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CRISPR-oriented genome editing to improve nutrients in crops: advancements and opportunities

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Abstract

Objective

This investigation targets to critically examine and summarise recent advancements in CRISPR-based genome editing technologies applied to raise the nutritional quality of major food crops. The centralize is on identifying particular gene targets, evaluating the outcomes of genetic modifications, and emphasizing future chances for sustainable agriculture and global food security.

Materials and methods

We analysed peer-reviewed research articles, case investigations, and institutional reports. The review concentrates on CRISPR/Cas9 and its progressive variants Cas12a, base editors, and prime editors that have been applied to modify genes related to nutrient biosynthesis, transport, and accumulation in crops. Key gene targets include *psy1* and *crtI* for provitamin A production, *o2* and lysine-rich proteins for increasing essential amino acids, and metal transporter genes like *OsNAS2* and members of the ZIP family for improving iron and zinc bioavailability. The methodologies examined also cover numerous guide RNA design platforms and delivery techniques, containing Agrobacterium-mediated transformation, particle bombardment, and protoplast-based systems.

Results

Meaningful improvements in crop nutritional profiles were observed. For instance, CRISPR-edited rice varieties showed increased iron and zinc content, maize exhibited elevated lysine levels, and tomato demonstrated improved concentrations of vitamins A and C. Base editing approaches facilitated accurate nucleotide replacement without the introduction of foreign DNA, thereby reducing regulatory hurdles and enhancing public acceptance. Furthermore, the regulatory landscape in countries like the United States and Japan has evolved to permit field testing and commercialization of gene-edited crops under relaxed GMO guidelines, further accelerating study and expansion.

Conclusions

CRISPR-based genome editing represents a transformative tool in the expansion of nutrient-dense food crops. When integrated with synthetic biology and computational bioinformatics, it proposes a rapid and aimed approach to crop development, which is crucial in the context of climate change and population growth. However, for the technology to achieve global impact, different challenges must be addressed. These include establishing harmonized biosafety regulations, managing ethical concerns, and enhancing public awareness and trust. Collaborative international frameworks and inclusive policy-making will be essential to ensure that CRISPR-driven innovations participate effectively to global food and nutritional security.

Keywords: Agricultural biotechnology, CRISPR/Cas9, Gene modification, Genome editing, Sustainable agriculture

Paper Type: Research Paper.

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Introduction

Fortifications (FFs) and biofortifications (BFs) are separate food-enriching methodologies that vary in strategies. This review addresses the fundamental challenge of global malnutrition, which stems from the low nutritional content of staple crops like rice, wheat, and maize and highlights how biofortification can propose a solution. These crops often lack sufficient iron, zinc, and vitamin A, which can lead to widespread deficiencies known as "hidden hunger." Traditional breeding and genetic modification methods have problems with accuracy and public acceptance (Mohammadabadi et al., 2024b). The review examines how CRISPR-based genome editing supplies an accurate, effective, and non-transgenic method to augment the nutritional quality of crops, with the objective of bolstering global initiatives targeted at enhancing food quality and addressing nutrient deficiencies (Singh et al., 2023). In the past, food fortifiers were typically added through the terminal stages of food processing. However, they are now integrated throughout the entire manufacturing process in food production facilities. Relative to fortification, biological fortification is economically advantageous as it needs a singular investment to cultivate a biofortified plant with minimal ongoing expenses. Bio-fortified plants show a hopeful solution to nutritional concerns (Bouis & Saltzman, 2017). Biofortification is a sustainable and enduring option for supplying micronutrient-dense plants to populations (Koç & Karayiğit, 2021). Plants are biofortified with necessary nutrients by nutrient treatments and selective breeding. Agronomic BF entails the deliberate utilization of minerals to raise the density of a special mineral in the consumable parts of plants (White & Broadley, 2009). Modern agromonic bio formulations should integrate with artificial nanomaterials, like nano fertilizers, to promote plant growth by promoting rhizobacteria to raise the nutrient efficiency and stimulate plant expansion (Chieb & Gachomo, 2023). Essential Quantitative Trait Loci (QTLs) are employed in breeding attempts to raise plant nutrient profiles (Maldonado-Taipe et al., 2022). Plant breeding, exclusively polyploid breeding, is a protracted and arduous process for progressing agricultural output (Trojak-Goluch et al., 2021). Certain plants have been biofortified with particular nutrients by genetic modifications utilizing genetic engineering. The drawbacks of Genetically Modified (GM) plants include human allergic responses and diminished nutritional value (Ghimire et al., 2023). They exert environmental impression by leaking toxins into the soil, inducing insect resistance, and disrupting plant diversification. Numerous ethical issues are linked to genetically modified plants (Maghari & Ardekani, 2011). Genome Editing (GE) technology has notable benefits, attending the drawbacks of GM plants (Wang et al., 2022). GE yields deterministic and heritable alterations in designated genomic areas, exhibiting little off-target effects and no incorporation of gene patterns. GE employs alterations, additions, solo-nucleotide replacements, and extended fragment replacements for DNA modifications (Zhang et al., 2018). Before the identifying of Clustered

Regularly Interspaced Short Palindromic Repeats (CRISPR) related proteins (Cas), tools for genome editing, like homing enzymes known as endonucleases or meganucleases (MN), Zinc Finger Nucleases (ZFNs), and other nucleases, were utilized (Ganger et al., 2023). The succinct overview of previously employed GE techniques is delineated below. MNs, or homing enzymes like endonucleases, are infrequently cutting enzymes show in every bacterial genome (Kazemipour et al., 2025). These enzymes recognize and sever extensive DNA patterns (typically 18-30 sets), leading to Dual-Stranding Breaks (DSBs) (Fujii et al., 2022). Numerous engineered MN variations exist to cleave special DNA regions so that GM can expand meaningful traits in plant species. The equipment of homing enzymes known as endonucleases has encountered technological challenges in producing these nucleases, like creating carriers for cellular entry and off-target effects. ZFNs are engineered nucleases that consist of a DNA-binding domain (zinc finger motifs) fused to a FokI nuclease domain. ZFN-based DSBs are subjected to DNA-repairing mechanisms, leading to highly particular mutagenesis and directed gene substitution. The ZFNs comprise four to 30-amino-acid motifs that can link to trinucleotide patterns, restricting the overall selectivity of DNA-binding areas to 10-16 nucleotide chains. ZFN technology has different drawbacks, containing a complex design process that needs custom proteins for each target DNA sequence, restricted flexibility, potential off-target effects, moderate efficiency, and inability to carry out RNA editing or accurate base alters. Transcriptional Activator-Like Effecting Enzymes (TALENs) are non-specifically DNA-cleaving enzymes related to a customizable DNA-binding region to target special amino acids (Christian et al., 2010). TALENs consist of a synthetic arrangement of TALE repeats combined with the nuclease domains and are utilized for GE. TALENs possess drawbacks, containing intricate design, reduced engineering practicality, diminished specificity, inadequate effectiveness, and incapacity for gene knockdown and RNA modification. In recent years, novel Cas variations, like CRISPR/Cpf1 (where CRISPR stands for Clustered Regularly Interspaced Short Palindromic Repeats)—have emerged as powerful tools for genome editing. This approach is a more progressive and effective GE tool than CRISPR/Cas9. The base editing approach is a novel complementary method to the HDR technique, facilitating the direct and irreversible alter from one base to the next without necessitating a double-stranded breakage or source DNA. Scientists have effectively expanded Adenine-Based Editing (ABE) and showcased the effectiveness of conversion utilizing the model within the rice genes. Likewise, additional researchers validated the effectiveness and accuracy by converting the target without any inserts, eliminations, or replacement alters at the intended sites, demonstrating its superior effectiveness in multiplexed base editing. A recent investigation has applied CRISPR/Cas9 and an activation-induced deaminase substance to create different herbicide-resistant variants (Li et al., 2018). Rice serves as a model plant for operational and structural genetics investigations owing to its compact genome size, elevated conversion effectiveness, availability of genetic resources, and increased genomic synchrony. Rice is effectively utilized to investigate numerous categories of rice GE within the CRISPR/Cas9 framework and ascertain the functional elements' roles. Different investigations have been published regarding the prospective employment of CRISPR/Cas9 in rice. Attend ing the swift and substantial proliferation of recent results on the CRISPR/Cas9 GE technology, a complete evaluation is necessary. This essay intends: To examine the simultaneous employment of CRISPR/Cas9 in rice investigations, specifically targeting CRISPR/Cas9 genes to raise rice plants; to examine the components and processes of CRISPR/Cas9; to emphasize the design of CRISPR/Cas9 vector assembly models and numerous online tools for targeting site expansion; and to evaluate CRISPR/Cas9 against alternative GE technologies (ZFNs and TALENs), exclusively the recently expanded Cas9 variations.

CRISPR for addressing hunger issues

GE is essential for producing high-yield, high-quality, climate-resilient, and environmentally friendly plants. This section examines the utilization of CRISPR/Cas9 structures for enhancing food yields and addressing malnutrition-related challenges. The study elucidates numerous plant enhancement strategies employing CRISPR-based GE technologies. The investigation contends that the secure implementation of CRISPR/Cas9 methods in agricultural enhancement can assist researchers in creating climate-resilient plant types, thus advancing the achievement of the Sustainable Development Goal (SDG), the objective of eradicating hunger (Oliva et al., 2019).

Enhancement of biotic stress resilience applying CRISPR/Cas9 technology: Plant infectious agents induce numerous crop illnesses that substantially diminish production; herbivorous animals, like insects, inflict direct harm and carry diseases (Pandey et al., 2017). The shifting climate is negatively impacting plants' resilience to numerous biotic stressors. Acute plant losses attributable to biotic stressors are estimated to vary from 21% to 42%. Numerous papers have examined the possible uses of the CRISPR/Cas9 framework for creating disease- and insect-resistant plants. This part critically examines numerous genomic alterations in food plants utilizing the CRISPR/Cas9 system to demonstrate its potential in reaching the SDG. Enhancing biotic resilience to stress shows meaningful potential for progressing disease resistance and reducing plant losses (Oliva et al., 2019). For instance, the direct targeting of viral genomes applying CRISPR/Cas9 proposes adaptable and long-lasting resistance. Tactics targeted against Su genomes necessitate the laborious discovery of Su genes for the special plant-virus relationship; advancements in genetics expedite the process. Further investigation is needed to mitigate expansion-security trade-offs in engineering impediments to diseases.

Enhancement of abiotic stress resilience via CRISPR/Cas9 technology: Alongside biotic challenges, plants encounter many abiotic variables, like extreme temperatures, salt, and drought, which impede plant growth and result in substantial, often catastrophic, yield reductions globally. Particular plant genes exacerbate the detrimental impacts of stress from antibiotics, which are referred to as sensitive genes (Se genes). Editing the genome technique is employed in many crops, including grain and vegetables. By and fruit trees, to raise resistance to abiotic stresses by targeting and deleting Se genes (Oliva et al., 2019). B-amylase (BMY) genes participate to resistance to cold in rice. They govern starch breakdown and maltose buildup to mitigate the effects of cold stress. Mutant lines possessing a 369-bp mutation in coding sequences exhibited resistance to drought, osmosis, and salinity stressors, credited with a decrease in stomatal and an improve in leaf area, enhancing retained water and light-use effectiveness.

CRISPR-increased rain yield and architecture: The grain yield characteristics of plants are intricate. The plant yield is regulated by QTLs that impression 1000-grain weight (which includes grain shape), grain count per panicle, floret count per panicle, and panicle count per plant. QTLs affecting the dimension of grains have been transcribed and described in rice. Among these notable transcriptional regulators, which generate a gamma component of heterotrimeric G-protein, making a potential serine/threonine protease with a repeat domain, adversely impact shape and hence affect production. CRISPR-mediated modification increased grain size, thus augmenting the 1k-grain and total output per rice crop. Multiplex deletion of three separate genes increased grain production in edited plants relative to the wild type. In an additional investigation, they were concurrently wiped out applying CRISPR/Cas9, creating high-yielding, drought-tolerant grain lines (Xie et al., 2018). Farmers employ herbicides not only for particular plants but to diminish competition with unwanted plants for humidity, sunlight, and energy. Herbicide-tolerant plants (HTP) demonstrated meaningful utility in simultaneous farming. Historically, creating a new HTP necessitated genetic engineering or considerable mutagenesis. In recent years, CRISPR/Cas9 base cutting and prime editing techniques were employed to improve Acetolactate Synthesis 1, enhancing resistance to herbicides in maize. The mixture of the Cas 9 endonuclease in rice permits the splitting of the genes, whereas concurrent repair of the gene confers resistance to herbicides in rice. Likewise, accurate nicking of the genome and restoration by primary editing techniques have increased rice herbicide immunity. Tolerance for herbicides was increased in oil-seed rape and tomato plants applying the proposed method (Xie et al., 2018). The grain yield characteristics of plants are intricate. The production of grains is regulated by QTLs that impression 1000-grain mass (which includes grain size), grain count per panicle, floret count per panicle, and panicle count per plant. Now, QTLs that regulate shape are synthesized and described CRISPR-mediated modification increased grain size, augmenting the 1k-grain mass and production per rice crop. Multiplex genetic modification of three genes increased grain production in edited plants relative to the wild type. In a separate investigation, they were concurrently knocked out applying CRISPR/Cas9, resulting in the expansion of high-yielding, drought-tolerant rice strains (Xie et al., 2018).

Enhancement of photosynthesis applying CRISPR/Cas9: Researchers investigating plants have dedicated years to expanding agricultural photosynthesis for improved yield by augmenting the flag area of leaves, raising CO_2 absorption capability, minimizing transpiration, and elevating flux via the Calvin cycle. Photosynthesis has been increased applying CRISPR-based GE because of its crucial task in expanding and growing plants, wheat and fruit production, or biomass generation. For instance, CRISPR-mediated modification of the Negative Regulation, a translation element-like genome that modulates the activity of photosynthesis-related genes, increased rice effectiveness, yield of grains, and biomass generation (Oliva et al., 2019).

Enhancement of nutrient use effectiveness (NUE) via CRISPR/Cas9: The extensive utilization of chemicals increased agricultural productivity through the Green Revolution, although it escalated expenses and participated to environmental harm from fertilizer discharge. The advancement of plants exhibiting increased effectiveness in applying NUE will diminish fertilizer use, augment farmers' income, and mitigate pollution. Increased NUE is attained by augmented nutrient absorption from the soil, optimized nutrient employment and transport within plants, and heightened plant expansion and efficiency. Particular genes prevent nutrient absorption, adversely affecting plant NUE (Xie et al., 2018).

Enhancement of grain quality applying CRISPR/Cas9: Grain quality is evaluated based on preparation and consumption characteristics, nutritional content, visual appeal, and milling attributes. The amount of amylose impresses the cooking process and palatability. In contrast, production is governed by the starch synthesizer, an enzyme carried by the genes. Scientists have expanded elite corn and rice lines with reduced amounts of amylose by applying CRISPR/Cas9 technology. The genes generated rice with decreasing levels. Editing Starches resulted in rice lines with elevated amylose contents (Oliva et al., 2019). A different method for enhancing eating habits is the biological fortification of grains and other plants. Applying CRISPR/Cas9, Golden Rice is fortified with carotene by inserting Green Rice 1 (GR1) and GR2 genomic plasmids. Likewise, vegetables, and fruit varieties increased by the add-in or deletion mechanisms of the CRISPR/Cas9 technology (Xie et al., 2018).

Genetic applications of CRISPR in crop improvement

CRISPR-based GE technologies have transformed the cultivation of plants. The advancement of breeding materials has grown more effective and resilient via CRISPR/Cas9 technologies. This document summarizes notable uses for CRISPR/Cas9 systems in breeding plants.

Male sterility induction: Recent CRISPR-based disruption of key fertility genes in rice has enabled the production of male-sterile lines for hybrid expansion. Hybrid plants can exhibit meaningful hybrid vigor, known as heterosis, resulting in improved yields and increased agronomic traits. Manufacturing hybrid seeds commercially is laborious due to the challenges of preventing the self-pollination of female parents, which is necessary to exclude heterozygous embryos (Oliva et al., 2019). An effective method to avoid self-pollination is the employment of strains. It was recently achieved by adding off rice. Similarly, the TaNPl gene, which regulates plant growth and pollen exine expansion in crops, was disrupted at homologous loci applying the CRISPR/Cas9 system, resulting in male-sterile grain plants.

Hybrid vigor stabilization: Stabilizing is an economical method for preserving hybrid lines. This method outcomes in plants producing seedlings that are genetic clones of the maternal progenitor. Heterogeneity was established via the process of mitosis instead of this process mechanism in rice by the concurrent editing of four genetic materials: OsPAIR (abolishes meiotic replication), OsREC8 (the segregation of sister chromosomes through the first meiotic split), OsOSD1 (permits the omission of the meiotic dividing), and OsMTL (performs a role in conception) (Liu et al., 2020). The concurrent modification of the genomes led to the establishment of hybrid strength, and the resulting plants were genetically reproduced via seed.

Haploid induction: The doubled haploid technique stabilizes the genetic structure of lines that are inbred by the era, in contrast to the six to eight grandchildren needed by traditional repeated self-pollinating Haploid production in rice was effectively achieved by knocking down OsMTL, a gene encoding a pollen-specific enzyme, utilizing the CRISPR/Cas9 structure, resulting in a haploid production rate of 2-6%. Recent study has elucidated the process responsible for removing uniparental chromosomal post-fertilization, attributed to spermatid chromatin disintegration, resulting in haploid induction (Chen et al., 2024). In a separate investigation, the corn genome Centromeric Histone3 (CENH3) was altered via the CRISPR/Cas9 system to generate paternal haploid cells (Chen et al., 2024). The knockout of this protein outcomes in maternal genome deletion and diploid formation due to impaired kinetochore formation and pole adhesion through division and mitosis. By targeting different genes, CRISPR/Cas9 technology is utilized for haploid production in wheat, maize, rice, and Arabidopsis thaliana plants (Oliva et al., 2019).

The domestication of wild relatives of plants and overlooked plants: De novo domestication facilitates the use of wild plant relatives and orphan crops, which are momentous sources of resilience to biotic and abiotic stresses and supply substantial nutritional value (Zsögön et al., 2018). Conventional cultivation of plants needs centuries; the CRISPR technique permits breeders of plants to expedite the breeding process via accurate manipulation of numerous loci. Multiplex genome editing (MGE) technologies have meaningfully accelerated the process of de novo domestication. Wild African rice indigenous peoples serve as superior sources of stress resilience and possess improved nutritional profiles compared to cultivated rice (Liu et al., 2020).

Trait stacking and pyramiding: Study on CRISPR/Cas9 facilitated gene knock-in, gene transfer, and chromosomal reversal, enabling advantageous gene accumulation within a plant variety. The utilization of gene knock-in applying the CRISPR/Cas9 platform is underexplored in plants, yet particular instances are documented in animals (Mohammadabadi et al., 2024a). Genetic add-in in monkeys was achieved by introducing the mCherry genome (monomeric red fluorescent protein) regulated by the promoter, which has meaningful expression in numerous organs and cells. The resulting mutants exhibited elevated mCherry production in explosions. Likewise, a genome assembly was managed for the firefly genome in emerald algae (Chen et al., 2024). The naturally occurring inversions and mutations through evolution have mutated numerous critical genes whose functionality can be restored applying CRISPR/Cas9-driven inversions of extensive chromosomal segments. The CRISPR/Cas9 platform facilitates crop genetic placement to address stressors and improve nutritional value. Instances underscore the effectiveness of the CRISPR/Cas9 method in accumulating beneficial genes (e.g., resistant to disease alleles) in a plant (Schmidt et al., 2019).

Self-incompatibility engineering: Crops have expanded self-compatibility to prevent self-fertilization; altering the process improves crop breeding or possibly averts self-fertilization in line generation. Self-compliance can be altered by eliminating self-incompatible behavior to create inbred paths for harnessing by containing self-incompatible growth to establish paths targeted at exploiting heterosis and producing fruits without seeds by parthenocarpy. Rice plants exhibit sterility at hot temperatures and are exploited to eliminate **self-incompatibility-inducing** proteins for increased yield (Oliva et al., 2019).

De Novo domestication of wild relatives: The accessibility of systems and the possibility for multiplication induction applying the CRISPR/Cas9 system have underscored the feasibility of creating novel organisms. Polyploid crops like wheat and cotton exhibit increased resilience and trait redundancy due to multiple homologous gene copies, facilitating stable genome editing outcomes. CRISPR/Cas9 technology can facilitate de novo speciation by inducing multiplication in diploid organisms via the disruption of meiosis, resulting in the formation of diploid embryos that fuse to create tetraploid embryos, with the potential for much greater ploidy rates (Liu et al., 2020).

Alternative breeding techniques: The primary reason of sterility in men is architectural and copy number variation between subtypes—the japonica variant, S_y, harbors pollen-momentous genes that generate a protein with a region. The indigo-allele, S_x, comprises replicas of 26-kb tandemly replicated sequences, harboring the S_y homolog regulated by separate regulators. In S_y/S_x mixtures, a higher level of the S_x allele in units relative to S_y outcomes in the selected aborting of S_y pollens. The allele transfer ratio of both populations is disturbed. The technique known as CRISPR/Cas9 can restore the inheritance ratio of both parental lines by eliminating replicas of the S_x, producing fertile crops from S_y pollen-donated mothers. These outcomes corroborate the task of the CRISPR/Cas9 system in alleviating genome-dosage-dependent incompatibility across closely related races (Chen et al., 2024). The disruption of incompatibility between the Indian rice strain and the American rice variant was achieved by plucking out the enzyme genes at the center point. The egg production of the resulting mixture was notably recovered.

An overview of CRISPR/Cas9 ecosystems

Most bacteria and Archaea possess an adaptive defense mechanism known as CRISPR/Cas9, which safeguards them against phages, viruses, and other extraneous genetic information. The primary components of the CRISPR-Cas9 system consist of the Cas9 protein and a single-guide RNA (sgRNA) that directs it to the target DNA sequence. CRISPR/Cas99 is among the most well-described and often employed groups within the CRISPR/Cas9 systems. The Cas9 protein includes two nuclease domains: the HNH domain, which cleaves the DNA strand complementary to the guide RNA, and the RuvC domain, which cleaves the non-complementary strand, producing a site-specific double-strand break (DSB). The plant's intrinsic repair mechanism autonomously rectifies DSBs in vivo, employing Homology-Guided Repair (HDR), leading to substantial insertions or fragment substitutions (Jinek et al., 2012). Figure 1 shows the schematic depiction of the CRISPR/Cas9 GE system utilized to expand GM biofortified plants.

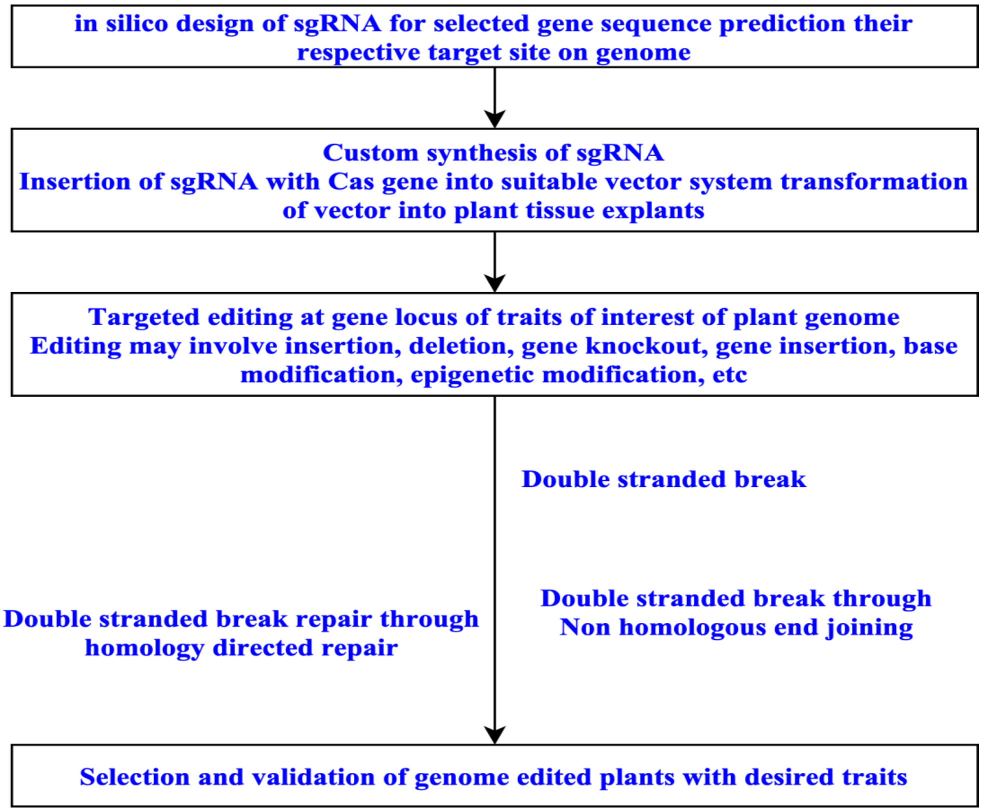

Figure 1. Workflow of CRISPR/Cas9 genome editing in crop biofortification, containing gRNA design, delivery methods, target mutation, and screening process

Regulations of CRISPR/Cas9-modified plants: A global discourse exists around the oversight of GE plants. Currently, the legal status of GE plants differs among numerous countries. Two primary models exist for the control of GE plants. The initial model governs the plant acquisition procedure. This framework asserts that the regulation of products derived from novel breeding techniques will depend on the methods employed in their creation. GE plants are subjected to the stringent rules applicable to GM Organisms (GMOs). The secondary, less rigorous regulatory framework emphasizes the terminal product instead of the methodology for creating GE plants. This plan emphasizes the novelty of the trait based on the particular technique applied in its expansion. This paradigm permits for labeling GE plants, supplied the result includes no foreign DNA, as shown in Figure 2.

As shown in Figure 2, the process-based regulations of GE plants in numerous nations, exclusively in the European Union, obstruct their progress since multinational study-oriented corporations are relocating their operations to countries with end-product-based oversight, like the United States. In a recent conversation with Reuters, it was asserted that plants created by the editing of genes should be regarded as separate from GMOs, contrary to the decision to subject these plants to stringent GMO regulations. Meaningful economies have established separate regulations for GE plants compared to GMOs. At the same time, the European Union might be poised to alter its regulatory approach. A commission was established in 2016 to expand recommendations for legalizing GE agricultural products, which stays a subject of ongoing discussion. Regarding Research and Development (R&D) activities and financing related to CRISPR initiatives, there is a global expectation for leniency towards GE plants and avoiding strict rules. These advancements underscore the hopeful future of GE plants and illustrate potential progress toward the zero hunger objectives.

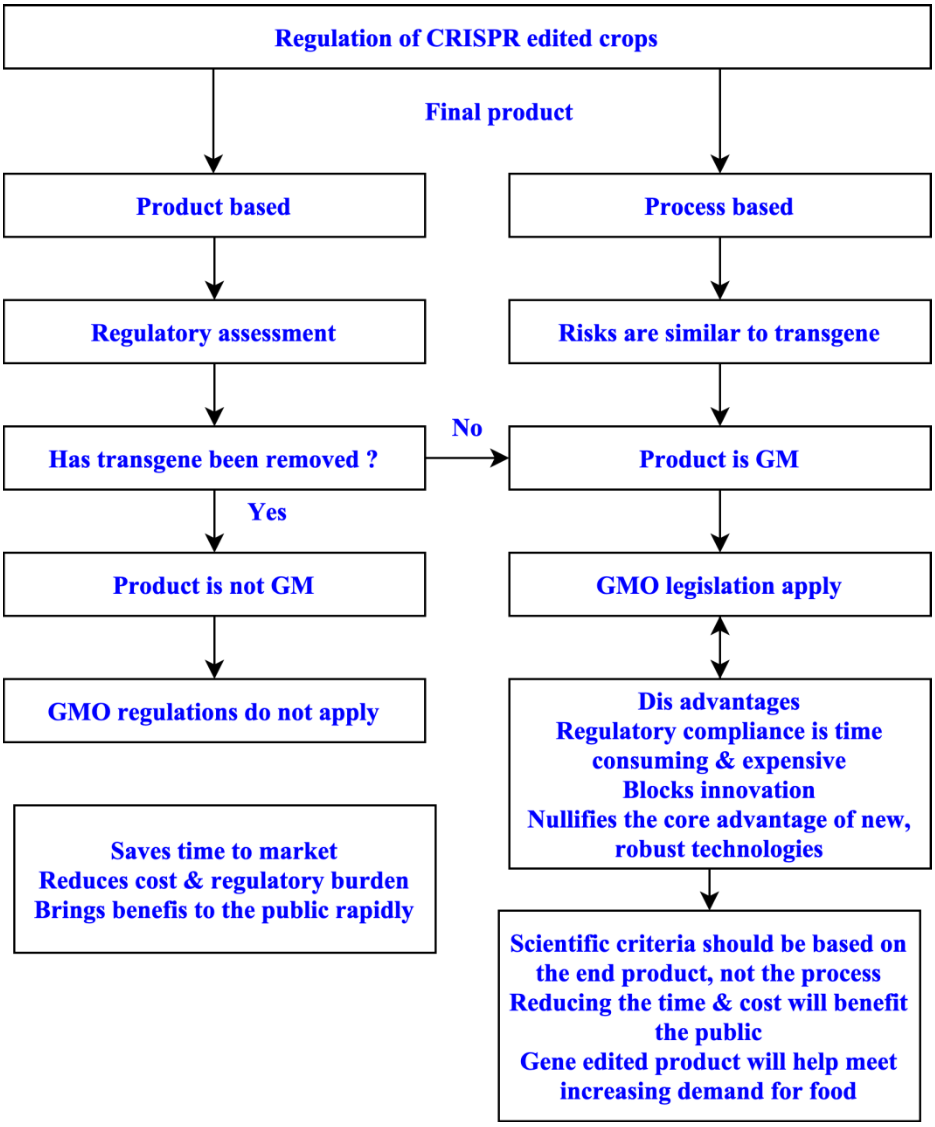

Figure 2. Comparison of regulatory models for genome-edited crops (EU, USA, Asia), emphasizing product- vs. process-based frameworks

Conclusions: Genome editing tools expansion and implementation specifically CRISPR-based technologies are redefining modern plant breeding with a precision that was unimaginable and efficiency at a fast pace. Out of those, CRISPR/Cas9 turned out to be the strongest tool for enhancing the nutritional quality of the crops, stress tolerance, productivity, and resource-use efficiency. Its coupling with synthetic biology, bioinformatics, and more progressive delivery systems introduces areas that promise to be the fastest routes to the realization of sustainable agricultural innovation. In spite of the progress, there is still a long way to go. Off-target effects, unclear regulatory issues, public acceptance, and ethics stay the hot topics that impress the introduction of genome-edited crops onto the market. Cas9 and Cas12a are the most broadly adopted nucleases in CRISP-based plant genome editing, but their properties and sustainability vary meaningfully depending on crop type and target locus. The blunt-end double-strand breaks were generated by Cas9 recognizes the NGG PAM, making it highly effective for gene knockouts in GC-rich regions. In contrast, Cas12a recognizes a T-rich PAM (TTTA), cuts with staggered ends, and needs only a single crRNA, which simplifies multiplex editing in AT-rich genomes. The Cas12a has shown higher specificity and high multiplexing potential in maize and barley, in the other side the Cas9 has shown higher efficiency in rice and tomato. Genome editing techniques are progressing, and a better perception of the biological impact of these tools, which will be enabled by extensive study and a clear regulatory framework, will be essential for their safe and reliable use. To conclude, the employment of CRISPR-based genome editing, specifically those like rice kernels, is on the power scale to address the nutritional problems of the world. The progress of this technology in agreement with ethical regulations and community requests will be crucial for renewable farming to evolve further.

Author contributions

Anshuman Jena expanded the abstract, outcomes, and important key results. Kuthalingam Venkadeshwaran expanded the main benefits of research work. Nittin Sharma expanded the main idea and Anshuman Jena participated to the expansion of the abstract, results section, and key results. Kuthalingam Venkadeshwaran was responsible for outlining the research significance and emphasizing the core benefits of the investigation. Nittin Sharma conceptualized the main idea and organized the overall structure of the manuscript. Prateek Garg managed the literature review on CRISPR utilizations and nutrient enhancement in crops. Mohamed Jaffar designed the investigation framework and gathered technical data. Dr. Linbathamizh prepared the figures and assisted in drafting the initial version of the manuscript. All authors reviewed and approved the final version of the manuscript.

Data availability statement

No new data were generated or analyzed through this investigation. All information presented is derived from previously published sources, which are appropriately cited.

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Ethical considerations

This investigation is based solely on a review of existing literature and does not involve any experiments on humans, animals, or genetically modified organisms managed by the authors. As such, ethical approval and informed consent were not needed. All references, data, and investigations have been properly cited by academic and publishing ethics.

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Conflicts of Interest

The authors declare no conflicts of interest.

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چکیده

هدف: این پژوهش با هدف بررسی انتقادی و خلاصه‌سازی پیشرفت‌های اخیر در فناوری‌های ویرایش ژنومی مبتنی بر CRISPR که برای ارتقای کیفیت تغذیه‌ای محصولات غذایی اصلی به کار گرفته شده‌اند، انجام شد. تمرکز اصلی بر شناسایی ژن‌های هدف خاص، ارزیابی پیامدهای تغییرات ژنتیکی، و برجسته‌سازی فرصت‌های آینده برای کشاورزی پایدار و امنیت غذایی جهانی بود.

مواد و روش‌ها: ما مقالات پژوهشی داوری‌شده، مطالعات موردی، و گزارش‌های نهادی را تحلیل کردیم. این مرور بر CRISPR/Cas9و گونه‌های پیشرفته آن مانند Cas12a، base editors و prime editors متمرکز است که برای اصلاح ژن‌های مرتبط با زیست‌سنتز، انتقال و تجمع مواد مغذی در گیاهان به کار رفته‌اند. ژن‌های کلیدی هدف شامل psy1 و crtI برای تولید پیش‌ویتامینA ، O2 و پروتئین‌های غنی از لیزین برای افزایش اسیدهای آمینه ضروری، و ژن‌های ناقل فلزی مانند OsNAS2و اعضای خانواده ZIP برای بهبود قابلیت زیست‌دسترس آهن و روی می‌باشند. همچنین روش‌های بررسی‌شده، پلتفرم‌های طراحی RNA راهنما و شیوه‌های انتقال شامل تراریختی واسطه آگروباکتریوم، بمباران ذره‌ای و سیستم‌های مبتنی بر پروتوپلاست را در بر می‌گیرند.

نتایج: بهبودهای چشمگیری در پروفایل تغذیه‌ای محصولات مشاهده شد. به عنوان نمونه، ارقام برنج ویرایش‌شده با CRISPR دارای محتوای بالاتر آهن و روی بودند، ذرت سطح بالاتری از لیزین نشان داد، و گوجه‌فرنگی غلظت بیشتری از ویتامین‌های A و Cداشت. رویکردهای ویرایش باز امکان جایگزینی دقیق نوکلئوتیدها را بدون وارد کردن DNA خارجی فراهم کردند که این امر موانع مقرراتی را کاهش داده و پذیرش عمومی را افزایش داد. علاوه بر این، چشم‌انداز مقرراتی در کشورهایی مانند ایالات متحده و ژاپن تغییر یافته و آزمایش میدانی و تجاری‌سازی محصولات ژن‌ویرایش‌شده را تحت دستورالعمل‌های تسهیل‌شده GMO مجاز کرده است که این موضوع پژوهش و توسعه را تسریع می‌کند.

نتیجه‌گیری: ویرایش ژنومی مبتنی بر CRISPR ابزاری تحول‌آفرین در توسعه محصولات غذایی غنی از مواد مغذی محسوب می‌شود. هنگامی که با زیست‌شناسی مصنوعی و بیوانفورماتیک محاسباتی ادغام شود، رویکردی سریع و هدفمند برای اصلاح محصولات ارائه می‌دهد که در زمینه تغییرات اقلیمی و رشد جمعیت حیاتی است. با این حال، برای دستیابی این فناوری به تأثیر جهانی، باید چالش‌های گوناگونی برطرف شوند. این چالش‌ها شامل ایجاد مقررات هماهنگ ایمنی زیستی، مدیریت دغدغه‌های اخلاقی، و افزایش آگاهی و اعتماد عمومی است. چارچوب‌های بین‌المللی مشارکتی و سیاست‌گذاری فراگیر برای تضمین آن‌که نوآوری‌های مبتنی بر CRISPR به‌طور مؤثر در امنیت غذایی و تغذیه‌ای جهانی نقش‌آفرینی کنند، ضروری خواهند بود.

کلمات کلیدی: اصلاح ژنی، زیست‌فناوری کشاورزی، کشاورزی پایدار، ویرایش ژنوم، CRISPR/Cas9

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