

Review

Mapping the growth of clustered regularly interspaced short palindromic repeat technology in plant science

Enrique E. BIÑAS, Jr.*

College of Agriculture, Faculty of Agronomy Department, Agusan del Sur State University, San Teodoro, Bunawan 8506, Agusan del Sur ebinas@adssu.edu.ph

*Correspondence: enriquejr.binas@wvsu.edu.ph and ebinas@asscat.edu.ph (Philippines)

Abstract: This study addresses the critical need to visualize the interdisciplinary advances and research trends of CRISPR-Cas technology in plant science, a rapidly evolving field at the intersection of biotechnology, genetics, and agriculture. Using a bibliometric analysis of 933 articles from the Scopus database ranging from 2010 to 2024, the study used VOSviewer 1.6.20 to analyze the following: (1) co-authorship of authors, organizations, and countries, (2) co-occurrence of all keywords, and (3) citations of documents. The analysis identified leading collaborative researchers (Qi, Yiping; Gao, Caixia; and Kumar, Ajay) as key contributors driving advancements. A dynamic, globally connected research landscape, with India and China as central hubs of innovation and collaboration, was observed. Dominant themes include precision technologies in gene editing, with a focus on base and prime editing, as well as an emphasis on ethical considerations and regulatory frameworks. The findings highlight CRISPR's transformative potential, which makes a positive contribution to crop improvement, climate resilience, and food security, while also addressing ongoing constraints and challenges, including regulatory barriers, off-target effects, and societal acceptance. Moving forward, the study emphasizes the importance of international partnerships, ethical governance, and public engagement to sustain the equitable adoption of CRISPR technology in agriculture.

Keywords: CRISPR-Cas Technology; Plant Science; Crop Improvement; Ethical Consideration

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1. Introduction

The application of CRISPR technology has a significant impact on the evolution of genetic engineering. This technology can be efficient, precise, and effective in gene editing, thus improving the resistance and tolerance of crops to diseases and stresses (Doudna and Charpentier, 2014; Zhou et al., 2024; Movahedi and Yang, 2025; Tuncel et al., 2025; Zhang et al., 2025). 'Li et al. (2018), Zhang

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et al. (2021), Faizal et al. (2024), and Azeem et al. (2025) noted that this helped optimize yield and improve the nutritional value.' This explains that this technology is a significant tool that contributes to the growth of agricultural biotechnology.

The expansion of CRISPR technology nowadays further achieves sustainable agriculture to ensure food security. 'Miglani (2017), Kolkur et al. (2024), and Kaur et al. (2025) highlighted the essence of capturing its progress and contribution in different research productions through bibliometric analysis.' Bibliometric analysis can provide a steadfast evaluation of research inclinations, impacts, and patterns (Wang et al., 2018; Kumar et al., 2024; and Jeddoub et al., 2025). The trajectories of publications are interesting in terms of their contributors, including authors, organizations, and countries, as well as their focuses and priorities in studies published in reputable journals. According to 'Zhang (2021) and Kolkur et al. (2024), this run can guide scientists and policymakers.'

Despite the evolution of CRISPR technology, there remains an incomplete understanding of its studies through bibliometric analysis, particularly regarding its influence and adoption for crop improvement. There are various studies regarding the application of CRISPR technology as a considered impactful and dynamic tool in agricultural biotechnology; however, the patterns among authors, organizations, countries, and other related analyses of thematic evolution and their influences are still limited. Thus, our understanding is restricted to the core topics of plant science through the adoption of CRISPR technology (Hwarari et al., 2024; Gao et al., 2025).

The visualization in the conduct of bibliometric analysis makes a great contribution worldwide. It is imperative to scrutinize the themes, whether contributing or trailing prominence, because according to 'Chen et al. (2017), there is a risk of undertakings being uneven and replicated.' It is crucial to structure well the conduct of bibliometric analysis to ensure the reliable synthesis of the information from the articles (Ozturk et al., 2024; Nowakowska, 2025; Stefanis et al., 2025).

Therefore, this bibliometric analysis was properly conducted to map the growth of CRISPR technology in plant science with the Scopus database. In this paper, the relevant observations on the structure, productivity, and direction of themes of this technology's evolution are presented, considering the evidence-based observations.

Generally, this study aimed to provide a comprehensive bibliometric analysis of CRISPR-Cas technology in plant science to map its growth, identify influential contributors, and highlight emerging trends. Specifically, it sought to analyze publication trends in CRISPR-Cas technology in plant science from 2010 to 2024 using the Scopus database, identify the most influential journals publishing CRISPR research, including citation metrics and impact factor, map co-authorship networks to identify key researchers and collaborative patterns in global CRISPR research, evaluate geographical contributions to CRISPR research, identifying leading institutions and countries in this domain, and assess key themes and topics through keyword co-occurrence analysis, identifying emerging research areas and gaps.

2. Materials and Methods

This study employed a bibliometric analysis to systematically evaluate the growth, trends, and global collaboration networks in research with CRISPR-Cas technology within the field and

scope of plant science. The methodology uses a structured approach, encompassing data collection, extraction, and analysis, utilizing VOSviewer (version 1.6.20) for visualization and interpretation.

2. 1. Database Selection

Scopus was selected as the key database outstanding due to its wide-ranging coverage of peer-reviewed scientific works across multiple disciplines and robust bibliometric tools. Scopus ensures comprehensive data access to journal articles, reviews, conference papers, and book chapters, enabling a reliable representation of CRISPR research trends in plant science. Scopus's wide-ranging multidisciplinary coverage and citation metrics provide a reliable basis for analyzing research productivity, collaboration patterns, and citation impact.

2.2. Search Strategy

A Boolean search string was constructed to capture relevant publications: ("Clustered Regularly Interspaced Short Palindromic Repeats" OR "CRISPR") AND ("Plant Science" OR "Plant Biology" OR "Agriculture") AND ("Growth" OR "Development" OR "Trends" OR "Mapping" OR "Advancements"). The "Growth", "Development", "Trends", "Mapping", and "Advancements" were included in the Boolean string to effectively retrieve studies that examine the evolution, research directions, and expansion of CRISPR technology in plant science. Therefore, incorporating these generic terms improved the comprehensiveness of the search and somehow increased the inclusion of relevant literature, highlighting the development and trajectory of CRISPR applications in plant-related fields. The search was limited to the period from 2010 to 2024 to capture the emergence and rapid development of CRISPR technology in plant science. The year 2010 marks the period when CRISPR technology began gaining significant traction in plant science research. Extending the study to 2024 ensures that the analysis captures the most recent trends, emerging themes, and collaborative dynamics.

2.3. Data Extraction

The search yielded 933 documents that met the selection criteria. The following bibliographic data were extracted in CSV format from Scopus: Document types (articles, reviews, conference papers, book chapters), Subject areas (biochemistry, genetics, agriculture), Year of publication (2010-2024), and CiteScore trends.

2.4. Analytical Tools and Visualization

VOSviewer (Version 1.6.20) was used for bibliometric analysis due to its robust capabilities in mapping and clustering bibliometric data (e.g., co-authorship, co-occurrence of keywords, citation patterns). The following analyses were conducted:

1. Co-authorship Analysis - Mapping collaborations among authors, institutions, and countries.
2. Co-occurrence Analysis - Identifying frequently occurring keywords and clustering them into thematic research areas.
3. Citation Analysis - Determining highly cited documents and identifying influential publications.
4. Network Visualization - Generating graphical representations of author networks, institutional and country collaborations, keyword occurrence clusters, and citations of documents. The threshold criteria for VOSviewer Analysis are shown in Table 1.

Table 1. Threshold Criteria for VOSviewer Analysis.

Type of Analysis	Unit of Analysis	Minimum Number of Documents	Selected Threshold
Co-authorship	Authors	1	1000
Co-authorship	Organizations	1	1000
Co-authorship	Countries	1	82
Co-occurrence	All Keywords	5	702
Citation	Documents	1	748

Thresholds were set to balance network clarity and data comprehensiveness. Lower thresholds could result in overly dense networks, making patterns difficult to interpret, while excessively high thresholds might exclude important connections.

2.5. Limitations of the Tools Used

While Scopus is comprehensive, it may exclude some region-specific or non-English publications, potentially leading to a slight geographic bias. The VOSviewer software may oversimplify complex relationships in highly dense datasets, limiting the granularity of network interpretations.

2.6. Interpretation Method

The generated figures of clusters, patterns, and collaboration networks from VOSviewer were analyzed and interpreted by the author with an AI-assisted language tool to improve the clarity of wording, refinement of academic language, and organization of explanations. The analytical decisions, especially the scientific interpretation of the results and validation of findings, were performed entirely by the author.

3. Results

3.1. Percentage of Documents by Type in the Scopus Database

The percentage of the documents by type is indicated in Figure 1. The highest percentage of documents involved in bibliometric analysis is from reviews with 41.2%, followed by articles (32.6%) and book chapters (18.2%). This implies that authors engaged more in critical analysis and evaluation of others' scholarly works and relied heavily on peer review. Innovative research and in-depth investigations of explicit topics are also highlighted through the proportions of articles and book chapters. These strong major sources are reliable for determining the network visualizations of the collaborative leading authors, keywords, institutions, and countries. The document types with a smaller percentage suggest that this collection might have been curated to focus on particular themes. This is also reported by Donthu et al. (2021) and Passas (2024) that the CRISPR technology studies were revealed in more review article publications, as used to scrutinize scientific articles by inspecting their external features.'

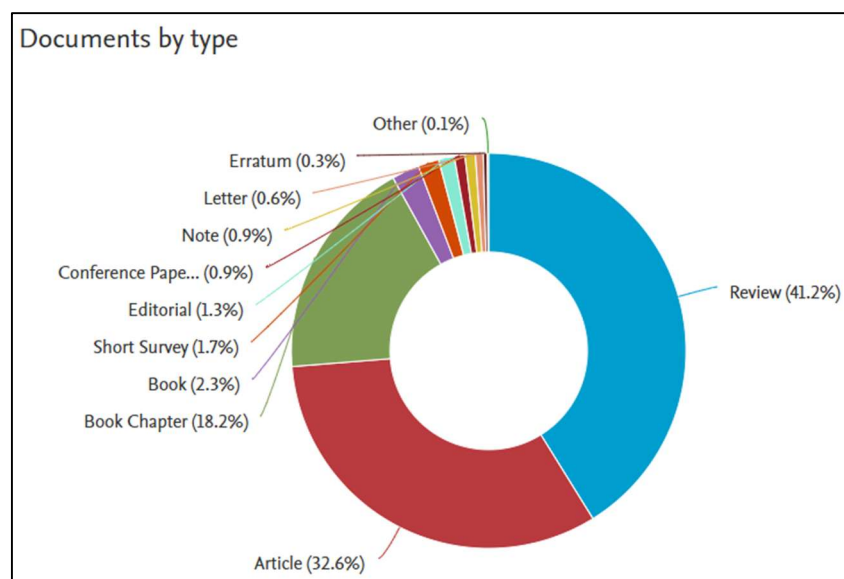


Figure 1. The percentage of documents by type of publication in the Scopus Database dominated by review articles was 41.2 percent.

3.2. Percentage of Documents by Area in the Scopus Database

The percentage of documents by subject area of publications is presented in Figure 2. It was observed that Biochemistry, Genetics, and Molecular Biology had the highest percentage of 27.2, reflecting CRISPR's fundamental role in genetic editing. On the other hand, the significant contribution of Agricultural and Biological Sciences with 24.2% highlights the practical applications in agriculture. The Engineering (7.4%), Immunology and Microbiology (6.7%), and Medicine (6.1%) indicate various groups that conceal several characteristics of health and technology. The publication that has a higher percentage may be due to the configuration with CRISPR technology, which can precisely make DNA modifications in crops and microbes that are faster, more precise, and more lucrative than traditional methods. 'Kolkur et al. (2024) also reported that CRISPR provides precise genetic editing in agriculture, auspicious solutions to food challenges.'

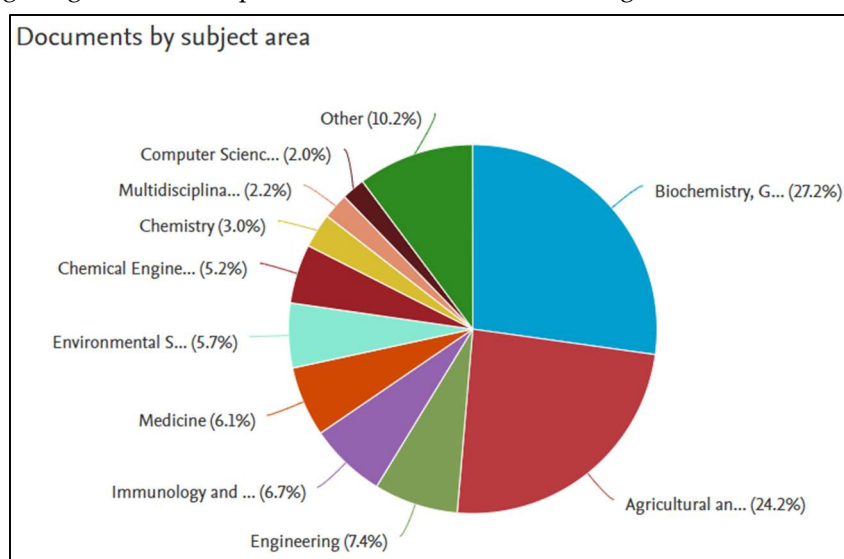


Figure 2. The percentage of the documents by subject area of publications in the Scopus Database, dominated by biochemistry, genetics, and molecular biology, was 27.2 percent.

3.3. Number of Documents Published by Year

The number of documents published by year is shown in Figure 3. Scopus database recorded that the CRISPR has progressively increased over the years, as proved by the documents published, with a significant peak in 2023. This implies that the activity in the field of adopting CRISPR technology is growing interestingly in improving crops, especially in 2023. This might be due to technological advancement, discoveries, changing research priorities, and funding support. Moreover, this might be influenced by the international conferences, scientific fora, and summits, changes in funding policies, breakthroughs, or discoveries. Thus, the CRISPR-Cas systems have been precisely developed as innovative tools for genetic modifications in plants that offer significant improvements in yield, resilience, and nutritional value, mostly in edible crops (Chen et al., 2024).

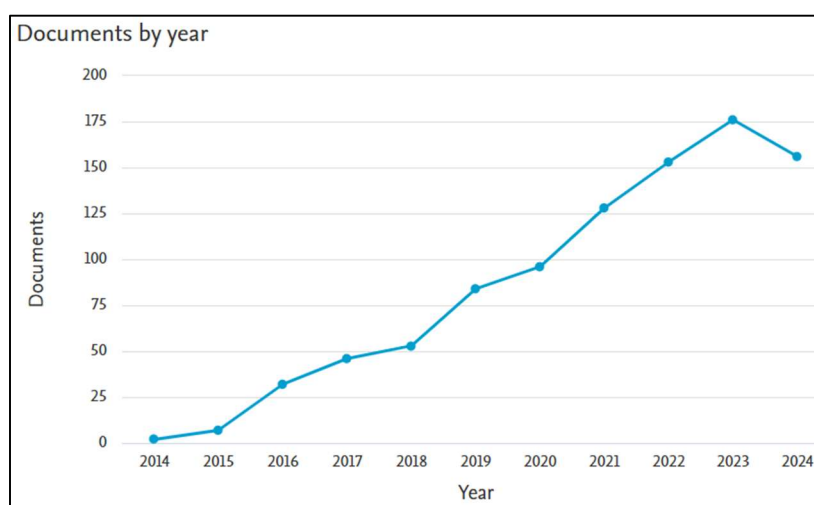


Figure 3. The number of documents published per year reached a peak in 2023.

3.4. CiteScore Publication by Year

The CiteScore publication by year is presented in Figure 4. The Scopus database revealed that most journals had to increase their CiteScore despite the noticeable fluctuation, thus increasing impact and citation rate. The rise in the CiteScore among journals corresponds with breakthroughs in the methodology of CRISPR. This might be due to the development of base-editing techniques and to the rise of research interest that focuses on biotechnology, genetics, molecular sciences, and plant science, which positively leads to further citations for articles published in these journals. The improvement of journal quality might also be one of the approaches to boost the quality of their publications, which encourages authors to submit their reputable research. It is also possible that the journals sought to increase their prominence by endorsing their articles on social media and contributing to indexing services. The published high-quality articles could attract citations, and this could contribute to the journals having a higher CiteScore.

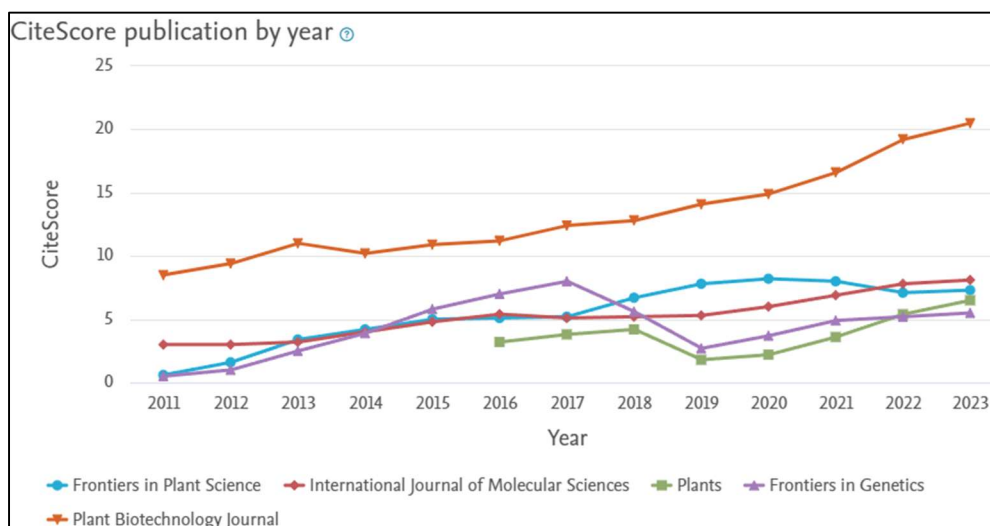


Figure 4. The CiteScore publication by year shows an upward trend for most journals, with the Plant Biotechnology Journal and the International Journal of Molecular Sciences demonstrating the most significant growth.

3.5. Network Visualization of the Co-Authorship of Authors

The co-authorship of the authors' network visualization is presented in Figure 5. The result reveals that there are eight major collaborative clusters that represent groups of authors with strong publication linkages. The blue cluster shows the group with a tightly knit collaboration with a wide range of studies on the application of CRISPR technology in plant science, composed of Kumar, Ajay, Fiaz, Sajid, Pan, Yunjun, and others in a smaller cluster linked with the blue. The purple cluster is anchored by Gao, Caixia, who connects with Zinta, Gaurav, and Mehta, Sahil, who focus on the technical development in genome editing. The light pink is led by Qi, Yiping, who links to multiple other clusters and suggests a bridging role across research groups. While the light brown, red, orange, green, and yellow are dominated by Ahmad, Aftab, Attwood, Graeme, Hegemann, Peter, Lin, Tao, and Jin, Shuangxia, respectively, who are also associated with the specialized subfields of CRISPR research. Their networks imply a global collaboration structure in the field of plant science using CRISPR technology, with predominantly linked authors who functioned as central hubs in CRISPR plant science.

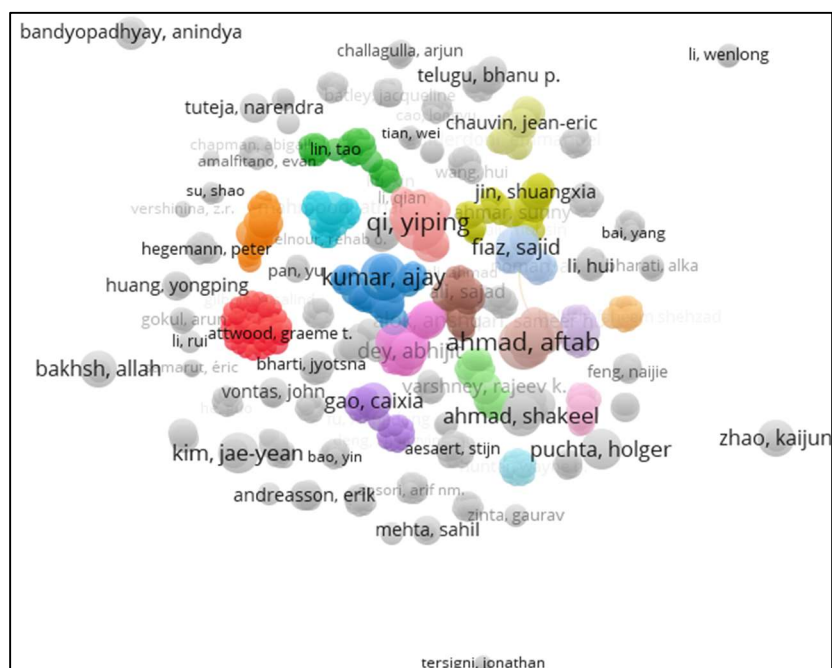


Figure 5. VOSviewer network visualization of the co-authorship of authors, in which Kumar, Ajay; Qi, Ying; Ahmad, Aftab; and Gao, Caixia, were identified as the leading authors in their respective link strengths.

3.6. Network Visualization of the Co-Authorship of Organizations

The co-authorship of the organization's network visualization is presented in Figure 6. The result visualizes the involvement of genome editing in agriculture, as it reveals a highly interconnected structure in the notable clusters formed by institutions with strong collaborative links. Based on the VOSviewer-generated figure, the University of Chinese Academy of Sciences, represented in light pink, is the most central and dominant organization, characterized by the largest node size and the highest number of connections, indicating extensive co-authorship activity. The other key institutions, like Cold Spring Harbor Laboratory in the orange cluster, had a distinct collaboration with the Department of Plant Science and Biotechnology, National Institute of Plant Genome Research, Department of Biochemistry, and the University of Nigeria. The University of Chinese Academy of Sciences seems to be closely linked with other Chinese institutions. The Department of Life Sciences and the Department of Biochemistry in the blue cluster indicate a biochemistry-focused research theme. AgResearch Limited in the green cluster had a strong collaboration with the Department of Plant Science in terms of strong contributions to applied plant research. The other smaller nodes are those institutions with fewer co-authorship links that suggest either focused on specialized research or limited collaborations.

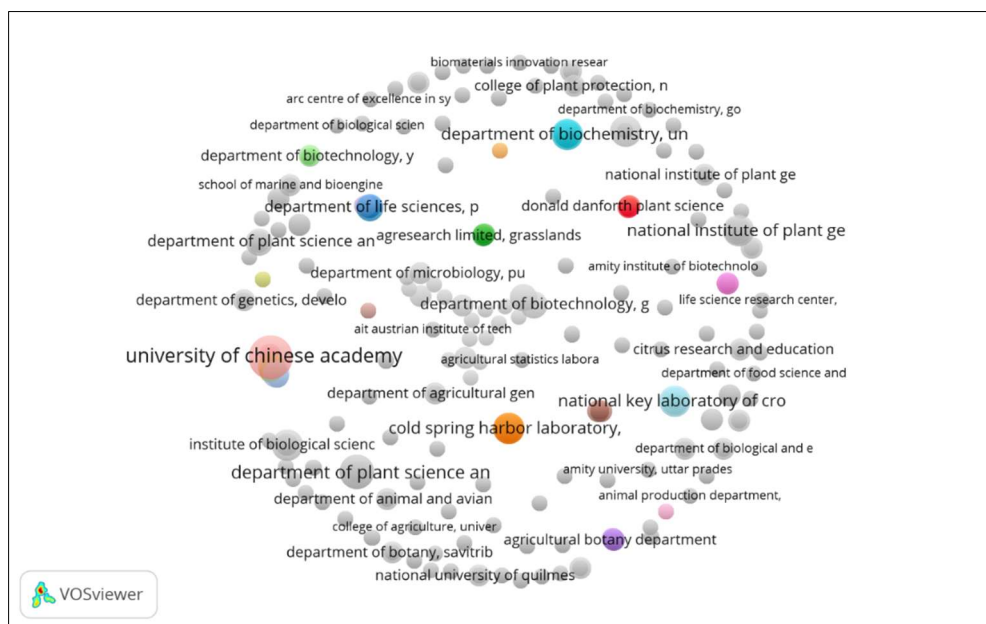


Figure 6. VOSviewer network visualization of the co-authorship of organizations in which the University of Chinese Academy is the most central and dominant organization, with a stronger connection to extensive co-authorship activity.

3.7. Network Visualization of the *Co-Authorship of Countries*

The co-authorship of the country's network visualization is presented in Figure 7. The result maps the CRISPR-related plant science national co-authorship patterns, which are interconnected with an international network. Countries such as India (light yellow cluster), China (light pink cluster), and Pakistan (blue cluster) have been the most prominent contributors to crop improvement through the adoption of CRISPR-Cas technology. The most central hub is the country of India, which maintains strong collaborations with Germany, Australia, Saudi Arabia, and even Russia. On the other hand, China also demonstrated global outreach extensively, especially with Pakistan, Australia, and South Korea. The country of Pakistan has a concentrated pattern of regional collaboration with Sri Lanka, Lebanon, the United Arab Emirates, and Egypt. Furthermore, the countries of Germany and France in the green cluster are expressed as European collaborators, which are bridging networks with India, Brazil, and Italy. The yellow cluster comprises India, South Korea, Australia, and Russia, which represent leadership in genome editing technologies. The cyan cluster comprises Pakistan and several South Asian and Middle Eastern countries, which reflect the regional research consolidation. The red cluster that consists of Canada, Spain, Turkey, and Brazil contributed to applied biotechnology cross-continently. The blue cluster consists of the United Kingdom, Italy, Belgium, Mexico, and Kenya, although they are smaller nodes and are also active contributors to crop-focused genome research.

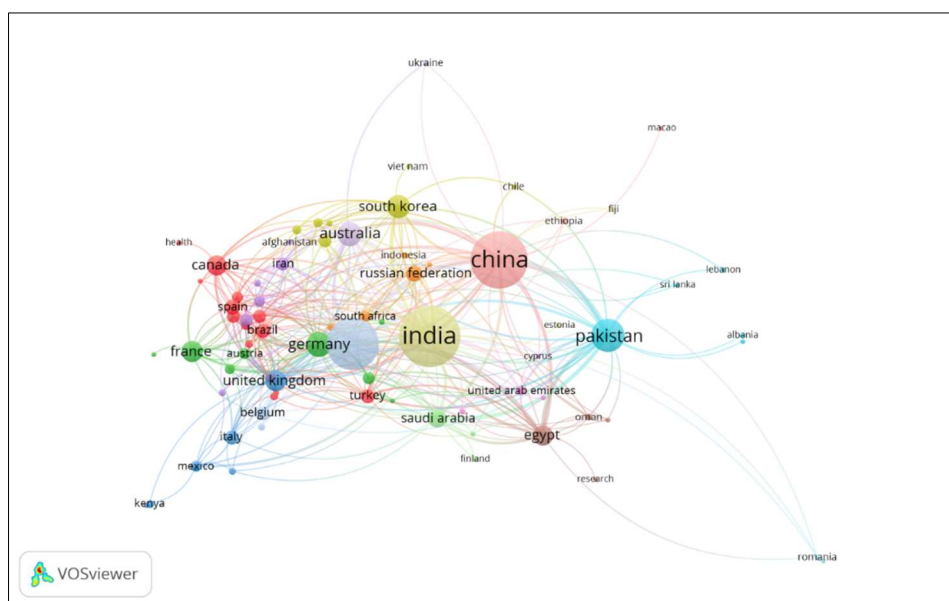


Figure 7. The VOSviewer network visualization of the co-authorship of the countries in which India, China, and Pakistan are anchored as the leading countries in terms of the research collaborations adopting CRISPR-Cas technology for crop improvement.

3.8. Network Visualization of the Co-Authorship of All Keywords

The co-occurrence of all keywords' network visualization is presented in Figure 8. The result shows that the most prominent keywords are genetics, gene editing, and genome editing, because they are positioned centrally, which reflects CRISPR's dual role as a cutting-edge molecular tool and also a unifying theme in plant science research. The purple cluster is led by genetics, which links with all other clusters, showing its role as a conceptual foundation. The yellow cluster has an integration of gene editing, genome editing, plant genome, gene targeting, and even governance-related terms (e.g., genetically modified food, legislation, and jurisprudence), which highlights both the regulatory and technical dimensions. The blue cluster consists of animals and core CRISPR-associated terms, especially the CRISPR-Cas system, which represents the technological advancements and precision genome editing. The green cluster contains metabolism, gene expression, and controlled study, which focuses on molecular and biochemical processes, and indicates the use of CRISPR in functional genomics and metabolic pathway engineering. The red cluster focuses on crop improvement and stress tolerance, as it contains plant growth, rice, maize, drought stress, climate change, phytohormones, crops, genomics, abiotic stress, and other related terms, suggesting the application of CRISPR to improve yield stability under environmental factors. The strong intercluster linkages imply that, in mainstream crop improvement and policy discourse, the application of CRISPR technology has expanded beyond model organisms.

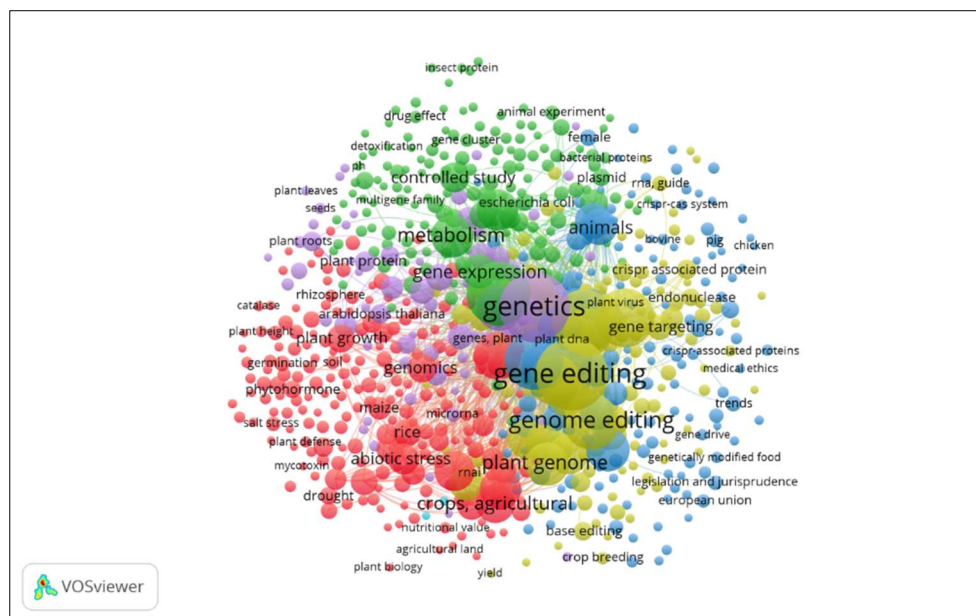


Figure 8. The VOSviewer network visualization of the co-occurrence of all keywords, where genetics, gene editing, and genome editing are prominent, suggests CRISPR's dual role as a cutting-edge molecular tool and also a unifying theme in plant science research.

3.9. Citations of Documents

The citation of the documents' network visualization is presented in Figure 9. The result expresses that several CRISPR studies in plant science were found in the identified core publications that form the intellectual foundation. The most cited publications were recorded for Bortesi (2015), Chen et al. (2019), Seshadri et al. (2018), Smanski (2016), Pham (2019), and Zhang (2019). This indicates their broad influence across technical development and theoretical discussions of CRISPR technology applied for crop improvement, as they are bridging multiple clusters. The Bortesi (2015) had the largest nodes of the green cluster, and the Chen (2019) in the yellow cluster, which are strongly linked with other frequently cited papers with Zhu (2018), Smanski (2016), Seshadri et al. (2018), Zhang (2019), Eshed (2019), Weeks (2016), Pham (2019), and other linked papers found in the gray nodes. Those papers performed their central role in persuading the use of CRISPR methodologies and applications in plants or crops. The distinction of the citation clustering reflects the specializations of theme, which includes CRISPR mechanism development that delivers strategies for treating the improvement in crops and regulatory perspectives.

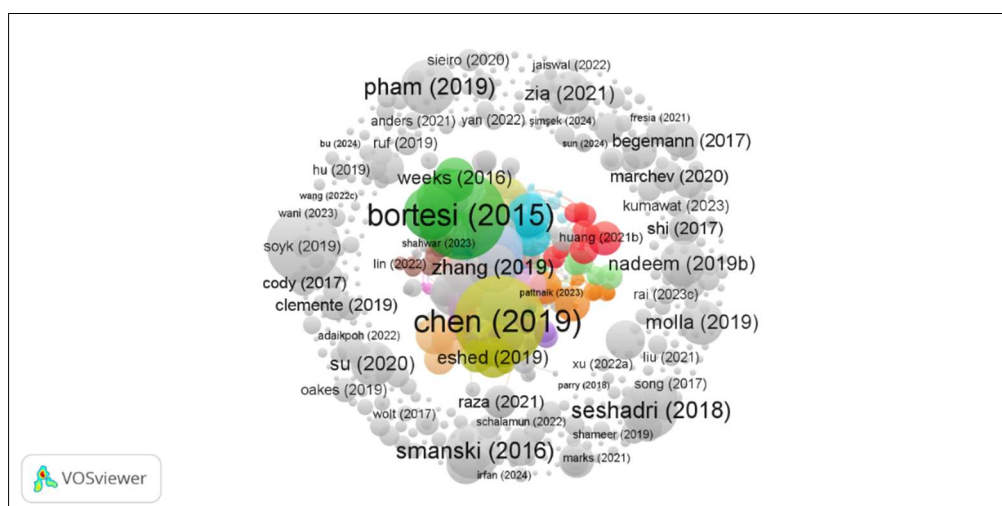


Figure 9. The VOSviewer network visualization of the citations of documents was Bortesi (2015) and Chen (2019) show the strong link strength of citations.

4. Discussion

A notable structural characteristic of the dataset is the high proportion of review articles, which comprised 41.2% of the total publications (384 documents). This outcome is closely related to the adopted search strategy, which intentionally included broad conceptual terms such as “growth,” “development,” “trends,” “mapping,” and “advancements.” These terms are frequently used in review and bibliometric literature that focuses on synthesizing research progress and technological evolution (Cheng et al., 2024; Shasha et al., 2025). The dominance of review articles may influence the configuration of collaboration networks by increasing the apparent centrality of prolific authors and leading institutions (Duan, 2024), as review papers often involve senior scholars, internationally recognized research groups, and multi-institutional collaborations (Hoang, 2025; Seifert and Hassan, 2025). Consequently, the authors and organizations may emerge as highly central within the network not only due to original research activity but also because of their prominent role in knowledge synthesis and agenda setting (Passas, 2024). This effect should be considered when interpreting collaboration patterns, as network centrality in this study may partially reflect the structural influence of review-based publications.

The network visualization of the co-authorship of authors demonstrates both global integration and specialization in CRISPR plant science research. Kumar, Ajay, and his collaborators were associated with CRISPR-based crop improvement, mostly in yield traits and abiotic stress tolerance, which is ‘consistent with prior work on molecular plant breeding according to Miglani (2017).’ Gao, Caixia, is recorded as a leader in advancing genome editing platforms for improving cereals, especially rice and wheat, for higher efficiency and high-fidelity editing systems, as reported also by Gao (2020). While Qi, Yiping, performs his crucial role in developing the toolkits of CRISPR that include the multiplex editing systems, delivery platforms, and Cas variants that bridge to methodological and applied research (Zhang et al., 2021). This mirrors the bibliometric findings of high international cooperation in CRISPR research, most especially among European, American, and Chinese institutions. This implies that the innovation of this analysis lies in overtly mapping thematic co-authorship clusters and seeing how these collaborative edifices align with subfields of CRISPR

plant research. Moreover, it is noticeable that the intra-cluster collaboration is strong, but there are less frequent in firm areas and suggests opportunities for bigger incorporation between technology inventors and field application specialists.

There are clear patterns of institutional collaboration in genome editing for agriculture in the investigation of co-authorship networks among organizations. China's major contribution to research output in the field is made by the University of the Chinese Academy of Sciences. This is consistent with the previous studies revealing the growth of China, which eventually influences agricultural biotechnology. The involvement of Cold Spring Harbor Laboratory and the National Institute of Plant Genome Research accentuates the global banquet of collaboration across Asia, North America, and Europe. These institutions are well known to be the hubs for innovation and interdisciplinary research, which reflects the nature of collaboration with multiple biotechnology and biochemistry departments, indicating an ongoing convergence between molecular biology and agricultural sciences. The analysis was notable in that fewer prominent institutions like AgResearch Limited and the Department of Agricultural Genetics also play essential roles in targeted research areas, for example, crop improvement and genomic resilience, even though there are more limited co-authorship networks (Miglani, 2017). The structure of the organizations' collaboration emphasizes the importance of institutional partnerships in solving the increasingly complex agricultural challenges. Moreover, they demonstrated engagement transnationally, which raises questions about how resource allocation and research infrastructure shape global cooperation in genome editing and policy environments.

The evolution of leadership and strategic partnerships in CRISPR plant science is highlighted by the co-authorship network of countries. The countries that dominate the research landscape are India and China, confirming their status as global leaders in terms of plant genome editing, mostly for crop improvement to be stress-tolerant and secure food. The central role of India connects to advanced economies of Germany and Australia as well as to regions (e.g., Pakistan and Sri Lanka), indicating its functional growth as a disseminator of knowledge of CRISPR-enabled plant science. On the other hand, Pakistan's regionally coordinated approach, by its close alignment with the Middle Eastern countries, was motivated by shared agricultural constraints (e.g., salinity and drought). European countries like Germany, the United Kingdom, and Italy collaboratively bridge between continents, underlining their role as a global hub in plant biotechnology research. The development of Australia and South Korea expands investment and partnership in high-impact strategic crop biotechnology. Their networks observed patterns beyond the capacity of the scientific scenario that reveal the strategic alignment of national priorities with global agricultural agendas of innovation. There are many countries that integrate genome editing into their agricultural research and development programs to make the production system modernized and for resilience and food security enhancement, and food security (Halimi et al., 2023). The relationship of global integration and regional clustering mostly influences the accessibility and innovation pathways of CRISPR technology in plant science (Xu, 2024; Asiamah et al., 2025).

The rapid integration of CRISPR technology into diverse plant science domains is demonstrated by the network visualization of keywords from collaborative authors and Scopus. This confirms that CRISPR is no longer limited to proof-of-concept studies but is actively applied in major food crops, such as maize and rice, which are near the CRISPR-Cas system, gene targeting, and base editing. It is consistent with recent global trends as reported by Nasti and Vovtas (2021) and Zhang et al. (2021).

The abiotic stresses were emphasized, such as drought stress, climate change, and salt stress, which are aligned with findings that CRISPR is increasingly used to develop climate-resilient varieties (Li et al., 2018; Gao, 2021). It was also found that the involvement of metabolism-related terms suggests the growth of CRISPR adoptions into biochemical trait engineering (e.g., nutritional enhancement and metabolic pathway modification (Borelli et al., 2018)). Furthermore, the occurrence of governance-related keywords, such as legislation and jurisprudence, within the networks of the European Union emphasizes the developing policy and biosafety considerations. This is spreading the observations from previous bibliometric analyses that CRISPR's regulatory landscape is growing alongside its progress in technical ways (Menz et al., 2020; Wei et al., 2022; Wei et al., 2023; Alomari et al., 2024). In comparison to the earlier bibliometric analyses, the research on stress and genome editing formed separate domains. On the other hand, the present results show a closer integration of interdisciplinary research, which indicates CRISPR as a central hub with connections to plant physiology, molecular biology, and regulatory science.

Bortesi (2015) confirms the foundational status of the reviews that consolidate the early knowledge on CRISPR applications in plants, which served as a key reference for subsequent studies (Yan et al., 2019). In the same case, *Chen* (2019) is profoundly cited for the methodological advances in the efficiency of genome editing, which influence both experimental methods and downstream trait development projects (Zhu et al., 2018). The patterns in the citations of document clusters showed that the early technical papers remain relevant, which suggests the continued underpinning of foundational methodology for newer applied research. The presence of other scholarly works in the network implies the expansion of rapid knowledge with newer studies that integrate advanced CRISPR variants like base and prime editors (Nasti and Vovtas, 2021). In comparison to similar bibliometric mappings, this research's network of document citations reveals a strong retention of key methodological literature alongside a continuous influx of applied studies, which reflects CRISPR's dual role as both a maturing and rapidly emerging technology in plant science for crop improvement.

5. Conclusions

There is a distinct thematic co-authorship cluster exhibited in the evolution of CRISPR technology in plant science, led by Kumar in crop improvement, Gao in genome editing platforms, and Qi in the methodological toolkits. The strong global and regional collaboration patterns among India and China, as dominant contributors, are also supported by the European countries, Australia, South Korea, Pakistan, and Middle Eastern partners, aimed at addressing the existing agricultural challenges. The University of Chinese Academy of Science, Cold Spring Harbor Laboratory, and the National Institute of Plant Genome Research are the key institutions that anchor innovation networks alongside organizations with a small extent of specialized expertise. The application of CRISPR technology has expanded beyond proof-of-concept to major crops as a source of food, climate resilience, and metabolic engineering, with the emerging critical dimension of policy and biosafety considerations. The foundational methodological studies are continuing as highly relevant, complemented by the newer advances, including base and prime editors, which reflect the dual role of CRISPR as both a platform established and evolving rapidly as a driver of agricultural innovation.

Therefore, the following are recommended:

1. More integration between technology developers like genome editing platform innovators and applied crop improvement specialists may be fostered to accelerate the translation of CRISPR breakthroughs into field solutions.
2. The joint projects between leading contributors and underrepresented regions may be encouraged to expand research diversity and address challenges in global food security.
3. The smaller research organizations that contribute specialized expertise in niche areas such as stress tolerance and metabolic engineering may be funded and provided with services like capacity-building.
4. The governance structures may be developed and harmonized to address ethical and biosafety issues and their legalities to enable smoother adoption of CRISPR innovations in agriculture.
5. The core CRISPR techniques may be continuously referenced and refined while investigating advanced variants such as base and prime editors to maintain both innovation and reliability.
6. The CRISPR projects may be prioritized and target abiotic stress tolerance, drought, and other stresses to enhance crop adaptation to climate change.

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Conflicts of Interest: The author declares no conflict of interest.

Data availability statement: The data used in this study were retrieved from the Scopus database (Elsevier). Due to licensing restrictions, the raw data cannot be publicly shared. Processed data are included in the manuscript, and additional data are available from the corresponding author upon reasonable request.

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