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Harnessing genome editing for post-harvest improvement of crops: a comprehensive bibliometric and literature review

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ABSTRACT

Post-harvest losses represent a critical challenge to global food security, necessitating innovative solutions to enhance crop longevity, quality, and resilience. This review provides a comprehensive analysis of the emerging applications of genome editing technologies, particularly CRISPR/Cas9, for post-harvest trait improvement in agricultural crops. Utilizing a dual-method approach of bibliometric analysis and systematic literature review, we mapped the trajectory and intellectual landscape of this field from 2012 to 2025. Initially, 1,172 Scopus publications were initially identified. After refining to the Agricultural and Biological Sciences subject area and retaining only documents at the "Final" publication stage, 845 documents were analyzed using Biblioshiny, revealing a striking annual growth rate of 22.17%, with China and India lead in research output, while European nations and the USA demonstrate significant per-article influence. Keyword co-occurrence and thematic analysis identified three central research clusters: (1) genetic regulation of ripening and physiology, (2) applications of editing tools in breeding, and (3) enhancement of nutritional quality and biofortification. The review synthesizes compelling evidence that precision editing of key genes, such as *RIN* in tomato for delayed ripening, *MeF6'H* in cassava to reduce physiological deterioration, *Vinv* in potato for improved sugar profiles, and *CsLOB1* in citrus for disease resistance, effectively mitigates the primary causes of post-harvest loss. We discuss how editing strategies are being deployed to extend shelf life, fortify nutritional content, enhance abiotic stress tolerance, and engineer resistance to fungal and bacterial pathogens, thereby reducing reliance on chemical interventions. We conclude that genome editing is a transformative force in post-harvest science, offering a precise and efficient alternative to conventional breeding. Future prospects lie in multiplex editing of complex traits, integration with AI and omics technologies, and navigating evolving regulatory landscapes. This technology holds immense promise for developing next-generation crops designed for durability and quality, ultimately contributing to more sustainable and resilient global food systems.

1. Introduction

Genome editing has emerged as a revolutionary technology in agricultural science, offering transformative potential for post-harvest management. Techniques such as CRISPR/Cas9 enable the precise modification of crop genomes to enhance traits critical for the post-harvest period, including disease resistance, delayed ripening, nutritional quality, and extended shelf-life (Chen et al., 2024; Hu et al., 2021; Ortega-Salazar et al., 2024). As global food security demands intensify, the deployment of genome editing to reduce post-harvest losses and improve food quality represents a crucial strategy for achieving sustainable agriculture (Idris et al., 2023; Kumari et al., 2022).

While the applications of genome editing in agriculture has been

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extensively studied (Ahmadikhah et al., 2025; Miladinovic et al., 2021), the specific field of post-harvest biology remains a nascent yet rapidly developing one (Shipman et al., 2021). Numerous reviews have addressed the technical mechanisms of gene editing, but systematic and macro-level reviews of the entire research landscape in the post-harvest context are lacking (Kolkur et al., 2024). Furthermore, although bibliometric studies exist in the broader agricultural field, they tend to be too general, failing to capture the novel and unique applications of genome editing intended to extend product shelf life and maintain post-harvest quality (Kusuma, 2023; Santos et al., 2025).

Therefore, this study offers a bibliometric analysis focused exclusively on the relationship between post-harvest and genome editing. First, we systematically map the intellectual landscape by analyzing publication trends, authors, institutions, and countries. Second, we identify biological insights at the gene level reported in the literature. This review aims to clarify which particular genes (such as those involved in ethylene biosynthesis, cell wall degradation, or oxidative stress pathways) are being targeted and how these targets are influencing the direction of post-harvest biotechnology by performing comprehensive analyses of keyword co-occurrence and clustering of research centers.

Ultimately, this study integrates the quantitative data with qualitative biological evidence while identifying important contributions and cooperative networks. This integrated approach elucidates the strategic connection between genome editing tools and the biological determinants of post-harvest crop quality, offering a unique roadmap that highlights current knowledge gaps and directs future innovation.

2. Methods

This study employed a systematic, three-stage bibliometric analysis to map the research landscape of genome editing applications in post-harvest management. The procedural framework, outlined in Fig. 1, consisted of: (1) data collection and extraction from the Scopus database; (2) quantitative bibliometric analysis using specialized software; and (3) data synthesis and visualization. The methodological approach was adapted from the frameworks established by Anshori et al. (Anshori et al., 2023) and Ardie et al. (Ardie et al., 2025).

2.1. Data collection and extraction

Literature data were retrieved from the Scopus database on February 10, 2025. Scopus was selected for its comprehensive coverage of high-quality, peer-reviewed literature across numerous scientific disciplines (Aghaei Chadegani et al., 2013).

A targeted search strategy was designed using keywords related to two core concepts: (1) Genome editing. Keywords included "genome edit*", "gene edit*", "CRISPR", "TALEN", "ZFN", and "base edit*"; (2) Post-harvest. Keywords included "postharvest", "post-harvest", "shelf-life", "shelf life", "storage", "ripening", and "food loss". These keywords were combined using Boolean operators within the [article title, abstract, and keywords] fields. The initial search query returned 1,172 documents. The search was not restricted by publication date or document type to ensure a comprehensive overview of the field. The exported data included complete bibliographic records (e.g., titles, authors, affiliations, citations, keywords) and abstracts for all retrieved documents.

From this initial set, a final corpus of 845 documents was derived by applying two filters: limiting to the "Agricultural and Biological Sciences" subject area and retaining only documents at the "Final" publication stage. These refinements ensured that the analysis focused on mature, relevant research within the scope of this study. The 845 documents were then exported to Biblioshiny for bibliometric analysis of country productivity and citation impact.

2.2. Bibliometric analysis

The final corpus of 845 publications was analyzed using a dual-software approach to ensure a robust and multi-faceted examination.

VOSviewer (version 1.6.20; Leiden University, The Netherlands) was used for constructing and visualizing bibliometric networks based on relational data units. Its strength in large-scale graphical representation allows for mapping the connections between research elements (van Eck & Waltman, 2010). We utilized VOSviewer specifically to generate networks for: (1) International Co-authorship to visualize collaboration clusters between countries; (2) Keyword Co-occurrence to identify and map the central research themes and their interrelationships; and (3) Citation Networks to analyze interactions between cited publishers and sources.

The Bibliometrix (version 0.3.0) package in RStudio (version 4.3.2, Posit Software, PBC) was employed for its comprehensive suite of bibliometric functions. This package is renowned for its ability to perform direct citation analysis, enhance reference matching with string-based algorithms, and employ a hybrid approach combining bibliometric and semantic techniques (Aria & Cuccurullo, 2017). The analysis was structured around three core dimensions: (1) general performance analysis (publication growth, key contributors), (2) analysis of the global conceptual structure (keyword co-occurrence, thematic evolution), and (3) in-depth, keyword-based topic development.

2.3. Counting methods

To analyze research productivity by country, this study employed the "Country Scientific Production" feature of Biblioshiny (bibliometrix R package). This feature utilizes a whole counting approach, where each author's institutional affiliation appearing on a publication is counted separately. Therefore, if one article has three authors from one country, the country is counted three times in this analysis. Consequently, the values reported for country productivity in this study represent the total frequency of author appearances, not the number of unique documents. This metric was chosen because it effectively captures the intensity of a

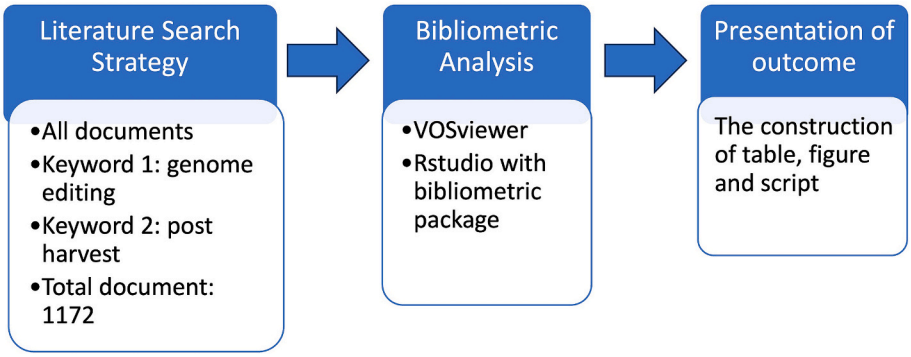

Fig. 1. Flowchart of the bibliometric analysis process for reviewing literature on genome editing for post-harvest applications.

country's research participation and its collaborative networks.

In contrast, citation impact was analyzed using the "Most Cited Countries" feature, which provides Total Citations (TC) and Average Article Citations based on unique articles. These two distinct units of analysis—author appearances for productivity and unique articles for impact—offer complementary perspectives on each country's contribution to the field. The average article citation is calculated by dividing the total citations by the number of unique articles involving authors from that country, ensuring consistency between the reported metrics. All analyses were conducted on the final refined dataset of 845 documents.

2.4. Data synthesis

The quantitative findings from the bibliometric analysis were synthesized to identify major research trends, collaborative networks, and emerging frontiers. This synthesis forms the basis for the results and discussion, providing a data-driven overview of the field's development and highlighting gaps for future research directions.

2.5. Sensitivity analysis

To test the robustness of the results and detect possible in the database, a sensitivity analysis was performed by comparing a random sample of publications from the Scopus database with those in the PubMed database. From the initial pool of publications in the Scopus database (n = [845]), 200 publications were randomly sampled using the random sampling option in Excel. Each publication was manually searched in the PubMed database using the DOI or the title. The presence of each publication in the database was verified. The overlap rate was calculated as the percentage of publications in the Scopus database that

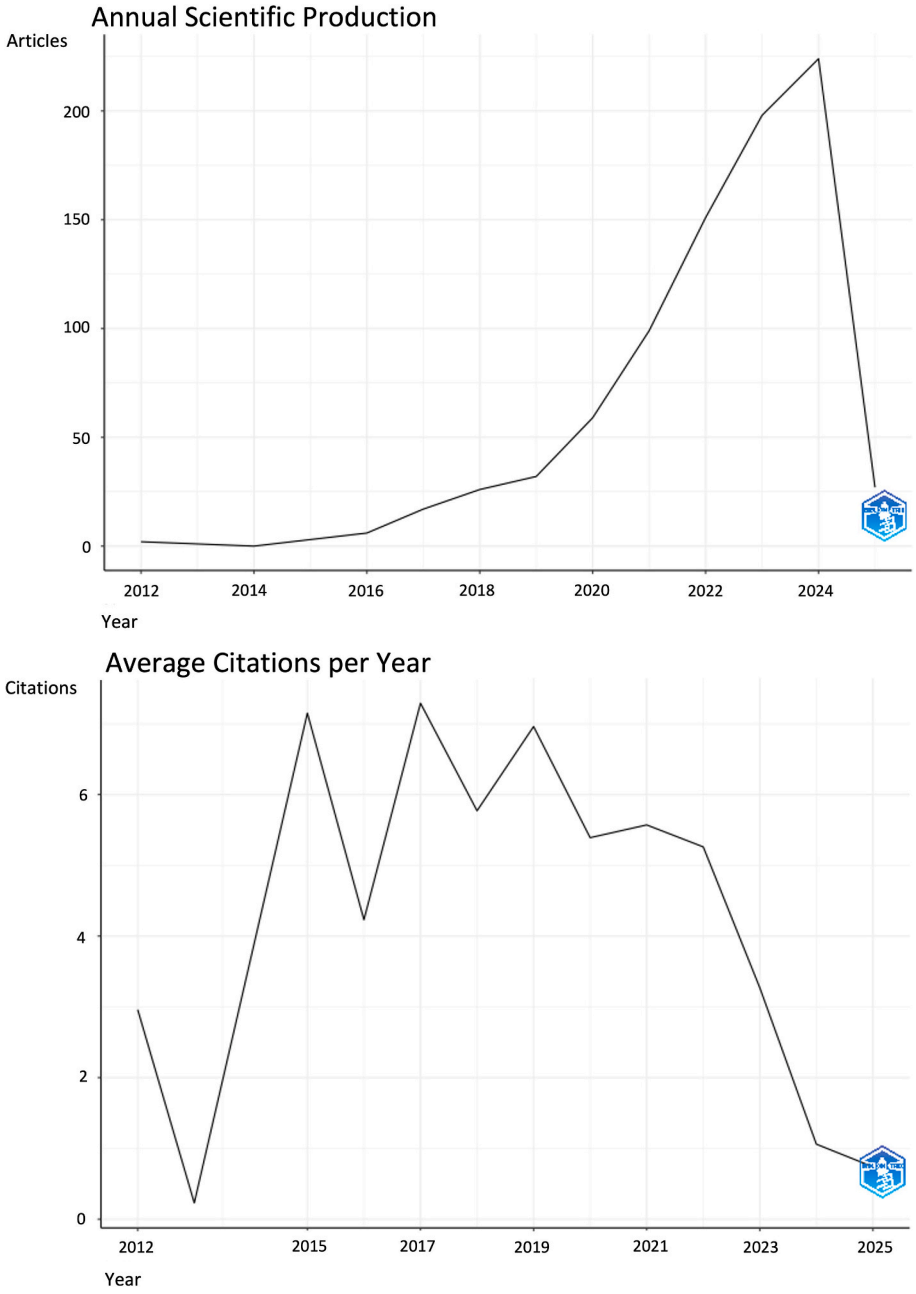

Fig. 2. Temporal trends in genome editing for post-harvest research. **(a)** The annual number of published documents from 2012 to early 2025. The 2025 data is incomplete due to the retrieval date (February 2025). **(b)** The trend in average citations per year for publications, highlighting the high impact of foundational early studies.

were detected in the PubMed database.

3. Results

3.1. Publication trends and impact

The bibliometric analysis of the Scopus dataset revealed a rapidly expanding and influential field of research. The initial Scopus search identified 1,172 documents on genome editing for post-harvest research. After refining the results to the Agricultural and Biological Sciences subject area and limiting them to the final publication stage, 845 documents were retained for bibliometric analysis. The field demonstrates vigorous growth, with an annual growth rate of 22.17%, and is characterized by strong collaboration, evidenced by an average of 6.29 co-authors per document and an international collaboration rate of 36.09%. The substantial average of 17.44 citations per document further underscores the significant impact of research in this domain.

The annual publication output, depicted in Fig. 2a, delineates the field's evolution. Publications first emerged in 2012, followed by a period of modest growth. A noticeable acceleration began in 2020 (59 articles), culminating in a peak of 224 articles in 2024. The apparent sharp decline for 2025 is an artifact of the data collection date (February 2025) and does not represent an actual yearly total.

Analysis of the temporal citation trend, presented in Fig. 2b, provides insight into the field's intellectual development. Early publications from 2012 to 2017, though few in number, received exceptionally high average citations per year. This pattern suggests these works were foundational and highly influential in establishing the research area. Conversely, the period of rapid publication growth from 2018 to 2024 coincides with a steady decline in the average number of citations per article per year. This trend is typical of maturing scientific fields and may indicate a diversification of research topics, an increase in incremental studies, or a natural lag between publication and citation accumulation for the most recent works.

3.2. Geographic and institutional research landscape

The analysis reveals a distinct global distribution of research output and influence in the applications of genome editing for post-harvest improvements. As presented in Table 1, which measures productivity using two complementary metrics, China and India are the unequivocal leaders in research participation. China recorded 1,487 total author appearances and 187 unique publications, while India contributed 957 author appearances and 126 unique publications—figures that vastly exceed those of the third-ranked United States (451 author appearances; 64 unique publications). However, an examination of citation metrics reveals a more nuanced picture of global impact. While China and India also lead in total citations (3,049 and 1,724, respectively), the average citations per article provides a clearer measure of influence per study. Here, European nations and the US demonstrate significant impact. The United Kingdom (31.3), Spain (28.7), the United States (26.4), and Italy (25.5) all boast a higher average citation rate than China (16.3) and India (13.6). This suggests that while Asian nations drive the volume of research, studies from several Western countries have, on average, a greater per-publication influence on the field.

This dominance in research volume is further reflected at the institutional level. As shown in Table 2, Chinese institutions comprise six of the top ten most prolific organizations, led by China Agricultural University (74 publications). The presence of US and Indian institutions (University of California, ICAR-Indian Agricultural Research) confirms the active role of these nations. The list is predominantly composed of agricultural universities, underscoring the applied nature of this research field and its direct relevance to the agricultural sector.

An examination of the global co-authorship network is shown in Fig. 3, which offers crucial information about the composition and geographic distribution of cooperative genome editing research for post-harvest enhancement. Visualization parameters, including node size, line thickness, and node color, reveal distinct patterns that support our core conclusions about the evolution of this field. The node size which represents publication volume, clearly identifies China, India, and USA as the dominant contributors in this research domain, with significantly larger nodes compared to European countries (Germany, the United Kingdom, Italy) and other Asian countries (Japan, India, South Korea). This quantitative dominance reflects these countries' substantial investment in agricultural biotechnology and genome editing over the past decade. Line thickness represents the strength of collaboration, with thicker lines indicating more frequent co-authorship between countries. Based on these collaborative linkages, the network identifies three major clusters: Cluster 1 (Red), centered in China, with strong links to the UK, Italy, Germany, France, and other European nations; Cluster 2 (Blue), centered in India, connecting with Australia, Spain, Japan, Indonesia, and other Asian countries; and Cluster 3 (Green), centered in the USA, with strong ties to Brazil, Nigeria, and Kenya.

This analysis gains a temporal dimension in Fig. 3B, where the average publication year of documents from each nation is represented by the color of the node, which is mapped on a gradient from purple (earlier publications, ~2020) to yellow (more recent publications, ~2024). A notable geographic shift in the momentum of research is revealed by this color gradient. The cooler shades (purple/blue) of the United States, United Kingdom, Italy, and Australia show that their contributions to the literature were greatest in the early years of the study period (2021–2022). China and India, on the other hand, are represented by warmer shades (yellow/orange), indicating that their

Table 1
Top 10 most productive countries in genome editing for post-harvest research based on Scopus database search for 2012-2025 period.

Country	Total Author Appearance	Total Citations	Average Article Citation	Total Publications
China	1,487	3,049	16.3	187
India	957	1,724	13.6	126
USA	451	1,715	26.4	64
Brazil	186	449	22.4	20
Pakistan	166	205	14.6	14
Italy	146	561	25.5	22
Spain	105	689	28.7	24
South Korea	91	249	13.1	19
Nigeria	90	174	21.8	7
UK	82	313	31.3	10

Notes: Total Author Appearance refers to the frequency of author affiliations from each country, calculated using the whole counting method in Biblioshiny's "Country Scientific Production" feature. If one article has multiple authors from the same country, that country is counted multiple times. Total Publications represents the estimated number of unique articles involving authors from each country, derived by dividing Total Citations by Average Article Citation. Total Citations is the total number of citations received by all articles involving authors from each country. Average Article Citation is calculated as Total Citations divided by Total Publications, indicating the mean impact per article.

Table 2
Top 10 most productive institutions in genome editing for post-harvest research.

Institution	Country	Total Publications
China Agricultural University	China	74
University of California	USA	64
Sichuan Agricultural University	China	61
Zhejiang University	China	54
Huazhong Agricultural University	China	49
Nanjing Agricultural University	China	46
Cornell University	USA	37
Mae Fah Luang University	Thailand	37
ICAR-Indian Agricultural Research	India	36
Shenyang Agricultural University	China	33

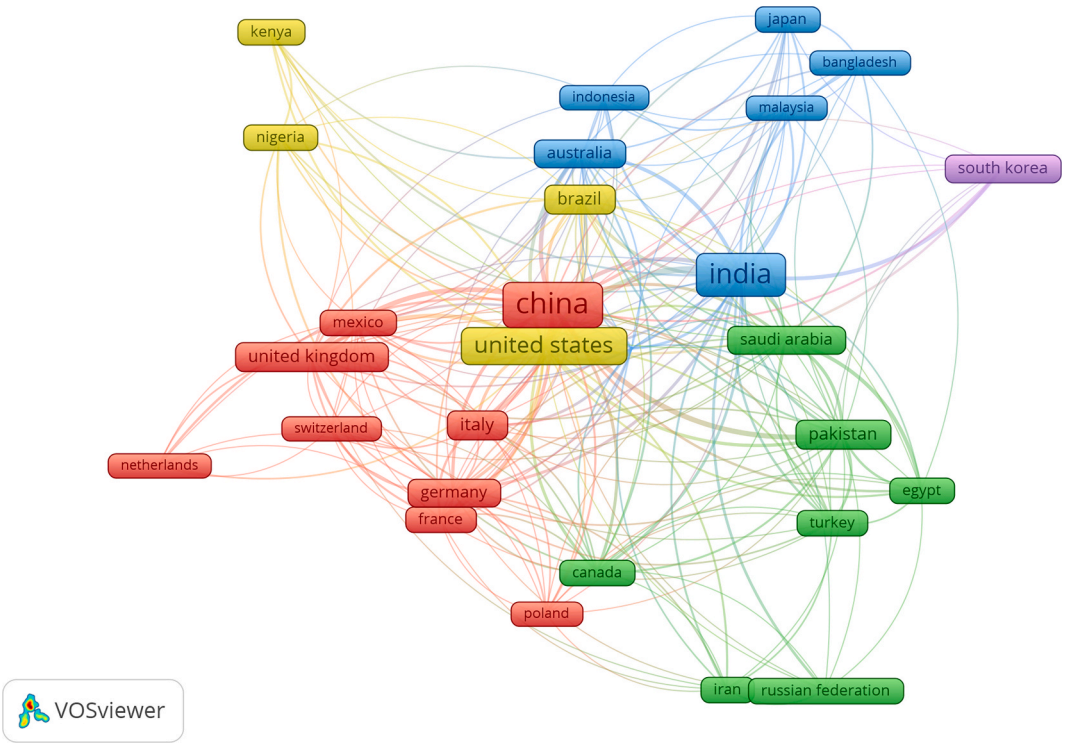

Fig. 3. International collaboration patterns in genome editing for post-harvest research. (A) Co-authorship network map showing collaborative relationships between countries. Node size is proportional to the number of publications originating from each country, with larger nodes (e.g., China, India, and US) indicating higher research output. Line thickness represents the strength of collaboration, with thicker lines indicating more frequent co-authorship between countries. (B) Temporal evolution of research activity, where node color indicates the average publication year of documents from each country, mapped on a gradient from purple (earlier publications, ~2010) to yellow (more recent publications, ~2025). The shift from purple/blue nodes in Western countries (USA, UK, Italy, Canada) toward yellow/orange nodes in Asian countries (China, India) visually demonstrates the geographic transition of research leadership in this field over the past decade. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

research output has increased more recently (2023–2024) and is currently at the top of the field.

3.3. Thematic evolution and keyword analysis

Keyword co-occurrence analysis reveals the intellectual structure and core research themes within the field. Applying a minimum threshold of 15 occurrences refined the dataset to 74 keywords, which were further streamlined to 51 highly interacting terms. These terms form three distinct, yet interconnected, clusters that define the current research landscape (Fig. 4). Cluster 1 (Green): Plant Physiology and Genetic Regulation. This cluster is centered on the fundamental biological processes governing post-harvest traits. Core keywords include physiology, gene expression, metabolism, fruit, and ethylene. Its strong connection to "CRISPR/Cas9″ and "gene editing" demonstrates that modern genome editing is primarily targeted at manipulating these very physiological pathways. For instance, editing genes involved in ethylene biosynthesis or signal transduction can directly delay ripening and extend shelf-life (Fu et al., 2021). For example, targeted mutagenesis of key ethylene biosynthesis genes such as 1-aminocyclopropane-1-carboxylic acid (*ACC*) synthetase 1 (*ACS1*) and ACC oxidase 1 (*ACO1*)], or ethylene receptors like *ETR1*, has been successfully employed in various crops to produce non-ripening or slow-ripening phenotypes (Adedeji et al., 2024; Holme et al., 2024; Xu et al., 2020). Furthermore, genes controlling cell wall remodeling, such as polygalacturonase (PG), are also prominent targets within this cluster to maintain fruit firmness during storage (Nie et al., 2022). The dominance of these physiological keywords confirms that the primary strategic goal is the systematic dismantling of the genetic programs that lead to spoilage. Therefore, this cluster represents the fundamental biological layer that underpins genome editing technology as the control knob of post-harvest biology. Subsequent clusters highlight more practical issues such as disease resistance and quality preservation, which require an understanding of these fundamental regulatory systems.

Cluster 2 (Red): Genome Editing Tools and Breeding Applications. This cluster encapsulates the technological and methodological core of the field, with central keywords including "genome editing", "plant breeding", "transgenic plants", "genomics", and "biotechnology". It represents the applications of tools like CRISPR/Cas9 to introduce precise genetic improvements. The critical link between this cluster and the "postharvest" keyword (Fig. 5) underscores a paradigm shift in breeding objectives. Modern breeding programs are no longer solely focused on yield and agronomic traits but are explicitly integrating post-harvest quality, durability, and marketability as primary targets for genetic improvement.

Cluster 3 (Blue): Post-Harvest Quality and Nutritional Enhancement. This cluster is focused on the end-goal traits: enhancing the quality and nutritional value of harvested produce. Key keywords are "postharvest", "antioxidants", "carotenoids", and "biofortification". This cluster is directly influenced by the tools in Cluster 2, which are used to achieve its goals. For example, genome editing is being deployed to boost the synthesis of health-promoting compounds like antioxidants and carotenoids, moving beyond shelf-life to create functionally enhanced foods (Chen et al., 2020; Krishna et al., 2022).

Fig. 5 depicts plant breeding as a fundamental framework or engine that combines numerous scientific disciplines and technologies to attain the desired outcome. Plant breeding serves as the central integrative engine that connects advanced genomics, transcriptomics, and genetic engineering to address global challenges such as climate change, drought, and biotic stress (Khan et al., 2016; Razzaq et al., 2021; Tyagi

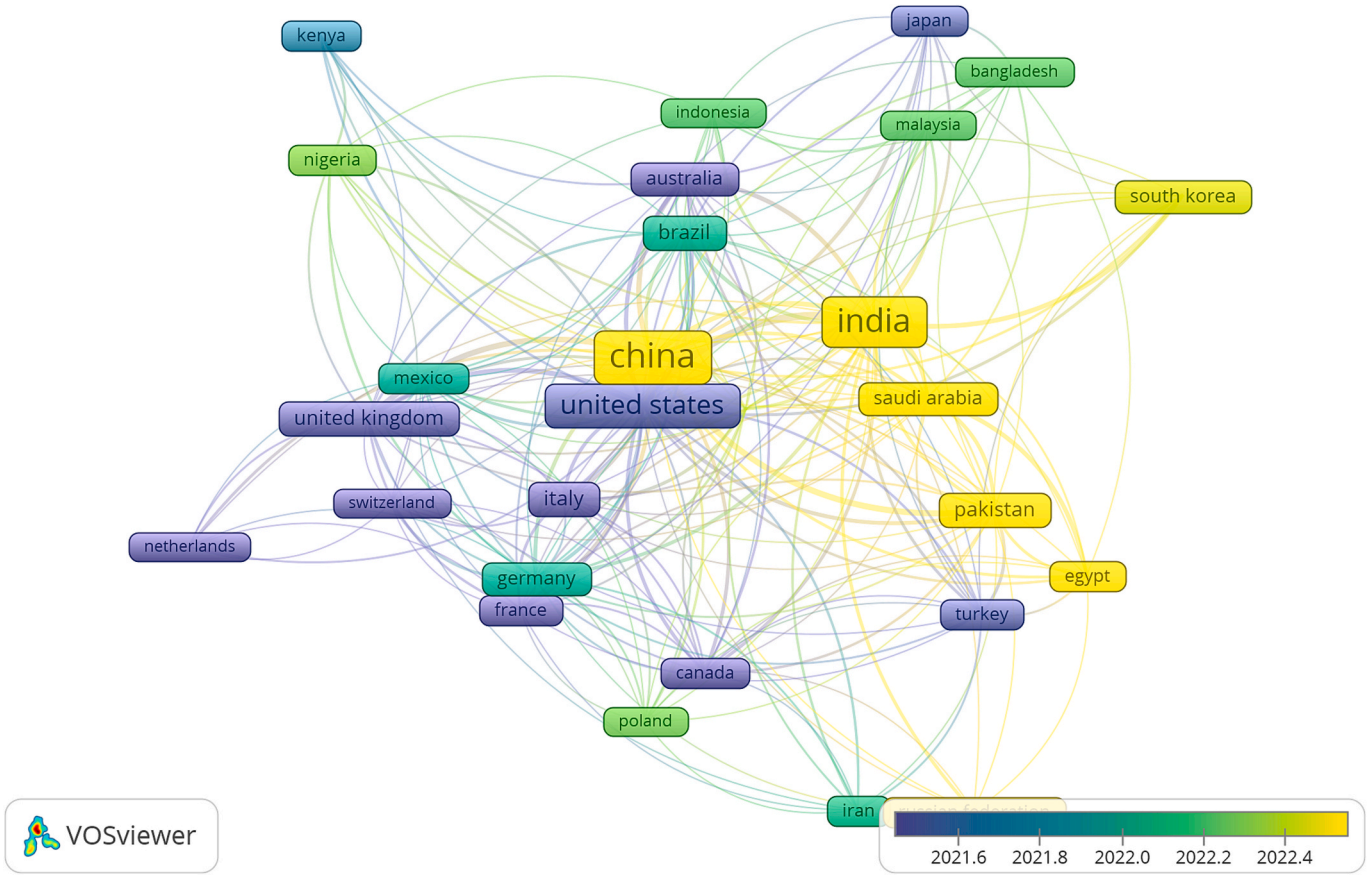

Fig. 3. (*continued*).

et al., 2024).

The network topology reveals several logical connections that illuminate how these domains intersect. The red cluster (Genome Editing Tools & Breeding Applications) contains keywords such as "CRISPR/Cas9″, "genome editing", "gene editing", and "genetic engineering", which are directly connected to the green cluster's physiological terms including "gene expression", "physiology", "metabolism", and "transcription factors." This proximity reflects the mechanistic reality that genome editing tools are employed to modify specific genes that regulate physiological pathways, for example: editing ethylene biosynthesis genes to control ripening, or targeting transcription factors that coordinate stress responses.

Critically, both the red and green clusters show strong co-occurrence linkages to the blue cluster (Post-Harvest Quality and Nutrition Enhancement), which contains applied keywords such as "nutrition", "biofortification" and "food safety". This three-part network structure provides quantitative evidence for the translational pathway underlying the field: a fundamental understanding of physiological processes (green cluster) enables precise genetic interventions (red cluster), which ultimately lead to tangible improvements in post-harvest performance (blue cluster).

The ultimate goal of this convergence is to achieve food security through crop improvements for staples such as potatoes, fruits, and cassava. By leveraging genetics and genome editing (e.g., Cas9), breeders now develop varieties with enhanced shelf life, slower ripening, and resistance to post-harvest diseases (Chen et al., 2024; Kumari et al., 2022; Mishra et al., 2021). This direct intervention at the genetic level, manipulating gene expression and phytohormone pathways, ensures that the improved nutrition and antioxidant content bred into crops are retained longer after harvest. Therefore, the interaction between plant breeding and post-harvest is a proactive strategy to reduce food loss, enhance food safety by reducing decay, and deliver the full benefits of high-quality produce to consumers, making breeding a critical tool for building a more resilient and efficient food system.

3.4. Conceptual structure and future directions

The conceptual structure of the field, analyzed via Multiple Correspondence Analysis (MCA), consolidates these themes into a unified framework (Fig. 6). The central and most diverse keywords, "CRISPR/Cas", "metabolomics", "carotenoids", "biotic stress", and "marker-assisted selection" represent the convergence of key concepts. These word's similarity is not accidental; rather, it illustrates the functional connection required for recent crop improvement. In particular: (1) The similarity between "CRISPR/Cas" and "metabolomics" reflects the increasing understanding that genome editing needs to be used in connection with suitable phenotyping tools to validate the functional impacts of genetic modification. For example, metabolomic profiling can be used to verify that edited strains truly accumulate desired nutritional compounds; (2) The connection between "CRISPR/Cas" and "carotenoids" represents the successful applications of genome editing to enhance nutritional quality, as demonstrated in recent studies where genes in the carotenoid biosynthesis pathway were targeted to increase provitamin A content in staple crops; (3) The linkage of "biotic stress" to both "CRISPR/Cas" and "marker-assisted selection" illustrates two complementary approaches to enhancing post-harvest disease resistance: direct editing of susceptibility genes (e.g., *NPR1* in raspberry) and accelerated introgression of resistance loci through marker-assisted breeding. The spatial distribution of these fundamental ideas supports our central claim, which is that genome editing works best when combined with advanced technology rather than alone. The integration of genome editing, precision analytics, quality traits, and stress resilience

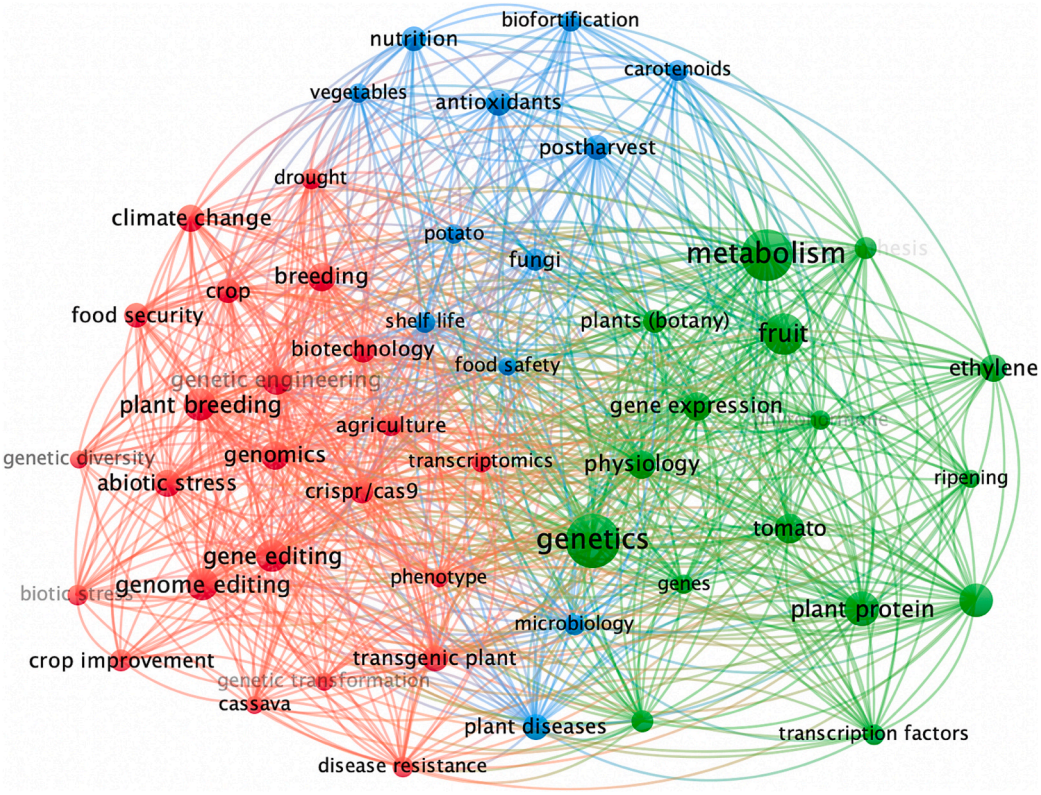

Fig. 4. Network visualization of keyword co-occurrence analysis, mapping the structure of genome editing research in post-harvest. Node size represents keyword frequency; larger nodes indicate terms that appear more frequently across the literature. Node colors indicate distinct research clusters identified through clustering analysis: Green (Cluster 1) represents Plant Physiology & Genetics; Red (Cluster 2) represents Genome Editing & Breeding; and Blue (Cluster 3) represents Post-Harvest Quality & Biofortification. Line (edges) between nodes indicate co-occurrence relationships, with thicker lines representing stronger co-occurrence frequencies (i.e., terms that appear together more frequently in the same publication).

in the conceptual core underscores the fact that the field has now moved beyond "proof of concept" to a holistic, systems-based approach to crop improvement.

4. Sensitivity analysis results

To test the robustness of the results against database selection bias, we compared 200 randomly sampled Scopus-indexed publications with the PubMed database. Out of the 200 publications, 70 (35%) were included in the PubMed database, while 130 (65%) were not. This moderate rate of overlap is because the Scopus database covers agricultural and plant science literature extensively, while PubMed primarily focuses on biomedical and life sciences (Ossom Williamson & Minter, 2019). Analysis of the non-overlapping articles (those present only in Scopus) revealed that 65% were published in specialized agricultural and plant science journals not within PubMed's core biomedical scope. This confirms that Scopus captures a broader range of applied agricultural research relevant to our study, including crop-specific genome editing applications that may fall outside PubMed's focus.

Nevertheless, the use of a single database presents limitations. These limitations suggest that our findings may not fully represent the entire body of research in this field. Future studies could enhance comprehensiveness by employing a multi-database approaches, including Web of Science, PubMed, and regional databases, as well as incorporating non-English publications and grey literature. Such an approach would provide a more inclusive and globally representative view of genome editing research for post-harvest applications.

5. Discussion

5.1. Genome Editing: A transformative tool for Mitigating global Post-Harvest challenges

Post-harvest losses represent a critical challenge to global food security, disproportionately affecting regions with inadequate storage and transportation infrastructure (Chauhan et al., 2021; Perdana et al., 2023). The primary goals of post-harvest research are to extend shelf-life, preserve nutritional and sensory quality, and reduce spoilage caused by pathogens and physiological deterioration (Baltazari et al., 2020; Schmidt et al., 2018). Achieving these goals is paramount not only for reducing waste but also for enhancing food safety, increasing farmer incomes, and promoting sustainable supply chains.

A central focus of this effort is managing the ripening and senescence of perishable produce, such as tomatoes, bananas, and leafy greens. While traditional methods like chemical treatments and conventional breeding have had partial success, they are often slow, imprecise, or face consumer skepticism. The rapid growth in scientific literature on genome editing for post-harvest applications, as evidenced by our bibliometric analysis (Fig. 2a), signals the emergence of a powerful new paradigm. Genome editing technologies, particularly CRISPR/Cas9, offer a precise and efficient alternative to conventional methods (Hillary & Ceasar, 2024). Unlike traditional breeding, CRISPR/Cas9 allows for targeted modifications of specific genes responsible for key post-harvest traits, such as ethylene synthesis, cell wall degradation, pathogen susceptibility, and nutrient biosynthesis (Bull et al., 2018; Mukami et al., 2024; Sharma et al., 2023).

This precision enables the development of crop varieties with inherently enhanced durability, extended freshness, and maintained nutritional quality throughout storage and transport. By addressing the

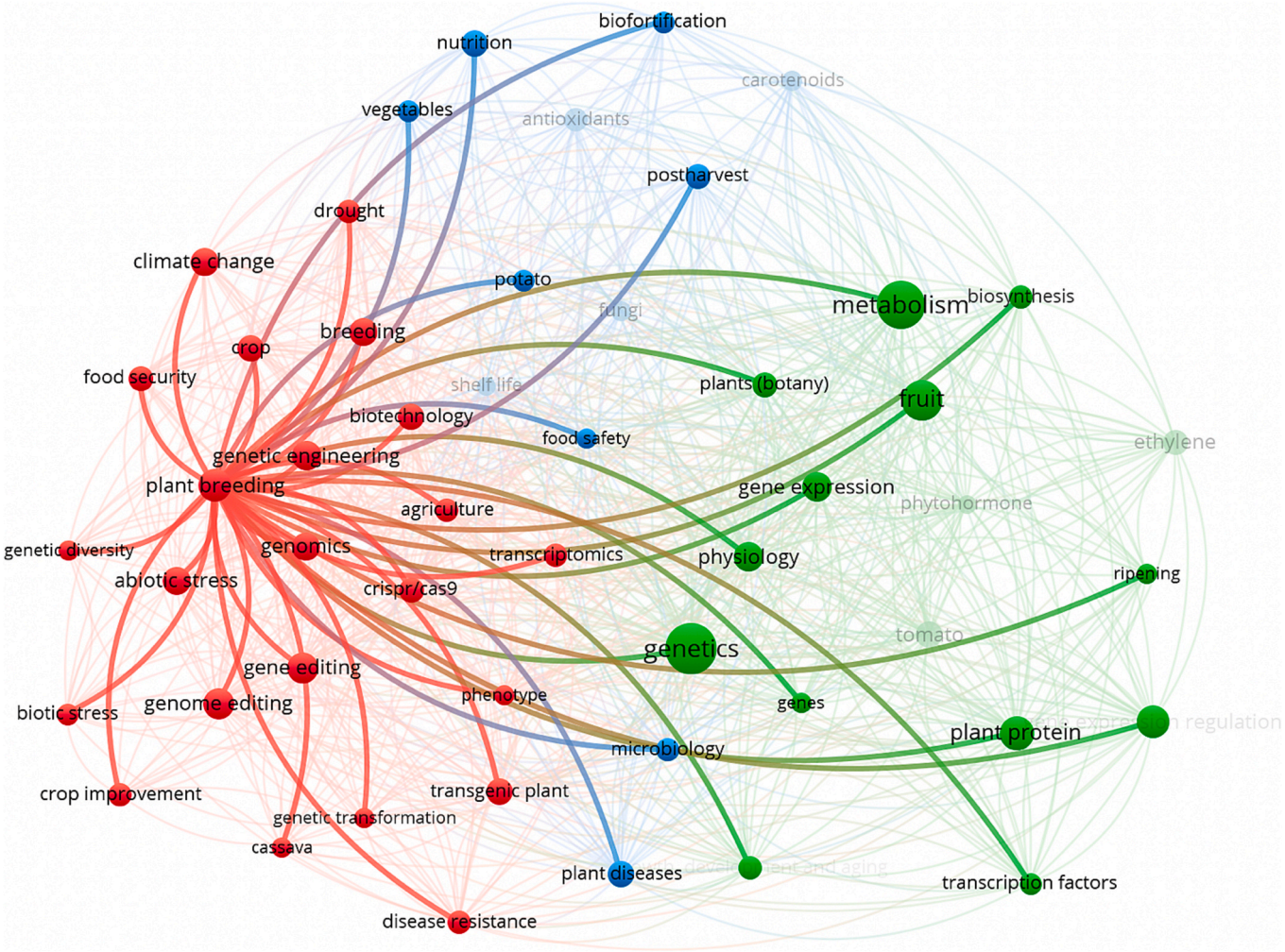

Fig. 5. Keyword co-occurrence network centered on "plant breeding," showing its role as an integrative hub connecting diverse disciplines to post-harvest outcomes. Derived from the full analysis in Fig. 4. Node size = keyword frequency. Node colors follow Fig. 4 clustering: Green (Plant Physiology and Genetic regulation), Red (Genome Editing Tools & Breeding Applications), Blue (Post-harvest Quality and Nutritional Enhancement). Lines indicate co-occurrence relationships. The network illustrates how plant breeding integrates genomics and genetic engineering (red) with physiological pathways (green) to achieve improved shelf-life, nutritional quality, and reduced post-harvest losses (blue), thereby enhancing food security.

genetic roots of spoilage, genome editing presents a promising pathway to significantly reduce post-harvest losses, diminish reliance on chemical interventions, and advance the goals of sustainable agriculture. Its escalating adoption, as mapped in this review, underscores its potential as a transformative tool in building a more resilient and efficient global food system.

5.2. *Enhancing nutritional and flavor quality through precision breeding*

The nutritional and sensory quality of horticultural crops, encompassing vitamins, minerals, antioxidants, and flavor compounds, is highly perishable and influenced by genetics, growing conditions, and post-harvest handling (Ahmed et al., 2024; Kumari et al., 2022). A primary post-harvest challenge is the rapid degradation of these desirable traits, leading to a loss of flavor, nutritional value, and the development of off-flavors during storage and transport. Genome editing provides a precise strategy to address this challenge at its genetic source, enabling the development of varieties that inherently maintain superior quality.

This approach is exemplified by successful applications in key crops, including (1) tomato where the *SlbZIP1* gene (Table 3), a central transcription factor regulating the synthesis of sugars and organic acids, has been targeted using CRISPR/Cas9. Editing this gene has successfully enhanced sweetness and overall flavor profiles, directly improving marketability by preserving sensory quality (Nguyen et al., 2023; Wang et al., 2021; Zhang et al., 2022). (2) rice where the nutritional quality and digestibility of rice are determined by its starch composition. Targeting the starch branching enzymes *SBEI* and *SBEIIb* allows for the modulation of amylose content. Edited lines with higher amylose offer not only potential health benefits (e.g., slower digestion) but also improved texture and flavor release upon cooking. (3) potato where cold storage often triggers the conversion of sucrose to glucose and fructose via the vacuolar invertase enzyme, encoded by the *Vinv* gene, leading to undesired sweetness and textural changes. Knockout of *Vinv* through genome editing suppresses this process, preserving the desired savory flavor and firm texture of potatoes for longer durations, thereby enhancing their culinary quality and consumer acceptability (Clasen et al., 2016; Ru et al., 2021; Wiberley-Bradford & Bethke, 2017; Yasmeen et al., 2022).

Beyond these major crops, genome editing has also been applied to improve the nutritional quality of minor but economically important cereals such as sorghum. In this climate resilient crop, the poor digestibility of grains, caused by the accumulation of protease-resistant γ-kafirin proteins encoded by the *K2G* gene, has been addressed through CRISPR/Cas9 editing. Mutant lines exhibited a 12.75%–19.22% reduction in γ-kafirin content and a remarkable 26.91%–74.31% increase in protein digestibility in raw flour, while maintaining grain

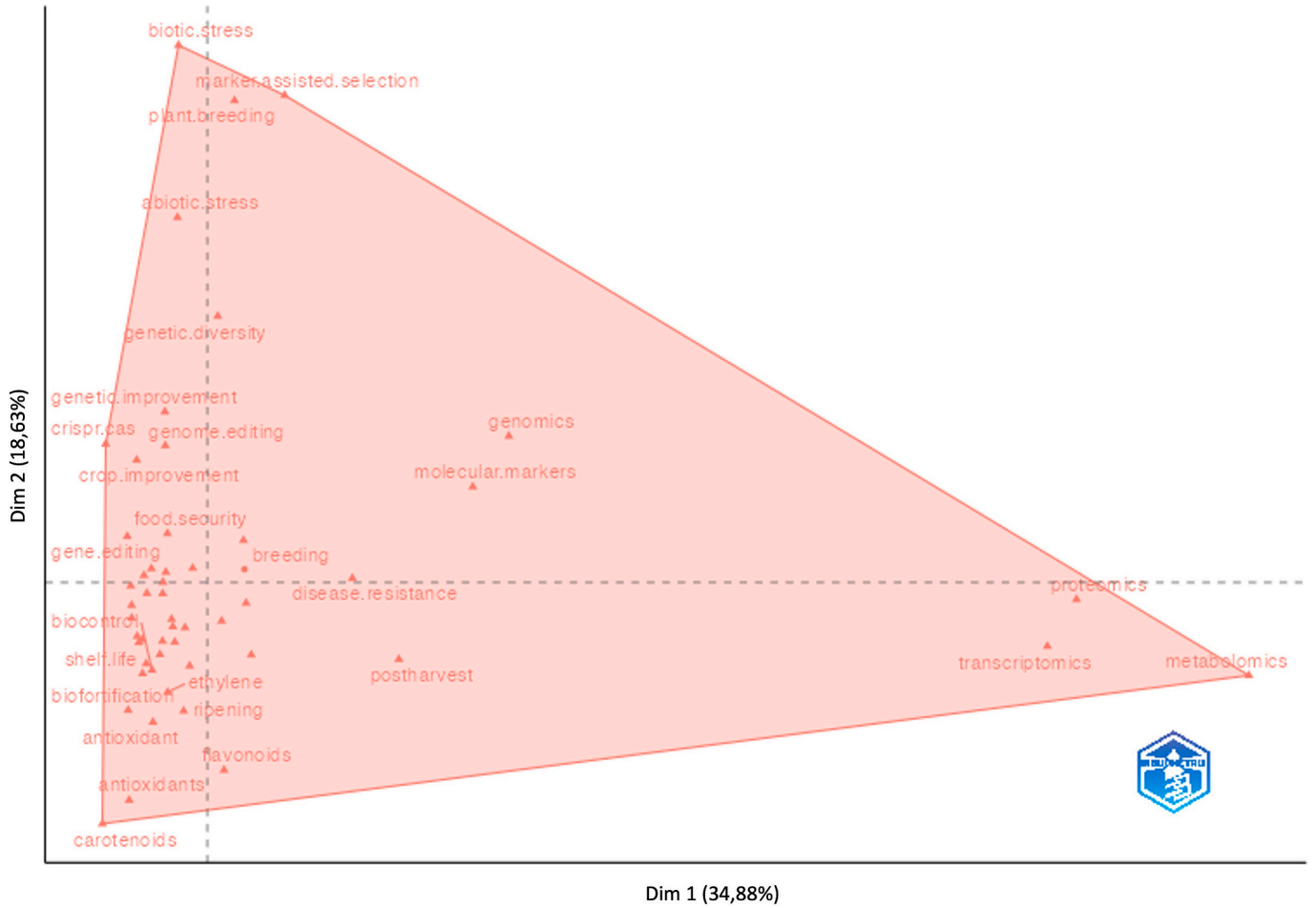

Fig. 6. Conceptual framework of the research field via Multiple Correspondence Analysis (MCA). The plot visualizes relationships among keywords in a two-dimensional space, where proximity reflects conceptual similarity and co-occurrence frequency in the literature. The horizontal axis (Dimension 1) captures the gradient from fundamental molecular research (left) to applied trait-oriented research (right). The vertical axis (Dimension 2) distinguishes cellular level approaches (bottom) from organismal and systems-level approaches (top). Keywords positioned near the center (e.g., "CRISPR-Cas," "metabolomics," "biotic stress") represent core integrating concepts that connect multiple research areas.

weight and exhibiting more vigorous vegetative growth (Li et al., 2023).

Collectively, these case studies underscore a paradigm shift from post-harvest intervention to pre-harvest genetic enhancement. By precisely manipulating genes controlling metabolic pathways, genome editing allows for the development of crops that are not only more resilient but also intrinsically endowed with superior and longer-lasting nutritional and sensory attributes.

5.3. Extending shelf life by targeting key physiological processes

A paramount applications of genome editing in post-harvest science is the direct extension of shelf life by targeting the genetic regulators of ripening and deterioration. This approach moves beyond managing symptoms to addressing the underlying causes of spoilage, offering a sustainable strategy to reduce waste.

The efficacy of this strategy is clearly demonstrated in tomato, a model climacteric fruit. Ripening in tomato is centrally controlled by the *RIN* gene, a master transcription factor that regulates ethylene biosynthesis, cell wall degradation, and pigment accumulation. By using CRISPR/Cas9 to manipulate the *RIN* gene, researchers have successfully decelerated the ripening process. This intervention results in tomatoes that maintain firmness and quality for significantly longer periods post-harvest, without substantially compromising their eventual flavor or nutritional content upon ripening.

Beyond highly perishable fruits, genome editing addresses critical shelf-life issues in staple crops. Cassava, a vital food source for millions, suffers from post-harvest physiological deterioration (PPD), a rapid spoilage process that renders roots unmarketable within 24–72 h of harvest. Recent research has implicated the *MeF6′H* gene cluster, which encodes enzymes critical for the biosynthesis of the coumarin scopoletin. While scopoletin plays a role in stress resistance, its accumulation is strongly correlated with the oxidative burst that drives PPD. Consequently, genome editing strategies aimed at downregulating the *MeF6′H* genes offer a promising route to delay PPD and drastically reduce cassava's post-harvest losses (Mbinda & Mukami, 2022; Mukami et al., 2024).

These case studies of *RIN* in tomato and *MeF6′H* in cassava exemplify a powerful new frontier: the precise management of post-harvest physiology at the genetic level. By targeting key genes controlling ripening and stress-response pathways, genome editing provides a direct method to enhance shelf life, improve food security, and increase the reliability of supply chains for both fresh produce and staple crops.

5.4. Engineering Resilience: Targeting Abiotic stress tolerance for improved Post-Harvest outcomes

Abiotic stresses, such as drought and cold, not only impact crop yield but also profoundly affect the quality and shelf-life of produce *after* harvest. Genome editing offers a strategic tool to fortify crops against these stresses, thereby preserving quality throughout the supply chain.

Table 3
Summary of genome editing applications for post-harvest trait improvement in crops.

Applications	Commodity	Target Gene	Cas Variant	Key Phenotypic Result	Molecular Function of Target Gene	References
Nutrition & Flavor	Tomato (*S. lycopersicum*)	*SlbZIP1*	SpCas9	Increased sugar and amino acid content	Transcription factor for sugar/amino acid biosynthesis	(Nguyen et al., 2023)
	Rice (*O. sativa*)	*SBEI, SBEIIb*	SpCas9	Increased resistant starch content	Enzymes regulating amylose/amylopectin ratio	(Sun et al., 2017)
	Potato (*S. tuberosum*)	*Vinv*	SpCas9	Reduced acrylamide, lower reducing sugars	Catalyzes sucrose hydrolysis to glucose/ fructose	(Clasen et al., 2016; Yasmeen et al., 2022)
	Sorgum (*Sorghum bicolor*)	*K2G*	SpCas9	increased protein digestibility in raw flour	encodes the protein γ-kafirin, which is one of the major storage proteins in sorghum grain.	(Li et al., 2023)
Shelf Life	Tomato (*S. lycopersicum*)	*RIN*	SpCas9	Delayed ripening, reduced ethylene production	Master regulator of ripening transcription factor	(Li et al., 2020b)
	Cassava (*M. esculenta*)	*MeF6′H* cluster	SpCas9	Reduced post-harvest physiological deterioration	Enzymes for scopoletin biosynthesis	(Mukami et al., 2024)
	Melon (*Cucumis melo*)	*CmACO1*	SpCas9 RNP	Extended shelf life The firmness of the fruit flesh is maintained	Catalyzes the final step of ethylene biosynthesis	(Sasaki et al., 2025)
Abiotic Stress	Rice (*O. sativa*)	*OsERA1*	SpCas9	Enhanced drought tolerance	Negative regulator of ABA signaling	(Ogata et al., 2020)
	Rice (*O. sativa*)	*OsAnn3*	SpCas9	Reduced cold tolerance (Functional study)	Stabilizes membranes during cold stress	(Shen et al., 2017)
	Tomato (*S. lycopersicum*)	*Slcbf1*	SpCas9	Reduced chilling tolerance (Functional study)	Regulates antioxidant activity under cold stress	(Li et al., 2018)
Disease Resistance	Pepper (*C. annuum*)	*CaERF28*	SpCas9	Enhanced resistance to *Colletotrichum*	AP2/ERF transcription factor for defense genes	(Mishra et al., 2021)
	Tomato (*S. lycopersicum*)	*SlDQD/ SDH2*	SpCas9	Resistance to *Botrytis cinerea*	Enzyme in phenylpropanoid/ antimicrobial pathway	(Wang et al., 2023)
		SlPAL2	dCas12a	Increased lignin content, Reduced pathogen load	Catalyzes the first committed step in the phenylpropanoid pathway	(Rivera-toro & Folter, 2025)
	Raspberry (*Rubus idaeus*)	*NPR1*	SpCas9 RNP	Resistance to *Botrytis cinerea*	Key regulators in the systemic acquired resistance (SAR) signaling pathway	(Creeth et al., 2025)
	Citrus (*Citrus* spp.)	*CsLOB1*	SpCas9	Resistance to citrus canker (*Xanthomonas citri* subsp. *citri*)	Susceptibility gene activated by pathogen	(Jia et al., 2016)
	Sweet potato (*Ipomoea batatas*)	SPCSV-*RNase3*	*RfxCas13d* and *LwaCas13a*	Resistance to sweet potato virus disease	Destroying plant basal antiviral defenses based on RNA interference (RNAi)	(Yu et al., 2022)

This approach is exemplified by research in key staple and horticultural crops.

The threat of drought, which can induce stress-related damage and quality loss even before harvest, is being addressed by targeting hormonal pathways. In rice, the *OsERA1* gene acts as a negative regulator of abscisic acid (ABA) signaling, a central hormone in drought response. CRISPR/Cas9-mediated knockout of *OsERA1* enhances ABA sensitivity, leading to improved stomatal closure, water retention, and ultimately, greater drought survival (Ogata et al., 2020; Yadav et al., 2023). This enhanced resilience during growth contributes to healthier, more robust plants that are less susceptible to quality degradation post-harvest.

Conversely, cold stress is a major cause of post-harvest spoilage for chilling-sensitive crops like tomato. Storage at low temperatures can lead to chilling injury, manifesting as surface pitting, accelerated rotting, and loss of flavor. Research on the *SlCBF1* gene, a master regulator of cold-induced gene expression, provides critical insights. Mutagenesis of *SlCBF1* via CRISPR/Cas9 has been shown to *compromise* the tomato's tolerance to low temperatures (Li et al., 2018). While this initially appears counterproductive, such research is invaluable; it precisely identifies key genetic players and helps elucidate the molecular mechanisms of chilling injury. This knowledge is the essential foundation for future strategies to *enhance* cold tolerance—for instance, by overexpressing *SlCBF1* or editing its upstream regulators—to develop tomato varieties that better withstand cold storage.

This reverse genetics approach—using gene knockouts to understand function—is further illustrated in rice for cold tolerance. Editing the *OsAnn3* gene, which encodes an annexin protein implicated in maintaining membrane stability during cold stress, resulted in reduced cold tolerance (Shen et al., 2017). This confirms its critical role in protecting cellular integrity under low-temperature duress.

Collectively, these examples demonstrate a dual applications of genome editing: firstly, to directly enhance tolerance to pre-harvest stresses like drought that impact post-harvest quality, and secondly, as a powerful discovery tool to map the genetic architecture of post-harvest disorders like chilling injury. This deeper understanding is a prerequisite for designing next-generation crops engineered for resilience across the entire field-to-table continuum.

5.5. *Engineering innate Immunity: Reducing Post-Harvest diseases by targeting susceptibility and defense*

Post-harvest losses caused by fungal and bacterial pathogens such as *Botrytis cinerea* and *Pectobacterium* spp. represent a major challenge to food security. Genome editing provides a sophisticated strategy to combat these losses by enhancing the plant's innate immunity, primarily through two approaches: (1) knocking out susceptibility (S) genes that pathogens exploit, or (2) fine-tuning defense-related pathways to bolster the plant's natural resistance, thereby reducing reliance on chemical fungicides.

The power of disrupting S genes is powerfully illustrated in citrus. The *CsLOB1* gene is a susceptibility factor for citrus canker; the pathogen *Xanthomonas citri* activates it to promote infection. CRISPR/Cas9-mediated editing of the *CsLOB1* promoter has successfully impaired this activation, leading to significantly reduced disease symptoms and enhanced resistance, directly improving post-harvest fruit quality (Jia et al., 2016; Zou et al., 2021).

This S gene knockout strategy has also been extended to address post-harvest fungal pathogens in soft fruits. In raspberry (*Rubus idaeus*), a high-value crop highly susceptible to gray mold (*Botrytis cinerea*), genome editing has been employed to target the *NPR*1 gene. While *NPR*1 is conventionally known as a positive regulator of defense, studies in tomato have revealed that its knockout can paradoxically enhance resistance to *B. cinerea* through modulation of reactive oxygen species (ROS) homeostasis and jasmonate/ethylene signaling pathways (Li

et al., 2020a). Creeth et al. (Creeth et al., 2025) successfully demonstrated DNA-free CRISPR-Cas9 editing of *NPR1* in raspberry protoplasts using ribonucleoprotein complexes (RNPs), achieving an editing efficiency of 6.0%. This establishes a foundation for developing raspberry cultivars with enhanced resistance to post-harvest fungal decay, directly addressing a major cause of post-harvest losses in this economically important crop (Creeth et al., 2025).

Conversely, genome editing can be used to amplify positive defense regulators. In pepper (*Capsicum annuum*), the *CaERF28* transcription factor is a positive regulator of ethylene and jasmonic acid-dependent defense pathways. Overexpression of *CaERF28*, achievable through CRISPR-activation techniques, has been shown to enhance resistance to anthracnose (*Colletotrichum* spp.) by upregulating pathogenesis-related (*PR*) genes, offering a strategy to fortify fruit against post-harvest rot (Ma et al., 2024; Mishra et al., 2021).

A third strategy involves rewiring metabolic pathways to enhance biochemical defenses. In tomato (*Solanum lycopersicum*), editing the Sl*DQD/SDH2* gene, which is involved in the phenylpropanoid pathway, has led to increased accumulation of antimicrobial phenolic compounds and lignin. This enhanced biochemical barrier results in greater resistance to bacterial soft rot (*Pectobacterium* spp.), demonstrating how editing metabolic genes can strengthen physical and chemical defenses post-harvest (Wang et al., 2023).

5.6. Diversity of CRISPR/Cas systems in post-harvest research

The case studies presented in this review have collectively shown the expanding of CRISPR systems available for post-harvest improvement, including three different classes of Cas effectors: DNA nucleases such as Cas9, DNA-binding epigenetic modifiers such as dCas12a, and RNA nucleases such as Cas13. This is because post-harvest improvement is a complex and multifaceted issue that covers different aspects of crop improvement, including genetic aspects such as ethylene biosynthesis and cell wall metabolism, biotic aspects such as virus infection, and regulatory aspects such as non-transgenic status.

The most widely used approach is still Cas9-based knockout of undesirable genes and its applications in melon *CmACO1*, tomato Sl*bZIP1*, rice *SBEI/SBEIIb*, and potato *VInv*. However, the emergence of dCas12a-based epigenome editing systems as shown by Rivera-Toro et al. (Rivera-toro & Folter, 2025) is a conceptual breakthrough in CRISPR-based post-harvest improvement because it does not involve gene knockout but instead modulates gene expression via histone methylation without affecting endogenous gene sequences and increases resistance to virus infection. This approach is highly desirable for traits that cannot be knocked out without undesirable side effects and is also desirable in terms of regulatory requirements for non-transgenic status.

However, the problem that Cas13-mediated RNA targeting solves is an entirely different dimension of post-harvest loss, which is the problem of viral diseases that occur in vegetatively propagated plants. Unlike DNA-targeting nucleases, which heritably change the plant genome, the Cas13-mediated degradation of the viral RNA transcript provides a reversible, environmentally sensitive response to the problem. The success with RfxCas13d in providing resistance to SPVD in sweet potato (Yu et al., 2022) shows that the CRISPR system can evade the viral suppressors of RNA silencing, which conventional approaches to RNA interference failed to achieve. This implies that the problem of other viral diseases that affect the quality of the post-harvest product in other crops, such as cassava, potato, and fruit trees, could be addressed with the help of the Cas13 system.

The parallel development of these different Cas systems in post-harvest biology emphasizes one of the main findings of this review: There is no one-size-fits-all genome editing tool. The best tool will depend on matching the tool with the Cas type, the biological target, and the outcome of interest, as well as knockout, activation, or degradation of RNA molecules. Future developments will likely involve new Cas variants that are more specific and smaller in size for easier delivery and new functions such as prime editing and base editing that are midway between knockout and precise editing.

5.7. Bridging bibliometric clusters to biological targets and post-harvest traits

Identifying research clusters through keyword co-occurrence provides a helpful macro-level perspective of the field's conceptual structure (Su & Lee, 2010). However, to turn these global trends into actionable insights for researchers and breeders, it is essential to break down each cluster into its basic biological components. Table 4 summarizes this integration by making a clear connection between specific genetic targets, crop models, and genome editing techniques and the topic clusters found by our bibliometric analysis.

The physiological themes of Cluster 1 (such as ethylene and ripening) are not merely theoretical ideas; rather, they correlate to well-established genetic pathways, as Table 4 shows. The prevalence of words like “gene expression” and “metabolism” in this cluster is indicative of the significant efforts made to use CRISPR/Cas9 to target particular genes like ACS, ACO, and PG. This demonstrates that directly modifying the genetic processes governing fruit ripening and softening is the primary objective of post-harvest genome editing.

Cluster 2 serves as a technological engine, providing methodological tools (CRISPR/Cas9, base editing) to manipulate the biological targets identified in Clusters 1 and 3. The strong linkages between these clusters (Fig. 5) indicate that breeding objectives now explicitly integrate post-harvest traits such as hardiness and nutritional quality, enabled by the precision of modern genome editing tools.

Furthermore, Cluster 3 demonstrates the extension of shelf life toward the concept of “functional foods.” The keywords “antioxidants,” “carotenoids,” and “biofortification” indicate a growing research focus on increasing the nutrient density of crop yields. This is achieved by editing key biosynthetic genes such as PSY (for provitamin A) or VTC2 (for vitamin C), thereby addressing food security and public health nutrition issues.

By providing this integrated framework, Table 4 serves as a strategic roadmap. It not only maps where research activity is concentrated but also explains the biological basis behind these trends and shows how future genome editing efforts can be optimally directed to reduce post-harvest losses and improve food quality.

5.8. A Comparative analysis of regulatory frameworks and commercialization hurdles for Gene-Edited crops

In the process of developing regulations for genome editing, genetic modified organism (GMO) regulations are highly relevant to consider, given that some genome editing methods also use genetic engineering techniques in the assembly process (Tachikawa & Matsuo, 2023). In general, countries worldwide regulate GMOs based on the nature of the product or the assembly process (Sprink et al., 2016). Process-based regulations such as the Cartagena Protocol specifically regulate products that are assembled through certain processes, while product-based regulations will not look at the assembly method, but will focus more on the nature of the product produced (Sprink et al., 2016). The special regulations implemented are in the form of biosafety studies, both in terms of human health and the environment (Sprink et al., 2016).

For countries that ratify the Cartagena Protocol, interpreting the status of gene-edited plants is crucial, particularly in the absence of specific regulations (Entine et al., 2021). Under the Protocol, a living modified organism (LMO) is defined by the use of modern techniques of biotechnology, which includes the use of recombinant DNA in vitro. The diversity of regulatory approaches to gene-edited crops globally is a key factor shaping the trajectory of their research and commercialization (Tachikawa & Matsuo, 2023). As summarized in Table 5, the fundamental differences lie in the regulatory philosophies themselves. Because the development of gene-editing plants, such as CRISPR/Cas9,

Table 4
Integration of Bibliometric Clusters with Biological Targets, Crops, and Editing Strategies for Post-Harvest Traits.

Bibliometric Cluster	Core Research Themes	Key Biological Targets (Genes/ Pathways)	Model/ Commercial Plants	Genome Editing Strategies & Expected Post-Harvest Traits	Representative Keywords of the Analysis
Cluster 1 (Green)	Plant Physiology and Genetic Regulation	Ethylene biosynthesis gene: 1-aminocyclo-propane-1-carboxylic acid (*ACC*) synthetase 1 (*ACS*1) and *ACC* oxidase 1 (ACO1)]; Ethylene receptor gene: *ETR*1; Cell wall gene: polygalacturonase (*PG*)	Tomato, pepper, banana, apple	Knockout of the *ACS/ACO/ETR1* gene to inhibits ethylene production or signaling for delays ripening and extends shelf life. Knockout of the *PG/PL* gene for slows fruit softening to maintains quality during storage.	ethylene, ripening, fruit, phytohormone, metabolism, physiology
Cluster 2 (Red)	Genome Editing Tools and Breeding Applications	Editing systems: CRISPR/Cas9, Cas12a (Cpf1), base editing, prime editing. Target validation: Various genes from Clusters 1 and 3 whose function has been validated through editing.	Various plants (model and commercial)	Development of transgene-free crops through editing, precision breeding for post-harvest traits, functional screening of genes to identify new targets.	Genetic engineering, genetic transformation, gene editing, CRISPR/Cas9
Cluster 3 (Blue)	Post-Harvest Quality and Nutritional Enhancement	Flavor regulation gene: *SlbZIP1*; Starch biosynthesis genes: *SBEI*, *SBEIIb*; Cold storage gene: *Vinv*; Protein digestibility gene: *K2G*	Tomato, rice, potato, sorghum	*SlbZIP1* gene editing: improves the sweetness and flavor profile of tomatoes; *SBEI/SBEIIb* gene editing: modifies starch composition for health and texture benefits. *Vinv* gene knockout: prevents cold-induced sweetening in potatoes, maintaining a savory flavor. *K2G* gene knockout: increases sorghum protein digestibility	Plant disease, post-harvest, biofortification, nutrition, carotenoids, antioxidants

Table 5
Regulatory Frameworks and Their Impact on Innovation in Gene-Edited Crops: A Regional Comparison.

Regulatory aspect	The European Union (and a Fragmented Britain)	North America (USA & Canada)
Regulatory Basis	Process-based: Focuses on how the product is made. Gene-edited crops are essentially considered GMOs.	Product-based: Focuses on the characteristics and risks of the final product, not the method.
Current Status	• European Union: In negotiations (trilogue) on the NGT (New Genomic Techniques) proposal, which would divide edited crops into two categories (Category 1 with minor modifications of < 20 bases, and Category 2 for the remainder). Patents and labeling are the main issues delaying agreement (Tachikawa et al., 2024). • United Kingdom: Has implemented the Genetic Technology (Precision Breeding) Act 2023, which effectively exempts precision-edited crops (without foreign DNA) from strict GMO regulations. However, Scotland and Wales still apply the old rules, creating fragmentation within the UK.	• United States: A coordinated, multi-agency approach. USDA-APHIS, through the SECURE rule (since 2020), significantly relaxed the rules for SDN-1 and SDN-2 crops. The FDA recently issued final guidance simplifying the path to market with the option of premarket meetings for low-risk products, but encouraging transparency and voluntary consultation (Tachikawa et al., 2024). • Canada: Focus on novelty. Gene-edited crops that do not contain foreign DNA and pose no new risks are less likely to be considered "novel foods," resulting in a faster path to market.
Impact on Innovators	Strict and uncertain regulations (especially in the EU) tend to be something only large companies with significant resources can cope with. Compliance costs are high.	Lighter and clearer regulations open the door for small companies, startups, and public research institutions to innovate. In the US, the development of crops like Pairwise's edited mustard greens is a prime example.

almost always involves in vitro steps, the resulting plants, regardless of whether the final product contains foreign DNA, can be interpreted as following existing GMO regulations (Eckerstorfer et al., 2019; Whelan & Lema, 2015). This interpretation was subsequently adopted by the European Court of Justice (ECJ) in 2018, which ruled that organisms resulting from mutagenesis (including gene editing) fall within the definition of GMOs and are subject to strict EU regulations (ECJ, 2018). This decision puts the European Union in the most restrictive position, where gene-edited crops are treated on a par with classic transgenic crops (Eckerstorfer et al., 2019).

This situation contrasts with countries that adopt a product-based approach, such as the United States (US), Canada, and several Latin American countries (e.g., Argentina, Brazil). In the US, regulation is driven by the presence or absence of specific risks (such as plant pathogenicity) or the use of pathogenic vectors, rather than by the method of production (Waltz, 2018). Consequently, many SDN-1 gene-edited products (which produce only point mutations without foreign DNA insertions) have been declared unregulated by biosafety authorities because they are considered equivalent to conventionally mutated plants (Waltz, 2018). In Canada, despite using a product-based trigger, the approach is different. Regulation in Canada is driven by the novelty of the trait (plant with novel trait, PNT), so both gene-edited plants and conventional breeding that produces novel, unprecedented traits are subject to risk assessment (Smyth, 2017).

These fundamental differences in the regulatory landscape create uneven barriers and opportunities for commercialization globally. For example, gene-edited tomatoes with increased levels of GABA (a calming amino acid) developed in Japan, or mushrooms that are less prone to bruising in the US, can reach market quickly due to relaxed regulations (Ishii, 2025; Waltz, 2016). However, similar products face long, expensive, and uncertain bureaucratic hurdles if they are to be exported or developed in countries with process-based regulations such as the European Union or New Zealand. This uncertainty not only discourages investment from the private sector, particularly startups, but also slows the potential benefits of these technologies, such as reduced food waste through longer shelf-life post-harvest products. Conversely, countries like Argentina that have adopted pragmatic and clear policies have seen a surge in innovation from a wide range of stakeholders, including public research institutions focused on local crops, due to lower regulatory compliance costs (Whelan & Lema, 2015). Thus, the clarity and type of regulation (process vs. product-based) directly shape the innovation landscape and are key determinants of which technologies will reach farmers and consumers, and how quickly.

6. Conclusion and future perspectives

Genome editing stands poised to revolutionize post-harvest management, offering unprecedented precision in addressing the global challenges of food loss, nutritional quality, and agricultural sustainability. As this review has detailed, technologies like CRISPR/Cas9 enable direct manipulation of key genes governing ripening, senescence, stress response, and pathogen defense, moving beyond the limitations of traditional breeding.

The future trajectory of this field will likely focus on several promising avenues, including (1) precision control of ripening and senescence. Fine-tuning hormonal signaling pathways, particularly ethylene and ABA, will allow for precise control over ripening initiation and pace. This could lead to crops with extended shelf life that maintain peak flavor and nutritional content until consumption, reducing reliance on artificial ripening agents and costly storage conditions. (2) targeting quality degradation. Editing genes encoding enzymes responsible for post-harvest spoilage, such as polyphenol oxidase (causing browning in cereals and fruits) and pectinases (leading to softening), offers a direct route to preserving the visual and textural appeal of produce throughout the supply chain. (3) Engineering durable disease resistance. Enhancing innate immunity by knocking out susceptibility genes or boosting defense pathways will be crucial for developing crops with inherent resistance to post-harvest pathogens. This can drastically reduce dependency on chemical fungicides, which is especially critical for regions lacking advanced storage infrastructure. (4) Multiplexed editing for complex traits: The ability to edit multiple genes simultaneously will be essential for tackling complex post-harvest traits influenced by numerous physiological and genetic factors. This allows for the holistic improvement of quality, longevity, and resilience in a single cultivar.

Looking ahead, the integration of genome editing with emerging technologies like artificial intelligence (for high-throughput phenotyping) and multi-omics analyses (genomics, transcriptomics, metabolomics) will enable a systems biology approach. This will shift the paradigm from editing single genes to optimizing entire metabolic networks responsible for post-harvest performance. Furthermore, evolving regulatory frameworks that distinguish transgene-free edited crops from GMOs are paving the way for smoother commercial adoption and public acceptance.

In conclusion, genome editing transcends being merely a novel tool; it represents a foundational shift in our approach to post-harvest biology. Its precision, efficiency, and versatility position it at the forefront of developing next-generation crops designed for resilience and quality from field to table. As research advances and adoption barriers diminish, genome editing is unequivocally positioned to become a cornerstone of sustainable and secure global food systems.

Declaration of generative AI and AI-assisted technologies in the manuscript preparation process

During the preparation of this work the authors used chat-gpt in order to improve English language in manuscript preparation. After using this tool/service, the authors reviewed and edited the content as needed and takes full responsibility for the content of the published article.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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References

Adedeji, O., Naing, A.H., Kang, H., Xu, J., Chung, M., Kim, C., 2024. Editing of the ethylene biosynthesis gene in carnation using CRISPR-Cas9 ribonucleoprotein complex. Plant Methods 20, 20–39. https://doi.org/10.1186/s13007-024-01143-0.

Aghaei Chadegani, A., Salehi, H., Md Yunus, M.M., Farhadi, H., Fooladi, M., Farhadi, M., Ale Ebrahim, N., 2013. A comparison between two main academic literature collections: Web of science and scopus databases. Asian Soc. Sci. 9 (5), 18–26. https://doi.org/10.5539/ass.v9n5p18.

Ahmadikhah, A., Zarabizadeh, H., Nayeri, S., Abbasi, M.S., 2025. Advancements in genome editing tools for genetic studies and crop improvement. Front. Plant Sci. 15–2024. https://doi.org/10.3389/fpls.2024.1370675.

Ahmed, N., Zhang, B., Chachar, Z., Li, J., Xiao, G., Wang, Q., Hayat, F., Deng, L., Narejo, M.-N., Bozdar, B., Tu, P., 2024. Micronutrients and their effects on Horticultural crop quality, productivity and sustainability. Sci. Hortic. 323, 112512. https://doi.org/10.1016/j.scienta.2023.112512.

Anshori, M.F., Dirpan, A., Sitaresmi, T., Rossi, R., Farid, M., Hairmansis, A., Purwoko, B., Suwarno, W.B., Nugraha, Y., 2023. An overview of image-based phenotyping as an adaptive 4.0 technology for studying plant abiotic stress: a bibliometric and literature review. Heliyon 9 (11), e21650. https://doi.org/10.1016/j.heliyon.2023.e21650.

Ardie, S.W., Bagus Nugroho, R., Dirpan, A., Anshori, M.F., 2025. Foxtail millet research in supporting climate change resilience efforts : Bibliometric analysis and focused literature review. Heliyon 11 (3), e42348. https://doi.org/10.1016/j.heliyon.2025.e42348.

Aria, M., Cuccurullo, C., 2017. bibliometrix: an R-tool for comprehensive science mapping analysis. J. Informet. 11 (4), 959–975. https://doi.org/10.1016/j.joi.2017.08.007.

Baltazari, A., Mtui, H.D., Mwatawala, M.W., Chove, L.M., Msogoya, T., Samwel, J., Subramanian, J., 2020. Effects of Storage Conditions, Storage Duration and Post-Harvest Treatments on Nutritional and Sensory Quality of Orange (*Citrus sinensis* (L) Osbeck) Fruits. International Journal of Fruit Science 20 (4), 737–749. https://doi.org/10.1080/15538362.2019.1673278.

Bull, S.E., Seung, D., Chanez, C., Mehta, D., Kuon, J.E., Truernit, E., Hochmuth, A., Zurkirchen, I., Zeeman, S.C., Gruissem, W., Vanderschuren, H., 2018. Accelerated ex situ breeding of GBSS- and PTST1-edited cassava for modified starch. Sci. Adv. 4 (9). https://doi.org/10.1126/sciadv.aat6086.

Chauhan, C., Dhir, A., Akram, M.U., Salo, J., 2021. Food loss and waste in food supply chains. a systematic literature review and framework development approach. J. Clean. Prod. 295, 126438. https://doi.org/10.1016/j.jclepro.2021.126438.

Chen, F., Chen, L., Yan, Z., Xu, J., Feng, L., He, N., Guo, M., Zhao, J., Chen, Z., Chen, H., Yao, G., Liu, C., 2024. Recent advances of CRISPR-based genome editing for enhancing staple crops. Front. Plant Sci. 15 (September), 1–21. https://doi.org/10.3389/fpls.2024.1478398.

Chen, Y., Mao, W., Liu, T., Feng, Q., Li, L., Li, B., 2020. Genome Editing as a Versatile Tool to Improve Horticultural Crop Qualities. Hortic. Plant J. 6 (6), 372–384. https://doi.org/10.1016/j.hpj.2020.11.004.

Clasen, B.M., Stoddard, T.J., Luo, S., Demorest, Z.L., Li, J., Cedrone, F., Tibebu, R., Davison, S., Ray, E.E., Daulhac, A., Coffman, A., Yabandith, A., Retterath, A., Haun, W., Baltes, N.J., Mathis, L., Voytas, D.F., Zhang, F., 2016. Improving cold storage and processing traits in potato through targeted gene knockout. Plant Biotechnol. J. 14 (1), 169–176. https://doi.org/10.1111/pbi.12370.

Creeth, R., Thompson, A., Kevei, Z., 2025. DNA-free CRISPR genome editing in raspberry (*Rubus idaeus*) protoplast through RNP-mediated transfection. Frontiers in Genome Editing 7–2025. https://doi.org/10.3389/fgeed.2025.1589431.

ECJ. (2018). *Judgement of the Court in Case C-528/16: Court of Justice of the European Union* (p. Available online at: http://curia.europa.eu/juris/). (Accessed Februari 25, 2026).

Eckerstorfer, M.F., Engelhard, M., Heissenberger, A., Simon, S., 2019. *Plants developed by New Genetic Modification Techniques — Comparison of existing Regulatory Frameworks in the EU and Non-EU*. Countries 7 (February). https://doi.org/10.3389/fbioe.2019.00026.

Entine, J., Felipe, M.S.S., Groenewald, J.-H., Kershen, D.L., Lema, M., McHughen, A., Nepomuceno, A.L., Ohsawa, R., Ordonio, R.L., Parrott, W.A., Quemada, H., Ramage, C., Slamet-Loedin, I., Smyth, S.J., Wray-Cahen, D., 2021. Regulatory approaches for genome edited agricultural plants in select countries and jurisdictions around the world. Transgenic Res. 30 (4), 551–584. https://doi.org/10.1007/s11248-021-00257-8.

Fu, B., Wang, W., Liu, X., Duan, X., Allan, A.C., Grierson, D., Yin, X., 2021. An ethylene-hypersensitive methionine sulfoxide reductase regulated by NAC transcription factors increases methionine pool size and ethylene production during kiwifruit ripening. New Phytol. 232 (1), 237–251. https://doi.org/10.1111/nph.17560.

Hillary, V.E., Ceasar, S.A., 2024. CRISPR/Cas system-mediated base editing in crops: recent developments and future prospects. Plant Cell Rep. 43 (11), 271. https://doi.org/10.1007/s00299-024-03346-0.

Holme, I.B., Ingvardsen, C.R., Dionisio, G., Podzimska-Sroka, D., Kristiansen, K., Feilberg, A., Brinch-Pedersen, H., 2024. CRISPR/Cas9-mediated mutation of Eil1 transcription factor genes affects exogenous ethylene tolerance and early flower senescence in Campanula portenschlagiana. Plant Biotechnol. J. 22 (2), 484–496. https://doi.org/10.1111/pbi.14200.

Hu, C., Sheng, O., Deng, G., He, W., Dong, T., Yang, Q., Dou, T., Li, C., Gao, H., Liu, S., Yi, G., Bi, F., 2021. CRISPR/Cas9-mediated genome editing of MaACO1

(aminocyclopropane-1-carboxylate oxidase 1) promotes the shelf life of banana fruit. Plant Biotechnol. J. 19 (4), 654–656. https://doi.org/10.1111/pbi.13534.
Idris, S.H., Mat Jalaluddin, N.S., Chang, L.W., 2023. Ethical and legal implications of gene editing in plant breeding: a systematic literature review. J. Zhejiang Univ. Sci. B 24 (12), 1093–1105. https://doi.org/10.1631/jzus.B2200601.
Ishii, T., 2025. Consumer choices regarding genome-edited food crops: lessons from Japan. Frontiers in Genome Editing 7, 1672358. https://doi.org/10.3389/fgeed.2025.1672358.
Jia, H., Zhang, Y., Orbović, V., Xu, J., White, F.F., Jones, J.B., Wang, N., 2016. Genome editing of the disease susceptibility gene CsLOB1 in citrus confers resistance to citrus canker. Plant Biotechnol. J. 15 (7), 817–823. https://doi.org/10.1111/pbi.12677.
Khan, A., Sovero, V., Gemenet, D., 2016. Genome-assisted Breeding for Drought Resistance. Curr. Genomics 17 (4), 330–342. https://doi.org/10.2174/1389202917999160211101417.
Kolkur, S.U., Sharma, A., Gouda, M.N.R., Praveen, K.V., Singh, A., 2024. CRISPR in agriculture and it's ethical implications: a bibliometric analysis. Food and Humanity 3, 100322. https://doi.org/10.1016/j.foohum.2024.100322.
Krishna, T.P.A., Maharajan, T., Ceasar, S.A., 2022. Application of CRISPR/Cas9 Genome Editing System to Reduce the Pre- and Post-Harvest Yield losses in Cereals. The Open Biotechnology Journal 16 (1), 1–9. https://doi.org/10.2174/18740707-v16-e2205190.
Kumari, C., Sharma, M., Kumar, V., Sharma, R., Kumar, V., Sharma, P., Kumar, P., Irfan, M., 2022. Genome Editing Technology for Genetic Amelioration of Fruits and vegetables for Alleviating Post-Harvest loss. Bioengineering 9 (4), 1–18. https://doi.org/10.3390/bioengineering9040176.
Kusuma, R. A. (2023). *A Bibliometric Analysis of Post-Harvest Research and Innovations in Tackling Grain Crisis using VOSviewer*. 582–593.
Li, R., Wang, L., Li, Y., Zhao, R., Zhang, Y., Sheng, J., Ma, P., Shen, L., 2020a. Knockout of SlNPR1 enhances tomato plants resistance against Botrytis cinerea by modulating ROS homeostasis and JA/ET signaling pathways. Physiol. Plant. 170 (4), 569–579. https://doi.org/10.1111/ppl.13194.
Li, R., Zhang, L., Wang, L., Chen, L., Zhao, R., Sheng, J., Shen, L., 2018. Reduction of Tomato-Plant Chilling Tolerance by CRISPR–Cas9-Mediated SlCBF1 Mutagenesis. J. Agric. Food Chem. 66 (34), 9042–9051. https://doi.org/10.1021/acs.jafc.8b02177.
Li, S., Zhu, B., Pirrello, J., Xu, C., Zhang, B., Bouzayen, M., Chen, K., Grierson, D., 2020b. Roles of RIN and ethylene in tomato fruit ripening and ripening-associated traits. New Phytol. 226 (2), 460–475. https://doi.org/10.1111/nph.16362.
Li, X., Liu, W., Wang, G., Yuan, L., Wang, J., & Sai-, S. (2023). *Improving digestibility of sorghum proteins by CRISPR / based genome editing. September*, 1–12. Doi:10.1002/fes3.506.
Ma, L., Shi, Q., Ma, Q., Wang, X., Chen, X., Han, P., Luo, Y., Hu, H., Fei, X., Wei, A., 2024. Genome-wide analysis of AP2/ERF transcription factors that regulate fruit development of chinese prickly ash. BMC Plant Biol. 24 (1), 565. https://doi.org/10.1186/s12870-024-05244-9.
Mbinda, W., Mukami, A., 2022. Breeding for postharvest physiological deterioration in cassava: problems and strategies. CABI Agric. Biosci. 3 (1), 30. https://doi.org/10.1186/s43170-022-00097-4.
Miladinovic, D., Antunes, D., Yildirim, K., Bakhsh, A., Cvejić, S., Kondić-Špika, A., Marjanovic Jeromela, A., Opsahl-Sorteberg, H.-G., Zambounis, A., Hilioti, Z., 2021. Targeted plant improvement through genome editing: from laboratory to field. Plant Cell Rep. 40 (6), 935–951. https://doi.org/10.1007/s00299-020-02655-4.
Mishra, R., Mohanty, J.N., Mahanty, B., Joshi, R.K., 2021. A single transcript CRISPR/Cas9 mediated mutagenesis of CaERF28 confers anthracnose resistance in chilli pepper (*Capsicum annuum* L.). Planta 254 (1), 1–17. https://doi.org/10.1007/s00425-021-03660-x.
Mukami, A., Juma, B. S., Mweu, C., Oduor, R., & Mbinda, W. (2024). CRISPR-Cas9-induced targeted mutagenesis of feruloyl CoA 6′-hydroxylase gene reduces postharvest physiological deterioration in cassava roots. *Postharvest Biology and Technology*, *208*(November 2023), 112649. 10.1016/j.postharvbio.2023.112649.
Nguyen, N.H., Bui, T.P., Le, N.T., Nguyen, C.X., Le, M.T.T., Dao, N.T., Phan, Q., Van Le, T., To, H.M.T., Pham, N.B., Chu, H.H., Do, P.T., 2023. Disrupting Sc-uORFs of a transcription factor bZIP1 using CRISPR/Cas9 enhances sugar and amino acid contents in tomato (Solanum lycopersicum). Planta 257 (3), 1–11. https://doi.org/10.1007/s00425-023-04089-0.
Nie, H., Shi, Y., Geng, X., Xing, G., 2022. CRISRP/Cas9-Mediated Targeted Mutagenesis of Tomato Polygalacturonase Gene (SlPG) Delays Fruit Softening. Front. Plant Sci. 13–2022. https://doi.org/10.3389/fpls.2022.729128.
Ogata, T., Ishizaki, T., Fujita, M., Fujita, Y., 2020. CRISPR/Cas9-targeted mutagenesis of OsERA1 confers enhanced responses to abscisic acid and drought stress and increased primary root growth under nonstressed conditions in rice. PLoS One 15 (12 December), 1–12. https://doi.org/10.1371/journal.pone.0243376.
Ortega-Salazar, I., Crum, D., Sbodio, A.O., Sugiyama, Y., Adaskaveg, A., Wang, D., Seymour, G.B., Li, X., Wang, S.C., Blanco-Ulate, B., 2024. Double CRISPR knockout of pectin degrading enzymes improves tomato shelf-life while ensuring fruit quality. Plants People Planet 6 (2), 330–340. https://doi.org/10.1002/ppp3.10445.
Ossom Williamson, P., Minter, C.I.J., 2019. Exploring PubMed as a reliable resource for scholarly communications services. Journal of the Medical Library Association : JMLA 107 (1), 16–29. https://doi.org/10.5195/jmla.2019.433.
Perdana, T., Kusnandar, K., Perdana, H.H., Hermiatin, F.R., 2023. Circular supply chain governance for sustainable fresh agricultural products: Minimizing food loss and utilizing agricultural waste. Sustainable Prod. Consumption 41, 391–403. https://doi.org/10.1016/j.spc.2023.09.001.
Razzaq, A., Kaur, P., Akhter, N., Wani, S.H., Saleem, F., 2021. Next-Generation Breeding strategies for Climate-Ready Crops. Front. Plant Sci. 12 (July), 1–27. https://doi.org/10.3389/fpls.2021.620420.
Rivera-toro, D. M., & Folter, S. De. (2025). *CRISPR / dCas12a-mediated activation of SlPAL2 enhances tomato resistance against bacterial canker disease*. 1–27. Doi:10.1371/journal.pone.0320436.
Ru, L., Chen, B., Li, Y., Wills, R.B.H., Lv, Z., Lu, G., Yang, H., 2021. Role of sucrose phosphate synthase and vacuolar invertase in postharvest sweetening of immature sweetpotato tuberous roots (Ipomoea batatas (L.) Lam cv 'Xinxiang'). Sci. Hortic. 282, 110007. https://doi.org/10.1016/j.scienta.2021.110007.
dos Santos, U.J., Rocha, A., dos Santos, A.E.O., Guimarães, G.H.C., Florêncio, R.R., 2025. Post-harvest fruit quality : a bibliometric analysis Qualidade pós-colheita de frutas : Uma análise bibliométrica. Research, Society and Development 2025, 1–22.
Sasaki, K., Urano, K., & Mimida, N. (2025). *A long shelf-life melon created via CRISPR / Cas9 RNP-based in planta genome editing. 2025*(June), 1–8. Doi:10.3389/fgeed.2025.1623097.
Schmidt, M., Zannini, E., Arendt, E.K., 2018. Recent advances in physical post-harvest treatments for shelf-life extension of cereal crops. Foods 7 (4), 1–22. https://doi.org/10.3390/foods7040045.
Sharma, P., Pandey, A., Malviya, R., Dey, S., Karmakar, S., Gayen, D., 2023. Genome editing for improving nutritional quality, post-harvest shelf life and stress tolerance of fruits, vegetables, and ornamentals. Frontiers in Genome Editing 5 (February), 1–19. https://doi.org/10.3389/fgeed.2023.1094965.
Shen, C., Que, Z., Xia, Y., Tang, N., Li, D., He, R., Cao, M., 2017. Knock out of the annexin gene OsAnn3 via CRISPR/Cas9-mediated genome editing decreased cold tolerance in rice. Journal of Plant Biology 60 (6), 539–547. https://doi.org/10.1007/s12374-016-0400-1.
Shipman, E.N., Yu, J., Zhou, J., Albornoz, K., Beckles, D.M., 2021. Can gene editing reduce postharvest waste and loss of fruit, vegetables, and ornamentals? Hortic. Res. 8 (1), 1. https://doi.org/10.1038/s41438-020-00428-4.
Smyth, S.J., 2017. Canadian regulatory perspectives on genome engineered crops. GM Crops Food 8 (1), 35–43. https://doi.org/10.1080/21645698.2016.1257468.
Sprink, T., Eriksson, D., Schiemann, J., Hartung, F., 2016. Regulatory hurdles for genome editing : process- vs . product-based approaches in different regulatory context. Plant Cell Rep. 35 (7), 1493–1506. https://doi.org/10.1007/s00299-016-1990-2.
Su, H., Lee, P.-C., 2010. Mapping knowledge structure by keyword co-occurrence: a first look at journal papers in Technology foresight. Scientometrics 85, 65–79. https://doi.org/10.1007/s11192-010-0259-8.
Sun, Y., Jiao, G., Liu, Z., Zhang, X., Li, J., Guo, X., Du, W., Du, J., Francis, F., Zhao, Y., Xia, L., 2017. Generation of high-amylose rice through CRISPR/Cas9-mediated targeted mutagenesis of starch branching enzymes. Front. Plant Sci. 8 (March), 1–15. https://doi.org/10.3389/fpls.2017.00298.
Tachikawa, M., Matsuo, M., 2023. Divergence and convergence in international regulatory policies regarding genome-edited food: how to find a middle ground. Front. Plant Sci. 14, 1105426. https://doi.org/10.3389/fpls.2023.1105426.
Tachikawa, M., Matsuo, M., & America, S. (2024). *Global regulatory trends of genome editing technology in agriculture and food*. *10*, 3–10. Doi:10.1270/jsbbs.23046.
Tyagi, A., Mir, Z.A., Almalki, M.A., Deshmukh, R., Ali, S., 2024. Genomics-Assisted Breeding: a Powerful Breeding Approach for improving Plant Growth and stress Resilience. Agronomy 14 (6), 1–21. https://doi.org/10.3390/agronomy14061128.
van Eck, N.J., Waltman, L., 2010. Software survey: VOSviewer, a computer program for bibliometric mapping. Scientometrics 84 (2), 523–538. https://doi.org/10.1007/s11192-009-0146-3.
Waltz, E., 2016. Gene-edited CRISPR mushroom escapes US regulation. In. Nature Vol. 532, Issue 7599. https://doi.org/10.1038/nature.2016.19754.
Waltz, E., 2018. With a free pass, CRISPR-edited plants reach market in record time. Nat. Biotechnol. 36 (1), 6–7. https://doi.org/10.1038/nbt0118-6b.
Wang, H., Zhang, Y., Norris, A., Jiang, C.-Z., 2021. S1-bZIP Transcription Factors Play Important Roles in the Regulation of Fruit Quality and stress Response. Front. Plant Sci. 12, 802802. https://doi.org/10.3389/fpls.2021.802802.
Wang, R., Liu, K., Tang, B., Su, D., He, X., Deng, H., Wu, M., Bouzayen, M., Grierson, D., Liu, M., 2023. The MADS-box protein SlTAGL1 regulates a ripening-associated SlDQD/SDH2 involved in flavonoid biosynthesis and resistance against Botrytis cinerea in post-harvest tomato fruit. Plant J. 115 (6), 1746–1757. https://doi.org/10.1111/tpj.16354.
Whelan, A.I., Lema, M.A., 2015. Regulatory framework for gene editing and other new breeding techniques (NBTs) in Argentina. GM Crops Food 6 (4), 253–265. https://doi.org/10.1080/21645698.2015.1114698.
Wiberley-Bradford, A., Bethke, P., 2017. Suppression of the vacuolar invertase gene delays senescent sweetening in chipping potatoes. J. Sci. Food Agric. 98. https://doi.org/10.1002/jsfa.8478.
Xu, J., Kang, B.-C., Naing, A.H., Bae, S.-J., Kim, J.-S., Kim, H., Kim, C.K., 2020. CRISPR/Cas9-mediated editing of 1-aminocyclopropane-1-carboxylate oxidase1 enhances Petunia flower longevity. Plant Biotechnol. J. 18 (1), 287–297. https://doi.org/10.1111/pbi.13197.
Yadav, R. K., Tripathi, M. K., Tiwari, S., Tripathi, N., Asati, R., Chauhan, S., Tiwari, P. N., & Payasi, D. K. (2023). Genome Editing and Improvement of Abiotic Stress Tolerance in Crop Plants. *Life (Basel, Switzerland)*, *13*(7). 10.3390/life13071456.
Yasmeen, A., Shakoor, S., Azam, S., Bakhsh, A., Shahid, N., Latif, A., Shahid, A.A., Husnain, T., Rao, A.Q., 2022. CRISPR/Cas-mediated knockdown of vacuolar invertase gene expression lowers the cold-induced sweetening in potatoes. Planta 256 (6), 1–15. https://doi.org/10.1007/s00425-022-04022-x.

Yu, Y., Pan, Z., Wang, X., Bian, X., Wang, W., Liang, Q., Kou, M., Ji, H., Li, Y., Ma, D., & Li, Z. (2022). *Targeting of SPCSV- - Cas13 confers resistance against sweet potato virus disease. April 2021*, 104–117. Doi:10.1111/mpp.13146.

Zhang, Y., Li, S., Chen, Y., Liu, Y., Lin, Y., Li, M., Wang, Y., He, W., Chen, Q., Zhang, Y., Luo, Y., Wang, X., Jiang, C.-Z., Tang, H., 2022. Heterologous overexpression of strawberry bZIP11 induces sugar accumulation and inhibits plant growth of tomato. Sci. Hortic. 292, 110634. https://doi.org/10.1016/j.scienta.2021.110634.

Zou, X., Du, M., Liu, Y., Wu, L., Xu, L., Long, Q., Peng, A., He, Y., Andrade, M., Chen, S., 2021. CsLOB1 regulates susceptibility to citrus canker through promoting cell proliferation in citrus. The Plant Journal: for Cell and Molecular Biology 106 (4), 1039–1057. https://doi.org/10.1111/tpj.15217.