

Review

A Bibliometric Review of Sorghum Breeding

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Abstract: Sorghum (*Sorghum bicolor* (L.) Moench) is a crucial food, biofuel, and forage crop significantly affected by global climate change. Frequent extreme heat and drought markedly affect sorghum production, reducing production and threatening global food security. Several studies have been conducted on sorghum breeding, but a comprehensive bibliometric review is still lacking. Therefore, we retrieved articles published between 2007 and 2023 on sorghum breeding from the Web of Science and used various tools such as VOSviewer and CiteSpace to analyze them. The analysis showed that the number of articles on sorghum breeding has steadily increased during this period. A strong collaboration was observed among the United States, India, China, and Australia. The research results published by Australian scholars provide significant findings in this field and have been widely cited. Most articles were published in the ‘Theoretical and Applied Genetics’, ‘Crop Science’, and ‘Genetics’ journals. Drought stress, high sugar sorghum, temperature and soil mineral tolerance, and marker-assisted breeding were the research hotspots in sorghum breeding. Future CRISPR/Cas9 gene editing and MAS technology should be incorporated in sorghum breeding strategies to achieve precise environment-friendly breeding. New sorghum varieties with robust stress resistance, high yield, and tailored to specific use can be cultivated through genetic manipulation to effectively meet the needs of modern agriculture and promote green agriculture. Increasing the research, investment, and application of these advanced technologies can promote sorghum breeding and ensure global food security.

Keywords: High-sugar Sorghum, QTL, Tolerance

1. Introduction

Sorghum is a gramineous plant and the world’s fifth major cereal crop after rice (*Oryza sativa* L.), wheat (*Triticum aestivum* L.), maize (*Zea mays* L.) and barley (*Hordeum vulgare* L.)^[1]. Sorghum is highly rich in nutrients. Sorghum is a major component of human food that promotes human health and has the potential as a functional food^[2-4]. In addition, sorghum is an herbaceous plant widely used as animal feed in many countries^[5]. The domestication of crops plays a key role in changing human lifestyle (from nomadic to sedentary)^[6]. Scholars explore the genetic diversity of wild, local and cultivated varieties to promote crop breeding using advanced biotechnology and re-domestication methods^[7,8]. Sorghum was domesticated in Africa about 4000-6000 years ago. Sorghum has several varieties, including bicolor, guinea, durra, caudatum, and kafir. These varieties thrive in different geographical origins and exhibit distinct morphological characteristics^[9,10]. Large-scale population genomics studies are required for the in-depth analysis of the domestication and genetic improvement of sorghum.

Sorghum has several uses, such as food, feed, fiber, and fuel sources^[11,12]. Therefore, the sorghum breeding goals vary based on the targeted use. In addition, breeding materials are diverse, including food-based grain sorghum, sweet sorghum with juicy stalks, and forage sorghum with many tillers^[12]. Sorghum breeding typically focuses on four primary areas: increasing biological stress resistance, enhancing abiotic stress tolerance,

breeding to optimize agronomic traits, and improving nutritional quality. The various breeding strategies are interrelated to ensure sorghum varieties are highly adaptable to various environments, resulting in higher yields and better quality ^[13].

Sorghum crops are affected by several biological factors, including infectious pathogens, diseases, parasitic weeds, and pests. These biological factors markedly affect sorghum crops, leading to significant economic losses and reduced agricultural production, and they directly affect farmers' income and food security ^[14]. Scholars use modern transgenic technology to accurately identify and transfer key genes to improve productivity and resistance, optimize overall performance, and ensure the safety and stability of agricultural production by developing stress-resistant sorghum varieties. Abiotic stress tolerance is a complex trait intricately regulated and influenced by numerous quantitative trait loci (QTLs) ^[15,16]. Although molecular breeding programs theoretically offer a basis for producing more resistant crop varieties, the track record of successfully breeding these excellent varieties in practice is still relatively limited. Scholars have explored genetic markers for various key traits, such as QTL ^[17-19], which is associated with drought stress and modulates sorghum overwintering ability. SbMATE is a key gene that controls aluminum tolerance, providing valuable genetic information for understanding sorghum stress resistance and adaptability ^[20-22]. Various agronomic traits, such as the number of tillers, number of whole grains per ear, and grain weight, determine sorghum yield ^[23-25]. Previous results indicate 340 QTLs associated with sorghum grain yield ^[26]. In addition, Burks et al. identified 42,926 single nucleotide polymorphisms (SNPs) associated with sugar yield in sweet sorghum ^[27]. These findings provide an essential genetic basis for improving sorghum grain yield and sugar yield. The protein digestibility of sorghum is lower than that of other grains, which is attributed to the cross-linking of disulfide bonds in β - and γ -caperine. A correlation analysis of grain quality in various sorghum varieties revealed a close relationship between SNPs in critical genes such as *SSIIa*, *pSB1700*, and *pSB0289* and grain quality ^[28]. These genes are essential genetic markers and provide a basis for developing potential strategies for optimizing sorghum grain quality. Sorghum breeding has several challenges, requiring global collaboration to share resources. International collaborations are needed to enhance the research on QTLs and the associated traits in sorghum. Global research teams can overcome breeding challenges by sharing resources and exchanging results, enhancing sorghum production.

Bibliometrics is a widely used strategy in literature analysis, and it was established as an independent discipline by Pritchard et al. (1969) ^[29,30]. It provides a quantitative tool for reviewing literature in a particular field ^[31] and reveals advances in a specific academic field ^[32]. Co-citation analysis is a comprehensive and intuitive method that reveals the internal links between different parameters, such as author groups, institutional research directions, and new theories. Co-citation analysis facilitates a clear understanding of the dynamics of academic research. Bibliometrics and visual analysis methods were used in this study to comprehensively explore the advances in sorghum breeding. This comprehensive analysis aimed to provide a valuable reference and guidance for future research on sorghum breeding.

2. Methods

2.1. Data acquisition

Data were retrieved using the Web of Science (WoS) core collection platform (Table 1). The WoS is the most authoritative indexing database for scientific and technical literature and an ideal data source for bibliometric research ^[33]. We selected SCI-EXPANDED AND SSCI as our indexes, and our research focus was on Sorghum Breeding, so our search strategy was directly TS=(“Sorghum “and” Breeding”). The period was set from January 1, 2007 to December 11, 2023. The search terms used in the study were “Sorghum “AND “Breeding”, with “English” set as the search language. The subject categories were “Genetics Heredity” or “Agronomy” or “Plant Science”. The Citation Topics Meso was Crop Science. The research areas included Biochemistry or Molecular Biology or Genetics Heredity or Agriculture or Plant Sciences or Biotechnology or Applied Microbiology or

Developmental Biology, or Evolutionary Biology. “Articles” was selected as the document type. Articles with complete records and cited references in plain text format were exported for the data extraction. A total of 649 articles were obtained. We reviewed the title and abstract and eliminated repeated and inconsistent studies, retaining 430 articles (Figure 1). Content analysis and bibliometric analysis were conducted to assess the progress and direction of these 430 studies.

2.2. Data analysis

The articles were classified, and the year of publication, citation, author citation, country, keywords, journals, and other bibliography information were recorded. CiteSpace and VOSviewer software were used to determine the frequency of each category of articles retrieved from the WOS database. The number of authors, countries, keywords, and co-citations were recorded. Visualization was conducted using CiteSpace, VOSviewer, and Gephi tools.

VOSviewer and Gephi tools were used for statistical analysis of the number of publications published by authors, journals, and countries. Subsequently, a collaborative network graph was generated to visualize the relationship among the published articles. The lines in Figure 3 and Figure 4 represent the collaborative relationship among the articles, the depth and thickness of the lines represent the collaboration intensity, and the size of the circle in Figure 3 indicates the number of publications. The proportion level of line segments in the line and line diagram represents the number of documents (Figure 4). Author co-citation and document co-citation graphs were generated using the VOSviewer tool. The node box size in Figure 5 and Figure 6 represents the co-citation frequency. A larger box corresponds to a higher frequency. The different colors represent different clustering. A keyword clustering knowledge map was generated based on the keyword co-occurrence frequency using the CiteSpace software. Different colors represent different clusters. The burst intensity of keywords, and the number of articles were determined using the CiteSpace tool.

Table 1. Summary of the data sources and selection process

Category	Specific Standard Requirements
Research database	Web of science core collection
Citation indexes	SSCI
Searching period	January 2007 to December 2023
Language	“English”
Searching keywords	(“Sorghum “ AND “Breeding”)
Subject categories	“Genetics Heredity” or “Agronomy” or “Plant Science”
Citation Topics Meso	Crop Science
Research Areas	Biochemistry or Molecular Biology or Genetics Heredity or Agriculture or Plant Sciences or Biotechnology or Applied Microbiology or Developmental Biology or Evolutionary Biology
Document types	“Articles”
Data extraction	Export articles with complete records and cited references in plain text format.
Sample size	649

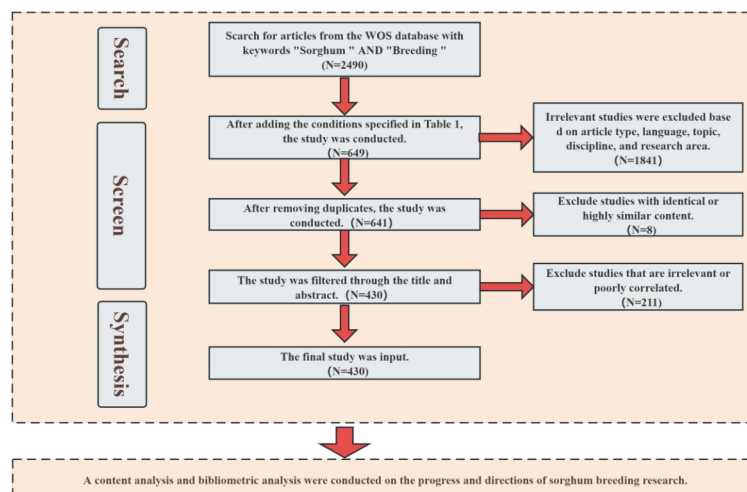


Figure 1. A flow chart illustrating the data retrieval and selection process

3. Results

3.1. Research age distribution

The analysis comprised 430 articles published by 1798 authors from 504 institutions in 67 countries. The articles were published in 104 different journals, and the authors cited 13,013 articles in 3,344 journals. The time distribution trend of articles published on sorghum breeding between 2007 and 2023 is illustrated in Figure 2. The number of articles published in this field has been increasing over the study period, with 5 articles published in 2007 and 46 published in 2023. This significant growth indicates that extensive research has been conducted on sorghum owing to the development and utilization of new sorghum varieties.

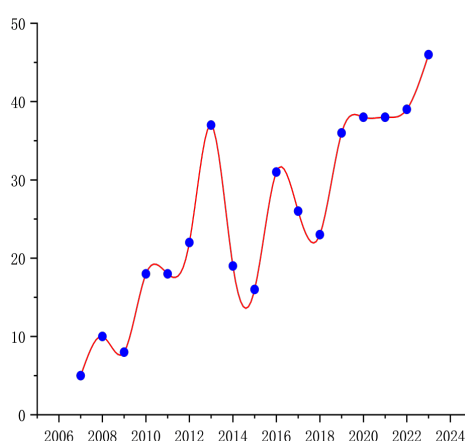


Figure 2. Time distribution of the number of published articles on sorghum breeding

3.2. Analysis of countries and institutions

The articles included in the study were published by 504 institutions focusing on sorghum breeding in 67 countries. The findings indicated that many countries and institutions were actively involved in sorghum breeding research, with some countries presenting remarkable results. The United States, India, and Australia had the

highest number of articles published on sorghum breeding (Table A1). The average number of citations of the articles published by the University of Queensland was approximately 39.69 times, showing a high contribution of this institution to sorghum breeding research. A sorghum breeding collaborative network of the top 30 countries was evaluated, and the United States, India, China, and Australia exhibited robust collaborations (Figure 4A). The collaboration enhances scientific research resources, technical exchanges, personnel training, and other levels to advance sorghum breeding and improve food security. The model fosters global collaboration and promotes industrial upgrading. The network analysis demonstrated the close collaboration among the top 27 institutions involved in sorghum breeding and their collaborative efforts to advance the field (Figure 4B). This robust collaboration ensures the sharing results, promotes prosperity, and highlights the importance of collaboration models.

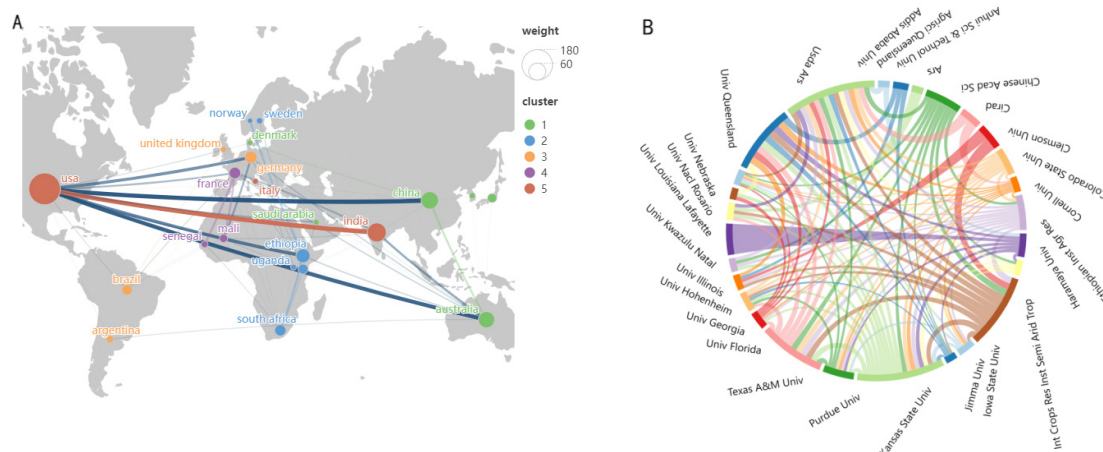


Figure 4. (A) collaboration network of the countries with more than 5 publications; (B) collaboration network diagram of the institutions with more than 7 publications.

3.3. Journal analysis

Statistical analysis was conducted on the journals focusing on sorghum breeding research literature. The results demonstrated that internationally renowned journals have published several high-quality studies in sorghum breeding, demonstrating its vast influence and academic depth. The top ten journals publishing articles on sorghum breeding were identified (Table A2). The top three journals were Crop Science, Theoretical and Applied Genetics, and Frontiers in Plant Science, with 34, 32, and 25 articles, respectively. The proportion of citations from the Theoretical and Applied Genetics journal was 41.84, indicating the high quality of the articles published in this journal, resulting in increased attention. Although few articles were published in Molecular Breeding journals such as Plant Genome and Molecular Breeding, these articles received a high number of citations, indicating that molecular breeding has attracted significant interest globally.

3.4. Generation and analysis of co-citation map

Co-citation analysis helps identify the frequently cited articles in the research field and the journals that publish these papers. A co-citation graph of journals and literature was generated using VOSviewer. The number of citations of the journals was set to at least 60 times and the number of citations for the various pieces of literature was set to at least 25 times. Consequently, 57 journals and 42 references were included in the co-citation analysis of the cited journals and papers. The final co-citation relationship diagram is presented in Figure 5.

The results demonstrated that the journal co-citation network comprised 4 clusters, indicated by 4 colors (Figure 5). The top three cited journals were Theoretical and Applied Genetics (1,563 citations), Crop Science (1,554 citations), and Genetics (552 citations). Theoretical and Applied Genetics is a prominent journal in the

JCR1 category. Crop Science and ‘Genetics are also excellent journals in the JCR2 category. Journals indicated in blue primarily publish articles focusing on agriculture and forestry sciences and emphasize new advances in crop systems research. Yellow indicates journals that mainly focus on bio-agronomy, genetics, and biotechnology. Red represents journals that published articles on genetics, from microbes to humans, showing a broad focus. Green represents bio-plant science journals that publish original research. These journals will strengthen interdisciplinary collaboration, promote data-driven research, promote open science, strengthen ethical responsibility, and jointly promote sustainable advancement in all fields. The highly cited literature was divided into two clusters: the red cluster represents the research hotspots from 2000 to 2010 (Figure 6). A genetic map of sorghum was constructed through SNP detection and bioinformatic analysis to promote the development of breeding and genetics. The green represents the research hotspots from 2010 to 2022. QTL mapping technology was used to locate sorghum genes and promote the cultivation of high-yield and high-quality stress-resistant varieties, highlighting the significance of biotechnology in crop breeding. The top ten highly cited articles are presented in Table A3. The article ‘Sorghum bicolor genome and the diversification of grasses’ exhibited the highest number of academic contributions, with 111 citations (Table A3).

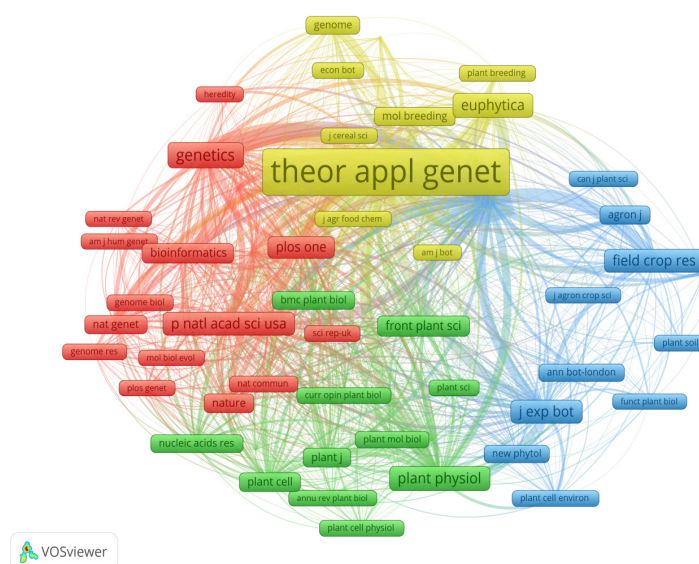


Figure 5. Co-citation map of journals with at least 60 citations

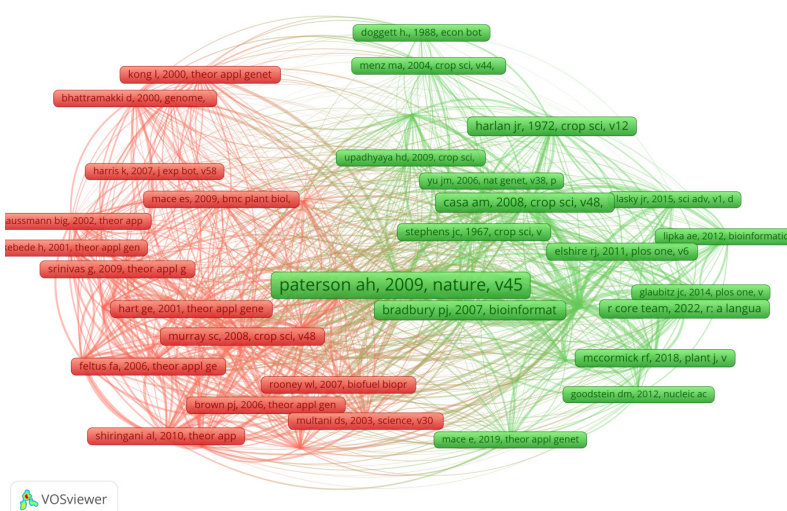


Figure 6. Co-citation map of articles cited at least 25 times

3.5. Keyword cluster analysis

A cluster analysis was conducted on the keywords to explore the substantial focus and research hotspots in sorghum breeding. The cluster analysis was conducted using the log-likelihood ratios (LLR) algorithm available in the CiteSpace tool and indicates the uniqueness and coverage direction of a research area^[34]. The labels were assigned according to the keywords. The mass Q of clustering was 0.4009, and the average contour S was 0.7456. The results indicated that the keywords were grouped into 6 clusters (Figure 7 and Table A4). The clusters were further divided into 3 primary research topics: tolerance studies (#0, #1, #4, #5), high-sugar sorghum studies (#2), and breeding methods (#3).

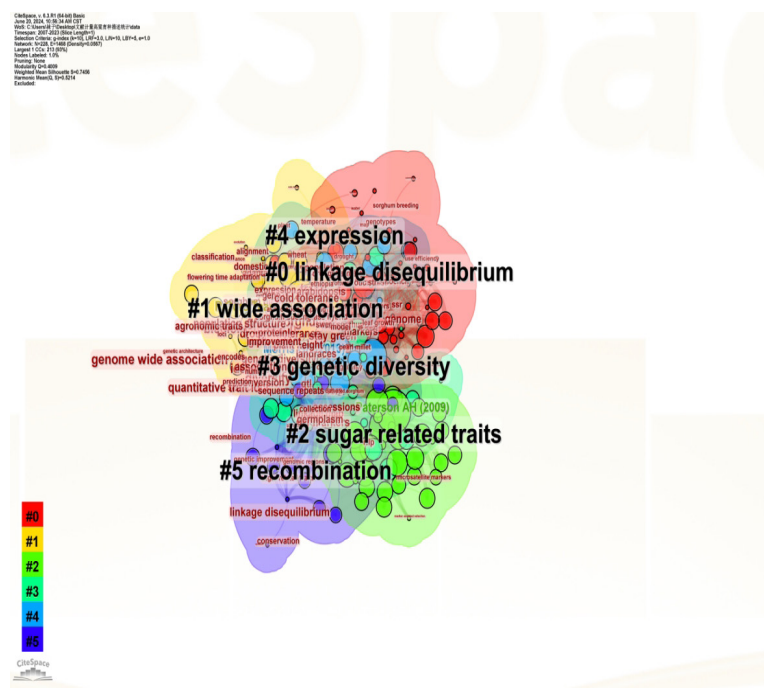


Figure 7. Keyword clustering diagram

3.6. Outburst word analysis

Burst analysis using CiteSpace tool to reveal the key breakout words and the latest trends to offer insight into the research hotspots of sorghum breeding (Figure 8). Burst analysis showed the development, frontier, and innovation points of the field, guiding future research (Figure 8). A linkage map showed a significantly high burst intensity (7.44) in sorghum breeding between 2008 and 2013. The analysis revealed a significant increase in sorghum breeding from 2008 to 2013. The findings indicated that molecular breeding was mainly conducted using Linkage map, SSR, and RFLP techniques during this period. QTL mapping technology was the primary research method between 2020 and 2023. The results demonstrate the significant adoption of quantitative trait gene mapping, which has more advantages than RLFP, Linkage map, and SSR methods.

Top 20 Keywords with the Strongest Citation Bursts

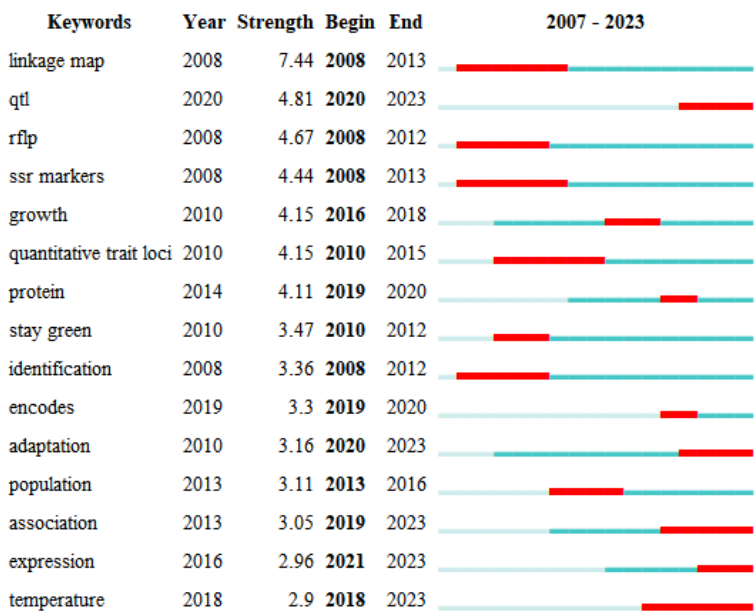


Figure 8. Analysis of keywords with high citation bursts

4. Discussion

4.1. Analysis of highly cited papers

The most cited studies used whole genome sequencing to explore the uniqueness of the sorghum genome and its evolutionary trajectory, offering a foundation for studying the diversity and genetic improvement of other plants related to sorghum^[35]. Sorghum is an essential food crop and bioenergy source. Consequently, the in-depth analysis of the sorghum genome can significantly enhance future breeding and cultivation. The top four most cited papers (2, 3, 7, 10) reported the latest sequence of the sorghum genome, conducting a comprehensive analysis, including sequencing, association analysis, reference genome comparison, and genetic variation analysis^[36-39]. The analyses reveal the genetic diversity and evolutionary trajectory of sorghum and lay a robust theoretical and data foundation for increased agricultural sorghum production and bioenergy generation. QTL analysis is a crucial method in the genetic improvement of sorghum. This technique allows accurate location of the genetic loci associated with various agronomic traits. The results help in selecting excellent varieties and revealing non-random QTL associations such as tiller height and number. These findings deepen the understanding of genetic variation and evolution of sorghum, provide new breeding resources and strategies, and promote the development of new varieties with excellent environmental adaptability^[40,41]. The 4th, 5th, and 8th rankings highlight the complementary synergistic effect of TASSEL, R language, and GBS in sorghum breeding. The TASSEL tool facilitates association analysis of complex traits^[42], R language is used for data processing and visualization^[43], and GBS allows accurate genotyping^[44]. The three tools enhance sorghum breeding research and accelerate the discovery and application of various genetic resources.

The highly cited papers comprehensively covered several vital fields, such as genomics, genetic diversity and evolution, QTL analysis and genetic improvement, and the application of tools and methods. Moreover, the articles discussed the internal relationships and potential applications of these fields, providing a robust theoretical foundation and key insights into the genetic improvement and sustainable production of sorghum.

4.2. Research on stress resistance

Drought is a significant stress factor that affects agricultural productivity in the tropical regions. The evaluated studies showed that fine-grained detection of drought-tolerant QTLs is a significant strategy in genetic improvement and provides key findings to ensure stable crop production globally. QTL mapping and MAS technology facilitate the accurate identification of genomic regions associated with crop growth traits. Moreover, these techniques are used to construct ideal allele combinations and provide robust scientific and technological to improve drought tolerance^[45]. "Staying green" is a significant indicator of a plant's ability to endure extreme drought. Sorghum adapts to drought conditions by increasing the chlorophyll content in leaves and slowing the decay of green leaves^[46]. Four key QTLs affect green retention in sorghum^[47,48]. Several studies report that QTL analysis is essential for enhancing drought tolerance of sorghum^[47,49]. These findings reveal that the drought resistance in sorghum can be enhanced by evaluating and selecting drought-tolerant germplasm and identifying QTLs associated with drought tolerance. The response of specific phenotypic traits to drought stress at the reproductive stage is heritable. Consequently, these traits are targeted in genomic studies to identify potential genes for improving drought tolerance in sorghum.

Temperature stress is a significant abiotic stress that affects crop growth, survival, productivity, and geographic distribution. Low temperature significantly reduces the germination rate and seedling vitality of cold-sensitive plants, ultimately limiting the overall growth of crops^[50,51]. Cold stress experienced at the early stage of growth is a major obstacle to expanding crop planting areas, especially high-latitude and high-altitude regions in the tropics. Several genes and their regulatory functions in low-temperature signaling and cold tolerance have been widely explored in *Arabidopsis thaliana* (L.) Heynh., a model plant. In addition, homologous genes with similar conservative functions have been identified in sorghum crops^[52]. Potential candidate genes that confer cold tolerance in seedlings have been identified through genome-wide association analysis. In contrast to the tenacious vitality observed under drought conditions, cold stress significantly inhibited the emergence and uniform growth of sorghum seedlings. This observation is attributed to the high sensitivity of sorghum to temperatures below 15 °C and the fact that it cannot survive under freezing conditions^[53]. Consequently, introducing sorghum into temperate regions as a stable crop is challenging. It is imperative to explore strategies to overcome the limitations associated with cold stress, and cultivating cold-tolerant sorghum strains has become our priority breeding goal.

Crops exhibit different adaptive responses to enhance their tolerance against stress caused by various minerals in the soil. In-depth studies on QTLs or SNP loci associated with abiotic stress tolerance in sorghum have been conducted to explore the functions and regulatory mechanisms of these loci [22,54-56]. The findings were used to develop new breeding strategies to improve sorghum's adaptability to changing environmental conditions, significantly improving crop yield and growth. Acidic soils (pH < 5.0) affect plant growth. Aluminum toxicity and low phosphorus levels significantly impact sorghum yield. These acidic conditions are particularly pronounced in tropical and subtropical regions, especially in Africa, where approximately 25% of the land has acidic soils^[57,58]. The unique weathering characteristics of acidic soils induce excessive enrichment of aluminum and iron in soils^[59], markedly affecting crop growth. In acidic soil, Al is converted into Al³⁺ ion, affecting the growth of roots into deeper soil layers^[60]. Aluminum toxicity limits other minerals and water absorption, significantly reducing food production^[61]. Low phosphorus levels reduce sorghum production. In soil, phosphorus reacts with Al and Fe oxides to form mineral complexes, minimizing the effective absorption of phosphorus by plants, thereby reducing crop yield^[62]. Notably, even if soil water content does not reach the threshold of drought stress, low water levels can affect phosphorus absorption by crops^[67]. However, some crops can detoxify aluminum and promote phosphorus absorption through the transporter *SbMATE*, alleviating the effects of low phosphorus levels^[20-22].

4.3. Research on high-sugar sorghum

The demand for high-sugar sorghum, an ideal raw material for biofuels, has markedly increased due to the increasing global demand for renewable energy ^[64,65]. Moreover, high-sugar sorghum has good palatability due to its high sugar content and is easy to digest and absorb, significantly promoting weight gain in cattle and sheep and enhancing its nutritional value ^[66]. Therefore, sorghum straw is widely used in livestock production ^[67-69]. Molecular marker technology and QTL mapping technology are advanced methods that are highly preferred by researchers in the breeding field ^[55,70-72]. Molecular markers have several advantages, such as high accuracy, breeding speed, environmental adaptability, detail processing, efficiency, affordable cost, and wide application range, promoting the sustainable development of agriculture and animal husbandry compared to the conventional breeding technology of QTL positioning.

The sugar content in sorghum stem juice is a key agronomic trait. This trait is directly correlated with the overall quality and energy conversion efficiency of sorghum. Several agronomic characteristics, especially sugar content, are modulated by complex mechanisms involving multiple genes. By accurately locating additive QTLs associated with sugar content, researchers can more accurately identify sorghum varieties with superior sugar content characteristics, significantly enhancing the breeding process. These QTLs explain the genetic mechanism of sugar content in sorghum stem juice and provide a theoretical foundation for subsequent genetic improvement and molecular breeding studies ^[73-74]. Moreover, molecular markers can be developed based on the QTLs related to sugar content to facilitate marker-assisted selection, resulting in precise selection of sorghum varieties with superior sugar content.

4.4. Breeding methods

In-depth analysis of genetic diversity, genetic distance, and genetic structure of sorghum provide crucial information for optimizing breeding strategies, significantly improving breeding efficiency, and effectively protecting precious germplasm resources ^[75-77]. Microsatellites are indispensable genetic tools that significantly improve sorghum breeding ^[75]. QTL mapping, genetic analysis, gene cloning, and functional analysis enable molecular marker-assisted selection and genome assembly and annotation in sorghum. Further studies and applications of linkage maps can greatly promote the rapid enhancement of sorghum breeding. QTL interactions can be used to optimize breeding strategies, such as selecting the best QTL combinations for desirable traits. Identification of pleiotropic QTLs can improve the breeding efficiency of sorghum and provide a reference for the breeding of other crops, broadening the application of this technology. RFLP technology can be used to select target traits, locate quantitative trait genes, assess genetic diversity, and accelerate the sorghum breeding process. Although several SNPs have been identified in sorghum, SSR/SV molecular markers can significantly enhance sorghum breeding due to their low cost and easy verification ^[78-80]. SSR markers have several advantages, such as wide genome distribution, easy operation, high polymorphism, and co-dominant inheritance, compared to RFLP, RAPD, and AFLP ^[88]. Consequently, they are widely used in genetic map construction, genetic diversity analysis, and molecular fingerprint construction ^[81-82].

5. Conclusion and prospects

5.1. CiteSpace and VOSviewer visualization results

The number of published articles on sorghum breeding has increased steadily since 2007, reaching 46 by 2023. This increase indicates a strong academic interest in developing new sorghum varieties. The United States, India, China, Australia, and other countries have established a core collaborative network to promote resource sharing, technology exchange, and personnel training, and enhance sorghum production. The contribution of the University of Queensland to sorghum research is outstanding. Several high-quality articles on

sorghum breeding have been published in internationally renowned journals such as ‘Crop Science’, ‘Theoretical and Applied Genetics’, and ‘Frontiers in Plant Science’. The vast influence and scholarly depth of these journals provide an essential communication platform for sorghum breeding research. Co-citation and keyword cluster analysis showed that tolerance research (including drought resistance, disease resistance, etc.) and high-sugar sorghum research are primary research directions in the field. Extensive development of breeding methods (such as molecular breeding technology) has facilitated the cultivation of high-yield and high-quality stress-resistant sorghum varieties. These research hotspots indicate the current need for sorghum breeding and provide an important reference for future research.

5.2. Recommendations for further research

It is imperative to further expand sorghum research in the future from the following dimensions to further improve sorghum breeding and ensure the sustainability of the sorghum industry:

1. Optimize molecular breeding strategies: This can be achieved by integrating the genomics, transcriptomics, and metabolomics strategies to ensure accurate QTL analysis. A strict verification system should be established to ensure the reliability of the research. Innovate genotyping technology should be adopted to provide efficient and precise tools for molecular breeding to obtain high-quality sorghum varieties.

2. Strengthen sorghum breeding for use as livestock feeds: It is necessary to explore sorghum germplasm resources to increase sorghum starch content, optimize protein composition, and reduce anti-nutrient factors in feeds. New high-yield, high-quality, and multi-resistance varieties should be cultivated to meet the urgent needs of the livestock feed industry. New sorghum varieties with attractive color, rich aroma, delicate taste, and health benefits such as anti-oxidation, lowering blood sugar, and lowering blood lipids should be cultivated for human consumption.

3. Promote in-depth identification and innovative utilization of germplasm resources: Novel sorghum germplasm resources should be identified, focusing on varieties with genes that encode high-quality phenotypes. A precise genotype and phenotype identification strategy should be established. Moreover, heterosis groups should be reconstructed and hybridization strategies should be optimized to improve the utilization efficiency significantly and enhance the level of sorghum heterosis.

4. Accelerate the green revolution of sorghum varieties: Strategies successfully used in wheat and other crops should be adopted to promote the green revolution of sorghum. Modern biotechnology methods, such as genetic engineering, should be used to enhance photosynthetic efficiency, plant varieties, and dense planting resistance, improve harvest index, and optimize the growth cycle.

5. Promote interdisciplinary talent training and international collaborations: An interdisciplinary education system should be established to develop professional, innovative, and practical breeding talents. International collaborations should be strengthened to enhance research and solve agricultural problems. These collaborations will facilitate the sharing of resources and the exchanging of experience and technical skills to promote sustainable production of sorghum and improve agriculture.

Author Contributions

X.Y. and Q.D. designed the experiments and wrote the manuscript. Q.D. and B.L. performed the data analysis. X.L. and L.L. contributed to the grammar and language revision of the paper. All authors have read and agreed to the published version of the manuscript.

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Institutional Review Board Statement

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Informed Consent Statement

Not applicable.

Conflicts of Interest

The authors declare no conflicts of interest.

Appendix

Table A1. Top 10 research institutions with the number of published documents

Rank	Organization	Country	Documents	Citations	Average Citation/Publication
1	Usda ars	USA	47	1140	24.26
2	Kansas State University	USA	45	1131	25.13
3	Int Crops Res Inst Arid Trop	India	38	839	22.08
4	Univ Queensland	Australia	35	1389	39.69
5	Texas A&M Univ	USA	34	1111	32.68
6	Ars	USA	19	397	20.89
7	Cornell Univ	USA	18	620	34.44
8	Purdue Univ	USA	16	594	37.13
9	Univ Kwazulu Natal	South Africa	16	131	8.19
10	Clemson Univ	USA	14	274	19.57

Table A2. Top 10 journals in terms of publication volume

Rank	Source	Documents	Citations	Average Citation/Publication
1	Crop Science	34	1022	30.06
2	Theoretical and Applied Genetics	32	1339	41.84
3	Frontiers in Plant Science	25	238	9.52
4	Field Crops Research	21	511	24.33
5	Euphytica	20	253	12.65
6	Plant Genome	19	522	27.47
7	Genetic Resources and Crop Evolution	15	104	6.93
8	Agronomy-Basel	14	74	5.29
9	Molecular Breeding	14	291	20.79
10	Journal of Plant Registrations	11	25	2.27

Table A3. Top 10 cited literatures

Id	Cited Reference	Citations
1	The Sorghum bicolor genome and the diversification of grasses	111
2	Population genomic and genome-wide association studies of agroclimatic traits in sorghum	85
3	Community Resources and Strategies for Association Mapping in Sorghum	56
4	TASSEL: software for association mapping of complex traits in diverse samples	55
5	R: A Language and Environment for Statistical Computing.	48

Id	Cited Reference	Citations
6	Genetic Improvement of Sorghum as a Biofuel Feedstock: I. QTL for Stem Sugar and Grain Nonstructural Carbohydrates	44
7	The Sorghum bicolor reference genome: improved assembly, gene annotations, a transcriptome atlas, and signatures of genome organization	43
8	A Robust, Simple Genotyping-by-Sequencing (GBS) Approach for High Diversity Species	37
9	Alignment of genetic maps and QTLs between inter- and intra-specific sorghum populations	37
10	Whole-genome sequencing reveals untapped genetic potential in Africa's indigenous cereal crop sorghum	37

Table A3. (Continued)

Table A4. Keyword clustering

ClusterID	Size	Silhouette	Mean (year)	Core Noun Terms
#0	56	0.641	2012	linkage disequilibrium ; drought stress; genome wide association; ssr markers; water
#1	46	0.711	2017	wide association; registration; drought tolerance; sudangrass; tolerance
#2	35	0.86	2009	sugar related traits; height; tiller number; ssr marker; glucose
#3	32	0.768	2015	genetic diversity; accessions; microsatellites; genetic structure; genetic distance
#4	25	0.793	2014	expression; arabidopsis; genome wide association; freezing tolerance; anthocyanin
#5	19	0.827	2008	recombination; diversity; selection; minerals; sorghum landraces

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