. Using information from this code, the cell makes proteins with the processes known as transcription and translation. DNA can be found in the nucleus of eukaryotic cells, but in simpler organisms such as bacteria, it is in the cytoplasm [4, 5]. The fact that DNA can replicate perfectly ensures that heredity takes place when a child inherits its parents' genes. For this reason, the DNA molecule is usually referred to as the "blueprint of life" since it carries the instructions needed to form and maintain an organism [6].

In 1869, Friedrich Miescher (Swiss biochemist) found DNA for the first time. He singled out a substance from inside the nuclei of white blood cells and gave it the name "nuclein." Back then, he found out its chemical properties but did not know what its role was. At this moment, research into DNA has started [7]. Levene found out which sugar (deoxyribose), phosphate, and four nitrogenous bases are present in DNA (early 1900s). He believed that there are repeating groups called nucleotides in DNA. Although Fraser thought that DNA could not store genetic data due to its simplicity, his studies set a base for future breakthroughs [8]. Erwin Chargaff (1950) examined DNA from many different organisms and found out that adenine and thymine were in equal amounts, and guanine and cytosine also matched. According to Chargaff's rules, DNA bases act

in pairs, which gave scientists the main clue in figuring out DNA's structure. Griffith discovered in 1928 that bacteria transfer genetic codes from one to another, which is called transformation. They used their experiments to find out that DNA, not protein, was the "transforming principle" in genes. In 1953, they said that DNA is made of two intertwining helices. The scientists pointed out that DNA was composed of two intertwined strands where the bases specifically matched: adenine with thymine and cytosine with guanine. It showed how DNA manages to reproduce and hold genetic information [9]. Rosalind Franklin and Raymond Gosling's critical X-ray diffraction pictures were important parts of the model created by Crick and Watson. Photo 51 was taken by Franklin and uncovered the helix shape of DNA. Even though Watson and Crick did not completely ask for her approval, their findings about the double helix rested on her work. After this discovery, biology was changed in a major way. Because it explained how genetic data is kept and copied, it paved the way for molecular genetics and biotechnology [10-12].

Many researchers groundbreaking studies in recent years for genomics and biotechnology have continued to deepen our understanding of how DNA functions in living organisms. Research published in journals like *Nature Genetics* and *Science* has highlighted the growing influence of personalized medicine, gene editing, and epigenetics in both clinical and agricultural settings. The integration of AI with genomics, as demonstrated by DeepMind's AlphaFold in predicting protein structures, and recent CRISPR-based clinical trials for conditions like sickle cell anemia and beta-thalassemia, underline how far the field has advanced [13]. These innovations build upon decades of foundational discoveries in molecular biology that began with the unveiling of the double helix structure of DNA. A key breakthrough

came in 1960 with the decoding of the genetic code. Researchers discovered that sequences of three nucleotide bases, known as codons, each correspond to a specific amino acid. This discovery clarified how DNA provides instructions for synthesizing proteins, the essential molecules that drive cellular functions [14].

The development of DNA sequencing technology was another major step forward. In 1977, Frederick Sanger introduced the chain termination method, enabling researchers to read DNA sequences accurately. However, it wasn't until the advent of next-generation sequencing (NGS) technologies in the early 2000s that DNA sequencing became faster, cheaper, and scalable. These high-throughput systems revolutionized research, allowing scientists to sequence entire genomes in a matter of days [15, 16]. Molecular cloning, recombinant DNA technology, and polymerase chain reaction (PCR) gave scientists the ability to replicate and study specific genes in detail. These tools are essential in diagnosing genetic disorders, conducting forensic analysis, and developing targeted treatments. PCR, for example, became indispensable not only in labs but also in clinical diagnostics, as seen during the COVID-19 pandemic for rapid viral detection. The emergence of CRISPR-Cas9 gene-editing technology in the 2010s marked a turning point in biotechnology. This precise and cost-effective method allows scientists to make targeted changes to DNA in living organisms [17]. Recent clinical trials have shown promising results using CRISPR to treat inherited blood disorders, eye diseases, and certain cancers. In agriculture, CRISPR is being used to develop crops that are more resilient to climate change and pests [18-21].

A landmark achievement in the field was the completion of the Human Genome Project in 2003. The mapping of all human genes, scientists gained a comprehensive reference for studying genetic diseases and

tailoring medical treatments to individual genetic profiles. This paved the way for the era of personalized medicine, where therapies are increasingly customized based on a patient's genetic makeup. The advances in DNA science continue to shape the future of healthcare, agriculture, and beyond. The decoding genetic instructions to editing the genome itself, recent innovations have turned what was once theoretical into practical, life-changing applications [22-24]. This review article highlights how mutation and variations in DNA sequences influence health, evolution and disease susceptibility. This review emphasizes how the integration of classical molecular genetics with cutting edge gene editing techniques offers a comprehensive understanding of DNA function for addressing agricultural and global health challenges.

DNA and its Chemical Composition

DNA is made up of smaller units known as nucleotides. Adenine (A), thymine (T), cytosine (C), or guanine (G) are the four nitrogenous bases that make up each nucleotide. The other two components are phosphate group and deoxyribose sugar. The phosphate and sugar chain that makes up DNA's robust structure is joined by phosphodiester linkages. Carrying the genetic code, the bases enter the strand. The sugar that is present in RNA is termed ribose, but because DNA does not include an oxygen atom, it is known as deoxyribose. This modification increases DNA's resistance to chemical reactions, enabling the long-term preservation of genetic information. The sugars are joined by phosphate groups to form a difficult-to-break sugar-phosphate chain. This backbone facilitates DNA's interaction with ions and proteins inside the cell since it is negatively charged [25, 26]. Each base has a certain structure that determines how it will collaborate with other bases. Cytosine and thymine are referred to as pyrimidines and have a single ring, in contrast to adenine and

guanine, which are categorized as purines. This variation shapes the production and function of DNA [27].

Double Helix and Antiparallel Orientation

The double helix shape of DNA has made it well known, and it was found by James Watson and Francis Crick in 1953. The double helix is made up of two strands that are wound around each other just like a twisted ladder. They run opposite each other and are called antiparallel. A strand goes from the 5' end to the 3' end, and another from the 3' end to the 5' end. DNA replication and transcription depend on this orientation since the enzymes can tell where each strand begins. The strands relate to each other by hydrogen bonds that form between matching bases. On the outside, the backbone has sugar and phosphate, while all the bases are on the inside and stack against each other. As a result of the DNA helical turn, major and minor grooves are present, which attract proteins that manage how genes operate [28, 29]. It is a flexible shape because its coils and curves fit inside the nucleus while leaving enough space for other cell tasks.

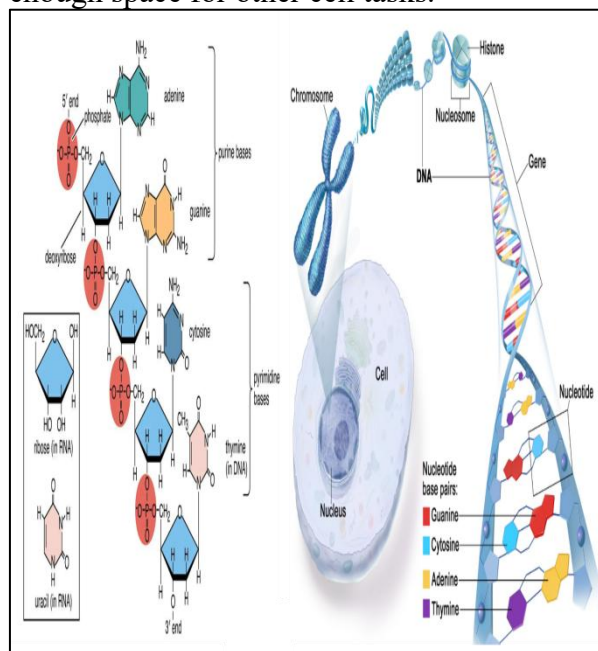


Fig 1: The double helix structure of DNA and its internal structure.

Base Pairing Rules and Hydrogen Bonding

Adenine always pairs with thymine through the help of two hydrogen bonds, and guanine always pairs with cytosine through the help of three hydrogen bonds. In 1950, Erwin Chargaff made the initial discovery, discovering that a DNA sample always has the same amounts of A, T, C, and G. Since hydrogen bonds are weak, the double helix's many bonds enable it to maintain its shape while splitting apart for transcription and replication. DNA can replicate itself without information errors when base pairing is ideal. The information that tells the other strand what sequence to create is found on one strand. In this manner, DNA can fulfill its primary function as the blueprint for life, as it depends on complementarity to securely transmit information [30, 31].

Different Conformations of DNA

The well-known B-form isn't always the shape of DNA. There are various forms DNA takes due to the surrounding conditions of humidity, levels of salt, and the sequence of nucleobases in the DNA strand.

B-DNA

The most common and biologically relevant form of DNA is B-DNA. This right-handed double helix typically contains about 10 base pairs per turn. It is the standard conformation found under physiological conditions and is the primary structure involved in protein-DNA interactions within living organisms [32].

A-DNA

A-DNA forms when DNA is dehydrated, losing a significant amount of water. Like B-DNA, it is also a right-handed helix, but it contains approximately 11 base pairs per turn. The helical structure is wider, with a more tilted base pair alignment [32]. A-DNA can also occur when DNA binds with RNA or when RNA forms double-stranded structures.

Z-DNA

Z-DNA has a left-handed helical

structure with a distinctive zig-zag backbone. It typically contains 12 base pairs per turn and is associated with sequences that alternate between purines and pyrimidines. According to researchers, Z-DNA may play a role in gene regulation and contribute to DNA stability [33, 34].

Table 1: Comparison of DNA Conformations.

Feature	B-DNA	A-DNA	Z-DNA
Helix Direction	Right-handed	Right-handed	Left-handed
Base Pairs/Turn	~10	~11	~12
Helix Diameter	2 nm	2.3 nm	1.8 nm
Sugar Pucker	C2'-endo	C3'-endo	Alternating C2'/C3'
Occurrence	Most common in cells	Dehydrated DNA	Certain gene regions
Biological Role	Standard genetic info	Structural form under stress	Gene regulation

The Impact of DNA Research on Modern Science and Medicine

The study of DNA has evolved into the study of contemporary biotechnology, biology, and medicine. In 1869, Swiss scientist Friedrich Miescher made the first significant discovery in DNA study when he identified a substance in white blood cells that he named nuclein. Totally unaware that he was leading the path to the discovery of DNA, he had taken this substance out of the pus cells' nuclei. Even though the function of nuclein was not determined until decades later, this discovery was crucial in directing scientific attention toward the comprehension of the molecular nature of heredity [35]. In the early 1900s, Phoebus Levene expanded on Miescher's work by clarifying the structure of nucleic acids, specifically differentiating between sugar, phosphate, and nitrogenous bases. Even if his tetra nucleotide hypothesis appeared to be mistaken about the direct nature of a simple, repeating structure, it cleared the path for a later discovery about the

structure's ultimate nature. The Avery-MacLeod-McCarty experiment in 1944 was a significant advance, demonstrating that DNA was the transformative principle that transferred genetic material between bacterial strains [7]. The Hershey-Chase experiment, which was conducted in 1952, was the last piece of evidence showing the bacteriophages use DNA, not protein, as their genetic material to infect bacteria [36].

The most drastic step in the study of DNA was taken in 1953 when James Watson and Francis Crick developed the double-helix theory of DNA based on Rosalind Franklin's X-ray crystallography results [37]. The solutions to the questions of how genetic information may be copied and passed on to the progeny were in their paradigm. Franklin's Photo 51 contributed to the establishment of the helical structure, which was initially unacknowledged. This raises another issue regarding female bias in research. Francis Crick later articulated the "central dogma of molecular biology," stating that DNA to RNA to protein is the transcriptional pathway of genetic information. These findings served as the foundation for modern molecular biology, genetics, and biotechnology. Genome sequencing became possible considerably more quickly and at a much lower cost as Next-Generation Sequencing (NGS) gained popularity. Within twenty-four hours, scientists may access entire genomes thanks to NGS technologies like Oxford Nanopore and Illumina. This has found extensive use in metagenomics, microbial diversity, and cancer genomics [38]. Prenatal screening and the identification of uncommon genetic diseases are two other significant uses for NGS. abnormalities, insertions, deletions, and substitutions. The study found that various diseases, including Tay-Sachs disease (CFTR gene), sickle cell anemia (HBB gene), and cystic fibrosis (HEXA gene), can be caused by a single mutation of some important genes. Treatments for these disorders can now be

targeted thanks to the development of new gene therapy techniques like the delivery of viral vectors and antisense oligonucleotides. Zolgensma, a gene therapy for spinal muscular atrophy, for instance, offers a healthy variant of the faulty SMN1 gene [39].

The CRISPR-Cas9 technology revealed yet another paradigm change. CRISPR offers a way to reprogrammed DNA to alter it at a specific location, perhaps achieving previously unheard-of levels of accuracy. In Duchenne muscular dystrophy, 6-thalassemia, and sickle cell disease, it has been used to fix a defective heredity. Base editing and prime editing are two examples of more precise techniques that can also provide fewer off-target impacts. As a Chinese scientist announced the birth of the first CRISPR-assisted babies in 2018, the ethical debate over gene editing peaked [40]. This behavior infuriated the global scientific community since it resulted in a breach of ethical standards and a lack of transparency in these procedures. Additionally, it sparked a global discussion on human genome editing regulation, which expedites the creation of new ethical standards by the WHO and other regulatory bodies. However, Alec Jeffreys' discovery of DNA fingerprinting in 1984 posed a significant obstacle to forensic science. Short tandem repeats (STRs), which are polymorphic genomic regions, are used to assign individuals distinct profiles. Numerous criminal cases, paternity tests, immigration, and animal conservation have all been resolved with this method [41].

DNA-based diagnostics and personalized treatment are quickly taking over clinical practice. Pharmacogenomics investigates how genetic differences impact drug metabolism to prevent adverse consequences. Patients with CYP2C19 gene variants get different side effects from the common antiplatelet drug clopidogrel. Concerns over data privacy and the accuracy of the results are raised by firms like 23andMe and AncestryDNA that provide

health and ancestry reports in addition to genetic data. In terms of pattern recognition, gene annotation, and disease prediction, artificial intelligence has already been embraced by genomics. Together with DeepVariant and AlphaFold, deep learning algorithms enabling specificity in the identification of genetic variations and the prediction of protein structure [42, 43].

The purpose of this paper is to cover DNA's chemical form, its physical structure, its actions in the body, and its major involvement in heredity. No matter if the scientific advance is old or recent, the objective is to record and summarize its outcomes. In this review, the main topics analyzed are chemicals found in DNA, DNA doubling, transcription, how genes are passed from parents to offspring, different types of mutations, and new technology called CRISPR-Cas9. Scientific articles that were peer-reviewed and published mostly in the past 30 years are the main source for the review. Nevertheless, the early contributions in the field of genetics are acknowledged as important.

The main articles were described in a table by giving the source, the year the article was published, the database, the topic, and the key findings.

Table 2: Summary of Key Selected Sources and Themes of previous studies on DNA.

Theme	Database	Key Findings	Year	Source
DNA Structure	Historical	Proposed double helix model	1953	Watson & Crick (1953)
Base Pairing	Historical	Base rules pairing (A=T, C=G)	1950	Chargaff (1950)
DNA Sequencing	PubMed	Developed chain termination	1977	Sanger et al. (1977)
Gene Editing (CRISPR)	Nature	CRISPR-Cas9 system discovered	2012	Jinek et al. (2012)

Genomics	ScienceDirect	Sequenced human genome	2003	Human Genome Project (2003)
DNA Packaging	PubMed	Structure of nucleosome	1997	Luger et al. (1997)
DNA Mutations & Diseases	ScienceDirect	The impact of a mutation on a protein function	2019	Li et al. (2019)

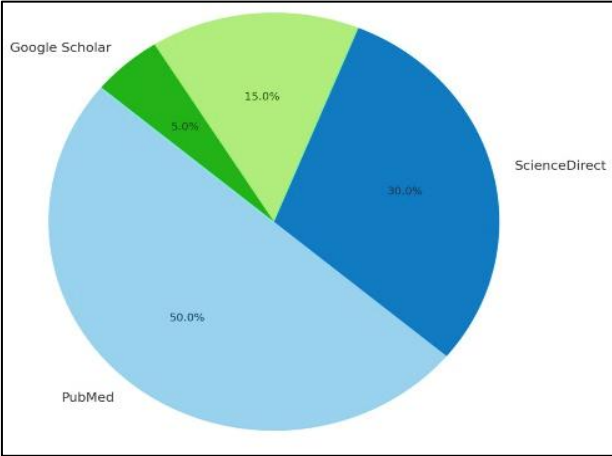


Fig 2: Percentage of articles published in recent years by database source.

DNA in Disease and Therapeutics

The diseases and modern medical approaches depend a lot on DNA. Disruptions caused by changes in DNA may result in diverse genetic conditions, some cancers, and a higher risk of catching diseases. Such technologies as gene therapy, CRISPR, and antisense oligonucleotides are now revolutionizing how medical treatments are done. A better understanding of how DNA affects illnesses and may be used in therapy has changed both biomedical science and medical practice [44]. A mutation is when the DNA sequence changes and it can happen on its own or through events like radiation, chemicals, or viruses. Some of the variations in DNA can be called point mutations, insertions, deletions, or frameshift mutations. As a result of these changes, functions might be lost, gained, or gene expression may alter, giving rise to different aspects of a disease. The substitution of one base pair in some

genes can have significant results. Hence, a one-letter change in the DNA of the HBB gene can bring about sickle cell anemia through the creation of a distorted hemoglobin. Any alteration in genes caused by frameshift mutations interferes with their reading sequence, which creates nonfunctional proteins and has been linked to Tay-Sachs and Duchenne muscular dystrophy diseases [45].

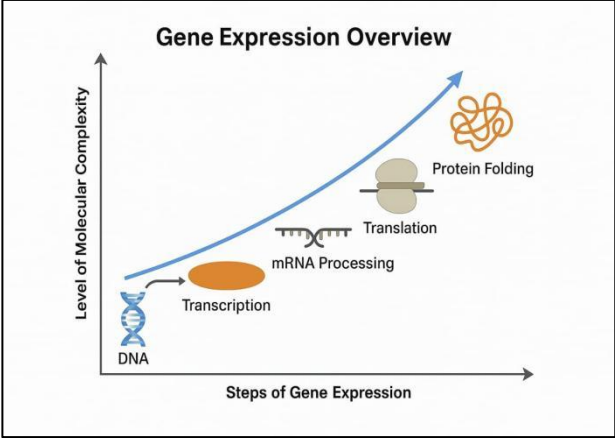


Fig 3: The graphical illustration of gene expression with the increasing complexity and regulation at each step, highlighting the involved key enzymes and processes.

Table 3: Common Diseases caused by DNA mutations.

Disease	Type of Mutation	Gene Involved	Symptoms
Sickle Cell Anemia	Point mutation	HBB	Anemia, pain, infection
Tay-Sachs Disease	Frameshift mutation	HEX A	Neurodegeneration, early death
Duchenne Muscular Dystrophy	Deletion mutation	DM D	Muscle weakness, mobility loss
Huntington's Disease	Trinucleotide repeats	HTT	Motor decline, psychiatric symptoms

Cancer as a Genetic Disease

The growth of cells in cancer is triggered by changes or mutations in several types of genes. They either come from birth or can be experienced during a person's life. A mutation in the TP53 gene is often identified in more than half of all human cancers. BRCA1/2 genes are another example; having certain types of mutations here can increase a person's chances of getting breast and ovarian cancers. The study of cancers using DNA sequencing has found mutations that help doctors apply targeted approaches for each cancer type. The usage of oncogenomics, the science of cancer genes, it is possible to learn how to use biomarkers to create targeted cancer drugs [46].

Modern Applications and Technologies

The advances in DNA exploration have become commonplace in the twenty-first century, molecular biology is undergoing significant transformation. Thanks to breakthrough technologies, scientists are now able to handle and alter genetic information at a level never before possible. These advancements have enhanced our understanding of biology and, therefore, various fields like agriculture, healthcare, and environmental work [30, 47]. These are the key technological developments that have a significant influence on DNA research.

DNA Sequencing

The process of determining the precise nucleotide sequence in DNA is known as DNA sequencing. The Sanger method, which signaled the advent of sequencing technologies, was created in the 1970s. To create fragments that can be isolated and analyzed, it halts the replication of DNA chains. However, when used for large workloads, Sanger sequencing is more expensive and takes a long time. Many DNA samples did not respond well to Sanger sequencing, researchers developed next-generation sequencing (NGS), which enables

the analysis of several DNA strands at once. A person's complete genome can be sequenced in a few hours and at a significantly lower cost thanks to technologies like Oxford Nanopore and Illumina. NGS now enables physicians to examine tumor DNA to choose and administer the best treatments, oncology has undergone significant transformation [48]. This has made it feasible to conduct extensive genomic research on a wide scale and practice personalized therapy. NGS is being used in new ways to find crucial information about microorganisms and to do early pregnancy screenings. Bioinformatics handles a vast volume of data to uncover information about diseases, genetic alterations, and evolution [49].

CRISPR-Cas9 and Gene Editing

The combination of CRISPR and Cas9 can be considered one of the major discoveries in the field of genetics. Because of its origins in bacterial defense, CRISPR-Cas9 lets scientists choose and remove exact parts of DNA. With this tool, some genes are turned off, genetic info is added, and mutations can be corrected. It is easy to use, affordable, and very precise, CRISPR is now found in laboratories everywhere. The discipline allows experts to study genetic diseases in animals, make crops strong, and look into ways of gene therapy. For illustration, CRISPR is being used to modify a particular mutation that brings on sickle cell anemia in stem cells as shown in Figure 4. The appearance of CRISPR-Cas12 and Cas13 means RNA and epigenetic elements can now be targeted too, which improves gene-regulation and diagnostic options. Since people are debating how ethical it is to alter embryos using CRISPR, it is necessary to have worldwide rules that control these technologies [50-52].

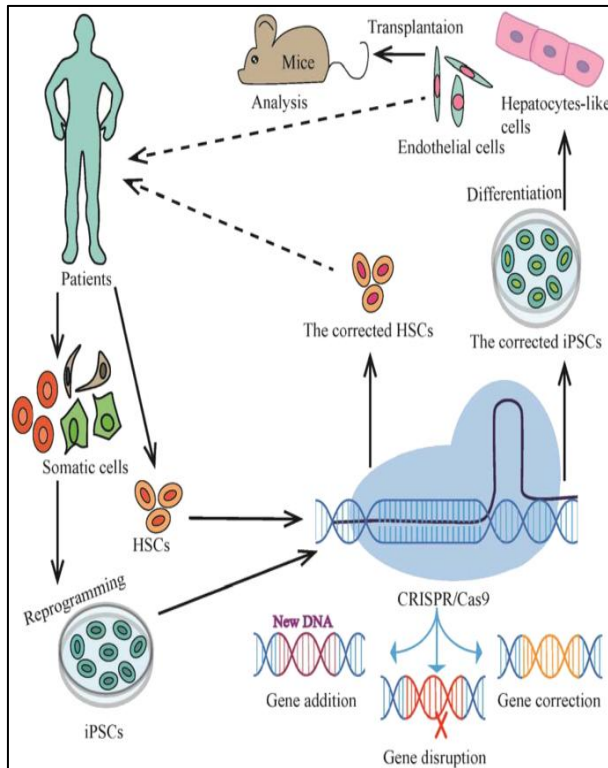


Fig 4: The genome editing using CRISPR-Cas9 to treat hereditary issues.

DNA Fingerprinting and Forensics

DNA profiling, which is the same as DNA fingerprinting, is used to identify people by their genetic analysis. Unlike the coding sections, non-coding areas like STRs can show massive distinctions between people. It was introduced in the 1980s by Sir Alec Jeffreys, and since then, DNA fingerprinting has greatly improved the justice and paternity systems. In this field, sections of DNA from blood, hair, or saliva found at the scene are checked against data from suspects [53]. Up-to-date methods rely on multiplying STR loci with PCR and using capillary electrophoresis to quickly and accurately get the results. Using databases of DNA, authorities are able to both solve unsolved cases and set free individuals who had been found guilty wrongly. Besides, DNA fingerprinting is applied in immigration cases, to identify the dead after natural disasters, and to check ancestry in the conservation of endangered species as shown in Figure 5. Forensic science has a huge effect on society since it combines

science and law with great success [54].

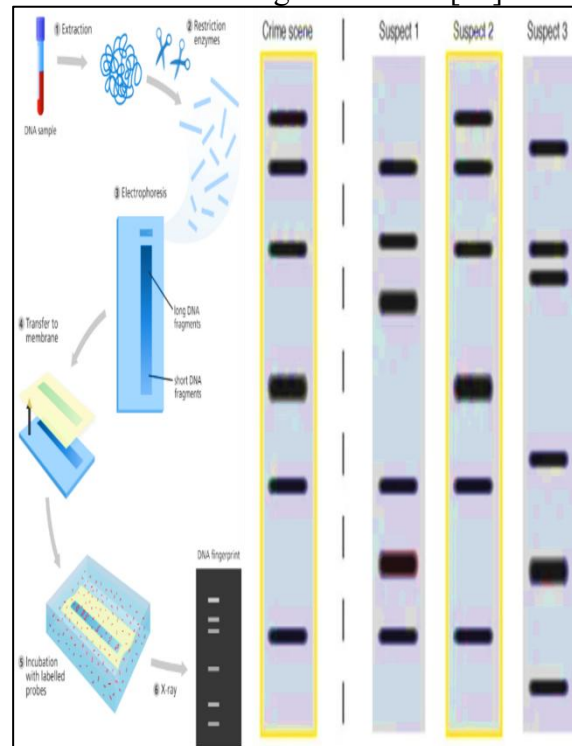


Fig 5: The visual representation of DNA fingerprinting and their forensic application.

Synthetic Biology

Synthetic biology uses engineering methods in the field of biology. Researchers make new genetic circuits, metabolic pathways, and organisms by engineering DNA as required. Synthetic biology stands out from traditional genetic engineering because it produces genes and genomic DNA from the beginning. Some uses of biotechnology are to make biofuels, invent biosensors, and build microorganisms to clean waste in the environment. To give an example, scientists have genetically modified *E. coli* to create artemisinin, which is key to its helpful medical effects against malaria [55]. Synthetic biology has an effect on making artificial vaccines and imitating cells in laboratories. Being able to design DNA on their own, experts can probe the edges of life and study possible reasons for the origin of cellular parts. Still, using this power can bring up issues about both biosafety and biosecurity, mainly when scientists create new organisms or

stronger pathogens [56].

Personalized and Predictive Medicine

Healthcare can now be based on patients' individual needs and anticipated future health problems. This method is designed to provide medical care based on a person's inherited genes. Clinicians can offer patients useful tips and treatments if they know that genetic factors increase the risk for cancer, diabetes, or disorders of the heart. Pharmacogenomics studies how genes alter the response of people to drugs, which helps prevent bad reactions and ensures each drug is given in an appropriate amount [57]. With the FDA's approval, people now use genetic tests for Warfarin and Clopidogrel, which improves the outcomes of their drug therapy. Early detection through special markers and the guidance of doctors becomes possible because of predictive medicine. Joining big data analytics has helped this approach bring changes to healthcare and cut down the expenses for patients needing ongoing care. The subject of privacy and access to genetic services is still a key focus for setting up genomics services [58].

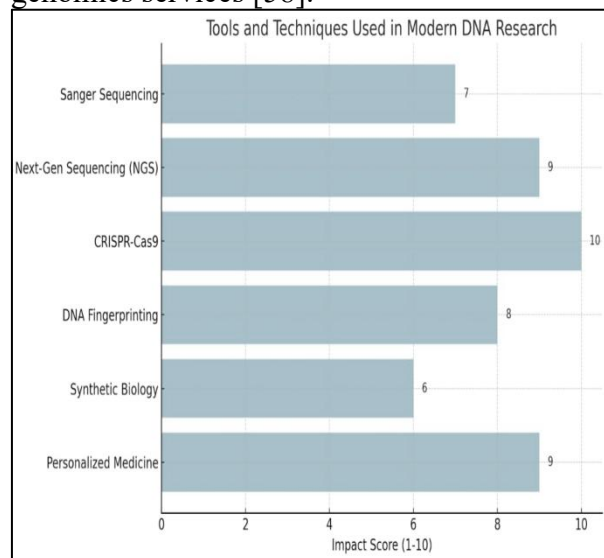


Fig 6: Tools and Techniques Used in Modern DNA Research

Conclusion and Future Perspectives

The modern understanding of DNA function and heredity has significantly

evolved through advancements in molecular genetics and technologies such as CRISPR. These breakthroughs have not only deepened our knowledge of gene structure and function but have also paved the way for precise genome editing. CRISPR-based methods, along with recent innovations like base editing and prime editing, are transforming the landscape of gene therapy by enabling accurate, targeted modifications with reduced risks, offering hope for treating previously incurable genetic disorders such as sickle cell anemia and Tay-Sachs disease.

The integration of artificial intelligence (AI) with molecular genetics marks a promising frontier. AI and machine learning algorithms are increasingly being utilized to identify genetic mutations, predict disease susceptibility, and design personalized treatments. These technologies enhance our ability to interpret large-scale genomic data with unprecedented accuracy, often detecting complex patterns and anomalies beyond human capacity. AI also holds immense potential in drug discovery by simulating the impact of gene mutations on protein function, thus accelerating the development of targeted therapeutics. Deep learning models can even anticipate cellular outcomes of gene edits, supporting safer and more effective clinical applications.

Moreover, the convergence of synthetic biology and AI could revolutionize the creation of novel biological systems. These may be designed to manufacture therapeutic compounds, degrade environmental pollutants, or serve as foundational elements of synthetic life. However, such powerful technologies raise ethical and safety concerns that demand interdisciplinary collaboration, involving not only geneticists and computer scientists but also ethicists, policymakers, and the public. As we move forward, a balanced approach that promotes innovation while ensuring safety and ethical integrity will be essential.

The future of DNA science lies in this synergy between biology, computation, and societal responsibility for a future full of promise for both medicine and humanity.

REFERENCES

1. Minchin, S. and J.J.E.i.b. Lodge, *Understanding biochemistry: structure and function of nucleic acids*. 2019. **63**(4): p. 433-456.
2. Fitz-James, M.H. and G.J.N.R.G. Cavalli, *Molecular mechanisms of transgenerational epigenetic inheritance*. 2022. **23**(6): p. 325-341.
3. Bailey, J., *Nucleosides, nucleotides, polynucleotides (RNA and DNA) and the genetic code*, in *Inventive Geniuses Who Changed the World: Fifty-Three Great British Scientists and Engineers and Five Centuries of Innovation*. 2021, Springer. p. 313-340.
4. Baluška, F. and S. Lyons, *Symbiotic origin of eukaryotic nucleus: from cell body to neo-energide*, in *Concepts in Cell Biology-History and Evolution*. 2018, Springer. p. 39-66.
5. Oborník, M.J.M.C., *In the beginning was the word: How terminology drives our understanding of endosymbiotic organelles*. 2019. **6**(2): p. 134.
6. Staley, J.T.J.O.b., *Domain Cell Theory supports the independent evolution of the Eukarya, Bacteria and Archaea and the Nuclear Compartment Commonality hypothesis*. 2017. **7**(6): p. 170041.
7. Veigl, S.J., O. Harman, and E.J.J.o.t.H.o.B. Lamm, *Friedrich Miescher's discovery in the historiography of genetics: from contamination to confusion, from nuclein to DNA*. 2020. **53**(3): p. 451-484.
8. Harding, S.E., G. Channell, and M.K.J.B.S.T. Phillips-Jones, *The discovery of hydrogen bonds in DNA and a re-evaluation of the 1948 Creeth two-chain model for its structure*. 2018. **46**(5): p. 1171-1182.
9. Fariselli, P., et al., *DNA sequence symmetries from randomness: the origin of the Chargaff's second parity rule*. 2021. **22**(2): p. 2172-2181.
10. Borus, A., *James Watson, Francis Crick, Rosalind Franklin, and Maurice Wilkins: The Scientists who Revealed the Structure of DNA*. 2020: The Rosen Publishing Group, Inc.
11. Shah, E., *Rosalind Franklin and her Science-in-the-Making: A situated, sexual, and existential portrait 1*, in *Who is the Scientist-Subject?* 2018, Routledge India. p. 113-133.
12. Steyaert, S., *Developing bioinformatics applications for the analysis of epigenetic next-generation sequencing data*. 2016, Ghent University.
13. Gregory, F.D. and B.D.J.A.S.I.o.N.A.o.Q.N.-P. Trump, *The Evolving Landscape of Biotechnology Research: Challenges and Opportunities in Acquisitions, Funding, Education, and Workforce Development for a Productive Bioeconomy*. 2023: p. 25-50.
14. Shahid, A., et al., *Appraisal of CRISPR Technology as an Innovative Screening to Therapeutic Toolkit for Genetic Disorders*. 2025: p. 1-24.
15. Heather, J.M. and B.J.G. Chain, *The sequence of sequencers: The history of sequencing DNA*. 2016. **107**(1): p. 1-8.
16. Kang, Y., et al., *History of nucleotide sequencing technologies: advances in exploring nucleotide sequences from Mendel to the 21st century*. 2019. **37**(5): p. 549-558.
17. Teymouri, M., et al., *Recent advances and challenges of RT-PCR tests for the diagnosis of COVID-19*. 2021. **221**: p. 153443.
18. Mardian, Y., et al., *Review of current COVID-19 diagnostics and opportunities for further development*. 2021. **8**: p. 615099.
19. Afzal, A.J.J.o.a.r., *Molecular diagnostic technologies for COVID-19: Limitations and challenges*. 2020. **26**: p. 149-159.
20. Da Silva, S.J.R., et al., *Clinical and laboratory diagnosis of SARS-CoV-2, the*

- virus causing COVID-19. 2020. **6**(9): p. 2319-2336.
21. Lippi, G., M.J.C.C. Plebani, and L. Medicine, *The critical role of laboratory medicine during coronavirus disease 2019 (COVID-19) and other viral outbreaks*. 2020. **58**(7): p. 1063-1069.
 22. Manero, A., et al., *Emerging Medical Technologies and Their Use in Bionic Repair and Human Augmentation*. 2024. **11**(7): p. 695.
 23. Mittos, A., *Analyzing the privacy and societal challenges stemming from the rise of personal genomic testing*. 2020, UCL (University College London).
 24. Yan, W.X., *Towards Therapeutic Applications of CRISPR-Cas Nucleases: Developing Technologies for In Vivo Gene Editing & Evaluating Genome-wide Specificity*. 2017: Harvard University.
 25. Corrêa, R.C.G., et al., *Biotechnological, nutritional and therapeutic uses of Pleurotus spp.(Oyster mushroom) related with its chemical composition: A review on the past decade findings*. 2016. **50**: p. 103-117.
 26. Dickson, P., T.J.O. Kodadek, and b. chemistry, *Chemical composition of DNA-encoded libraries, past present and future*. 2019. **17**(19): p. 4676-4688.
 27. Xu, J.-G., et al., *Chemical composition, antibacterial properties and mechanism of action of essential oil from clove buds against Staphylococcus aureus*. 2016. **21**(9): p. 1194.
 28. Subramanian, H. and R.A.J.S.R. Gatenby, *Evolutionary advantage of anti-parallel strand orientation of duplex DNA*. 2020. **10**(1): p. 9883.
 29. Sawada, T., et al., *Parallel and antiparallel peptide double β -helices controlled by metal-induced folding and assembly*. 2021. **1**(1): p. e10008.
 30. Tompkins, J.D.J.J.o.t.H.o.B., *Discovering DNA methylation, the history and future of the writing on DNA*. 2022. **55**(4): p. 865-887.
 31. Song, X., et al., *Design rules of hydrogen-bonded organic frameworks with high chemical and thermal stabilities*. 2022. **144**(24): p. 10663-10687.
 32. Kulkarni, M., A.J.P.i.b. Mukherjee, and m. biology, *Understanding B-DNA to A-DNA transition in the right-handed DNA helix: Perspective from a local to global transition*. 2017. **128**: p. 63-73.
 33. Sahayasheela, V.J., et al., *Z-DNA at the crossroads: untangling its role in genome dynamics*. 2025.
 34. Herbert, A.J.R.S.O.S., *The ancient Z-DNA and Z-RNA specific Za fold has evolved modern roles in immunity and transcription through the natural selection of flipons*. 2024. **11**(6): p. 240080.
 35. Hall, K. and N.J.T.B.J.f.t.H.o.S. Sankaran, *DNA translated: Friedrich Miescher's discovery of nuclein in its original context*. 2021. **54**(1): p. 99-107.
 36. Moraes, F., A.J.B. Góes, and M.B. Education, *A decade of human genome project conclusion: Scientific diffusion about our genome knowledge*. 2016. **44**(3): p. 215-223.
 37. Small, H.J.Q.S.S., *Bayesian history of science: The case of Watson and Crick and the structure of DNA*. 2023. **4**(1): p. 209-228.
 38. Candela, E., *Mid-Century Molecular: The Material Culture of X-ray Crystallographic Visualisation across Postwar British Science and Industrial Design*. 2015: Royal College of Art (United Kingdom).
 39. Cring, M.R. and V.C.J.G.t. Sheffield, *Gene therapy and gene correction: targets, progress, and challenges for treating human diseases*. 2022. **29**(1): p. 3-12.
 40. Chanchal, D.K., et al., *CRISPR-based therapies: Revolutionizing drug development and precision medicine*. 2024. **24**(3): p. 193-207.
 41. Al-Kabani, A., et al., *Exploring Experimental Models of Colorectal Cancer: A Critical Appraisal from 2D Cell Systems to*

- Organoids, Humanized Mouse Avatars, Organ-on-Chip, CRISPR Engineering, and AI-Driven Platforms—Challenges and Opportunities for Translational Precision Oncology*. 2025. **17**(13): p. 2163.
42. Brown, S.-A. and N.J.J.o.p.m. Pereira, *Pharmacogenomic impact of CYP2C19 variation on clopidogrel therapy in precision cardiovascular medicine*. 2018. **8**(1): p. 8.
43. Djordjevic, N.J.E.O.o.D.M. and Toxicology, *Genotyping genetic variants of CYP2C19 for precision antiplatelet dosing: state of the art and future perspectives*. 2022. **18**(12): p. 817-830.
44. Sussman, C., R.A. Liberatore, and M.M.J.P. Drozd, *Delivery of DNA-based therapeutics for treatment of chronic diseases*. 2024. **16**(4): p. 535.
45. Natoli, M.E., *Isothermal Nucleic Acid Assays for the Detection of HIV Drug Resistance and Sick Cell Disease in Low-Resource Settings*. 2020, Rice University.
46. Bouaoun, L., et al., *TP53 variations in human cancers: new lessons from the IARC TP53 database and genomics data*. 2016. **37**(9): p. 865-876.
47. Jeger, M., et al., *Global challenges facing plant pathology: multidisciplinary approaches to meet the food security and environmental challenges in the mid-twenty-first century*. 2021. **2**(1): p. 1-18.
48. Chen, W., H. Lin, and K.-C.J.M.B. Chou, *Pseudo nucleotide composition or PseKNC: an effective formulation for analyzing genomic sequences*. 2015. **11**(10): p. 2620-2634.
49. Emms, A., et al., *Next generation sequencing after invasive prenatal testing in fetuses with congenital malformations: prenatal or neonatal investigation*. 2022. **13**(9): p. 1517.
50. Tahir, T., et al., *The journey of CRISPR-Cas9 from bacterial defense mechanism to a gene editing tool in both animals and plants*. 2020. **2020**(10.54112).
51. Wan, F., et al., *Novel strategy to combat antibiotic resistance: a sight into the combination of CRISPR/Cas9 and nanoparticles*. 2021. **13**(3): p. 352.
52. Jiang, W. and L.A.J.A.r.o.m. Marraffini, *CRISPR-Cas: new tools for genetic manipulations from bacterial immunity systems*. 2015. **69**(1): p. 209-228.
53. Bivins, R.J.S., Technology, and H. Values, *Forgone, Not Forgotten: "DNA Fingerprinting," Migration Control and Britain's DNA Profiling Pilot Project*. 2024. **49**(1): p. 3-27.
54. Bell, S., *Forensic science: an introduction to scientific and investigative techniques*. 2019: CRC press.
55. Dehghan, H., et al., *Evaluation of anti-malaria potency of wild and genetically modified Enterobacter cloacae expressing effector proteins in Anopheles stephensi*. 2022. **15**(1): p. 63.
56. Huang, W., et al., *Biosynthesis investigations of terpenoid, alkaloid, and flavonoid antimicrobial agents derived from medicinal plants*. 2022. **11**(10): p. 1380.
57. Alessandrini, M., et al., *Pharmacogenomics and global precision medicine in the context of adverse drug reactions: Top 10 opportunities and challenges for the next decade*. 2016. **20**(10): p. 593-603.
58. Malsagova, K.A., et al., *Pharmacogenetic testing: a tool for personalized drug therapy optimization*. 2020. **12**(12): p. 1240.