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REVIEW ARTICLE

Trends and advancements in cucumber (*Cucumis sativus* L.) breeding: A bibliometric review

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Abstract

Cucumber (*Cucumis sativus* L.) is one of the most important vegetable crops in the world and faces several challenges in global agriculture, such as climate change, pest outbreaks and sustainable production. The species' narrow genetic base further constrains breeding efforts, making the development of stable and resilient cultivars particularly difficult. These challenges underscore the importance of evaluating ongoing research progress in cucumber breeding. In the present study, a bibliometric analysis was conducted to evaluate the publication process and trend of the cucumber breeding technologies. A total of 166 papers between 2015 and 2024 were retrieved from the Scopus database and, analysed using Bibliometrix R, Biblioshiny and VOS viewer. The results revealed a steady growth in annual publications, which peaked in 2024. China contributed most, in terms of the number and citations of publications. Frontiers in Plant Science was the most productive journal and study of CRISPR-associated protein 9 (CRISPR/Cas9) had the highest number of citations. Networks of collaboration between authors and countries, helped find focused research clusters. Thematic analysis showed that the major subjects of research are molecular breeding, quantitative trait locus (QTL) mapping, transcriptomic profiling, disease resistance and gene expression. This bibliography analysis provides a quantitative reference for future cucumber breeding research prospects, research hotspots and the pattern of cooperation.

Keywords: bibliometric analysis; cucumber; molecular breeding; Scopus

Introduction

Cucumber (*Cucumis sativus* L.) is an important vegetable crop worldwide, due to its nutrition, economic and horticultural value. The fruits are a rich source of nutrients such as protein, multivitamins, cucurbitacin, calcium, iron, propanol diacid and other vital dietary components (1). Polysaccharides and flavonoids contained in the fruit possess antioxidant effects, helping scavenge free radicals, enhance immunity and delay the aging process (2, 3). Cucurbitacin C, found in the fruit, has been demonstrated to inhibit tumour growth (4) and to exhibit hepatoprotective and anti-inflammatory properties (5).

In 2023, cucumber was cultivated on approximately 2.19 million hectares globally. China ranked first among global producers with a production of 80.22 million tonnes or about 82.01 % of total world's production followed by Turkey (1.87 million tonnes) and Russia (1.68 million tonnes) (6).

In the last few decades, conventional genetic breeding work has largely contributed to the generation of new cucumber varieties with high yield and good quality such as green fruit peel, fruit wart, fruit spin and flesh thickness (7). Parameters such as yield, fruit diameter, length and weight were critical for maximising production potential (8, 9). Skin and flesh thickness are key quality characteristics targeted in marketing and consumer acceptability (8, 10). Disease resistance, particularly against pathogens like powdery mildew caused by *Podosphaera xanthii* and *Erysiphe cichoracearum* and downy mildew caused by *Pseudoperonospora cubensis*, is crucial to ensuring crop health and reducing losses (11, 12). These traits are the focus of breeding efforts to improve cucumber varieties (13, 14).

However, the narrow genetic base and limited genetic diversity in cucumber hinder the development of stable genetic traits and well-defined genotypes (15). While traditional breeding has brought tremendous changes, new challenges such as climate change, resistant strains and sustainable agriculture demand sophisticated solutions. The narrow genetic base of cucumber germplasm makes it difficult to breed stable and distinct varieties; Furthermore, the effect of traditional breeding is not ideal. Consequently, cucumber breeding has evolved from traditional selection method to increasingly complex science founded methods. The rapid development of molecular biotechnologies (7) has facilitated the use of advanced molecular techniques and bioengineering technologies to improve cucumber production.

The genomic tools and resources that are currently available in the post-genomic era are propelling us into the use of new and very effective strategies for plant breeding, because they can efficiently assist the analysis of genotype and its correspondence/relationship with phenotype especially when dealing with complex traits (16). Additionally, research in cucumber breeding has advanced significantly since the completion of cucumber genome sequencing (7). Through the use of molecular markers and genome-wide association analysis (GWAS), transgenic and gene editing technologies, breeders have made improvements in the fruit quality, yield potential, resistance to biotic and abiotic stresses as well as cucurbit plant sex differentiation and flower development, fruit development and shoot branching (7). Furthermore, advances in bioinformatics tools and next-generation sequencing technologies have improved understanding of cucumber genomics and trait inheritance, enabling more precise breeding for traits such as disease resistance, fruit quality, stress tolerance and yield improvement (7).

Considering the current research trends in this field also helps define growing trends, blank spots in knowledge and future research priorities. Bibliometric analysis thus comprises a set of statistical, mathematical and algorithmic techniques to process data and sort out and analyse large datasets. Bibliometric analysis is used as a powerful means to quantify various aspects regarding the subject area such as productivity and impact of scientific literature, research productivity, collaboration pattern, science mapping, co-citation, co-occurrence analysis and how the central theme has evolved over time (17). Quantitative studies of published literature would provide a better understanding for researchers and decision makers on the dynamics, performance and direction of cucumber breeding research. A bibliometric analysis on cucumber breeding for the last 10 years is presented in this research. It seeks to examine the quantity and significance of publications, the primary authors, patterns of collaboration and the primary themes under investigation. This will help plan future breeding programs and research initiatives and provide a comprehensive picture of the research landscape.

Materials and Methods

The bibliometric review was conducted by collecting research articles from Scopus database. The methodology was divided into three divisions i.e. development of search string, document screening and database analysis.

Search string construction

The construction of the search string was a crucial process that brought all research articles relevant to the current research topic to the Scopus database. For constructing a search string, it was important to identify the relevant keywords and their synonyms commonly used in published literature related to cucumber breeding research. A typical format was followed in the search string where the keywords were written in the inverted commas and 'AND' was used in between the keywords, whereas 'OR' was used to denote the synonyms of the keywords. Only article titles were considered during the keyword search. The search string used in the Scopus database for the current study is presented below.

"cucumber" OR "Cucumis sativus" AND "crop improvement" OR "breeding" OR "biotechnology" OR "genetic improvement" OR "genetic diversity" OR "recent advancement" OR "molecular breeding"

Screening of database

The search string applied in the Scopus database yielded 1993 relevant documents. Further, the documents were screened based on the requirements of the current study. For the bibliometric review, the article selected according to the time framed of the published years between 2015 and 2024. A total of 1109 documents remained after the scrutiny based on published years. Next, the subject areas were chosen based on the relevance to the research topic, so that the most accurate research article were included in the study. Agricultural and biological sciences and biochemistry, genetics and molecular biology are the subject area used to define the screening of the articles. After scrutinising based on the subject area 968 documents remained and those articles were subjected for the further screening. Subsequently, the database was screened based on the document type required for the research, where only research articles were selected for the current study. The document was reduced to 823 in the screening for document type. The preferred language for the research papers in the Scopus database is to be English thus 743 English-language documents were retained and others were discarded in the screening. Then the documents were further screened for source type, among that only the journal was selected. The number of documents were reduced to 736 in their source type. Next, the documents were screened for open access, only 385 open access research papers were retained. Then the documents are screened based on the key words, keywords such as sea cucumber, Holothuroidea, spawning, juvenile etc., were eliminated and 264 documents were selected for the further scrutiny. Next, the screened database was downloaded in comma-separated values (CSV) format for further processing. During the final screening, all the research papers were manually selected based on the title and theme of the article. The papers which were sticked to the keywords or to the main theme were retained and remaining papers were eliminated in the screening process. In the final scrutiny, the research articles were drastically reduced from 264 to 166. Finally, the bibliometric analysis was performed using 166 research articles from Scopus database that are most relevant to the present study. Conceptual framework for the cucumber breeding bibliometric analysis is given in Fig. 1.

Database analysis

Bibliometrix R (R-studio v.4.3.1) and biblioshiny are used to analyse the CSV file of the shortlisted research publications for the bibliometric study. The VOS viewer software analyses the CSV file to provide a visual representation of bibliometric networks and relationships.

Results and Discussion

Main information and annual scientific production

The Scopus database provided 166 documents from the cucumber breeding literature for bibliometric analysis (Table 1). The 166 documents had 71 sources, all of which were scientific journals. In total, 716 authors used 8193 references. There are two (1.16 %) single -authored documents and 164 (98.83 %) multi-authored documents. This data suggests that research on cucumber breeding is a very collaborative field. The dataset contains 499 author keywords in total, while the number of the keywords plus is 800. The international collaboration among the authors is 18.67 %. The growth rate throughout the entire period is 14.31 % (Table 1). The number of publications produced each year directly reflects research progress and its significance in a particular scientific discipline.

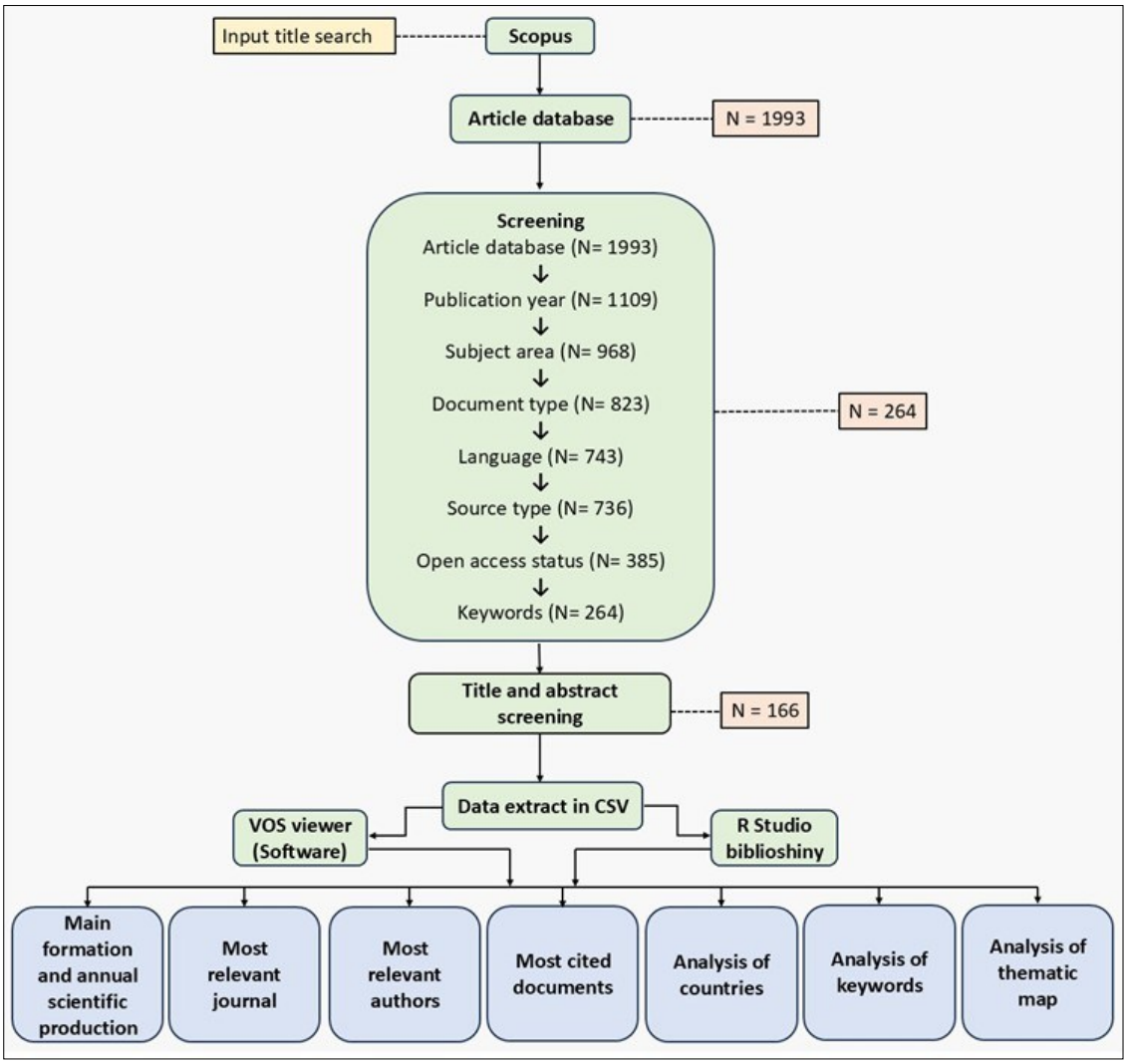


Fig. 1. Conceptual framework for the cucumber breeding bibliometric analysis.

Table 1. Main information of the cucumber breeding bibliometric data in the period from 2015 to 2024

Description	Results
Main information about data	
Timespan	2015–24
Sources (Journals, Books, etc)	71
Documents	166
Annual growth rate %	14.31
Document average age	4.31
Average citations per doc	21.61
References	8193
Document contents	
Keywords plus (ID)	800
Author's keywords (DE)	499
Author information	
Authors	716
Authors of single-authored docs	2
Authors collaboration	
Single-authored docs	2
Co-authors per doc	7.24
International co-authorships %	18.67
Document types	
Article	166

To understand the trend and growth of research in a specific academic discipline, one useful metric is the quantity of research papers that have been published. The number of publications on breeding cucumbers has steadily increased between 2015 and 2024 (Fig. 2). The number of publications was in the single digits during the initial years of study, often falling as low as 10 per year. The number has significantly increased from 2017 (n = 10) and in 2024 it reached its greatest number of publications, which is 30 articles in a year. Publications increased by 29.51 % over the study's first 5 years (2015–19), but they increased by an impressive 70.48 % during the following five years (2020–24). The upward trend in the number of annual publications indicates increased research activity and scientific interest in cucumber breeding, particularly in molecular breeding, trait improvement and the development of better genotypes.

Most relevant journals

The articles on cucumber breeding were published in 71 different journals. Table 2. summarises 10 of the most popular journals. Frontiers in Plant Science is the most relevant and productive journal with largest number of articles (n = 20), followed by Horticulture Research (n = 10), Agronomy (n = 9), BMC Plant Biology (n = 8), Horticultural Plant Journal (n = 7), International Journal of Molecular Sciences (n = 7), Plants (n = 7), Genes (n = 6), BMC Genomics (n = 4) and Electronic Journal of Plant Breeding (n = 3).

Articles from Molecular Plant Pathology received the most of citations (n = 744), followed by Frontiers in Plant Science (n = 499),

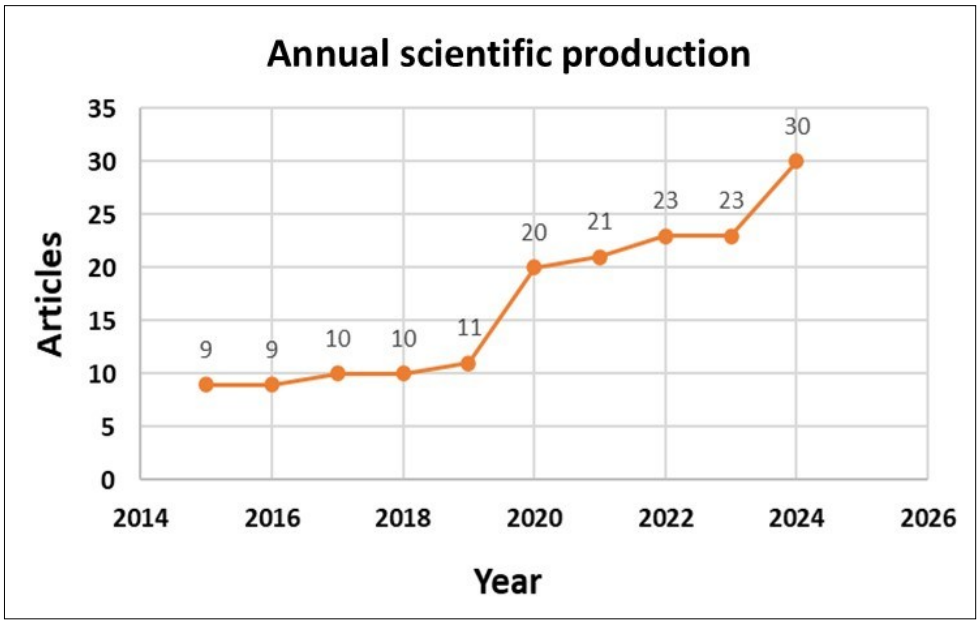


Fig. 2. Annual scientific production on cucumber breeding litrature in the period from 2015 to 2024.

Table 2. The 10 most relevant and cited journals related to cucumber breeding litrature in the period from 2015 to 2024

Relevant journal	n	2024 IF	Quartiles ranking	Cited journal	n	2024 IF	Quartiles ranking	H-index
Frontiers in Plant Science	20	4.8	Q1	Molecular Plant Pathology	744	4.9	Q1	138
Horticulture Research	10	8.7	Q1	Frontiers in Plant Science	499	4.8	Q1	248
Agronomy	9	2.0	Q2	Horticulture Research	295	8.7	Q1	82
BMC Plant Biology	8	4.8	Q1	Plant Cell	257	11.6	Q1	412
Horticultural Plant Journal	7	6.2	Q1	BMC Plant Biology	250	4.8	Q1	159
International Journal of Molecular Sciences	7	4.9	Q1	International Journal of Molecular Science	120	4.9	Q1	314
Plants	7	4.1	Q1	Agronomy	113	2.0	Q2	159
Genes	6	2.8	Q2	Nature Communications	110	15.7	Q1	577
BMC Genomics	4	3.7	Q2	Plants	105	4.1	Q1	116
Electronic Journal of Plant Breeding	3	-	-	Molecular Plant	104	24.1	Q1	178

Horticulture Research (n = 295), Plant Cell (n = 257), BMC Plant Biology (n = 250), International Journal of Molecular Sciences (n = 120), Agronomy (n = 113), Nature Communications (n = 110), Plants (n = 105) and Molecular Plant (n = 104) (Table 2).

The citation map for journals is depicted in Fig. 3. Only 7 journals met the threshold and were displayed on the term map with two clusters. Cluster 1 (red) contains Frontiers in Plant Science (Total link strengths (TLS) = 3241), Plants (TLS = 1167), International Journal of Molecular Sciences (TLS = 1109), Horticulture Research (TLS = 1081) and Agronomy (TLS = 592). Cluster 2 (grey) contains two journals, BMC Genomics (TLS = 1992) and Genes (TLS = 586). Higher TLS values indicate a stronger citation connection and more influence from a journal in the research network for cucumber breeding. The high TLS value of Frontiers in Plant Science indicates that it is a primary journal for connecting relevant studies and disseminating research in cucumber breeding.

Most relevant authors

For the authors who mostly studied cucumber breeding, Liu X. (n = 19) from China ranked first in the number of publications with nineteen articles, followed by Chen X. (n = 15), Chen J., Miao H. and Wang Y. all three with 11 articles (Table 3). In terms of citation, the most cited author is Weng Y. (n = 116), followed by Li S. (n = 111), Chen X. (n = 110), Li S. (n = 104), Wang Y. (n = 87), Wang Y. (n = 80), Chen X. (n = 79), Chen X. (n = 69), Chen X. (n = 64) and Wang Y. (n = 61) (Table 3).

The author collaboration network is presented in Fig. 4a. Of the 716 participating authors, only 10 met the threshold for inclusion in the network map, forming three clusters. The first cluster (red) comprised two authors: Chen J. and Li J. The second one included 5 authors (blue colour): Liu X., Chen X., Wang Y., Li S. and Weng Y., while the third clusters comprise 3 authors (green colour): Miao H., Gu X. and Zhang S. The authors citation term map consists of two cluster and it is depicted in Fig. 4b. The first cluster consisted of 8 authors (blue colour): Liu X., Chen J., Miao H., Wang Y., Gu X., Zhang S., Li J. and Weng Y. The second one included 2 authors (grey colour): Chen X. and Li S. The authors with highest TLS are Wang Y. (TLS = 9863), Weng Y. (TLS = 8311), Miao H. (TLS = 7234), Gu X. (TLS = 6409) and Liu X. (TLS = 5617).

Most cited documents

Citations are a reliable quantitative indicator of a paper's impact (18). The document 'Development of broad virus resistance in non-transgenic cucumber using CRISPR/Cas9 technology' (19) as the most cited article followed by 'A Functional Allele of CsFUL1 regulates fruit length through repressing CsSUP and inhibiting auxin transport in cucumber' (20), 'Genome-wide mapping of structural variations reveals a copy number variant that determines reproductive morphology in cucumber' (21), 'Graph-based pan-genome reveals structural and sequence variations related to agronomic traits and

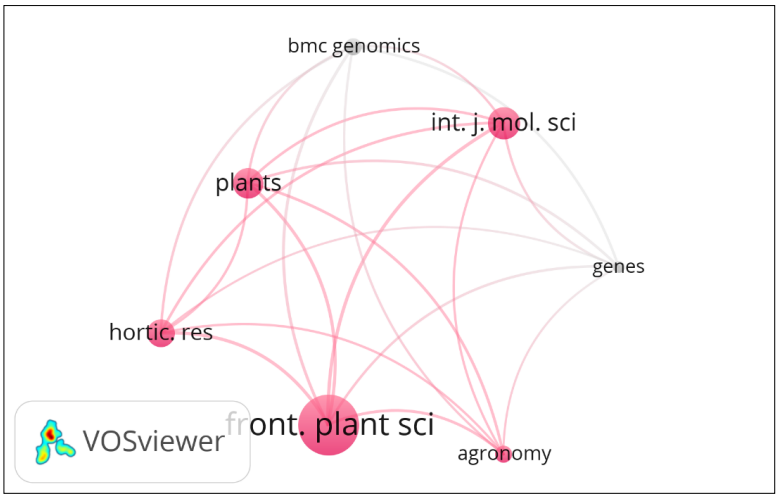


Fig. 3. The citation term map of the journal on cucumber breeding literature in the period from 2015 to 2024.

Table 3. Author analysis in terms of productivity and number of citations within the cucumber breeding research area

Author	Number of articles (n)	Total link strength	Author	Total citations
Liu X	19	5617	Weng Y	116
Chen X	15	4665	Li S	111
Chen J	11	4424	Chen X	110
Miao H	11	7234	Li S	104
Wang Y	11	9863	Wang Y	87
Gu X	10	6409	Wang Y	80
Li S	10	3154	Chen X	79
Zhang S	10	4399	Chen X	69
Li J	9	5360	Chen X	64
Weng Y	9	8311	Wang Y	61

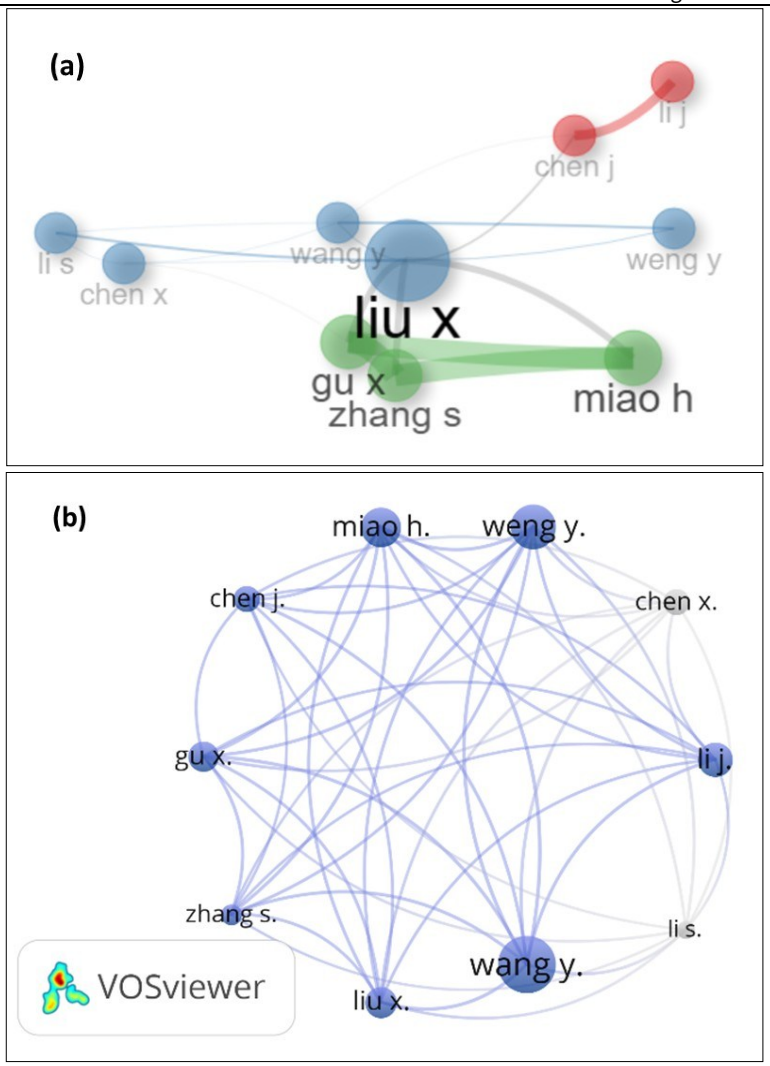


Fig. 4. Author collaboration and citation network maps of the cucumber breeding literature published during 2015–24. a: author collaboration network map; b: author citation network map.

domestication in cucumber' (22), 'An ACC oxidase gene essential for cucumber carpel development' (23), 'Genome-wide identification and transcriptional expression analysis of cucumber superoxide dismutase (SOD) family in response to various abiotic stresses' (24), 'Loss-of-function mutations in CsMLO1 confer durable powdery mildew resistance in cucumber (*Cucumis sativus* L.)' (25), 'The USDA cucumber (*C. sativus*) collection: genetic diversity, population structure, genome-wide association studies, and core collection development' (26), 'A high-density genetic map of cucumber derived from specific length amplified fragment sequencing (SLAF-seq)' (27) and 'Comparative proteomic analysis provides insight into the key proteins involved in cucumber (*C. sativus*) adventitious root emergence under waterlogging stress' (28). The 10 most cited articles are listed in Table 4.

Country-wise analysis

In total, 28 countries are active in the field of cucumber breeding (Fig. 5a). Most of publications were contributed from the China (n = 783), followed by India (n = 81), USA (n = 73), South Korea (n = 39), Poland (n = 27), Japan (n = 23), Turkey (n = 22), Spain (n = 20), Thailand (n = 19) and Pakistan (n = 15). The papers published by authors from the China had the most citations (n = 2148), followed by the USA (n = 170), Korea (n = 98), Spain (n = 70), Nigeria (n = 53), India (n = 52), Chile (n = 39), Pakistan (n = 35), Poland (n = 30) and Bangladesh (n = 21) (Fig. 5b).

To graphically summarise the collaboration among countries, Fig. 5c presents the collaboration network map of countries involved in cucumber breeding research. All the countries are grouped into 5 clusters Fig. 5c. The first cluster consisted of 5 countries (red-colored): Pakistan, Bangladesh, Egypt, Australia and Saudi Arabia. The second group consisted of four countries (blue colour): Poland, Turkey, Thailand and United Kingdom. The third cluster included 7 countries (green colour): China, the USA, France, the Netherlands, South Africa, Kenya and Hong Kong. The fourth cluster included two countries (purple colour): Japan and Germany. The last one consisted of two countries (orange colour): Iran and Chile.

Analysis of keywords

Keywords reflect scientific study methods and findings. For a better grasp of research trends and possible research gaps, it can be helpful to understand frequently appearing keywords. The co-occurrence term map of the author keywords is displayed in Fig. 6. Out of a total of 499 author keywords, only 36 meet the threshold and are used in the term map construction. The available keywords are presented on the map, as well as in Table 5. The first cluster (navy blue colour) comprises terms aphid resistance, cucumber, gene expression, genetic diversity, low temperature tolerance, simple sequence repeat (SSR) markers, volatile organic compounds and waterlogging. Second cluster (green colour) comprises terms combining ability, downy mildew, gene action, heterosis, powdery mildew and resistance. Third cluster (sea blue colour) including the keyword terms: abiotic stress, biotic stress, breeding, *Cucumis sativus* L. and disease resistance. Fourth cluster (yellow colour) comprises terms fusarium wilt, metabolome, RNA-seq and transcriptome. Fifth cluster (purple colour) comprises terms genetic analysis, germplasm and parthenocarpy. Cluster six (aqua blue colour) comprises terms cucumber angular leaf spot, quantitative trait locus (QTL) mapping and single nucleotide polymorphism (SNP). Cluster seven (orange colour) comprises terms begomovirus, marker-assisted breeding and tomato leaf curl New Delhi virus (ToLCNDV). Cluster eight (brown colour) comprises terms clustered regularly interspaced short palindromic repeats/CRISPR-associated protein 9 (CRISPR/Cas9), virus resistance and zucchini yellow mosaic virus (ZYMV).

The keywords clusters revealed cucumber (cluster 1) as the most frequently mentioned keyword (114 times). The most frequent keywords representing the advancement in cucumber breeding were *C. sativus* (cluster 3), gene expression (cluster 1), disease resistance (cluster 3), transcriptome (cluster 4), breeding (cluster 3), abiotic stress (cluster 3), biotic stress (cluster 3) and genetic analysis (cluster 5). The analysis reveals a notable lack of synergy between conventional breeding and modern genomics, as well as severe dispersion across cucumber research fields. Progressing resilient and effective cucumber improvement requires bridging these barriers through cross-disciplinary approaches.

Table 4. The 10 most cited articles on cucumber breeding literature in the period from 2015 to 2024

Author(s)	Title	Journal	Year	Global citations	Reference
Chandrasekaran et al.	Development of broad virus resistance in non-transgenic cucumber using CRISPR/Cas9 technology	Molecular Plant Pathology	2016	744	(19)
Zhao et al.	A Functional Allele of CsFUL1 regulates fruit length through repressing CsSUP and inhibiting auxin transport in cucumber	Plant Cell	2019	116	(20)
Zhang et al.	Genome-wide mapping of structural variations reveals a copy number variant that determines reproductive morphology in cucumber	Plant Cell	2015	111	(21)
Li et al.	Graph-based pan-genome reveals structural and sequence variations related to agronomic traits and domestication in cucumber	Nature Communications	2022	110	(22)
Chen et al.	An ACC Oxidase Gene Essential for Cucumber Carpel Development	Molecular Plant	2016	104	(23)
Zhou et al.	Genome-Wide Identification and Transcriptional Expression Analysis of Cucumber Superoxide Dismutase (SOD) Family in Response to Various Abiotic Stresses	International Journal of Genomics	2017	91	(24)
Nie et al.	Loss-of-function mutations in CsMLO1 confer durable powdery mildew resistance in cucumber (*Cucumis sativus* L.)	Frontiers in Plant Science	2015	87	(25)
Wang et al.	The USDA cucumber (*Cucumis sativus* L.) collection: genetic diversity, population structure, genome-wide association studies and core collection development	Horticulture Research	2018	80	(26)
Xu et al.	A high-density genetic map of cucumber derived from specific length amplified fragment sequencing (SLAF-seq)	Frontiers in Plant Science	2015	79	(27)
Xu et al.	Comparative proteomic analysis provides insight into the key proteins involved in cucumber (*Cucumis sativus* L.) adventitious root emergence under waterlogging stress	Frontiers in Plant Science	2016	69	(28)

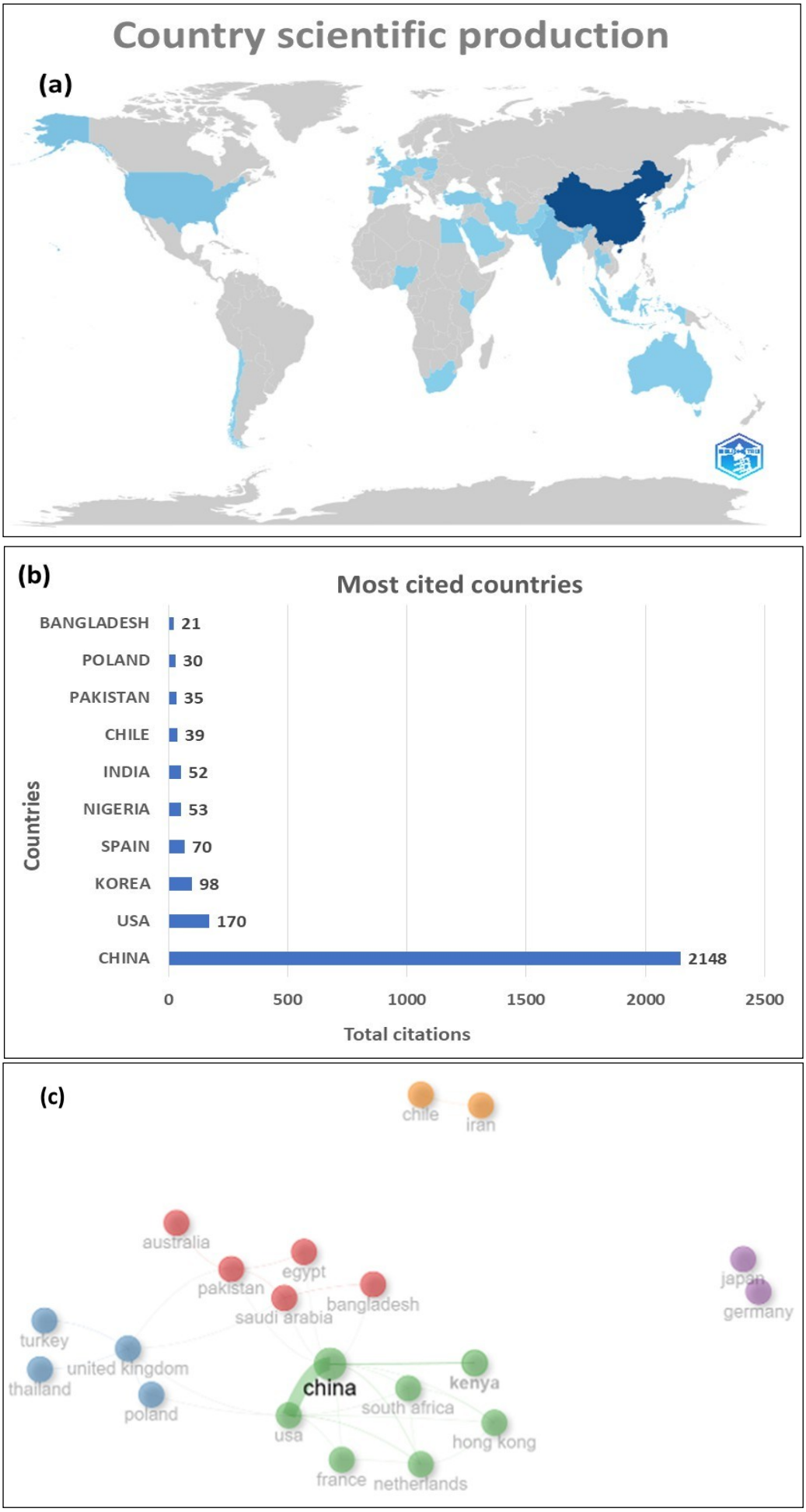


Fig. 5. Scientific production, most cited countries and international collaboration in cucumber breeding research published during 2015–2024. a: scientific production by countries; b: most cited countries; c: international collaboration among countries.

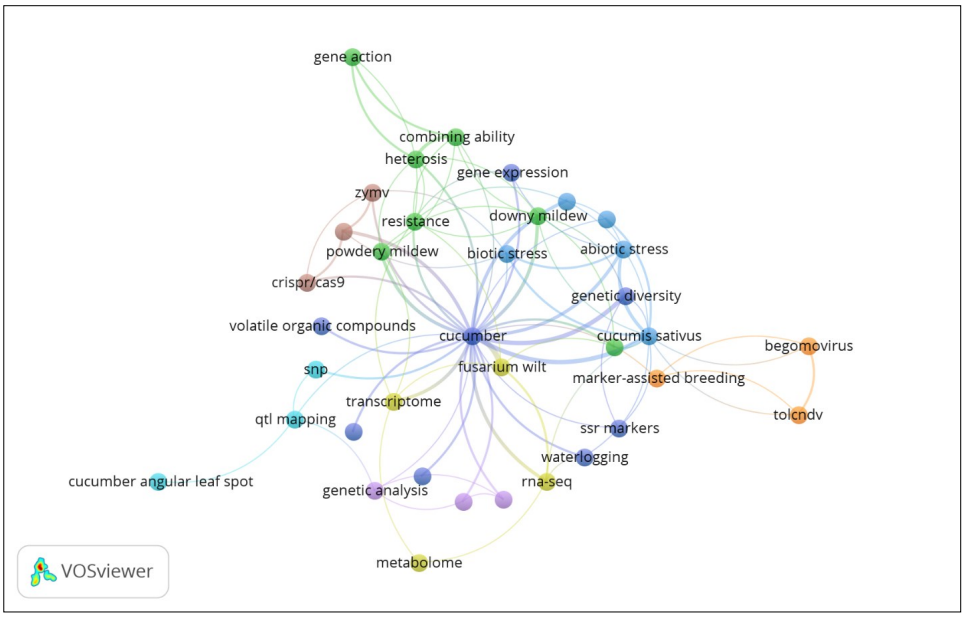


Fig. 6. The co-occurrence term map of the author keywords showing the highly occuring keywords within the cucumber breeeding.

Table 5. The clusters of keywords related to cucumber breeding based on the co-occurrence term map

Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8
Aphid resistance (2)	Combining ability (3)	Abiotic stress (9)	Fusarium wilt (5)	Genetic analysis (7)	Cucumber angular leaf spot (2)	Begomovirus (2)	CRISPR/Cas9 (2)
Cucumber (114)	Downy mildew (6)	Biotic stress (9)	Metabolome (2)	Germplasm (4)	QTL mapping (4)	Marker-assisted breeding (2)	Virus resistance (3)
Gene expression (20)	Gene action (2)	Breeding (12)	RNA-seq (6)	Parthenocarpy (3)	SNP (2)	ToLCNDV (2)	ZYMV (2)
Genetic diversity (6)	Heterosis (5)	*Cucumis sativus* (68)	Transcriptome (12)				
Low temperature tolerance (2)	Inheritance (4)	Disease resistance (13)					
SSR markers (2)	Powdery mildew (5)						
Volatile organic compounds (2)	Resistance (6)						
Waterlogging (4)							

CRISPR: clustered regularly interspaced short palindromic repeats; Cas9: CRISPR-associated protein 9; QTL: quantitative trait locus; RNA-seq: RNA sequencing; SNP: single nucleotide polymorphism; SSR: simple sequence repeat; ToLCNDV: tomato leaf curl New Delhi virus; ZYMV: zucchini yellow mosaic virus. The most frequently mentioned keywords are denoted inside the "()".

Analysis of thematic map

The thematic map was constructed from the co-occurrence network of authors' keywords. The centrality (x-axis) and density (y-axis) describe the themes, which represent the relevance and development of the themes, respectively (Fig. 7).

The motor themes (upper right quadrant) which include genetics, gene expression, metabolism and QTL) are the most developed and central topics regarding cucumber breeding research. Their prominence shows the strong integration of molecular and genomic approaches in breeding programs, consistent with previous studies that highlight the increasing importance of genomics-assisted breeding in crop improvement (29, 30). However, the focus on these themes around gene-level analysis indicates a research bias towards molecular mechanisms with relatively little attention on field-level validation and environmental interactions (31).

The Basic Themes (lower-right quadrant), including QTL mapping, molecular markers, resistance, heterosis and *C. sativus*, are highly relevant but less internally developed. These themes are the conceptual basis of cucumber breeding and link classical breeding strategies with modern genomic tools. Their relatively low density indicates that methodological integration and innovation in these areas is still limited, although they are important (32).

The niche themes (upper left quadrant) are well developed but weakly connected to the overall research field, for example CRISPR-Cas systems, virus resistance and cucurbit downy mildew. This indicates that there are specific groups of researchers involved in advanced technologies like genome editing, which has been reported more often as an emergent, but not yet fully incorporated, method in plant breeding systems (33, 34).

The emerging or declining themes (lower-left quadrant) with low centrality and density are characterised by weak development and marginal relevance and include themes such as aphid resistance and diversity and specific length amplified fragment sequencing (SLAF-seq). Some of these topics may indicate decreasing research areas, while others, particularly those related to high-throughput sequencing and genetic diversity, may suggest emerging directions that have not yet reached wider usage (35). The distribution of resistance-related topics across several quadrants also suggests fragmentation in this research domain and the need for more integrated research efforts.

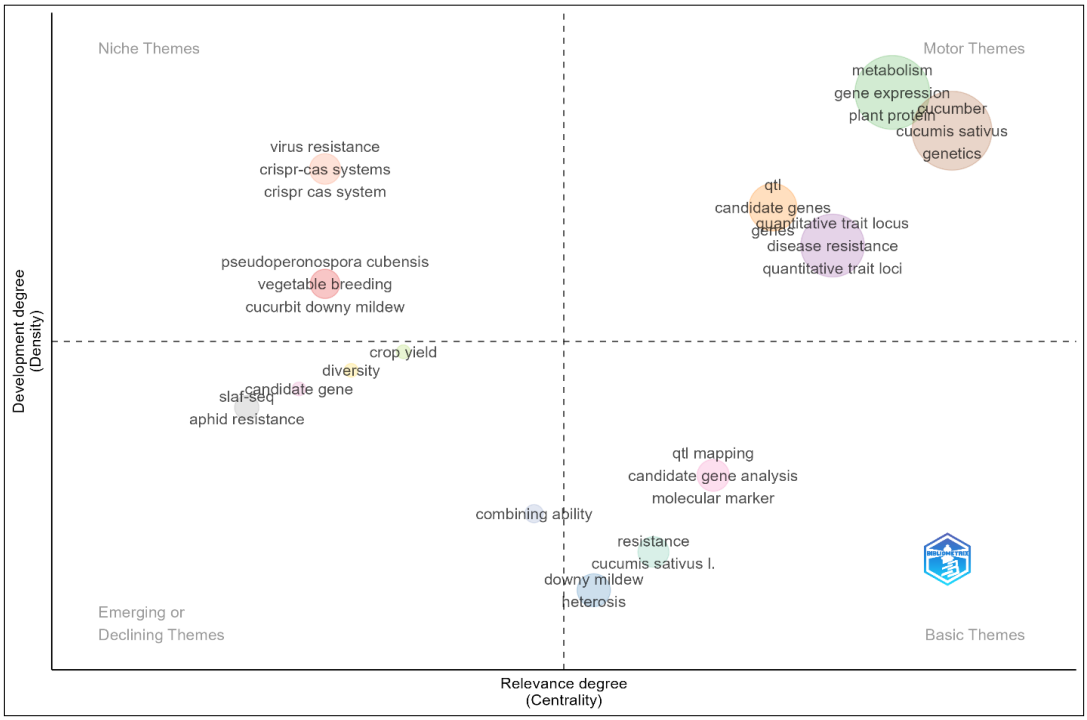


Fig. 7. Thematic map on cucumber breeding litrature in the period from 2015 to 2024.

Conclusion

This bibliometric study provides a quantitative analysis of the global research trends on cucumber breeding for the period 2015 to 2024. Results indicate a steady increase in scientific output reflecting an increasing research interest in the field. In both publications and citations, China was the most important contributor, showing its leading position in cucumber breeding research. The high proportion of multi-authored publications also demonstrates the collaborative nature of the domain.

According to thematic and keyword analyses, molecular breeding, quantitative trait locus (QTL) mapping, gene expression and disease resistance are the most central and mature research areas. Concurrently, new topics such as CRISPR-associated protein 9 (CRISPR/Cas9), transcriptomics and metabolomics remain niche and not yet fully integrated in the broader research framework. Some areas, such as genetic diversity and aphid resistance, appear to have research gaps and seem under-developed. Overall, the findings suggest an increasing trend of genomics-driven research and a need for better integration of emerging technologies into applied breeding strategies.

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Authors' contributions

KRA and RV conceptualised the study. KRA, RV and JKT developed the methodology and carried out the investigation, validation, visualisation and formal analysis. KRA prepared the original draft of the manuscript. KRA, RV, JKT, AD, SN and GS reviewed and edited the manuscript. RV and JKT supervised the study. All authors have read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interests to declare.

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During the preparation of this work the authors used Quillbot v32.1.3 in order to enhance the language and grammar. After using this tool, the authors reviewed and edited the content as needed and take full responsibility for the content of the publication.

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