Current Trends in Biotechnology and Pharmacy
Vol. 20 (Supplementry Issue 1A), March 2026, ISSN 0973-8916 (Print)., 2230-7303 (Online)
10.5530/ctbp.2026.1s.11

Global Regulatory Frameworks for Multiplex Genome Editing: A Bibliometric Analysis

Egambaram Gowtham, Jevanantham Senthamarai Kiruthika, and Palanisamy Suresh Babu*

Department of Biotechnology, Saveetha School of Engineering, Saveetha Institute of Medical and Technical Sciences (SIMATS), Thandalam, Chennai - 602105, Tamil Nadu, India
*Corresponding author: sureshbabup.sse@saveetha.com

Abstract

The demand for efficient and sustainable food production systems has increased due to the world’s growing population and shrinking arable lands. The creation of high-yielding, nutritionally improved, and stress-tolerant cultivars has become crucial in order to meet these challenges. With the introduction of sophisticated genome editing tools, particularly Multiplex Genome Editing (MGE). methods like CRISPR-Cas9, traditional breeding practices and early genetics alteration tactics have changed. These technologies provide promising strategies for enhancing crop resilience against pests, diseases, and environmental stressors by enabling precise and simultaneous changes at numerous genetic loci. This study uses bibliometric analysis to explore the landscape of MGE research in crop improvement using data from Web of Science and Scopus (2016-2025), tools like VOSviewer and Bibliometrix in R studio are used to generate visualizations of collaboration networks, co-authorship, keywords trends, and citation patterns. The analysis reveals major research domains that are driving progress in the field, such as yield enhancement, trait stacking, metabolic engineering, and gene regulation, as well as leading authors, institutions, and journals that are driving this field. Therefore, a thorough bibliometric analysis of MGE in crop improvement utilizing CRISPR-cas9 over the last ten years is needed. The current efforts attempt to close this research gap by providing academics with multi-dimensional insights into current and future developments in the promising field.

Keywords: Genome editing, CRISPR-Cas9, Plant Breeding, Bibliometric, crop improvement

Introduction

Demand for high-yielding, sustainable agricultural methods is growing as the world’s population rises and arable land shrinks. Despite their value, early genetic alteration approaches and traditional breeding procedures have limitations in terms of scalability and precision. By increasing productivity, disease resistance, and stress tolerance, Multiplex Genome Editing (MGE) technologies in particular, CRISPR-Cas9 offer hitherto unheard-of possibilities for targeted crop development (1). A thorough bibliometric study that synthesizes research trends, important contributors, thematic focus areas, and technological advancements over the past ten years is still absent, despite the expanding body of research on MGE applications in agriculture. This gap limits the ability of researchers and policymakers to identify progress, challenges, and future directions in the field. Therefore, there is a critical need to conduct a structured bibliometric review of MGE research, especially CRISPR-Cas9 applications in crop improvement, to map the evolution of this field and guide future research and innovation.

As the world's population grows and the amount of arable land shrinks, the need for food is rising daily. It is necessary to create high-yielding, nutritionally enhanced, and stress-tolerant cultivars in order to satisfy this growing demand. Numerous methods, including translocation breeding, intergeneric crosses, and mutagenesis, are advanced to improve crop quality. Later, as genetic engineering advanced, genetically modified crops established the transgene insertion technique, which helps them survive harsh environments. Genetically modified crops are regulated using process- or product-focused approaches, which take into account the risks to the environment and public health. Multiplex Genome Editing (MGE) methodologies are newly developed multipurpose bioengineering tools for adapting two or more specific DNA loci in a genome with high accuracy. Such genome editing gears have significantly increased the viability of introducing desired variations at numerous nucleotide degrees into a target genome (2).

In the current genomic era, the choice of incapacitating these strains for a food crop has expanded due to the widespread availability of genomic resources and genome editing technologies like Transcription Activation-like Effector Nucleases (TALENs), Zinc Finger Nucleases (ZFN), and Clustered-Regularly Interspaced Palindromic Repeats and its associated proteins (CRISPR/Cas). By introducing or removing DNA sequences of the target gene or genes from the genome, these methods have made gene editing easier to handle and more accessible at the embryonic level. The CRISPR construct is made up of a solitary guide RNA that complements the target gene sequence's nucleotide segments and has an adjacent protospacer motif. To get the desired traits of interest, the Cas9 endonuclease then cleaves the target sequence in the organism's genome. The elements, working, and varieties of CRISPR-Cas methods are discussed in the current review, along with how this technology has aided in the functional characterization of genes linked to different biotic and abiotic stressors in a target organism. The use of CRISPR-Cas tools to target these challenges in crops by knocking down or deleting related genes (3).

Owing to the plethora of applications, MGE technique increases crop resilience to pests, diseases, and climate changes, which guarantees increased yields and better sustainability in agriculture and food security. It revolutionizes disease treatment in medicine and human health by facilitating the creation of gene therapies, the repair of genetic diseases, and advances in personalized medicine (4). Genome editing helps biodiversity and conservation efforts by controlling invading populations and safeguarding endangered species. It is essential to the production of biofuel, synthetic biology, and microbial engineering for environmental solutions in industrial biotechnology. These developments, however, bring up moral and legal questions, including the possibility of unforeseen genetic repercussions, challenges to biosecurity, and concerns about fair access (5).

Bibliometric Analysis design

Bibliometric analysis is a qualitative technique that uses statistical analysis of literature to comprehend research trends, patterns and the general organization of a field. So, this analysis is useful for showing how a certain subject of study has changed over a number of years or even decades. Reviewing scientific research developments on certain issues can be done in a number of ways. The two main types of these approaches are relational and evaluative reviews. The quantitative examination of the total research impacts of research papers, authors, organizations, and nations is done through evaluative reviews. This analysis includes a range of production metrics, including the number of journals, annual publications, citations and more (6, 7).

The present study uses relational and evaluative methods to provide a sensible bibliometric analysis of research in MGE in crop improvement. Important information about the research outcomes of individual authors and their affiliated organizations, the networks of collaboration and citations among documents, organizations, authors, and location, keywords and trending topics, top publishing journals, inter-journal linkages and additional are usually obtained from these analyses (8). VOSviewer was used for quantifiable data analysis and visualization of MGE in crop improvement using CRISPR-cas9 issued articles in the Web of Science (WoS) from (2016 to 2025). and SCOPUS from (2016 to 2015). Grounded on bibliometric analysis of collaboration and citation data, VOSviewer (version 1.6.20). creates keyword, author and journal linkage maps. It can also generate keyword networks that validate the relationship between numerous co-occurring phrases in a study topic. R Studio (version 4.4.3). Biliometrix is used for bibliometric analysis, including citation mapping, co-authorship networks, and keywords trend visualization. Bibliographic data from sources such as Web of science and Scopus is processed and cleaned with its assistance. Science mapping, topic evolution analysis, and the generation of performance measures such as impact factors and h-index are all made possible by the program (9, 10).

The objective of the studies have concentrated on bibliometric analysis of MGE in crop improvement using CRISPR-cas9 within comparatively specific domains like yield enhancement, metabolic engineering, disease resistance, trait stacking, stress tolerance, and gene regulation. Therefore, a thorough bibliometric analysis of MGE in crop improvement utilizing CRISPR-cas9 over the last ten years is needed. The current efforts attempt to close this study gap by providing academics with multi-dimensional perceptions into present and future progresses in the promising field.

Methodology

The current study employed a bibliometric analysis approach to examine the global research landscape on regulatory frameworks for multiplex genome editing, integrating quantitative methods to map publication trends, citation patterns, and thematic structures. The research was conducted using RStudio (version 4.4.3). with the Bibliometrix and Biblioshiny packages, alongside VOSviewer for visualizing keyword clustering and co-occurrence networks. The data collection began with a clearly defined research objective, focusing on the intersection of genome editing technologies (such as CRISPR-Cas9). and their associated regulatory, ethical, and policy frameworks. Bibliographic data were sourced from reputable scientific databases-Scopus and Web of Science-using a targeted search query: ("Multiplex Genome Editing" OR "CRISPR-Cas9" OR "Gene Editing") AND ("Regulation" OR "Governance" OR "Policy" OR "Ethics"). The search was restricted to English-language documents published between 2016 and 2025, including articles, reviews, and conference papers relevant to policy, bioethics, and regulation.

The retrieved bibliographic data were exported in two formats: CSV format and plain text format for analysis in RStudio and .csv for use in VOSviewer (version 1.6.20) (11). Prior to analysis, the dataset was eviscerated to remove duplicates, unify author and institution names, and standardize keyword terminology. In RStudio, the Bibliometrix package was used to perform a range of quantitative analyses such as annual scientific production, citation trends per year, most relevant authors and affiliations, most cited countries, collaboration networks, and keyword co-occurrence patterns. Through the Biblioshiny GUI, interactive visualizations were generated, including trend topic analysis, thematic mapping, and conceptual structure mapping using Multiple Correspondence Analysis (MCA) (12).

For deeper insight into thematic relationships, keyword co-occurrence data were exported and analyzed using VOSviewer (13). The software was used to create network visualizations by selecting co-occurrence based on “all keywords” with a lowest threshold of five keyword occurrences. The resulting maps included density plots, network diagrams, and cluster visualizations, revealing how keywords such as “CRISPR regulation”, “ethics”, “germline editing” and “international governance” were interlinked. Each cluster was color-coded, allowing for the identification of core research themes and their interconnections. The combined use of RStudio and VOSviewer provided a robust methodology for mapping the evolution and structure of research on genome editing regulation. The final output integrated statistical insights and visual representations to identify global leaders in research, collaboration patterns, emerging policy concerns, and the conceptual foundations of the field, forming a strong empirical basis for understanding current trends and gaps in the regulatory discourse surrounding multiplex genome editing (14).

Results

Annual Scientific Production

Research output on the topic of Global Regulatory Frameworks for Multiplex Genome Editing increased significantly between 2019 and 2021 (Fig. 1), reaching a peak of more than 100 articles in 2021, according to the field's annual scientific production graph (15). This increase most likely reflects a rise in interest in the moral, legal, and biotechnological ramifications of genome editing using CRISPR on a worldwide scale. Publication rates stayed comparatively high until 2023, despite a minor decline in 2022, indicating ongoing scholarly activity. Between 2024 and 2025, there is a discernible drop, which could be brought on by changes in research priorities or publication delays. The peak period (2021-2023) coincides with increased regulatory scrutiny and advances in multiplex editing tools for agriculture, medicine, and synthetic biology. The basic accumulation of literature is shown by the early growth phase (2019–2020), while the current decline might call for more research. All things considered, the pattern demonstrates that multiplex genome editing has been a major area of study for the last five years due to both scientific advancement and policy significance (16).

Most Citation Country

According to a bibliometric analysis of the international literature on multiplex genome editing regulatory frameworks, the United States leads in total citations, which is indicative of its significant influence in forming the scientific and regulatory discourse through important organizations like the FDA and NIH as well important publications on bioethics, CRISPR governance, and genome oversight. The UK large amount of research, has a s in second with the maximum average number of citations per document, highlighting the extraordinary impact of fewer but significant contributions, especially from organizations like the Nuffield Council on bioethics and academic institutions like

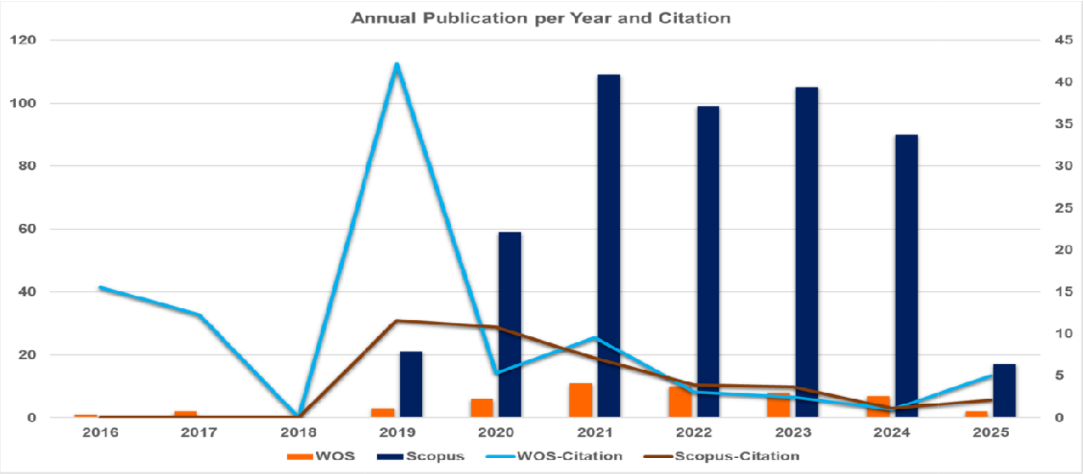

Fig 1: depicts year-wise publication along with number of cumulative citations

Oxford and Cambridge that have written extensively about ethical governance, public involvement, and legal clarity in human genome editing.

Germany holds a prominent position with high impact contributions that emphasize legal and constitutional perspectives, with organizations such as the Max Planck Institute publishing widely cited analyses on the regulation of gene editing within democratic frameworks. China, despite producing a relatively lower average citation rate, reflecting a growing but still maturing impact (Fig. 2). Other European nations, such as France, the Netherlands, and Italy, make significant contributions through the European Union's harmonized policy efforts, with EU-wide regulatory reports and precautionary legal frameworks being frequently cited across jurisdictions. Because of their well-known policy analysis papers and globally cited regulatory models-such as Australia's Gene Technology Regulatory Frameworks and Canada's Tei-council Policy Statement which are frequently cited for their organized risk based methodologies and ethical consent procedures, nations like these exhibit high average citation counts (17). Japan and South Korea, meantime, are becoming more well known for their careful incorporation of ethical and cultural considerations into gene governance, offering complex viewpoints through their expanding literature.

The most frequently cited nations are those that actively influence global policy and ethical norms in addition to advancing science, highlighting the significance of regulatory leadership, interdisciplinary cooperation, and international policy engagement in the rapidly changing field of multiplex genome editing(18). The analysis of the most referenced countries shows that, with 3,797 citations overall, China tops the world in multiplex genome editing research output, demonstrating its significant contribution to both collaborative and scientific innovation (19). With 1,789 citations, the US comes in second, demonstrating its significant influence in early CRISPR research and regulatory debates. With 1,709 citations, India comes in third place, demonstrating its growing sway in the sector, especially in agricultural applications and policy engagement. Australia (478 citations) and South Korea (897 citations) both make substantial contributions to cutting-edge research, particularly in the areas of agriculture development and CRISPR technology. Despite their increasing involvement, nations like Germany (179), Kenya (349), and Pakistan (456), remain less well-known worldwide. Although the presence of both established and developing countries indicates a diverse research environment, the majority of the most frequently cited countries continue to focus on technical and application-based research (20). This highlights an ongoing deficiency in ethical and regulatory research, which is essential for internationally standardized genome editing regulation.

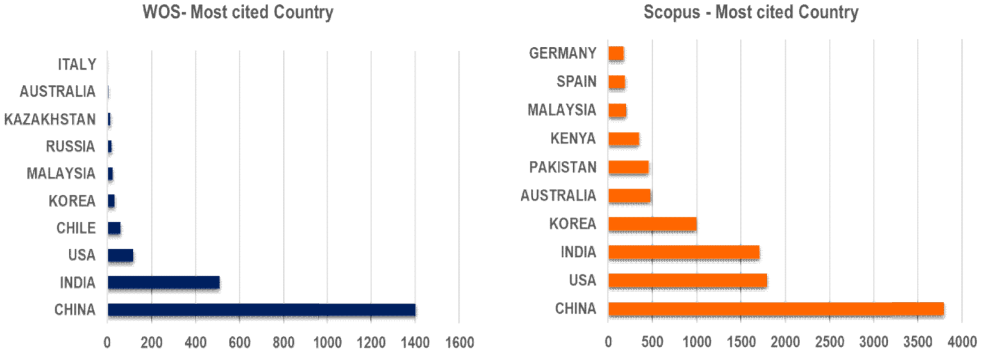

Fig 2: Most cited countries

Tree Map

The most common keywords in the literature on multiplex genome editing and regulatory frameworks are shown in the tree map visualization. A high technical and scientific focus is indicated by the dominating terms, which include gene editing (13%), CRISPR-Cas systems (6–7%) and genetics (6%) (Fig. 3). Research on agricultural uses is shown in keywords like "plant breeding," "transgenic plant," and "crop improvement." But the underrepresentation of ethical and regulatory terminology highlights a disconnect between the discourse on governance and technology innovation. This shows that more comprehensive research on the ethical, legal, and policy aspects of genome editing is required (21).

Trends Topic

Research on multiplex genome editing from 2020 to 2022 was primarily centered on fundamental technical phrases such as "genome editing", "CRISPR-Cas system" and "gene editing" according to the trend topic analysis (Fig. 4). Peak scientific involvement was indicated by the highest frequency of these phrases. A move toward agricultural and environmental applications was reflected in the emergence of fresh themes such as "climate change," "environmental stress," and "breeding method" starting in 2022 (22). More interest in sophisticated editing techniques is shown by recent terms like "cytosine deaminase" and "CRISPR-associated protein." Throughout, the discussion of genetic variety and genetically modified plants was constant. There was a lack in governance-focused studies, though, as concepts pertaining to ethics, legislation, and policy were conspicuously missing (23). This implies that future research should incorporate regulatory discourse more thoroughly.

Coupling map

Different groups of closely connected research subjects within the field of multiplex genome editing are revealed by the document coupling map (24). Dominant clusters like "gene editing", "CRISPR-Cas system", and "CRISPR-Cas systems" are found in the upper-right quadrant, which combines high centrality and high impact (Fig. 5). These clusters each contribute more than 25–30% of the total thematic coupling, demonstrating their crucial significance in advancing the field (25).

Moderately influential but less prominent themes like "plant breeding" and "plant genome" are included in the upper-left quadrant, emphasizing their applicability in agricultural settings. Clusters such as

Fig. 3: Tree Map showing all author's keywords and its frequency

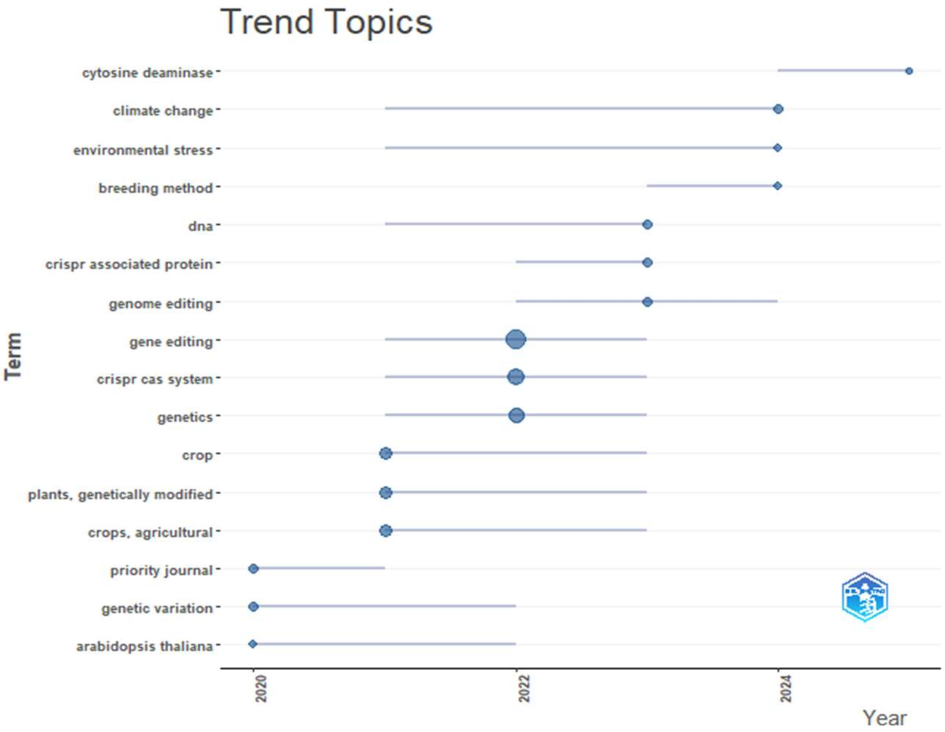

Fig 4: Trending topics

"biotechnology" which have a low centrality but a moderate influence, are found in the lower-right quadrant, indicating new but undeveloped connections to the main discourse. The middle zone's central but low-impact clusters, such as "genetic engineering" and "gene editing," point to underlying issues that are being revisited with growing significance (26). Overall, the map shows that although the area is dominated by basic technical concerns, there is still a need for interdisciplinary expansion because of the insufficient integration of more general regulatory or governance topics (27).

Thematic Map

Research subjects are categorized using thematic map analysis according to density (development) and centrality (relevance). "Gene editing", "CRISPR-Cas system", and "genetics" are included in the bottom-right quadrant (Basic Themes), indicating that these are fundamental and closely related subjects in the literature, albeit still evolving in complexity. "Crop improvement," "abiotic stress," and "review" are found in the top-right quadrant (Motor Themes)., suggesting that these are both extremely pertinent and well-developed, propelling the field ahead. Terms like "metabolism," "guide RNA," and "article" are well-developed but have no meaning in the top-left quadrant (Niche Themes); they may be specialized subtopics (28). Lastly, "crops", "gene", and "genome editing" are found in the bottom-left quadrant (Emerging or Declining Themes), indicating that although these were previously important, they may now be waning or require more research (Fig. 6). Overall, the map shows that while regulatory or policy-related themes are missing, key technical phrases continue to be structurally significant, indicating a gap in the literature that must be filled for thorough governance studies in genome editing (29).

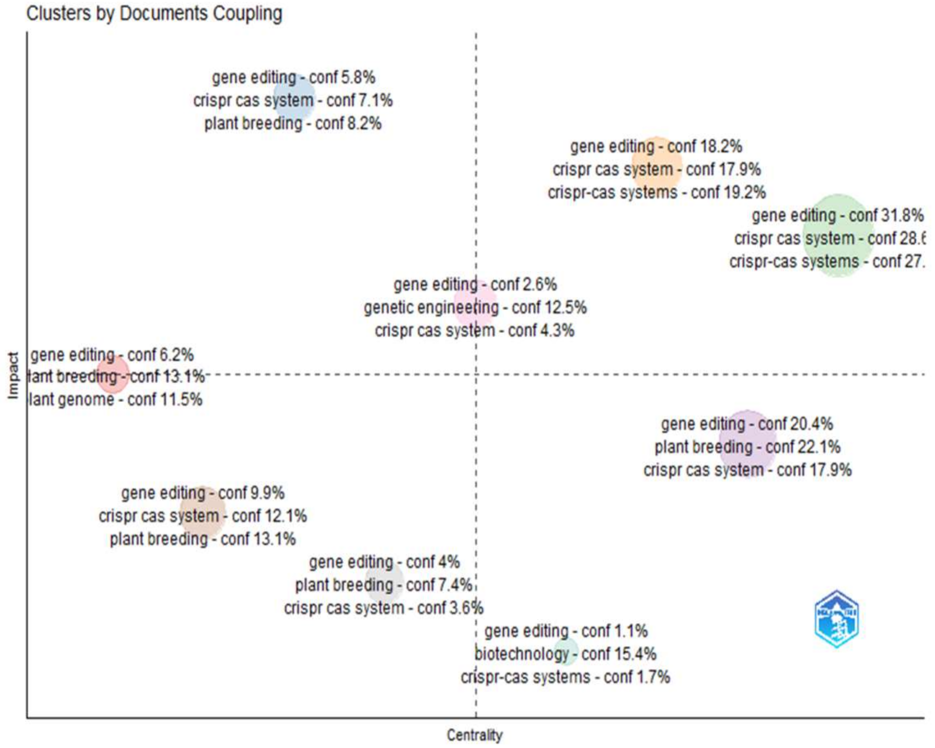

Fig 5: Technical coupling theme map

Factorial Analysis

The factorial analysis finds important topic groupings in the multiplex genome editing study by combining Hierarchical Clustering and Multiple Correspondence Analysis (MCA) (30). Significant term clusters that represent crucial conceptual domains including "plant breeding," "crop improvement," "biosafety," "genetic engineering," and "CRISPR-based techniques" like CRISPR-Cas9, prime editing, and base editing are revealed by the MCA plot (Fig. 7). These clusters also contain emerging issues like food security, abiotic stress, and climate change, demonstrating the increasing convergence of genomic technologies with international agricultural sustainability objectives (31). The use of phrases like "biosafety," "gene targeting," and "regulatory tools" suggests that the ethical and governance ramifications of genome editing are receiving more attention.

Country Scientific Production

A geographical overview of the amount of multiplex genome editing research output is given by the country's scientific production map. With the darkest blue hues, China and India are clearly the leading contributors, demonstrating their dominance in the publication of substantial amounts of scholarly material on the subject. The United States is closely behind these nations and produces a significant amount of work as well, particularly in the areas of technology development and genome editing regulations. Australia, Brazil, Germany, South Korea, and a number of European countries are among the other regions with moderate to high scientific productivity, indicating a worldwide spread of interest in the field. Africa, Central Asia, and portions of South America, on the other hand, have lighter hues, suggesting comparatively less research effort. The map

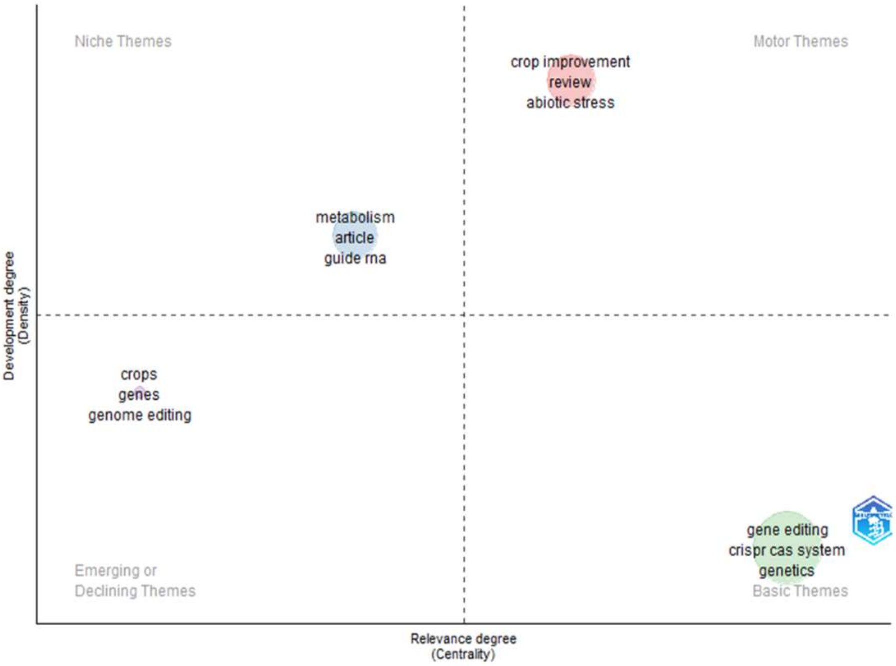

Fig 6: Themes conceptual Map

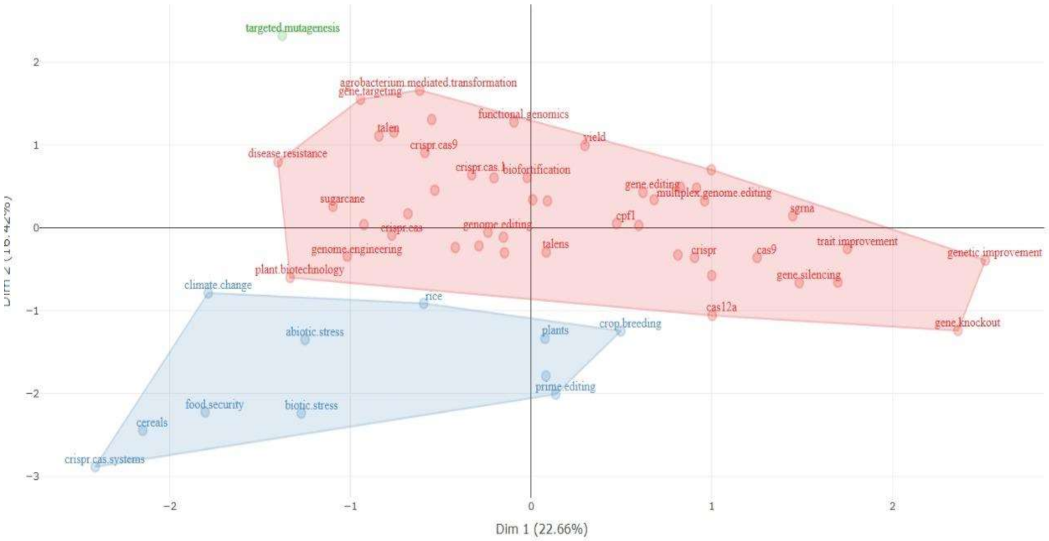

Fig 7: Factorial Analysis

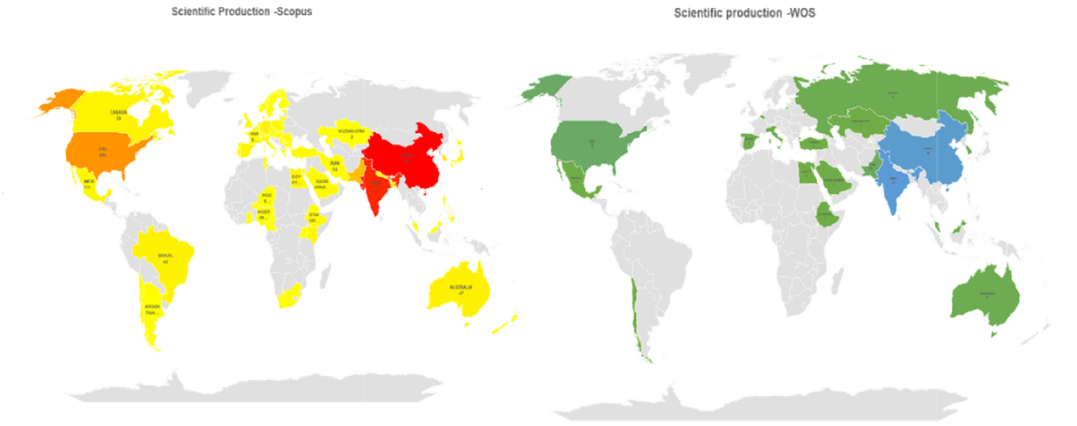

Fig. 8: Country's Scientific production

shows that although genome editing research is becoming more and more international, its regulatory aspects are frequently focused in a small number of high-output nations, highlighting the need for more international participation in talks on genetic technology governance and policy (Fig. 8).

Most Globally Cited Documents

The most widely referenced papers are important scientific findings that have had a big impact on the field of multiplex genome editing research. With 343 citations, Ahmad S.'s (2020). publication in the International Journal of Molecular Sciences is the most referenced, demonstrating its significant influence on the subject. Other notable works are Tripathi N.J. (2020) in Germplasm Biology (257 citations) and Molla K.A. (2019) in Trends in Biotechnology (284 citations) CRISPR-based systems, gene targeting strategies, and biotechnological rules in genome editing are the main topics of these studies (Fig. 9).

Global trends and technological breakthroughs, particularly in agricultural applications and biosafety regulation, are highlighted in documents by Bose A., Kumari Y., and Zhang Y., each of which has been mentioned more than 200 times. In addition to their high citation counts, these seminal works are significant because they provide thorough analyses of the moral, legal, and policy concerns related to genome editing. When taken as a whole, they serve as the basic literature for scholars studying the field's international regulatory dynamics.

Corresponding Author's Countries

According to the corresponding author nations study, China is the leader in multiplex genome editing research. This is evident from the country's high domestic research output, which is reflected in its dominant share of single-country publications (SCP). India comes in second place, demonstrating strong international cooperation with a notable balance between single and multiple-country publications (MCP). Despite having less publications overall than China and India, the US has a greater percentage of MCPs, indicating its robust international research collaborations. With a good balance of joint and independent research outputs, South Korea and Pakistan also make noteworthy contributions.

Moderate contributions from nations like Australia, Canada, Germany, and Kenya support their positions within the international research network (Fig. 9). Despite having fewer documents overall, the UK has a higher MCP ratio, indicating a greater level of integration into international programs. Overall, the graph shows that matching authorship is

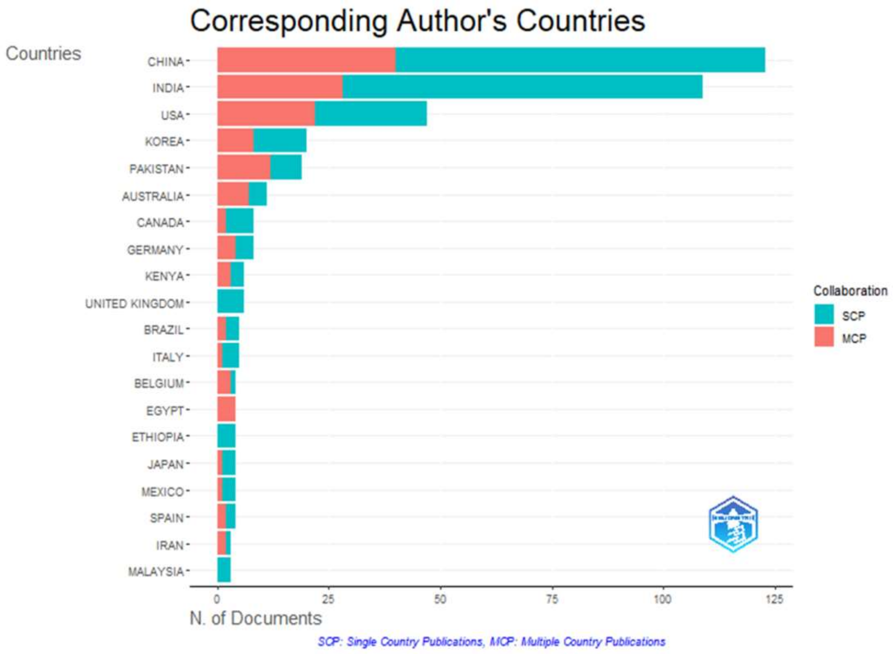

Fig 9: Country -Author correspondence

geographically concentrated in Asia and North America, whereas Europe and Africa are becoming more involved in the technological and regulatory discussion around genome editing.

VOS viewer

In multiplex genome editing research, the VOSviewer visualizations show essential keyword clusters. The terms "genome editing," "CRISPR," and "plant" stand out as key terms, demonstrating their critical involvement in the field. Strong thematic connections between genome editing methods (CRISPR/Cas9, prime editing, double-strand breaks) and agricultural uses including crop enhancement, resistance, and drought tolerance are demonstrated by the first network (Figs. 10 & 11). As precise molecular technologies are incorporated into plant science, homologous recombination and mutagenesis also emerge as key research areas.

The development of genome editing beyond plants is highlighted by the second map, which highlights multidisciplinary links between CRISPR and plant breeding, genetic transformation, biofortification, and human-related applications. Emerging technologies are indicated by smaller but important nodes such as "base editors," "nanotechnology," and "epigenetics. The color-coded clusters indicate theme specialization, which is the intersection of genomic biology, molecular technology, and agricultural development. All things considered, these networks show a quickly changing research environment propelled by CRISPR-based technologies with expanding cross-sector uses.

Collaboration World Map

The global research networks in multiplex genome editing are highlighted on the collaboration world map (Fig. 12), with strong bilateral and multilateral links evident across important scientific nations (32). With

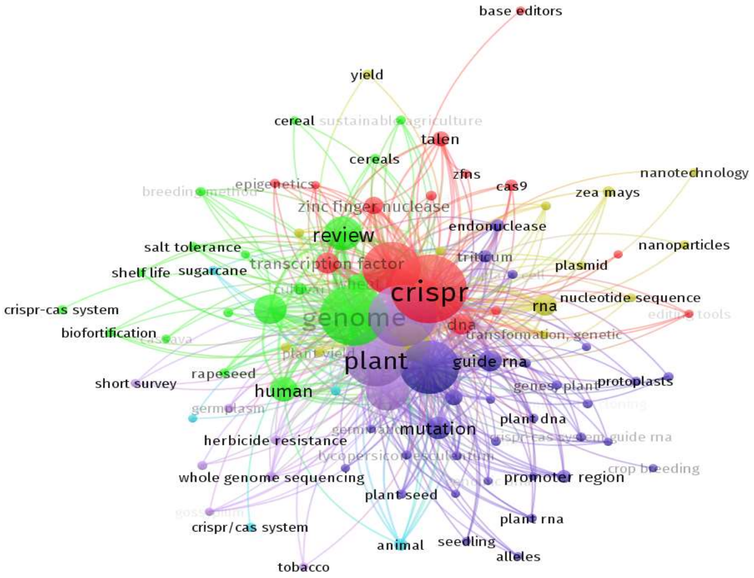

Fig 10: Keyword cluster- network

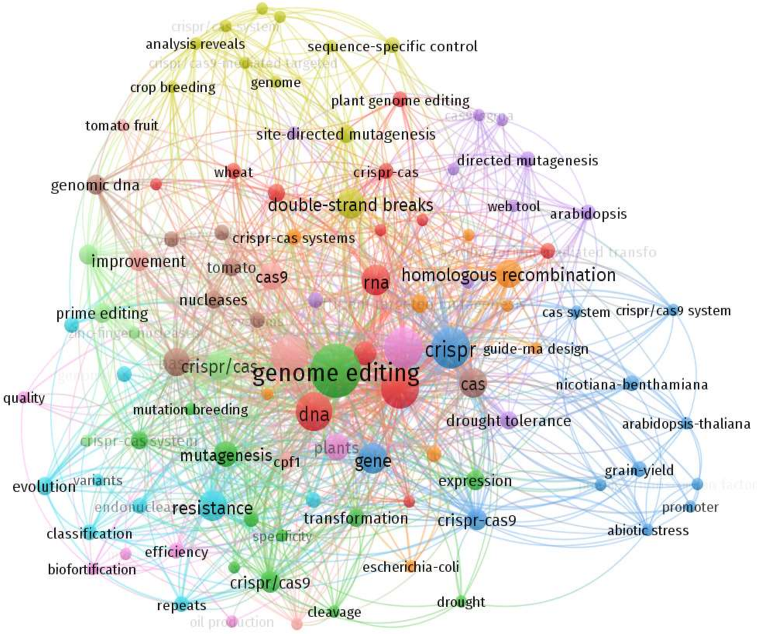

Fig 11: Author Keyword - networking

Global Regulatory Frameworks

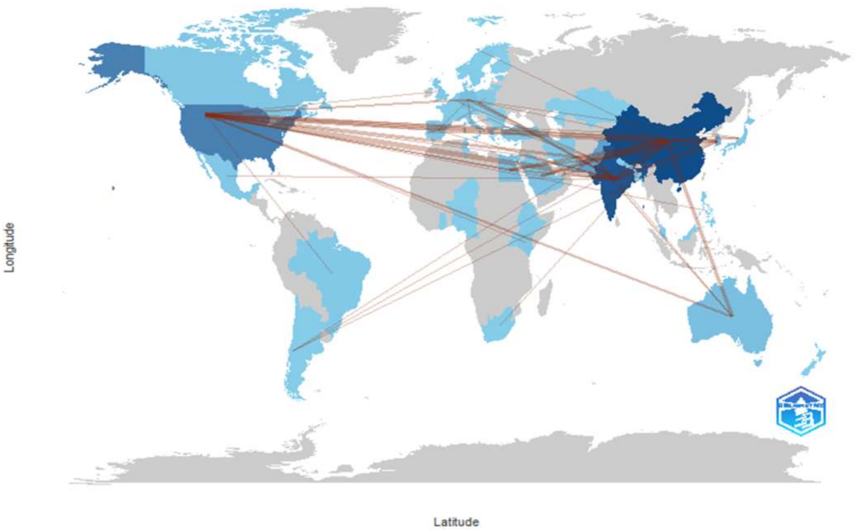

Fig 12: Collaborative world map

their darker hues and thicker link lines, China, India, and the US stand out as the top hubs, signifying a high volume of publications and strong cross-border cooperation. Notably, China has close relations to the United States, Australia, and a number of European countries, which reflects its pivotal role in advancing cooperative genome editing research. Strong ties between India and North America, Europe, and Asia further highlight the country's expanding scientific influence worldwide.

Lower collaboration intensity, which suggests regional underrepresentation, is seen in lighter blue regions, such as those in South America, Africa, and portions of Southeast Asia. In spite of this, there are a few new partnerships that show promise for expansion. While highlighting the worldwide interconnectedness of multiplex genome editing, the map also highlights regional differences in research participation and policy engagement. A crucial need for future international policy integration is highlighted by the fact that the predominant collaboration trends are primarily technological and agricultural, with little apparent worldwide cooperation on research centered on regulation or governance (33).

Discussion

Research on worldwide regulatory frameworks for multiplex genome editing has demonstrated a steady development trajectory, with a noteworthy uptick following 2015, spurred by advancements in CRISPR-Cas9. This is according to the combined analysis from Bibliometrix and VOSviewer. The United Kingdom has the highest citation impact per publication, demonstrating the importance of fewer but very significant contributions, whereas the United States leads in total citations, suggesting its pivotal role in forming regulatory discourse, according to Bibliometrix research. With significant investments in biotechnology, China and India also exhibit large publication volumes. With thematic maps showing "genome editing regulation" and "bioethics" as essential themes and "policy" and "public perception" as developing areas of interest, annual citation trends highlight the growing emphasis on bioethics, governance, and policy issues. In support of this, VOSviewer keyword clustering identifies three main research clusters: application-driven research (agriculture, disease resistance), technical foundations (CRISPR/Cas9, gene knockouts), and governance issues (bioethics, regulation). Density maps show the close ties between policy discourse and technological advancements. When combined, these tools offer a thorough understanding of the field's evolution toward a balance between scientific innovation and ethical, legal, and societal considerations in forming global genome editing governance. Bibliometrix provides quantitative insights into productivity, impact, and geographic trends, while VOSviewer reveals the conceptual and thematic landscape.

Conclusion

The Global Regulatory Frameworks for Multiplex Genome Editing bibliometric and VOSviewer analysis shows a notable increase in scientific output, especially after 2015, which corresponds with significant developments in CRISPR-Cas9 technology that prompted both experimental applications and regulatory discussion. However, China and India exhibit substantial increases in publication volume, suggesting expanding research capability and engagement in governance issues, while the United States leads in total citations and plays a central role through important organizations like the FDA and NIH. Despite having fewer publications, the UK has a high citation impact, demonstrating the work's worldwide relevance and frequent connection to legal and bioethical frameworks. Thematic trends show that integrated conversations about ethics, safety, public trust, and equal access are replacing technical problem-solving. The integration of legal, ethical, and technical themes is highlighted by VOSviewer clustering, demonstrating the interdependence of science and policy in the regulation of genome editing. There is a trend toward global harmonization of regulatory procedures, as seen by the growing interconnectedness of collaboration networks between nations and institutions. However, the pace of legislative adaption still lags behind rapid technical innovation, generating dangers of governance gaps. Setting globally accepted standards, encouraging open stakeholder participation, and guaranteeing fair access to technology are all necessary to meet these issues. The results imply that striking a balance between innovation and social protections will be essential to the administration of genome editing in the future. This will entail promoting inclusive international discourse, enhancing policy responsiveness, and bridging scientific breakthroughs with ethical considerations. Scientific leadership and fair governance can work together to promote responsible advancement in the field while lowering risks. Finally, this research emphasizes how urgently a unified, internationally recognized regulatory framework is required to maintain innovation and safeguard public confidence.

References

1. Mana AA, Allouhi A, Hamrani A, Rehman S, el Jamaoui I, Jayachandran K (2024) Sustainable AI-based production agriculture: Exploring AI applications and implications in agricultural practices. Smart Agric Technol 7:100416
2. Abdelrahman M, Wei Z, Rohila JS, Zhao K (2021) Multiplex genome-editing technologies for revolutionizing plant biology and crop improvement. Front Plant Sci 12:721203
3. Singh J, Sharma D, Brar GS, Sandhu KS, Wani SH, Kashyap R, Kour A, Singh S (2022) CRISPR/Cas tool designs for multiplex genome editing and its applications in developing biotic and abiotic stress-resistant crop plants. Mol Biol Rep 49:11443–11467
4. Kavitha Shree GG, Arokiamary S, Kamaraj M, Aravind J (2025) Biorefinery approaches for converting fruit and vegetable waste into sustainable products (2025). International Journal of Environmental Science and Technology 22:7211–7230
5. Patel A, Miles A, Strackhouse T, Cook L, Leng S, Patel S, Klinger K, Rudrabhatla S, Potlakayala SD (2023) Methods of crop improvement and applications towards

fortifying food security. Front Genome Ed 5:1171969
6. Ji H-J, Zhou X-H, Wu H-Y, Liu H-X, Zhang G-Z (2023) A bibliometric and thematic analysis of the trends in the research on ginkgo biloba extract from 1985 to 2022. Heliyon 9:e21214
7. Kamaraj M, Kiruthika N, Naganathan T, Saranya T, Aravind J (2025) Bibliometric analysis and impact of heavy metals contamination in soils. Global Journal of Environmental Science and Management 11:321–342
8. Didegah F, Thelwall M (2013) Which factors help authors produce the highest impact research? Collaboration, journal and document properties. J Informetr 7:861–873
9. Sharma D, Mittal R, Sekhar R, Shah P, Renz M (2023) A bibliometric analysis of cyber security and cyber forensics research. Results in Control and Optimization 10:100204
10. Balakumar SB, Bala S, Mahesh N, Kamaraj M, Aravind J (2025) Harnessing artificial intelligence for sustainable environmental remediation a review (2025). International Journal of Environmental Science and Technology 22:13189–13206
11. Yu Y, Li Y, Zhang Z, Gu Z, Zhong H, Zha Q, Yang L, Zhu C, Chen E (2020) A bibliometric analysis using VOSviewer of publications on COVID-19. Ann Transl Med 8:816
12. Maulidiya D, Nugroho B, Santoso HB, Hasibuan ZA (2024) Thematic evolution of smart learning environments, insights and directions from a 20-year research milestones: A bibliometric analysis. Heliyon 10:e26191
13. Can Gao, Wang R, Zhang L, Yue C (2021) Visualization analysis of CRISPR gene-editing knowledge map based on CiteSpace. Biol Bull Russ Acad Sci 48:705–720
14. Marchi H, Fuchs C (2024) Hurdle-QAP models overcome dependency and sparsity in scientific collaboration count networks. J Math Sociol 48:100–127
15. Wei X, Pu A, Liu Q, et al (2022) The bibliometric landscape of gene editing innovation and regulation in the worldwide. Cells 11:2682
16. Li X, Gao Y, Zhang Z, et al (2025) Biosafety considerations triggered by genome-editing technologies. Biosaf Health 7:141–151
17. Jones MGK, Fosu-Nyarko J, Iqbal S, et al (2022) Enabling trade in gene-edited produce in Asia and Australasia: The developing regulatory landscape and future perspectives. Plants 11:2538
18. Rubeis G, Steger F (2018) Risks and benefits of human germline genome editing: An ethical analysis. Asian Bioeth Rev 10:133–141
19. Anari E, Anari R, Pazoki-Toroudi H (2025) A decade of scientific advancements and collaborations on CRISPR-Cas9 application in cancer research: a bibliometric review. Discov Oncol 16:1232
20. Ardoin NM, Bowers AW, Gaillard E (2020) Environmental education outcomes for conservation: A systematic review. Biol Conserv 241:108224
21. Azeez SS, Hamad RS, Hamad BK, Shekha MS, Bergsten P (2024) Advances in CRISPR-Cas technology and its applications: revolutionising precision medicine. Front Genome Ed 6:1509924
22. Korav S, Department of Agronomy, CCSHAU Hisar, Haryana-125004 (2020) Review- zero budget natural farming a key to sustainable agriculture: Challenges, opportunities and policy intervention. Ind J Pure App Biosci 8:285–295
23. McHughen A (2016) A critical assessment of regulatory triggers for products of biotechnology: Product vs. process. GM Crops Food 7:125–158
24. Lorenzo CD, Debray K, Herwegh D, et al (2023) BREEDIT: a multiplex genome editing strategy to improve complex quantitative traits in maize. Plant Cell 35:218–238
25. Pandey DK, Hassan MK, Kumari V, Zaied YB, Rai VK (2024) Mapping the landscape of FinTech in banking and finance:

A bibliometric review. Res Int Bus Fin 67:102116

26. Hamdan MF, Tan BC (2024) Genetic modification techniques in plant breeding: A comparative review of CRISPR/Cas and GM technologies. Hortic Plant J. https://doi.org/10.1016/j.hpj.2024.02.012

27. Zuiderwijk A, Chen Y-C, Salem F (2021) Implications of the use of artificial intelligence in public governance: A systematic literature review and a research agenda. Gov Inf Q 38:101577

28. Hasanzadeh A, Hamblin MR, Kiani J, Noori H, Hardie JM, Karimi M, Shafiee H (2022) Could artificial intelligence revolutionize the development of nanovectors for gene therapy and mRNA vaccines? Nano Today 47:101665

29. Entine J, Felipe MSS, Groenewald J-H, et al (2021) Regulatory approaches for genome edited agricultural plants in select countries and jurisdictions around the world. Transgenic Res 30:551–584

30. Bejaei M, Cliff MA, Singh A (2020) Multiple correspondence and hierarchical cluster analyses for the profiling of fresh apple customers using data from two marketplaces. Foods 9:873

31. Sahoo S, Singha C, Govind A, Moghimi A (2025) Review of climate-resilient agriculture for ensuring food security: Sustainability opportunities and challenges of India. Environmental and Sustainability Indicators 25:100544

32. Kumar A, Anju T, Kumar S, Chhapekar SS, Sreedharan S, Singh S, Choi SR, Ramchiary N, Lim YP (2021) Integrating omics and gene editing tools for rapid improvement of Traditional Food Plants for diversified and sustainable food security. Int J Mol Sci 22:8093

33. Abiri R, Rizan N, Balasundram SK, Shahbazi AB, Abdul-Hamid H (2023) Application of digital technologies for ensuring agricultural productivity. Heliyon 9:e22601