www.ijarp.com ISSN 2456-9992 Page: 01-16

Research Article

International Journal Advanced Research Publications

Volume: 02
Issue: 11

GENOME EDITING TECHNOLOGIES AND LIVESTOCK PRODUCTION; RECENT ADVANCES AND FUTURE PROSPECTS

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Article Received: 23 September 2026, Article Revised: 13 October 2026, Published on: 02 November 2026

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Doi: https://doi-doi.org/101555/ijarp.7803

ABSTRACT

Genome editing has emerged as an important biotechnology for accelerating genetic improvement in livestock and addressing major challenges facing animal agriculture, including increasing demand for animal protein, disease pressures, climate change, and the need for sustainable production. In this review, major genome-editing technologies used in livestock, with particular emphasis on zinc finger nucleases (ZFNs), transcription activator-like effector nucleases (TALENs), and the CRISPR/Cas9 system were examined. Their structures, mechanisms of action, and dependence on cellular DNA repair pathways, particularly non-homologous end joining (NHEJ) and homology-directed repair (HDR), are discussed. The review further highlights some applications of genome editing in livestock improvement, including the development of disease-resistant animals, enhanced growth and meat production, improved tolerance to heat and cold stress, modification of milk composition, and animal welfare. Recent advances in CRISPR-based technologies, particularly base editing (BE) and prime editing (PE), have expanded the precision and versatility of genome modification by enabling targeted genetic changes without dependence on double-strand DNA breaks. Despite these advances, challenges such as off-target effects, unintended genomic alterations, delivery efficiency, high costs, regulatory requirements, and public acceptance continue to limit widespread application. The integration of artificial intelligence and machine learning with genome editing offers further opportunities for improving target selection, predicting editing outcomes, and optimizing the efficiency of gene editing. Overall, genome editing represents a promising complementary approach to

conventional livestock breeding, with considerable potential to improve productivity, disease resistance, climate resilience, and product quality when applied safely and responsibly.

KEYWORDS: Genome editing, CRISPR/Cas9, ZFNs, TALENs, base editing, prime editing, livestock improvements, and artificial intelligence.

1.0 INTRODUCTION

Animal agriculture faces unprecedented challenges, including the need to increase productivity to meet up the increasing demands for high quality protein while combating increasing pest and disease pressures, improving animal welfare, adapting to changing climate, and reducing the environmental impact of animal agriculture (Wray-Cahen *et al*., 2022). The traditional and conventional selection has contributed significantly to increases in growth rate, milk yield, reproductive performance and disease resistance, but its effectiveness depends on naturally occurring genetic variation and may require several generations to achieve substantial genetic change. Genome editing provides an alternative approach because specific DNA sequences can be modified directly and relatively rapidly. In recent years, changing public opinion and regulatory frameworks have permitted the integration of genetically edited animals into production systems, and for human consumption. Programs like the FDA in the USA regulate and evaluate the risk of intentional genomic alterations (IGAs) in animals before they are allowed to enter the food supply or the environment (Rodriguez-Villamil *et al*., 2024).

Owing to the fact that most of the economically important traits in animals are controlled by many genes (quantitative), livestock improvement via genetic manipulations often requires editing at multiple sites, which, using the traditional gene manipulation technologies will unavoidably be challenging, and expensive (Raza *et al*., 2022). Also, genome editing in livestock in the past, relied mostly on gene knockouts and knockdown techniques that were both inefficient and often difficult to implement, partly due to the lack of germline embryonic stem cells (Naik *et al*., 2021). To achieve real translational impact in enhanced livestock production, modern alternative gene editing technologies are required to specifically and efficiently edit multiple gene loci across the genome of any host species (Raza *et al*., 2022).

Gene editing is a powerful technique that enables the precise modification of specific gene sequences, enabling gene knockout or knockin. The principle behind gene editing technology is the use of engineered nucleases that introduce double-strand breaks (DSBs) at designated genomic sites. Earlier platforms for genome editing included zinc finger nucleases (ZFNs)

and transcription activation-like effector nucleases (TALENs), whereas CRISPR/Cas systems have become dominant because guide RNA molecules can be designed to direct nucleases to specific genomic sequences and implement modification. Recent assessment of gene editing in agriculture showed CRISPR/Cas9 as the most frequently used system, with yield, reproduction and disease resistance among the most commonly targeted traits (Rodriguez *et al*., 2024).

2.0 Major Genome Editing Technologies

The major gene editing technologies often being used in livestock improvements include zinc finger nucleases (ZFNs), transcription activator-like effector nucleases (TALENs), and clusters of regularly interspaced short palindromic repeats (CRISPR)/Cas9 system. Early-generation ZFNs and TALENs, have been instrumental in establishing methods for targeted genetic modifications. Both tools utilizes engineered nucleases to create DSBs at specific DNA locations, which subsequently induces the cell's own natural DNA repair mechanisms, often resulting in gene knockout and insertions (Ju *et al*., 2025).

2.1 Structure of Zinc Finger Nucleases (ZFNs)

ZFNs are chimeric nucleases made of a specific binding domain consisting of Zinc Finger protein motifs that bind to specific DNA sequence, fused to a cleavage domain of nonspecific FokI endonuclease (Cheit and Zeidan, 2025). A fully assembled ZF protein mainly consists of 3 tandem ZF modules, each with the capacity to recognize 3 DNA bases. A pair of ZFN therefore has left and right-assembled ZF proteins; hence, they recognize a total of 18 DNA bases (Katayama *et al*., 2025). The conceptual framework of ZFNs rooted from the earlier identification of zinc finger (ZF) domains modular protein motifs that recognizes specific DNA sequences within the transcription factor IIIA of *Xenopus laevis* oocytes (Sari *et al*., 2025).

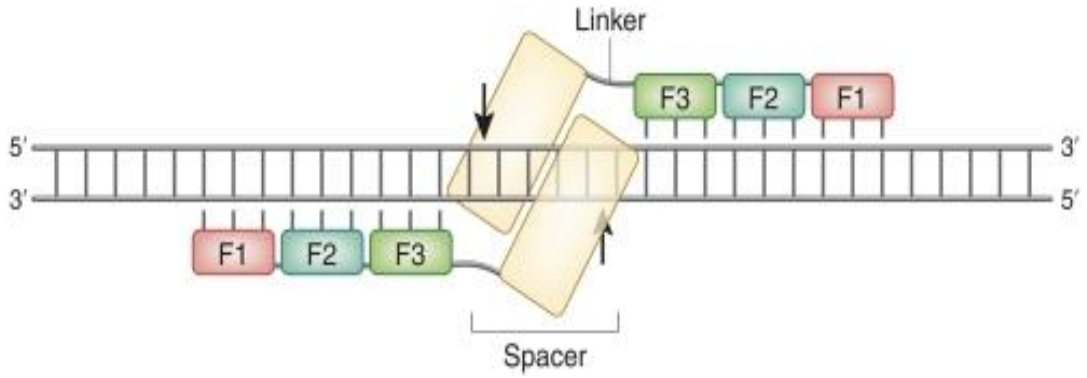


Figure 1: showing the structure of Zinc Finger Nucleases. (ZFNs)

Source; Carroll, (2011)

The cleavage part of ZFNs is a catalytic domain of FokI, a type IIS restriction endonuclease isolated from *Flavobacterium okeanokoites* used to customize zinc finger DNA-binding module by fusion. It is a modular construct of two functional domains linked via a peptide bond (linker) composed of two modular domains which offers the ability to link multiple Zinc Fingers, and for the creation of custom DNA-binding proteins, tailored to bind virtually any DNA sequence (Chivukula et al., 2025).

This results in custom-designed enzymes capable of binding to the target DNA sequence and inducing a double-strand break (DSB), by breaking the phosphorous sugar backbone of the DNA at the desired site (Cheit and Zeidan, 2025). The DNA-binding specificity of ZFNs is coupled with the nuclease domain *Fok1,* which can effectively cleave DNA after binding. ZFNs have been widely applied to produce knockout pig models with specific genetic modifications. Although ZFNs technology have been used for efficient modifications in somatic cells, their application has some challenges (Manikishore et al., 2025).

3.0 Mechanism of ZFNs Action

The general principle behind most gene editing technologies is essentially employing customized nucleases, engineered to bind to a specific sequence of DNA within the genome. Each ZFN contains a three zinc-finger tail, which ensure specific binding to the sense or the antisense strand of a particular target DNA sequence within the gene of interest. The head, which is a *Fok*I restriction endonuclease only become activated when both ZF proteins effectively binds to the complementary strands of the gene of interest with overlapping heads (Rodriguez-Villamil *et al*., 2024).

The DNA cleavage process occurs only after DNA recognition by the ZF domain, and the FokI dimerization. In the event of the existence of both the particular DNA and the Zn divalent ion, two FokI molecules cut double-stranded DNA (Khan *et al*., 2025). The creation of a DSB is a critical step since it is a molecular signal that activates the cell's endogenous DNA repair machinery. The cell repairs such breaks via two main pathways, and the efficacy of the editing is more a function of which pathway prevails (Manikishore *et al*., 2025).

The introduction of DSBs activate two key DNA repair pathways in the cell: homology-directed repair (HDR) and non-homologous end joining (NHEJ) (Wang *et al*., 2025a). HDR repair is a template-dependent repair mechanism that primarily occurs during the mitotic phase of the cell cycle, using exogenous DNA templates with homologous arms to accurately repair or replace the damaged DNA sequence, which enables precise gene insertion or point mutation correction. NHEJ on the other hand, is a template-independent mechanism that

repairs without a template, often introducing insertion/deletions (indels), which can disrupt gene function and thus achieve gene knockout (Wang *et al*., 2025b).

4.0 Structure of TALENs

Transcription activator-like effector nucleases (TALENs) are programmable nucleases that combine FokI endonuclease with modular DNA binding domain of TALEs (Yuan *et al*., 2024). Just like ZFNs, TALENs also consist of a DNA-binding domain and cleavage domain, with a pair of TALENs required to induce DSBs. The DNA-binding domain of TALENs is a transcription activator-like effector (TALE), which was first discovered in effector proteins secreted by *Xanthomonas* spp. TALE usually contain 30 tandem repeats of 33–35 amino acids, with each repeat domain recognizing individual base pairs. An artificial TALE is then linked with the single-strand DNA-cleaving domain of FokI to form a powerful tool called TALEN that combines the characteristics of TALE and FokI. (Park, 2023; Khan *et al*., 2025).

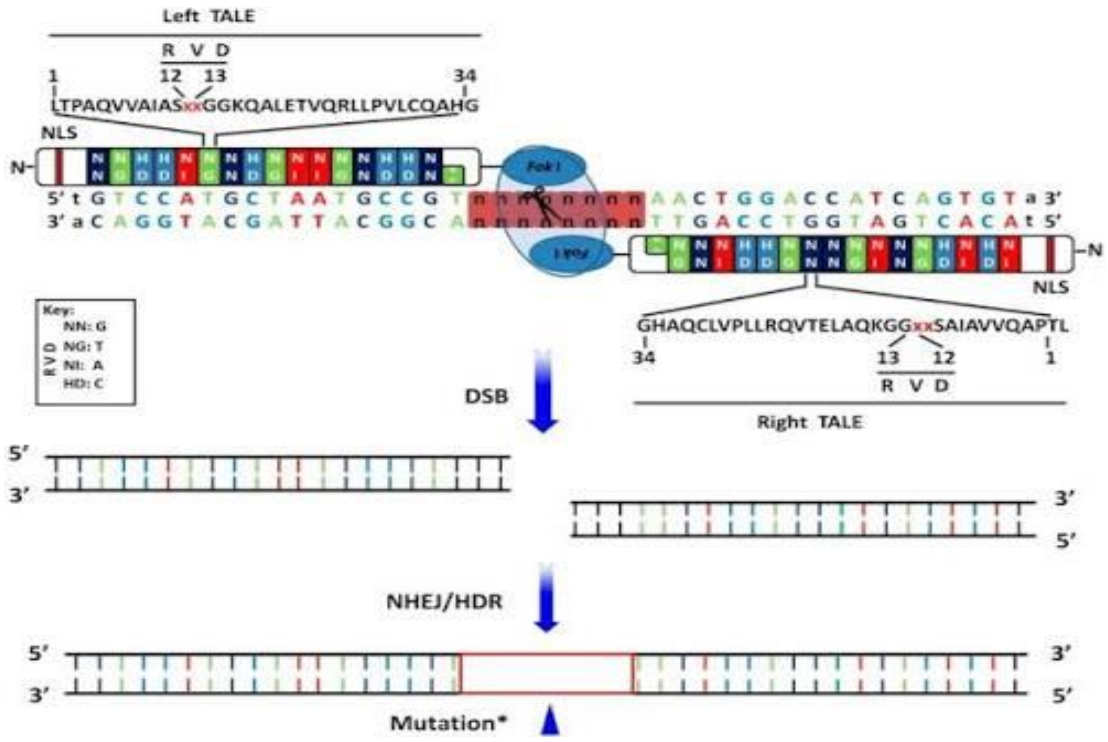


Figure 2: Schematic structure of TALENs. Source; (Xiong *et al.*, 2015).

5.0 Mechanism of action of TALENs

The target sequence of TALEN is recognized by the left and right half TALE monomer with each consisting of a tandem repeat of TALE. Each TALE repeat comprises a 34 amino acid (aa) unit that differs at two hypervariable aa located at the 12th and 13th positions, known as

the repeat variable di-residue (RVD), which determine the recognition specificity of each TALE repeat (Xiong *et al.,* 2015; Wang *et al*., 2025).

The TALEN monomer also consists of an N-terminal domain containing a nuclear localization signal (NLS), a recognition domain typically composed of tandem TALE repeats, and a C-terminal cleavage domain that comprises the *Fok* I endonuclease. Just like ZFNs, simultaneous bindings of the left and right TALE enable dimerization of the *Fok* I cleavage domain, resulting in DSBs of the target DNA. Like ZFNs, the induced DSBs of the target DNA activate cells' own DNA repair pathways NHEJ or HDR resulting in gene mutations that bring about indels, or substitution around the cleavage site (Wang *et al*., 2025).

Despite the achievements recorded in the application of ZFNs and TALENs, the technologies have exhibited certain limitations related to efficiency, specificity, and high cost. For instance, a significant number of ZFN motifs are always required for specific genomic modifications (Raza *et al*., 2022). TALENs offer higher targeting specificity and are easier to design due to the straightforward one-to-one correspondence between RVDs and DNA bases. However, the construction of TALE arrays remains labour-intensive and expensive, and their large size limits their delivery efficiency, thereby restricting their broad range application in certain biological settings (Urban *et al*., 2026).

Novel technology, clustered regulatory interspaced short palindromic repeats/CRISPR-associated protein 9 (CRISPR/Cas9) system has emerged as a more promising gene editing methods. CRISPR/Cas9 has an advantage over other gene editing methods because of its simple design and the ease of modifying multiple target sites. The technology also allows for the creation of in vitro and in vivo models for various applications (Ju *et al*., 2025).

6.0 Components of CRISPR/Cas9 System

The components of CRISPR/Cas9 system consist of the leader sequence, the Cas protein, and the CRISPR array. The leader sequences are 20 to 534 base pairs in length, rich in adenine (A) and thymine (T), and contain promoter elements localized at the 5′ end of the repeat spacer sequence. The Cas protein is a nuclease, consisting of two key structural domains, HNH and RuvC, responsible for cleaving DNA strands complementary to CRISPR RNA (crRNA) and non-complementary strands. CRISPR arrays consist of a sequences of discontinuous repeats and spacers of similar length, arranged in a specific order, together forming the CRISPR gene structure (Ma *et al*., 2025).

The CRISPR/Cas9 complex was first discovered as a primitive acquired immune system of some bacteria species and most of the archaea against foreign DNA of bacteriophage. This

mechanism consisted of two phases: immunization and immunity phases. In the immunization phase, Cas endonucleases recognize and break the viral genome into small fragments and insert them into the bacterial genome as repeat-spacer units (Wang *et al*., 2025). In the event of subsequent viral invasion (immunity phase), the bacteria produce precursor-CRISPR RNA (pre-crRNA) based on the previously captured repeat-spacer units. This will bring about the formation of sgRNA and complex with Ca9 (CRISPR/Cas9) for targeting that promotes DSB of invading DNA (Perisse *et al*., 2021).

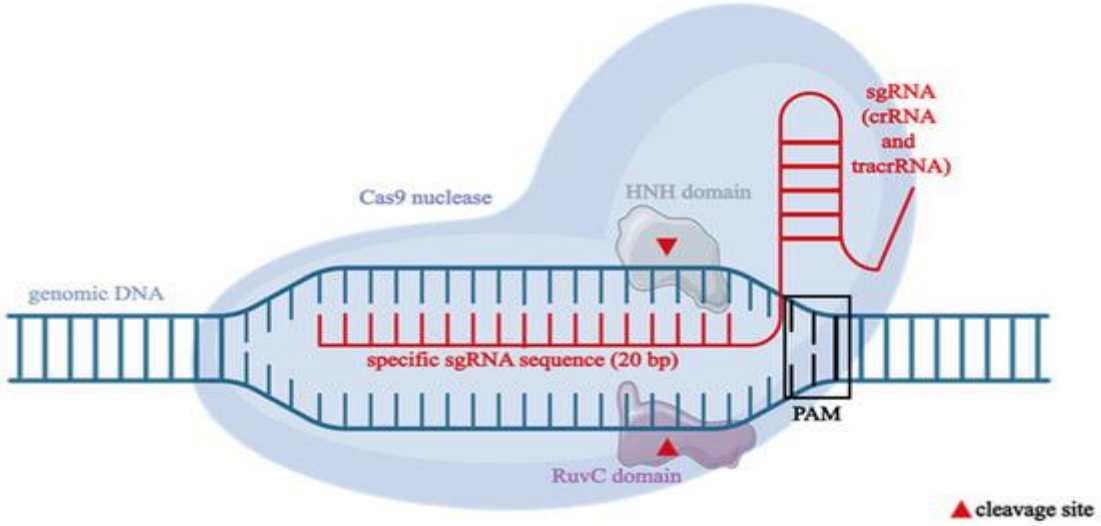


Figure 3; Schematic view of CRISPR/Cas9 system.

Source; Urban *et al. (2026)*.

7.0 Mechanism of CRISPR/Cas9 Action

CRISPR-Cas9 operates through a precise molecular mechanism comprising the Cas9 endonuclease, a single-guide RNA (sgRNA), and cellular DNA repair pathways. The sgRNA, a synthetic fusion of CRISPR RNA (crRNA) and trans-activating CRISPR RNA (tracr RNA), which guides Cas9 to a specific DNA sequence by base-pairing with the target genes (Nandal *et al*., 2025; Karimi *et al*., 2026).

A protospacer-adjacent motif (PAM) near the target sequence is essential for Cas9 binding and cleavage. The Cas9 protein, made up of a recognition and nuclease lobes with HNH and RuvC domains, unwinds DNA at the target site with a suitable PAM, forming an RNA-DNA hybrid and subsequently cleaves the complementary and non-complementary DNA strands, respectively, thereby creating a DSB. The cell repairs the DSB either via NHEJ, brings about indels that disrupt gene function, or HDR, which in the presence of template, that enable precise gene correction or insertion (Nandal *et al*., 2025). The PAM sequence length is a

short, conserved DNA motif located downstream of the cleavage site that varies among bacterial species (Karimi *et al*., 2026).

The CRISPR/Cas9 system is a simple and versatile procedure compared to ZFNs and TALENs approaches in which there is need for the assembly of the associated engineered proteins for each application. CRISPR-based gene editing technology is so efficient to the point that it allows the simultaneous editing of multiple target genes, making it the method of choice for introduction of specific genomic modifications in livestock species (Perisse *et al*., 2021).

8.0 Application of Genome Editing in Livestock Improvements

In the past decades, different genome editing technologies such as ZFNs, TALENs, and CRISPR/Cas9 systems have been applied in different fields of livestock production to improve productivity and profitability of associated industries in many ways, including breeding disease-resistant animals, improving animal performance, enriching milk composition, and producing hornless animals (Raza *et al*., 2022).

8.1 Disease Resistance Improvements

Amongst the most notable application of genome editing technology in livestock is the knock out of the scavenger receptor cysteine-rich receptor (CD163) to produce pigs that are resistant to Porcine Reproductive and Respiratory Syndrome (PRRS virus). Since deleting CD163 genes in pigs through genome editing confers a complete resistant to PRRS virus, such pigs can be used to reduce significant economic loss due to PRRS and improve the profitability of pig production (Raza *et al*., 2022). Genome editing using Cas9 nickase was equally used to produce cattle resistant to *Mycobacterium bovis* infection. *Mycobacterium bovis* causes significant economic losses to livestock industries, and poses zoonotic risks. Cas9 nickase system was applied in this case to induce the overexpression of *NRAMP1,* genes for natural resistance to infection due *M. bovis* in cattle (Raza *et al*., 2022).

8.2 Growth Performance and Meat production Improvements

CRISPR-based genome editing has been applied to improve traits associated with growth performance, feed efficiency, and product quality. Gene modifications linked to muscle development, fat deposition, and metabolic regulation offer opportunities to improve meat yield and nutritional value while optimizing resource use. It is important to note, these genetic improvements are achieved more rapidly and precisely than via conventional natural selection, which is often limited by long generation intervals (Sokra *et al*., 2026).

In another genome editing application for productivity improvements, CRISPR/Cas9 technology was used to knock out the myostatin (MSTN) gene in sheep and Yellow cattle, obtaining MSTN double allele knockout animal variants with improved growth and muscle mass. The significantly improved growth rate and muscle mass, therefore corresponds with improved meat production (Kim *et al*., 2026).

8.3 Climate Resilience Improvements

The effects of climate change has presented an additional challenge to animal production, necessitating the development of livestock that are heat and stress tolerant, and variable environmental conditions. Genome editing strategies targeting pathways involved in thermoregulation, oxidative stress, and energy metabolism have been proposed as means of enhancing animal resilience under increasing temperature extremes. Overall, these applications have placed CRISPR/Cas9 as a key enabling technology for the future of climate adaptive and sustainable livestock production (Sokra *et al*., 2026).

Members of the heat shock protein (HSP) family, such as HSP70 and HSF1, are key regulators of cellular response to heat stress in cattle. ATP1A1- and HSF1-knockout bovine fibroblast cell lines were produced using CRISPR/Cas9 technology. Both genes are crucial for heat shock resilience at the cellular level. Also, editing of PRLR gene, naturally associated with slick coats and thermos-tolerance in certain cattle breeds, has shown promise for improving heat tolerance in non-slick breeds such as Angus and Jersey (Wang *et al*., 2025).

The insertion of the UCP1 gene, encoding uncoupling protein1 using CRISPR/Cas9 technology, enhanced non-shivering thermogenesis in brown adipose tissue, thereby improving cold tolerance in pigs (Urban *et al*., 2026). UCP1 is a gene encoding uncoupling protein 1 (thermogenin), which is a mitochondrial protein found in brown adipose tissue. Instead of making ATP, the tissue generates heat by burning energy from fats. Pigs naturally lack functional UCP1 gene, which explains why they cannot generate heat from brown fat without shivering, they solely rely on shivering to stay warm under cold conditions (Berg *et al*., 2006).

8.4 Milk Production Improvements

CRISPR/Cas9 system has been used to modify the β-Lactoglobulin (BLG) gene to silence the β-Lactoglobulin (BLG) gene from the milk of dairy animals and make the milk less allergic while its nutritional values are retained. BLG is an allergenic protein which occurs in the mammary glands of ruminants and some monogastric animals, which causes serious allergic reaction in humans (Hadri *et al*., 2025). CRISPR-Cas9 offers the potential to refine the dairy

composition, and produce milk with enhanced nutritional profiles, such as increasing the concentrations of casein, a beneficial milk protein, or reduce the lactose content of milk, or produce modified protein structures, ultimately contributing to both animal health and product quality (Urban *et al*., 2026).

8.5 Animal Welfare Improvements

Polled (hornless) variants from the genome of Angus species was integrated into dairy cattle using genome editing tools. This became necessary since in modern livestock, daily management of horned cattle poses a high risk of injury for each other, as well as for the farmers. Physical dehorning of cattle is used to protect animals and farmers from accidental injury but is often associated with stress and painful experiences, application of gene editing to silence the associated genes is therefore valuable (Liu *et al*., 2022). The presence of some substances in male pork such as androstenedione and methyl-indole made the 'boar taint' and affect the taste of pork. To improve pork quality and to facilitate production management, boars are usually castrated after birth which exposed the animals to stress and unnecessary pains. CRISPR/Cas9 technology was used to knock-out the KISSR gene responsible for testicular development in pigs, to block testicular development and achieve the effect of depopulation, improve pork quality and to facilitate production management (Liu *et al*., 2022).

9.0 Advancements in CRISPR/Cas Technology

Since adaptation, genome editing has significantly transformed biology, despite the rapid progress, however, refinements in accuracy, delivery, versatility, efficiency, and accessibility are essential for expanding the impact and minimize the risks involved (Wang *et al*., 2025). Research in CRISPR/Cas technology showed that mismatch tolerance can result in editing similar sequences, and rare large incidences of deletions, rearrangements, or translocations, which are challenges that require urgent attention (Dudeja *et al*., 2025). Double-strand breaks (DSBs) can introduce unwanted DNA damage responses, and also promote genotoxicity for cells (Wang *et al*., 2025). Also, reliance on cellular DNA repair pathways and PAM sequence requirements, makes precise insertions or corrections inefficient and restrict targetable sites in many cells (Davis and Yeddula, 2024; Haider *et al*., 2026).

In this regard, significant improvements in CRISPR/Cas genome editing have shifted narrative of the technology from the basic double-strand DNA cutting to ultra-precise, non-cutting genetic and epigenetic modifications such as base editors (BE) and prime editing (PE). These systems utilizes modified Cas enzymes linked to specific enzymes to convert

single DNA (C-to-T or A-to-G) directly (point mutation), or, function as a 'search-and-replace' word processor for genomes, which allows targeted insertions, deletions, and all types of base conversions, without inducing DSBs reducing risky chromosomal breaks (Davis and Yeddula, 2024).

9.1 Base Editing (BE)

Base editing was the first breakthrough in the gene editing field after CRISPR/Cas9 due to the ability to perform precise point-mutation without a DSB. Base editing enables the direct, irreversible conversion of one DNA base to another without introducing DSBs or HDR. It comprises two main types: cytosine base editing (CBE) and adenine base editing (ABE). The first generation of base editor (BE) was BE1, a CRISPR/dCas9 fused at the *N*-terminus with a cytidine deaminase that produced a direct conversion of cytidine to uridine, therefore effecting a C → T or G → A base substitution. The BE1 targets deamination of nucleotides positioned within 4–8 base pairs that includes the PAM sequence (Wang *et al*., 2025).

Base editors combine catalytically impaired Cas proteins with deaminase enzymes to enable direct conversion of a single nucleotide to another without generating DSBs. BE stands out as a cutting-edge genome editing technique. In this process, engineered forms of CRISPR/Cas9 are fused to deaminase enzymes, permitting the conversion of specific nucleotides (such as cytosine to thymine or adenine to guanine) without inducing double-strand DNA breaks (DSBs) (Haider *et al*., 2026).

The system comprises two main types: cytosine base editing (CBE) and adenine base editing (ABE). CBE is achieved by fusing a cytidine deaminase to a Cas9 nickase (nCas9) and an uracil glycosylase inhibitor (UGI). Guided by sgRNA, the complex targets a specific DNA region, where cytosine is deaminated to uracil. UGI inhibits uracil DNA glycosylase (UDG) from removing uracil, allowing it to be interpreted as thymine during DNA replication or repair, resulting in C→T substitution (Wang *et al*., 2025). ABE follows a similar principle, using an engineered adenine deaminase fused to nCas9. At the target site, the adenine deaminase converts T to inosine (I) where I is recognized as G, and through DNA repair, I is ultimately converted to G (Wang *et al*., 2025).

9.2 Prime Editing (PE)

Prime editing (PE) represents an advancement, and evolution in precision genome engineering. PE, which is the coupling of Cas9 nickase (Cas9n) with a reverse transcriptase and a prime editing guide RNA (pegRNA) allows targeted insertions, deletions, and all types of base substitutions without reliance on donor DNA templates or the introduction of DSBs.

This versatility greatly expands the scope of feasible genomic modifications, particularly for complex traits requiring fine-scale genetic control (Sokra *et al*., 2026).

PE function as a 'search-and-replace' word processor for genomes, which allows targeted insertions, deletions, and all types of base conversions (Davis and Yeddula, 2024). This "search-and-replace" approach employs a modified Cas9 (nickase) fused to a reverse transcriptase, guided by a prime-editing guide RNA (pegRNA) which is capable of directing editing of complex genes including multiple nucleotide changes at a locus. The PE is a unique architecture which ensures that specific genetic alterations are made with minimal risk of undesired mutations or genomic instability (Haider *et al*., 2026).

10.0 Limitations of genome editing technologies

Off-target effects remain a critical concern in gene-editing technologies. These occur when the editing tool modifies unintended genomic loci of the DNA due to sequence similarities or imperfect targeting (Dudeja *et al*., 2025). Effective delivery of gene editing tools into target cells is critical in the success of gene editing. Current delivery mechanisms, including viral vectors (use of lentiviruses and Adeno Associated Viruses) and non-viral systems like lipid nanoparticles, often face limitations in tissue specificity, efficiency, and immune compatibility (Wang *et al*., 2025). The immune system may recognize the introduced gene-editing components, such as Cas proteins or viral vectors, as foreign, which can result in inflammation, reduced efficacy of therapy, or severe immune-related adverse events (Pacesa *et al*., 2024). Gene-editing techniques are expensive, with costs running into hundreds of thousands of dollars per patient. These high costs stem from the sophisticated manufacturing processes, and the resources required (Ajutor et al., 2024).

11.0 Way forward

The application of AI is imperative and holds the promise to further revolutionize gene editing technologies. Integration of AI with CRISPR can improve the overall genome editing pipeline, providing new insights, capabilities, and opportunities for manipulating and understanding the genetic code (Ajutor *et al*., 2024). The recent advances in multi-omics technologies for big data from genes, RNA, proteins, and DNA modifications, have made AI necessary for analysing information. Also, deep learning (DL) and Machine Learning (ML) models have been used to analyze large and complex genomic data sets, which prove valuable in identifying more appropriate features for AI models. ML algorithm called SPROUT has been developed which can predict the repair outcomes of genome editing in

primary T cells with high accuracy. SPROUT was trained on a large dataset of CRISPR-Cas9 editing events, and it can be used to design CRISPR experiments to maximize the desired editing outcome (Dixit *et al*., 2024).

12.0 CONCLUSION

Genome editing has transformed the prospects for genetic improvement in livestock by enabling targeted modification of specific genes associated with economically and biologically important traits. ZFNs and TALENs provided important foundations for precise genome modification, while CRISPR/Cas9 has become a widely adopted platform because of its relative simplicity, versatility, efficiency, and ability to target multiple genomic sites. Application of these technologies have proven to enhance economic productivity, climate resilience, the composition and quality of animal products.

The development of base editing and prime editing technologies has further expanded the capabilities of genome engineering. These newer technologies can introduce specific nucleotide changes and other targeted modifications with greater precision without introducing potentially toxic DSBs. However, the application of genome editing in livestock is being challenged by off-target effects, unintended genomic changes, inefficient delivery, high development costs, regulatory requirements, and public acceptance, which requiring careful attention.

Future progress such as integrating genome editing with AI, ML, and multi-omics technologies, can improve the identification of desirable genetic targets, prediction of editing outcomes, guide-RNA design, and overall editing efficiency. Also, genome editing should be considered a complementary tool to conventional breeding rather than a complete replacement for the established genetic improvement methods. With continued improvements in precision, safety, efficiency, affordability, and regulatory oversight, genome editing has considerable potential to contribute to productive, disease-resilient, climate-smart, and sustainable livestock production systems.

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