Journal of Advances in Biology & Biotechnology

Volume 27, Issue 8, Page 543-558, 2024; Article no.JABB.120433
ISSN: 2394-1081

The Role of Genome Editing Technologies in Sustainable Agriculture

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

DOI: https://doi.org/10.9734/jabb/2024/v27i81168

Open Peer Review History:
This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: https://www.sdiarticle5.com/review-history/120433

Review Article

Received: 21/05/2024
Accepted: 26/07/2024
Published: 26/07/2024

ABSTRACT

Genome editing technologies have emerged as powerful tools for making precise and targeted modifications in the DNA of living organisms, offering unprecedented opportunities to revolutionize agriculture amidst global challenges such as population growth, climate change, and diminishing resources. This review provides an overview of genome editing principles, its comparison with traditional breeding and genetic engineering methods, and the regulatory landscape governing its application. The CRISPR/Cas9 system, in particular, has revolutionized genome editing due to its efficiency, affordability, and versatility. By harnessing this system, researchers can induce specific modifications in plant genomes, enhancing traits such as yield, quality, and resilience to biotic and

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Cite as: *Waghmode, Prajyot, Chetariya Chana Pitha, and Vaishnavi Banka. 2024. "The Role of Genome Editing Technologies in Sustainable Agriculture". Journal of Advances in Biology & Biotechnology 27 (8):543-58. https://doi.org/10.9734/jabb/2024/v27i81168.*

abiotic stresses. The review highlights recent advancements in CRISPR/Cas9 technology, including its adaptation for base editing and prime editing, which allow for precise nucleotide substitutions and broaden the scope of genetic modifications possible in crops. Addressing the regulatory environment surrounding genome-edited crops, the paper discusses existing regulations, international agreements, and ethical considerations. It emphasizes the need for science-informed regulations that balance innovation with transparency and public safety, crucial for fostering societal acceptance and facilitating global trade in genetically modified agricultural products. Furthermore, the review explores case studies and trends in genome editing applications across different crop species, illustrating how these technologies are being employed to address challenges in agriculture. From improving disease resistance to optimizing nutrient content and environmental adaptation, genome editing offers a pathway towards sustainable crop improvement. Looking forward, the review outlines future prospects and challenges in the field, including potential limitations such as off-target effects and the need for enhanced precision in editing techniques. It underscores the importance of integrating genome editing with conventional breeding methods to optimize agricultural productivity and resilience in the face of evolving environmental pressures. Genome editing holds immense promise for enhancing global food security and sustainability. By elucidating the current landscape of genome editing technologies and their applications in agriculture, this review aims to provide a comprehensive resource for policymakers, regulators, researchers, and the public, facilitating informed decision-making and supporting the responsible deployment of these transformative technologies in agriculture.

Keywords: Genome editing; CRISPR/Cas9; disease resistance; nutrient content; food security; sustainability.

1. INTRODUCTION

Genome editing technologies represent a pivotal advancement in modern agriculture, poised to address the complex challenges posed by climate change, burgeoning populations, and the increasing demand for diverse and sustainable food sources [1]. As agriculture navigates these turbulent waters, the integration of cutting-edge biotechnologies offers a promising pathway towards enhancing crop yield, improving nutritional quality, and fortifying plant resilience against environmental stresses. At the forefront of this technological revolution lies genome editing, a precise tool that enables scientists to introduce targeted modifications within the DNA of crops [2]. Unlike traditional breeding methods, which rely on natural genetic variation and can be time-consuming, genome editing allows for the direct alteration of specific genetic sequences, thereby facilitating the precise modulation of desirable traits. Among the various genome editing techniques, CRISPR/Cas9 has emerged as a game-changer in plant biology. This technology harnesses the power of a bacterial enzyme, Cas9, guided by RNA, to make precise cuts in the DNA strands at targeted locations [3]. These cuts can then be repaired by the cell's natural DNA repair mechanisms, leading to genetic modifications such as gene knockout, gene insertion, or even precise nucleotide substitutions. The simplicity, cost-effectiveness, and efficiency of CRISPR/Cas9 have galvanized plant scientists worldwide, driving rapid advancements in crop improvement over the past decade [4]. This enthusiasm is underpinned by its potential to revolutionize agricultural practices, from enhancing yield and quality to conferring resistance against pests, diseases, and adverse environmental conditions. Moreover, the versatility of CRISPR/Cas9 extends beyond simple gene editing; innovations like base editing and prime editing now allow for more nuanced alterations, further expanding the scope of possibilities for crop enhancement.

Recent research has underscored the breadth of applications for genome editing in agriculture. Studies have demonstrated its efficacy in bolstering abiotic stress tolerance, such as drought or heat resistance [5], and enhancing biotic stress resistance against pathogens and pests. For instance, Maximiano and Franco highlight the strategic applications of CRISPR/Cas systems in fortifying plant defenses, paving the way for more sustainable agricultural production systems that are less reliant on chemical interventions [6]. However, alongside these transformative potentials, genome editing also raises significant ethical, regulatory, and safety considerations. The precise nature of CRISPR/Cas9 can sometimes lead to unintended genetic alterations at off-target sites, albeit at lower frequencies compared to conventional breeding methods [7]. Addressing these concerns is crucial to ensure the safety and acceptance of gene-edited crops among consumers and regulatory bodies worldwide. Moreover, the regulatory landscape surrounding genome-edited crops varies widely across different countries. While some nations have embraced these technologies and enacted supportive policies, others proceed with caution, balancing innovation with stringent safety protocols and public scrutiny. Wei et al. underscore the global disparities in regulatory frameworks, noting significant progress in countries like the United States, China, and parts of Europe, where genome-edited crops are increasingly integrated into agricultural practices [8]. These developments are crucial as they shape the trajectory of commercialization and public acceptance of genetically modified organisms derived from genome editing technologies.

In tandem with regulatory challenges, technological advancements continue to propel the field forward. Researchers have grappled with improving the efficiency of genome editing in complex crops like polyploid species, where multiple sets of chromosomes complicate the editing process. Strategies such as heat shock treatments have shown promise in enhancing editing efficiency in crops like wheat, underscoring the dynamic interplay between biotechnological innovation and agricultural productivity. The application of genome editing is not limited to enhancing crop traits alone but also extends to broader agricultural contexts [9]. For instance, the development of herbicide-tolerant crops through targeted genome editing presents a sustainable solution to weed management, reducing reliance on environmentally harmful herbicides while boosting crop yields. Looking ahead, genome editing holds the potential to unlock new frontiers in agricultural sustainability, from improving nutrient content in staple crops to engineering resilience against climatic fluctuations. Its integration into mainstream agriculture promises not only to bolster food security but also to reduce the ecological footprint of farming practices worldwide. As the global population continues to grow, and as environmental pressures intensify, the imperative to harness the full potential of genome editing for sustainable agriculture becomes increasingly urgent [10]. The advent of genome editing technologies marks a transformative chapter in agricultural innovation. By enabling precise and targeted modifications in crop genomes, these technologies offer unprecedented opportunities to address pressing global challenges while ushering in a new era of sustainable food production. As research progresses and regulatory frameworks evolve, the promise of genome editing in agriculture is poised to reshape the landscape of food security, environmental stewardship, and societal well-being on a global scale.

In the face of increasing global food demand driven by population growth and environmental challenges such as climate change, agriculture stands at a critical juncture. Traditional breeding methods have been instrumental in enhancing crop yields and quality over centuries. However, the pace and scale of modern agricultural demands necessitate more precise and efficient tools. Genome editing technologies have emerged as transformative tools in crop improvement, offering unprecedented precision and speed in modifying plant genomes [11]. This review explores the principles, applications, advancements, and challenges of genome editing technologies in agricultural innovation.

2. UNDERSTANDING GENOME EDITING TECHNOLOGIES

Genome editing refers to the precise alteration of DNA sequences within an organism's genome. This section delves into the foundational concepts and mechanisms behind various genome editing technologies, emphasizing their application in agricultural contexts. Genome editing technologies represent a revolutionary approach to altering genetic information with unprecedented precision [12]. At its core, genome editing involves targeted modifications to DNA sequences within an organism's genome using specialized molecular tools known as sequence-specific nucleases (SSNs). These SSNs, which include zinc finger nucleases (ZFNs), transcription activator-like effector nucleases (TALENs), and clustered regularly interspaced short palindromic repeats (CRISPR)-associated nucleases (Cas), enable researchers to introduce specific changes at desired locations within the genome. Among these tools, CRISPR/Cas systems, particularly CRISPR/Cas9, have garnered significant attention due to their simplicity, efficiency, and versatility in generating double-stranded breaks (DSBs) at precise genomic locations guided by complementary guide RNAs (gRNAs) [13].

In agricultural contexts, genome editing holds immense promise for advancing crop improvement by precisely modifying genes associated with desired traits such as yield, quality, stress tolerance, and nutritional content. By harnessing these technologies, researchers can engineer crops more rapidly and precisely compared to traditional breeding methods, which often rely on random mutations and crossing techniques. The ability to tailor genetic traits through genome editing not only accelerates the development of novel crop varieties but also enhances their resilience to environmental challenges, thereby contributing to sustainable agriculture practices. As genome editing tools continue to evolve and improve, their integration into agricultural biotechnology promises to revolutionize crop breeding strategies and address global challenges in food security and agricultural sustainability [14]. The integration of simplicity and adaptability has propelled zinc-finger nucleases (ZFNs), transcription activator-like effector nucleases (TALENs), and clustered regularly interspaced short palindromic repeats (CRISPR) to the forefront of genetic engineering (Fig. 1).

2.1 Principles of Genome Editing

Genome editing technologies utilize sequence-specific nucleases (SSNs) to induce targeted modifications in DNA. The primary SSNs include zinc finger nucleases (ZFNs), transcription activator-like effector nucleases (TALENs), and clustered regularly interspaced short palindromic repeats (CRISPR)-associated nucleases (Cas). Among these, CRISPR/Cas systems, particularly CRISPR/Cas9, have gained prominence due to their ease of use, efficiency, and versatility in generating site-specific double-stranded breaks (DSBs). Genome editing technologies revolutionize genetic manipulation by employing sequence-specific nucleases (SSNs) to precisely modify DNA sequences within an organism's genome [15]. These SSNs, which include zinc finger nucleases (ZFNs), transcription activator-like effector nucleases (TALENs), and CRISPR-associated nucleases (Cas), enable targeted alterations at specific genomic loci. Among them, CRISPR/Cas systems have emerged as the forefront tool, particularly CRISPR/Cas9, due to their simplicity, efficiency, and versatility in creating site-specific double-stranded breaks (DSBs) in DNA [16].

Zinc finger nucleases (ZFNs) were among the first SSNs developed, consisting of engineered zinc finger DNA-binding domains fused to the DNA-cleavage domain of the FokI endonuclease. These proteins can be customized to bind specific DNA sequences, allowing targeted cleavage and subsequent repair via cellular DNA repair mechanisms. Transcription activator-like effector nucleases (TALENs) operate similarly to ZFNs but use transcription activator-like effectors (TALEs) instead of zinc fingers for DNA recognition [17]. TALENs have been widely used for genome editing in various organisms, offering a programmable platform for introducing specific genetic modifications. However, the advent of CRISPR/Cas systems has revolutionized genome editing due to their superior ease of design and implementation [18]. CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats) are segments of prokaryotic DNA containing short, repetitive base

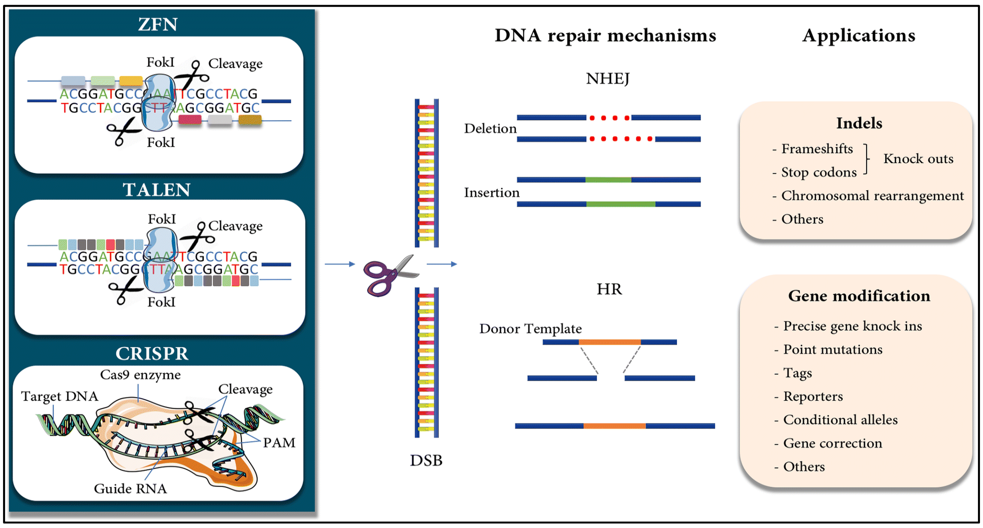

Fig. 1. The nuclease genome editing technologies with its mechanisms and applications [14]

sequences, interspaced with unique sequences known as spacers derived from viral or plasmid DNA. CRISPR-associated nucleases (Cas proteins) utilize these spacer sequences as guides to target and cleave specific complementary DNA sequences. Among Cas proteins, Cas9 from *Streptococcus pyogenes* is the most commonly used due to its robust activity and well-characterized mechanisms. CRISPR/Cas9-based genome editing involves designing a single-guide RNA (sgRNA) complementary to the target DNA sequence, directing Cas9 to induce a DSB precisely at the desired genomic site. This DSB triggers cellular DNA repair mechanisms, primarily non-homologous end joining (NHEJ) or homology-directed repair (HDR), which can introduce gene knockouts, insertions, or substitutions with high efficiency [19]. The simplicity and efficiency of CRISPR/Cas9 have democratized genome editing, making it accessible across diverse organisms and accelerating research in fields ranging from agriculture to medicine.

2.2 Mechanisms of CRISPR/Cas Systems

CRISPR/Cas systems are guided by short RNA sequences (guide RNAs or gRNAs) to target specific DNA sequences complementary to the gRNA. Upon binding, the Cas nuclease induces DSBs at the target site, triggering DNA repair mechanisms [20]. These repairs can result in gene knockout via error-prone non-homologous end joining (NHEJ) or precise gene editing through homology-directed repair (HDR). CRISPR/Cas systems constitute a powerful tool for precise genome editing, guided by short RNA sequences known as guide RNAs (gRNAs) to target specific DNA sequences complementary to the gRNA sequence (Fig. 2). The CRISPR array within a prokaryotic genome contains these short, repetitive sequences interspersed with unique spacer sequences derived from previous encounters with foreign genetic material, such as viruses or plasmids [21]. These spacers serve as a memory of past infections and guide the Cas nuclease to recognize and cleave complementary DNA sequences.

The mechanism begins with the formation of a complex between the Cas nuclease (e.g., Cas9) and the gRNA, which directs the complex to the target DNA site through base pairing between the gRNA sequence and the target DNA sequence. Once bound, Cas9 induces a double-stranded break (DSB) at the target site by cleaving both DNA strands. This DSB triggers cellular DNA repair mechanisms, primarily non-homologous end joining (NHEJ) or homology-directed repair (HDR). Non-homologous end joining (NHEJ) is an error-prone repair pathway that often results in small insertions or deletions (indels) at the DSB site [22]. These indels can disrupt the open reading frame of a gene, leading to a loss-of-function mutation or gene knockout. NHEJ is particularly useful for creating gene knockouts in a straightforward and efficient manner. Alternatively, homology-directed repair (HDR) is a more precise repair pathway that utilizes a donor DNA template with homologous sequences flanking the DSB site. HDR allows for the introduction of specific nucleotide changes or insertions at the target locus, facilitating precise gene editing [23]. HDR is advantageous for introducing precise modifications such as point mutations, insertions of new genetic sequences, or corrections of disease-causing mutations. Overall, the versatility of CRISPR/Cas systems lies in their ability to be easily programmed to target virtually any DNA sequence of interest by designing complementary gRNAs. This specificity, combined with the efficiency of inducing DSBs and the ability to harness cellular repair pathways like NHEJ and HDR, has made CRISPR/Cas a transformative technology in genome editing, advancing research across biological disciplines including agriculture, medicine, and biotechnology.

2.3 Advancements in CRISPR Technology

Recent advancements have expanded the CRISPR toolbox beyond Cas9, including Cas12a (Cpf1) and Cas13 (C2c2), each with unique capabilities such as cleaving DNA or RNA, respectively. Moreover, innovations in base editing and prime editing have enabled precise nucleotide substitutions and insertions/deletions without requiring DSBs. Recent advancements in CRISPR technology have significantly broadened its applicability and precision in genome editing beyond the traditional Cas9 nuclease. One notable advancement is the development and utilization of Cas12a, also known as Cpf1, and Cas13, also known as C2c2 [24]. These enzymes offer unique functionalities that complement and extend the capabilities of the original Cas9 system. Cas12a (Cpf1) differs from Cas9 in several key aspects. Unlike Cas9, which generates blunt-ended DSBs, Cas12a creates staggered cuts in the target DNA, resulting in sticky ends. This characteristic can be advantageous in certain genome editing applications, particularly in facilitating precise DNA modifications and enabling the insertion

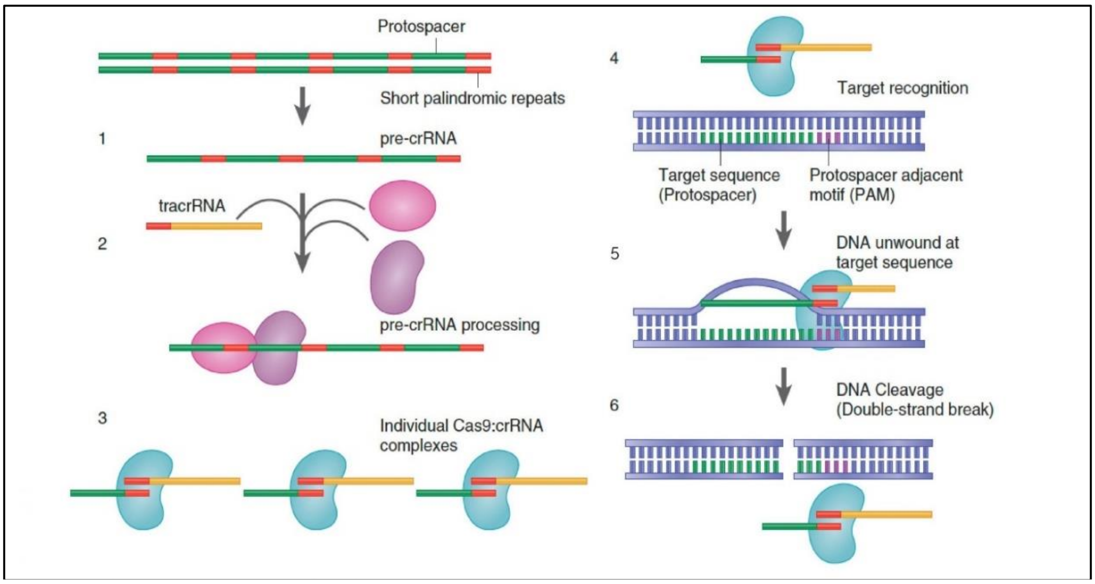

Fig. 2. Mechanisms of CRISPR/Cas Systems

of larger genetic sequences. Cas12a has been successfully employed in various organisms, expanding the toolkit for genome editing beyond what Cas9 can achieve alone.

On the other hand, Cas13 (C2c2) represents a breakthrough in RNA-targeting CRISPR systems. Unlike Cas9 and Cas12a, which target DNA, Cas13 specifically targets RNA molecules. This capability opens up new avenues for manipulating RNA transcripts within cells, which is crucial for applications such as gene regulation, RNA editing, and studying RNA biology. Cas13 has shown promise in applications ranging from RNA knockdown to diagnostic tools for detecting RNA viruses. In addition to expanding the range of CRISPR tools, recent innovations have focused on enhancing the precision of genome editing techniques [25]. Base editing and prime editing are two such advancements that offer alternatives to traditional CRISPR-mediated DSBs. Base editing enables the direct conversion of one DNA base pair into another without inducing DSBs, using engineered fusion proteins that combine a catalytically inactive Cas protein with a deaminase enzyme. This approach allows for precise nucleotide substitutions, offering potential applications in correcting point mutations associated with genetic diseases.

Similarly, prime editing represents a further refinement in genome editing technology by allowing targeted insertions, deletions, and base substitutions without creating DSBs. Prime editing combines a Cas nuclease (usually Cas9) with an engineered reverse transcriptase enzyme and a prime editing guide RNA (pegRNA). The pegRNA directs the Cas enzyme to the target site and specifies the desired edit, while the reverse transcriptase synthesizes new DNA sequences based on the RNA template provided by the pegRNA. These advancements in CRISPR technology—encompassing the development of Cas12a and Cas13, as well as innovations in base editing and prime editing—underscore the rapid evolution of genome editing tools. These tools not only expand the scope of applications in genetic research and biotechnology but also enhance the precision and efficiency of genome editing, paving the way for transformative advancements in agriculture, medicine, and beyond.

3. APPLICATIONS OF GENOME EDITING IN CROP IMPROVEMENT

Genome editing technologies offer unparalleled opportunities for enhancing crop traits related to yield, quality, stress tolerance, and nutritional content. This section explores diverse applications and case studies highlighting the impact of genome editing in modern agriculture. Genome editing technologies have revolutionized crop improvement by offering precise and targeted methods to modify genetic sequences, thereby enhancing various agronomic traits critical for sustainable agriculture. These technologies are increasingly applied across different crops to address challenges related to yield, quality, stress tolerance, and nutritional content, thus ushering in a new era of agricultural innovation.

3.1 Enhancing Yield and Quality

Genome editing has been instrumental in enhancing crop yield and quality through targeted modifications of genes involved in plant growth and development. For instance, researchers have successfully employed CRISPR/Cas systems to manipulate genes responsible for flowering time, fruit size, and grain yield in crops like rice, maize, and wheat. By optimizing these traits, genome-edited crops can potentially yield higher quantities of superior-quality produce, meeting the escalating demands of global food security amidst changing climatic conditions [26,27]. Enhancing crop yield and quality through genome editing represents a significant advancement in agricultural biotechnology, offering precise tools to address the challenges of food security and environmental sustainability. Researchers have leveraged CRISPR/Cas systems to manipulate key genes that influence various aspects of plant growth and development, thereby improving overall productivity and product quality. One notable application of genome editing is the manipulation of genes controlling flowering time, fruit size, and grain yield in major crops such as rice, maize, and wheat. By precisely modifying these genes, scientists aim to optimize traits critical for crop yield. For example, delaying flowering time can extend the vegetative phase, allowing plants to accumulate more biomass and nutrients before entering reproductive stages. This approach not only increases overall plant productivity but also enhances yield stability under variable environmental conditions.

In addition to flowering time, genome editing has been used to enhance fruit size and grain yield in crops. For instance, editing genes involved in cell division, hormone signaling pathways, and fruit development can lead to larger and more uniform fruits, which are not only visually appealing but also commercially desirable. Similarly, modifications in genes related to grain filling and nutrient transport have resulted in improved grain yield and nutritional content, addressing the dual challenge of quantity and quality in crop production. Furthermore, genome-edited crops have the potential to meet the escalating demands of global food security amidst changing climatic conditions. By deploying precise genetic modifications, researchers can develop varieties that are more resilient to environmental stresses such as drought, heat, and salinity, thereby ensuring stable yields even in challenging agricultural landscapes [28]. Overall, genome editing holds promise for revolutionizing agriculture by enabling the development of high-yielding, resilient crops with enhanced nutritional quality and reduced environmental impact. As advancements in biotechnology continue to expand, the application of genome editing in crop improvement is poised to play a pivotal role in achieving sustainable food production systems capable of feeding a growing global population.

3.1.1 Genome editing in legume crops for enhanced varieties

Genome editing through CRISPR-Cas technology has opened new avenues for improving legume crops, offering precise manipulation of targeted genes to enhance desirable traits. CRISPR-Cas operates with the Cas9 endonuclease and a guide RNA (gRNA), which includes a crisper RNA (crRNA) binding the target sequence and a transactivating RNA (tracer RNA) that facilitates recognition and cleavage [23]. This process allows for a wide range of applications, from improving crop yield to enhancing resistance to pests and diseases. However, there are challenges in applying CRISPR-Cas to legume crops, primarily due to the complexities of transformation and callus regeneration. *Agrobacterium*-mediated transformation with seed tissues has shown success in some legumes, especially in soybean and model species like *Medicago truncatula* and *Lotus japonicas* [24]. While the focus of many studies has been on nutrient delivery to the soil and plant through CRISPR-edited legumes, further research is required to establish comprehensive protocols for successful transformation and regeneration.

Despite these challenges, CRISPR-Cas-based genome editing has yielded positive results. In soybean, genome editing has led to improved isoflavone content and resistance to Soybean mosaic virus (SMV), as well as better seed-oil composition with an 80% increase in oleic acid content [25,26]. In chickpea, CRISPR-Cas was optimized with 42% mutation efficiency, indicated by albino phenotypes, while in pea, mutation efficiencies ranged from 16% to 45% [28]. Peanut and alfalfa have also been targets for genome editing, focusing on improving oleic acid content and understanding genes associated with plant growth and biomass development, respectively Genome Editing in Legume Crops for Enhanced Varieties tabulated in (Table 1). The advancements in genome editing hold significant promise for enhancing legume crops, contributing to more resilient, high-yielding, and sustainable agricultural practices.

Table 1. Genome editing in legume crops for enhanced varieties

Legume Plant	Desired Trait	Targeted Genes	Results	References
Soybean	Increased isoflavone content and resistance to Soybean mosaic virus (SMV)	GmF3H1, GmF3H2, & GmFNSII-1	stable inheritance; doubled isoflavone content in leaves; reduction (1/3) of SMV coat protein	[29]
Soybean	Understanding flowering time & adaptation to diverse environments	GmFT2a, & GmFT5a	Both genes collectively regulate flowering time; GmFT2a critical for short day conditions; GmFT5a essential for long day and adaptation in higher latitudes	[30]
Soybean	Improvement in seed-oil composition	GmFAD2-1A, & GmFAD21-B	80% increase in oleic acid; 1.3–1.7% reduction in linoleic acid	[31]
Soybean	Attempt to modify storage-protein composition of seeds	Nine soybean seed storage protein coding genes	three genes successfully mutated: Glyma.20 g148400, Glyma.03 g163500, Glyma.19 g164900	[32]
Soybean	Improvement in plant architecture	GmSPL9, GmSPL9a, GmSPL9b, & GmSPL9c	PL9a/b showed shorter plastochron length	[33]
Soybean	Improved taste	LOX1, LOX2, & LOX3	reduced lipoxygenase activity	[34]
Cowpea	Develop asexual plant lineage	Meiosis controlling gene VuSPO11-1	4.5–37% mutation efficiency	[35]
Chickpea	CRISPR-based genome editing and understanding drought tolerance	4CL, & RVE7	RNP complex-based editing of chickpea protoplast;	[36]
Chickpea	Optimization of genome editing through CRISPR-Cas	PsPDS	visible albino phenotypes	[37]
Pea	Optimization of genome editing through CRISPR-Cas	PsPDS	different vector constructs	[38]
Peanut	Enhanced oleic acid content	ahFAD2a, & ahFAD2b	higher oleic acid content	[39]
Alfalfa	Achieving genome editing through CRISPR	uidA, & NOD26	GUS gene successfully mutated	[40]
Alfalfa	Understanding genes for growth and biomass development	MsSPL8	early flowering, decreased internodal length, and plant height	[41-43]

3.2 Improving Stress Tolerance

One of the most promising applications of genome editing in agriculture is improving stress tolerance in crops. Abiotic stresses such as drought, salinity, and extreme temperatures pose significant challenges to crop productivity worldwide. Through genome editing, researchers have targeted genes involved in stress response pathways to develop crops capable of thriving under adverse environmental conditions. For example, editing genes related to water use efficiency, osmotic regulation, and heat shock proteins has enabled the production of drought-tolerant and heat-resistant varieties of crops like maize and soybeans. These advancements not only safeguard yield stability but also reduce the environmental footprint associated with excessive irrigation and agrochemical use. Improving stress tolerance in crops through genome editing represents a pivotal advancement in agricultural biotechnology, aimed at mitigating the detrimental effects of abiotic stresses such as drought, salinity, and extreme temperatures on crop productivity worldwide. These stresses pose significant challenges to agriculture, threatening food security and economic stability in many regions. Genome editing technologies, particularly CRISPR/Cas systems, have enabled researchers to precisely target and modify genes involved in stress response pathways [43]. By manipulating these genes, scientists have developed crops that exhibit enhanced resilience to adverse environmental conditions. For instance, in maize and soybeans, genes related to water use efficiency, osmotic regulation, and heat shock proteins have been edited to confer drought tolerance and heat resistance.

One notable example is the enhancement of drought tolerance in crops. Through genome editing, researchers have altered genes responsible for regulating stomatal closure and opening, thereby improving water use efficiency. This genetic modification allows plants to maintain adequate hydration levels during periods of water scarcity, ensuring sustained growth and productivity even in arid conditions. Similarly, editing genes involved in osmotic regulation helps crops tolerate high soil salinity by maintaining cellular ion balance and minimizing the toxic effects of salt accumulation. Moreover, genome editing has been instrumental in enhancing heat tolerance in crops. By manipulating heat shock proteins and other thermotolerance-related genes, scientists have developed varieties capable of withstanding elevated temperatures without compromising growth and yield. This adaptation is crucial as global climate change intensifies, leading to more frequent and severe heatwaves that threaten agricultural productivity. The development of stress-tolerant crops through genome editing not only safeguards yield stability but also promotes sustainable agriculture by reducing reliance on irrigation and agrochemical inputs. By enhancing the innate ability of crops to withstand environmental stresses, farmers can cultivate resilient varieties that require fewer resources and minimize environmental degradation [44]. In conclusion, genome editing offers unprecedented opportunities to enhance stress tolerance in crops, thereby bolstering global food security in the face of climate change and environmental pressures. Continued advancements in biotechnology and genomic research hold promise for further improving crop resilience and developing sustainable agricultural practices that ensure food production under challenging conditions.

3.3 Enhancing Nutritional Content

Genome editing offers a promising avenue to enhance the nutritional content of crops, thereby addressing malnutrition and dietary deficiencies prevalent in many parts of the world. By precisely modifying genes involved in nutrient metabolism and accumulation, researchers have successfully enriched crops with essential vitamins, minerals, and beneficial phytochemicals. For instance, biofortification efforts using genome editing have increased the levels of vitamin A in rice, iron and zinc in wheat and maize, and omega-3 fatty acids in soybeans [45]. These nutrient-enriched crops not only contribute to improving public health outcomes but also support sustainable agriculture by reducing reliance on external nutrient supplementation. Enhancing the nutritional content of crops through genome editing represents a transformative approach in agricultural biotechnology, offering significant potential to combat malnutrition and dietary deficiencies worldwide. By precisely modifying genes involved in nutrient metabolism and accumulation, researchers have successfully enriched crops with essential vitamins, minerals, and beneficial phytochemicals. One of the pioneering applications of genome editing in enhancing nutritional content is biofortification, which aims to increase the levels of key nutrients in staple crops. For example, in rice, scientists have utilized genome editing to enhance the biosynthesis pathway of beta-carotene, leading to the production of Golden Rice—a variety enriched with provitamin A. This advancement addresses vitamin A deficiency, a significant health issue in many developing countries where rice is a dietary staple.

Similarly, in wheat and maize, genome editing has been employed to enhance the accumulation of iron and zinc, essential minerals that are often deficient in diets lacking diverse food sources. Iron deficiency, in particular, is a global health concern affecting millions, especially in regions where cereal-based diets predominate. By increasing the bioavailability of these minerals in staple crops, genome-edited varieties contribute to improving nutritional status and reducing the prevalence of related health disorders. Another notable example is the enhancement of omega-3 fatty acids in soybeans through genome editing. Omega-3 fatty acids are essential for cardiovascular health and brain function, yet their availability in plant-based diets is limited. By introducing genetic modifications, researchers have boosted the production of these beneficial fatty acids in soybeans, offering a sustainable source of omega-3s for vegetarian and vegan populations [26,36]. Moreover, genome editing facilitates the enhancement of phytochemicals with antioxidant properties, such as flavonoids and polyphenols, which contribute to human health by protecting against chronic diseases. These compounds are crucial components of a balanced diet and can be augmented in crops through targeted genetic modifications, thereby promoting overall well-being and longevity. Beyond improving public health outcomes, genome-edited crops for enhanced nutritional content support sustainable agriculture by reducing the need for external nutrient supplementation. By fortifying staple crops with essential nutrients, farmers can cultivate varieties that provide greater nutritional value per harvest, potentially reducing food insecurity and improving dietary diversity [22]. In conclusion, genome editing offers a powerful tool to address global nutritional challenges by enhancing the nutrient content of crops. Continued research and development in this field hold promise for further innovations in biofortification and sustainable agriculture, contributing to improved public health and food security worldwide.

Encouraging farmers to adopt and cultivate biofortified cereal crops may require education and incentives. Understanding and overcoming the barriers to farmer adoption, which can include factors like access to seeds and training, is an essential component of successful biofortification initiatives [2]. Sustainability is a long-term concern in biofortification efforts. This includes maintaining genetic diversity in cereal crops and ensuring that biofortified varieties remain resilient and productive over time, especially in changing environmental conditions. Finally, identifying and addressing research gaps is an ongoing challenge in the field of biofortification. Continued scientific inquiry is essential to push the boundaries of what's possible in terms of improving nutritional quality

Table 2. List of genomic approaches in biofortification in cereals (rice, wheat, and maize)

Crop	Genome-Editing	Nutrients	Gene	Methods of Transformation	Vectors Used
Rice	Crispr/cas9	Carotenoid	–	Particle bombardment	–
		High amylose	SBEIIb	*Agrobacterium* mediated	*pCXUN-Cas9*
		Low phytic acid	OsITPK6		*pH_itpk6*
		Beta- carotene	Osor		–
		Amylose	Waxy	*Agrobacterium* transformation	*CRISPR/Cas9 vector*
		Sucrose efflux transporter	OsSWEET11, OsSWEET14		*pTOPO/D*
		Amylase synthase	OsU3, OsU6a, OsU6b, OsU6c		*pCAMBIA1300*
Wheat	Crispr/cas9	Low gluten	Alpha gliadin	Biolistic transformation	*pANIC-6E destination vector*
	Crispr/cas9	Fe, mg	TaVIT2	*Agrobacterium* mediated	*pBract202*
Maize	Cripsr/cas9	Carotenoid	Phytoene synthase		*pMD18-T*
	Cripsr/cas9	Low phytic acid content	Phytic acid synthesis	*Agrobacterium* transformation	*pEasy blunt vector*

in cereal crops and addressing the challenges that lie ahead. Genomic approaches in biofortification in cereals tabulated in Table 2.

4. CHALLENGES AND LIMITATIONS

Genome editing technologies in agriculture hold immense promise for addressing global challenges like food security and climate resilience. However, alongside their transformative potential, several challenges and ethical considerations must be addressed to ensure safe and responsible deployment.

4.1 Off-Target Effects

A primary concern in genome editing is off-target mutations, unintended changes in DNA sequences occurring outside the intended target site. Off-target effects can potentially lead to genetic instability, unintended phenotypic changes, or even safety risks if critical genes are altered. Mitigating these risks requires advancements in gRNA design and nuclease engineering to enhance specificity. New generations of CRISPR systems, such as Cas variants with improved fidelity, are being developed to minimize off-target effects [45]. Additionally, robust detection methods like high-throughput sequencing are crucial for accurately assessing and minimizing off-target mutations before genome-edited crops are released for commercial cultivation.

4.2 Regulatory Hurdles

The regulatory landscape for genome-edited crops varies globally, posing significant challenges to their commercialization and acceptance. In some regions, genome-edited crops are subject to regulations similar to those governing genetically modified organisms (GMOs), despite differences in the underlying technology and outcomes. Unclear regulatory definitions and inconsistent policies can create barriers to market entry, hindering agricultural innovation and delaying potential benefits to farmers and consumers. Efforts are underway to harmonize regulatory frameworks and update policies to reflect the nuances of genome editing. Stakeholders, including scientists, policymakers, and industry leaders, advocate for science-based regulations that prioritize safety while enabling timely approval and adoption of genome-edited crops. Collaborative initiatives are essential to navigate regulatory complexities and establish transparent, predictable pathways for regulatory approval that foster innovation and ensure consumer confidence.

4.3 Public Perception and Ethical Considerations

Public perception of genome-edited crops, influenced by perceptions of GMOs and concerns about health, environment, and ethical implications, remains a significant challenge. Misinformation and lack of understanding about the technology can lead to skepticism and resistance among consumers, influencing market acceptance and adoption by farmers. Addressing these challenges requires transparent communication, robust risk assessment, and stakeholder engagement throughout the research, development, and regulatory approval process. Ethical considerations, including environmental impact assessments, socio-economic implications, and equitable access to benefits, are integral to responsible innovation in agriculture. Educational initiatives and public dialogues are essential to foster informed decision-making and build trust in genome editing technologies. Engaging stakeholders—from farmers and consumers to policymakers and civil society organizations—ensures diverse perspectives are considered in shaping regulatory frameworks and deployment strategies. By addressing ethical concerns and promoting transparency in communication, stakeholders can collaboratively navigate the complexities of genome editing and build public confidence in its potential to contribute positively to sustainable agriculture and global food security.

Genome editing technologies represent a paradigm shift in agricultural innovation, offering unprecedented opportunities to enhance crop traits, improve nutritional content, and increase resilience to environmental stresses. However, realizing these benefits requires addressing challenges related to off-target effects, navigating regulatory landscapes, and fostering public trust and acceptance. Ongoing advancements in genome editing tools and techniques, coupled with clear regulatory frameworks and proactive engagement with stakeholders, are crucial for overcoming these challenges. By prioritizing safety, transparency, and ethical considerations, stakeholders can collectively harness the potential of genome editing to meet the complex challenges facing global agriculture while ensuring sustainable and equitable outcomes for society.

5. FUTURE PERSPECTIVES AND INNOVATIONS

Genome editing technologies are poised to revolutionize agriculture by addressing pressing challenges such as climate resilience, food security, and sustainable intensification. This section explores emerging trends, future innovations, and potential applications that are shaping the landscape of agricultural biotechnology.

5.1 Next-Generation Genome Editing Tools

The field of genome editing continues to evolve rapidly with ongoing efforts to enhance precision, efficiency, and versatility of editing tools. Technologies beyond CRISPR/Cas9, such as base editing, prime editing, and epigenome editing, offer novel capabilities for precise nucleotide substitutions, insertions, deletions, and modifications of gene expression without inducing double-strand breaks (DSBs). Base editing, for instance, allows targeted conversion of one DNA base pair into another, enabling precise changes to nucleotide sequences with reduced off-target effects compared to traditional CRISPR systems. Similarly, prime editing combines reverse transcriptase and Cas9 nickase to introduce targeted sequence alterations with high efficiency and minimal DNA damage, opening new avenues for complex genome engineering in crops [46,47]. These advancements are pivotal in accelerating trait discovery and crop improvement programs by enabling scientists to modify genetic sequences with unprecedented accuracy and control.

5.2 Integration with Other Agricultural Technologies

The convergence of genome editing with other cutting-edge agricultural technologies, including precision farming, artificial intelligence (AI), and omics technologies (genomics, transcriptomics, proteomics), holds immense potential for optimizing agricultural practices and enhancing crop productivity. Precision farming techniques, facilitated by AI and remote sensing technologies, enable farmers to monitor crop health, predict yield fluctuations, and optimize resource use based on real-time data. Integrating genome editing with precision agriculture allows for tailored modifications of crop genomes to maximize resilience against environmental stresses, improve nutrient use efficiency, and enhance overall agronomic performance [48]. Furthermore, omics technologies provide comprehensive insights into the molecular mechanisms underlying crop traits, facilitating targeted genome edits to optimize yield, quality, and nutritional content of crops under varying environmental conditions. These synergistic approaches are critical for accelerating breeding cycles and developing resilient crop varieties capable of meeting future food demands sustainably.

5.3 Addressing Global Agricultural Challenges

Genome editing offers precise solutions to global agricultural challenges by addressing key priorities such as sustainable intensification, resource conservation, and resilience to climate variability. By enhancing stress tolerance, disease resistance, and nutritional content in crops, genome-edited varieties can contribute to reducing chemical inputs, improving soil health, and mitigating environmental impacts associated with conventional farming practices [49]. Multidisciplinary collaborations and international partnerships are essential for leveraging genome editing technologies to develop region-specific crop varieties adapted to diverse agroecological zones and socio-economic contexts. Moreover, advancing regulatory frameworks that align with scientific advancements and societal values is crucial for enabling responsible deployment of genome-edited crops globally, ensuring equitable access to safe and sustainable agricultural innovations [50-52].

The future of agriculture hinges on harnessing the transformative potential of genome editing technologies to address complex global challenges and secure food supplies for a growing population [53]. By advancing next-generation editing tools, integrating with innovative agricultural technologies, and fostering collaborative efforts across disciplines and borders, stakeholders can unlock new opportunities for sustainable agriculture and resilient food systems.

6. CONCLUSION

In conclusion, genome editing technologies stand at the forefront of agricultural innovation, offering precise, efficient, and versatile tools to tackle pressing challenges in global food production. By enabling targeted modifications in the DNA of crops, these technologies hold immense potential to enhance yield, quality, and resilience against environmental stresses. The advent of CRISPR/Cas9 has revolutionized genome editing with its accessibility and adaptability, paving the way for advancements such as base editing and prime editing that further expand the scope of genetic modifications in agriculture. This review has underscored the transformative impact of genome editing across various crop species, demonstrating its ability to improve disease resistance, optimize nutritional content, and facilitate environmental adaptation. Despite these advancements, navigating the regulatory landscape remains a critical challenge, necessitating robust frameworks that balance innovation with safety and ethical considerations. Transparent communication and engagement with stakeholders are essential to foster public trust and acceptance of genome-edited crops, crucial for global adoption and trade. Looking forward, integrating genome editing with traditional breeding methods holds promise for synergistic improvements in agricultural productivity and sustainability. Continued research efforts aimed at minimizing off-target effects and enhancing editing precision will be pivotal in realizing the full potential of genome editing technologies. As the field evolves, interdisciplinary collaborations and international cooperation will be instrumental in overcoming challenges and leveraging genome editing to build resilient and nutritious food systems. In conclusion, genome editing represents a paradigm shift in agriculture, offering solutions to meet future food demands amidst escalating global challenges. By providing a comprehensive overview of current advancements, applications, and regulatory considerations, this review aims to inform decision-makers and stakeholders, guiding the responsible deployment and adoption of genome editing technologies to secure sustainable food production for generations to come.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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Peer-review history:
The peer review history for this paper can be accessed here:
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