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BIBLIOMETRIC ANALYSIS OF THE PAST RESEARCH BASED ON MAS TECHNOLOGY IN COTTON IMPROVEMENT

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SUMMARY

Marker-assisted selection (MAS) is a fundamental approach for enhancing the cotton crop quality. However, the comprehensive bibliometric analysis within this research domain is still lacking. In August 2023, we conducted a scientific, computer-assisted review methodology based on the bibliometric record use of the Scopus dataset. Employing an innovative research methodology has gathered the data to descend prevailing research trends, influential journals, document types, prolific authors, and key countries related to MAS application in cotton research. The bibliometric analysis helped determine the current general research direction and trend of publications about MAS application in cotton research in the most prolific and distinguished journals and document types with years, authors, countries, and keywords. Data extraction, integration, and visualization employed the VOS-viewer, Microsoft Excel, and Map-chart. The presented review referred to 273 research manuscripts published in 72 journals retrieved from the Scopus database, with China and the United States identified as the most productive nations. Authors, including Zhan T, Zhang J, Guo W, Fan DD, and Yuan Y, emerged as influential contributors to MAS studies. The most important fields were agricultural and biological science, biochemistry, genetics, and molecular biology. The latest review research will objectively assess the current state of MAS utilization in cotton research, offering valuable insights for individuals seeking information on MAS techniques in cotton and serving as a reference guide for researchers exploring further studies in this domain.

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Keywords: Bibliometric analysis, marker-assisted selection (MAS), cotton, Scopus database, collaborative network, co-accurate network, subject area

Key findings: The study provides a comprehensive overview of MAS research in cotton, emphasizing the leadership of China and the USA. Developing countries should strengthen MAS initiatives by collaborating with chief authors and organizations crucial for further advancements in this field.

INTRODUCTION

Marker-assisted selection (MAS) is one of the most effective approaches to developing superior crop cultivars, especially cotton crops (Abdurakhmonov *et al.*, 2007; Kushanov *et al.*, 2021; Turaev *et al.*, 2023). MAS can help considerably improve the effectiveness of breeding by decreasing the period required for different breeding processes and resources (Kushanov *et al.*, 2022; Suvarna and Yashaswini, 2023). For multi-locus quantitative trait locus (QTL) polymorphism, a reasonable allocation of marker combinations has intensely improved the selection effect (Chakraborty *et al.*, 2023).

The progression of molecular marker technologies and genomic sequencing has significantly advanced cotton breeding. Malik *et al.* (2014) highlighted the shift toward advanced genetic analysis methods, such as linkage disequilibrium and association mapping, facilitated by draft genome sequences and next-generation sequencing. Identifying QTL alleles associated with economically important traits enabled their direct utilization in MAS as DNA markers in cotton (Li *et al.*, 2018; Kushanov *et al.*, 2017; Khidirov *et al.*, 2023). The selection processes for F₂ hybrid plants began with three methods, i.e., a) phenotype-based selection, b) MAS, a combination of marker-genotype and phenotype, and c) genotype-based selection (Shavkiev *et al.*, 2022; Zeng *et al.*, 2022). Pedigree backcrossing and MAS techniques can effectively enhance the breeding values of different strains, incorporating a relatively small number of genes from a few outstanding parental lines by selecting particular combinations of advantageous QTL alleles (Jia *et al.*, 2014; Suvarna and Yashaswini, 2023; Bakhadirov *et al.*, 2024).

The past 20 years have shown a rapid rise in the MAS method used in plant breeding (Zeng *et al.*, 2022). Several scientists have led numerous research projects using the MAS technique (Wu *et al.*, 2007; Xiao *et al.*, 2010; Yu *et al.*, 2013; Zhu and Kuraparthi, 2014; Zhang *et al.*, 2003). Maheswari *et al.* (2023) concentrated on selecting bivoltine silkworm *B. mori* genetic resources with higher survival rates and high output. They utilized SSR markers associated with thermo-tolerance in silkworms. Monica S. and her team compared the MAS and traditional breeding methods to know their differences. As a result, they also highlighted the advantages of the MAS method. Suvarna and Yashaswini (2023) suggested that the MAS technology is essential for working out repeated choices and improving breeding in different crop species. Growing resistant cultivars can significantly enhance cotton yield and reduce production costs (Abdelraheem *et al.*, 2020). Developing high-throughput molecular markers, as detailed by Ijaz *et al.* (2019), revolutionized the breeding process through the MAS and enabled targeted improvements in fiber quality. Subsequent studies by Darmanov *et al.* (2022) and Zeng *et al.* (2022) further validated the efficacy of MAS over traditional phenotype selections in enhancing fiber quality. Darmanov *et al.* (2022) reported on creating the first cotton cultivar series 'Ravnaq' with superior fiber quality using MAS technology. Cotton breeding line production has also emerged for root-knot nematode resistance in early-generation hybrid plants using MAS (Lopes *et al.*, 2020). According to Nayak *et al.* (2017), MAS is the most efficient approach in plant breeding in selecting desired individuals in a breeding program engaging molecular markers, with or without considering its relative importance. This method works

particularly well for developing resistant species (Ayubov *et al.*, 2021; Umedova and Rakhmankulov, 2021; Baboeva *et al.*, 2023).

The completion of *Gossypium* genome sequencing, as Sabev *et al.* (2020) noted, opened new possibilities for exploiting genetic diversity and underscored the importance of molecular markers in selecting superior traits. This series of advancements underscores a significant evolution in cotton breeding strategies, focusing on precision and efficiency to meet the demands for improved cotton fiber quality and yield (Darmanov *et al.*, 2022; Seytnazarova *et al.*, 2024). Bibliometry is a statistical technique for examining scientific literature to determine the most significant and well-known research in a specific study field (Zyoud *et al.*, 2023). Researchers use bibliometric analysis for various purposes, including studying the intellectual framework of an existing field and identifying developing trends in article and journal performance, cooperation patterns, and various research components (Donthu *et al.*, 2020). Through quantitative analysis of the knowledge, bibliometry combines science, mathematics, and statistics to produce comprehensive data (Wilsa *et al.*, 2023).

The data that dominates the bibliometric analysis tends to be massive (hundreds or even thousands) and objective (number of citations and publications, circumstances of keywords and motifs). However, the interpretation frequently relies on both ideal (performance analysis) and private (thematic analysis) evaluations established through knowledgeable procedures (Donthu *et al.*, 2021). Therefore, bibliometric tools can be practical to evaluate the productivity and research patterns of different authors, journals, nations, and institutions, as well as recognize and measure collaborative patterns between them (Van-Nunen *et al.*, 2018).

Inferring the interdisciplinary nature of a research domain and the diversity of journals publishing research articles on a given topic is simple from the subject categories assigned to publications and the number of journals involved. According to Wang *et al.* (2014), bibliometric analysis can better highlight the

most recent developments in the research directions and hot subjects in a specific study area. Bibliometric analysis also enables gap identification in a particular field of study, both conceptually and geographically (Gall *et al.*, 2015).

Moreover, it is also crucial in the scientific decision-making process, often used to evaluate the effectiveness of journals, nations, and institutions and rank the candidates for academic employment. Bibliometric findings can assist decision-makers and funding organizations in fund allocation of future research (Ugolini *et al.*, 2015). Thus, the presented study sought to identify the literature on MAS and describe the characteristics of the MAS method work. Bibliometric analysis used in this study helped understand research trends in agriculture, focusing on cotton growing using the MAS method.

MATERIALS AND METHODS

This study methodology was quantitatively descriptive. Research manuscripts attained from the Scopus database on August 16, 2023, spanned 28 years, from 1995 to 2023. The search equation formed used keywords combination from the field of cotton cultivation and Boolean operators. In particular, it was Title-ABS-KEY 'Cotton,' 'Marker-Assisted Selection,' and 'Limit to (Language English).' The different stages of the descriptive research method used are available in Figure 1.

The initial search yielded 273 documents in agricultural and biological sciences. During the compilation phase, run the ris.file to analyze the whole data and identify the information on the publisher, source of publication, and the year published. Consequently, this study employed Microsoft Excel for bibliometric analysis. The VOSViewer (Leiden University, Leiden, Netherlands) tool within Microsoft Excel (Microsoft, Redmond, Washington) and Mapchart (<https://www.mapchart.net/world.html>) aided in analyzing and visualizing the bibliometric network (Van-Eck and Waltman, 2010).

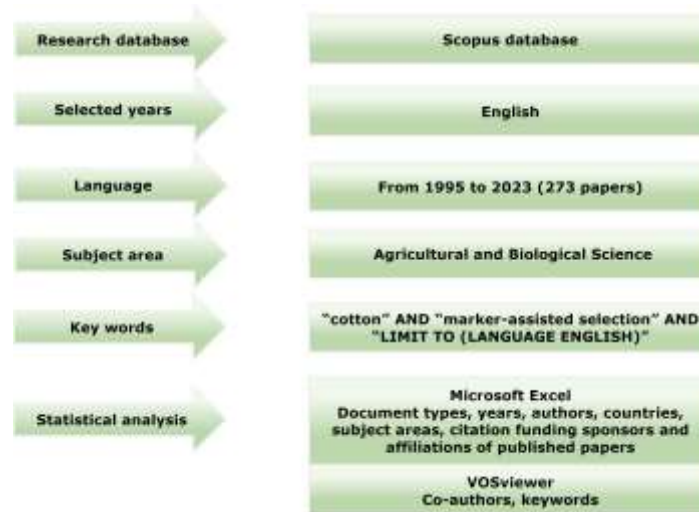


Figure 1. Methodology flowchart for the research.

The following indicators based on the documents included in this dataset underwent calculation:

- List of the journals on marker-assisted selection in cotton
- Percentage of document type
- Countries that published papers on MAS
- Publications by year
- Subject area
- Highest number of articles per author published
- A map of the countries with the highest number of publications in this field
- The temporal co-occurrence network of the most frequently used terms
- Most co-authored authors
- List of top 10 most cited papers

RESULTS

The Scopus dataset revealed 273 research manuscripts on marker-assisted selection (MAS) in cotton published between 1995 and August 2023. Before 1995, no research publications existed on MAS in cotton. The first research article published on MAS in cotton was in the United States in 1998. About 71 diverse peer-reviewed journals identified had

more than half-publishing and no more than one (57.7%) or two (12.7%) relevant papers. The journal with the maximum number of publications was *Euphytica* (15.0%), followed by *Theoretical and Applied Genetics* (7.7%), and then *Frontiers in Plant Science* (6.6%) (Table 1).

The present findings relied on the limited number of research manuscripts, and the results from such analyses should require treatment with utmost caution. The latest results seem to demonstrate that publications included 87% (237) original research articles, 7% (18) review articles, 5% (14) books, 1% (3) conference papers, and 0% (1) notes (Figure 2).

Given the number of research publications across the years, most published articles were in 2014 (Figure 3). In 2008, the publication number was three. In 2009, this indicator increased sharply to 11. In 2009–2011, the publications score rose to 10. The number of publications increased to 17 in 2013, with the highest score reaching 25 in 2014–2015. Research manuscripts started declining in 2016, eventually falling to 14 in 2017. The publishing indicator strengthened in 2018, with a gradual decline beginning in 2019.

Table 1. List of the journals on marker-assisted selection in cotton.

Scopus Source title	Number of papers	Scopus Source title	Number of papers
Euphytica	41	Crop Breeding and Applied Biotechnology	1
Theoretical and Applied Genetics	21	Crop Journal	1
Frontiers in Plant Science	18	Czech Journal of Genetics and Plant Breeding	1
BMC Genomics	15	DNA Research	1
Molecular Breeding	15	Frontiers of Economics and Globalization	1
Crop Science	14	Functional and Integrative Genomics	1
Molecular Genetics and Genomics	12	Genes	1
Plant Breeding	10	Genes and Genomics	1
Plos One	8	Genetics	1
BMC Plant Biology	5	Genomics	1
Journal of Cotton Science	5	Genomics Insights	1
Journal of Genetics	5	Gm Crops Food	1
Journal of Cotton Research	4	Heliyon	1
Journal of Plant Registrations	4	Indian Journal of Plant Physiology	1
Breeding Science	3	Journal of Genetics and Genomics	1
Chinese Science Bulletin	3	Journal of Heredity	1
G3 Genes Genomes Genetics	3	Journal of Nematology	1
Industrial Crops and Products	3	Journal of New Seeds	1
Journal of Integrative Plant Biology	3	Molecular Biology Reports	1
Pakistan Journal of Botany	3	Pathogens	1
Plant Science	3	Physiologia Plantarum	1
Agronomy	2	Physiology and Molecular Biology of Plants	1
Australian Journal of Agricultural Research	2	Phytopathology	1
Bulgarian Journal of Agricultural Science	2	Plant Biotechnology Journal	1
Frontiers in Genetics	2	Plant Cell Tissue and Organ Culture	1
Journal of Agricultural Science	2	Plant Molecular Biology Reporter	1
Journal of Integrative Agriculture	2	Scientific Reports	1
Journal of Plant Biochemistry and Biotechnology	2	Scientific World Journal	1
Plants	2	Seed Science Research	1
Turkish Journal of Agriculture and Forestry	2	Springerplus	1
Acta Agronomica Sinica	1	Tag Theoretical and Applied Genetics	1
Acta Genetica Sinica	1	Theoretische und Angewandte Genetik	1
African Journal of Biotechnology	1	Trends in Biotechnology	1
BMC Genetics	1	Turkish Journal of Biochemistry	1
Biotechniques	1	Turkish Journal of Botany	1
Biotechnology Annual Review	1	Turkish Journal of Field Crops	1
		World Applied Sciences Journal	1

Looking back on the subject area of scientific research published on the Scopus database, the main component was agricultural and biological science networks comprising 200 (46%). Biochemistry, genetics, and molecular biology contribute 184 (42%) to the science networks (Figure 4). The remaining 18% came from other areas, including multidisciplinary fields, such as medicine, ecology, livestock, engineering, biochemistry, and molecular biology.

Considered crucial to study authors who researched using the MAS technology in cotton cultivation is imperative. Studying these authors can monitor valuable developments in this field and be aware of emerging problems. The latest analysis showed that 160 authors from 27 countries have published scientific manuscripts using the MAS method in agriculture. The top authors listed with the most published articles in this area appear in Figure 5. By determining the number of

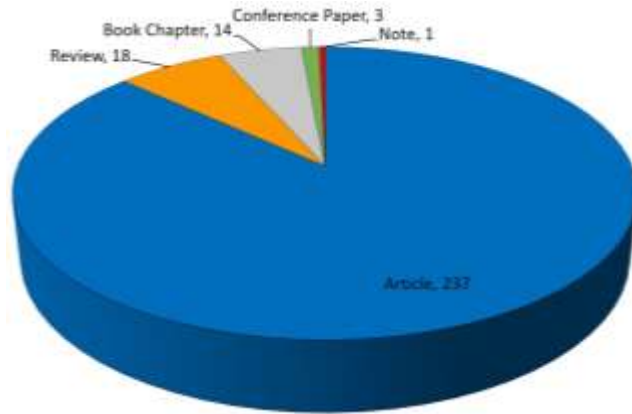


Figure 2. Document type of publications.

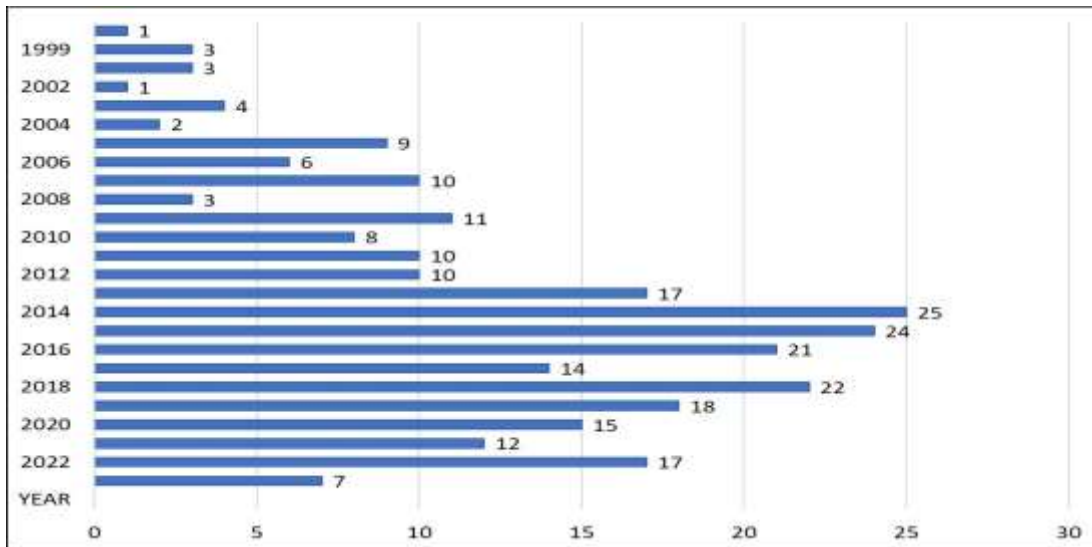


Figure 3. Publications by year.

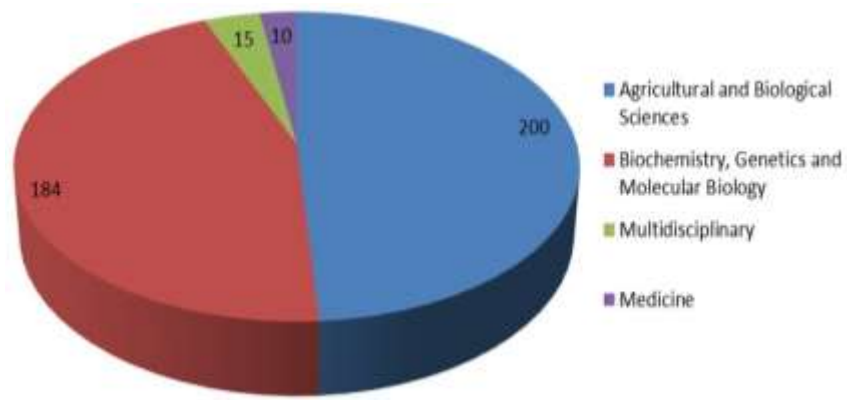


Figure 4. Subject area.

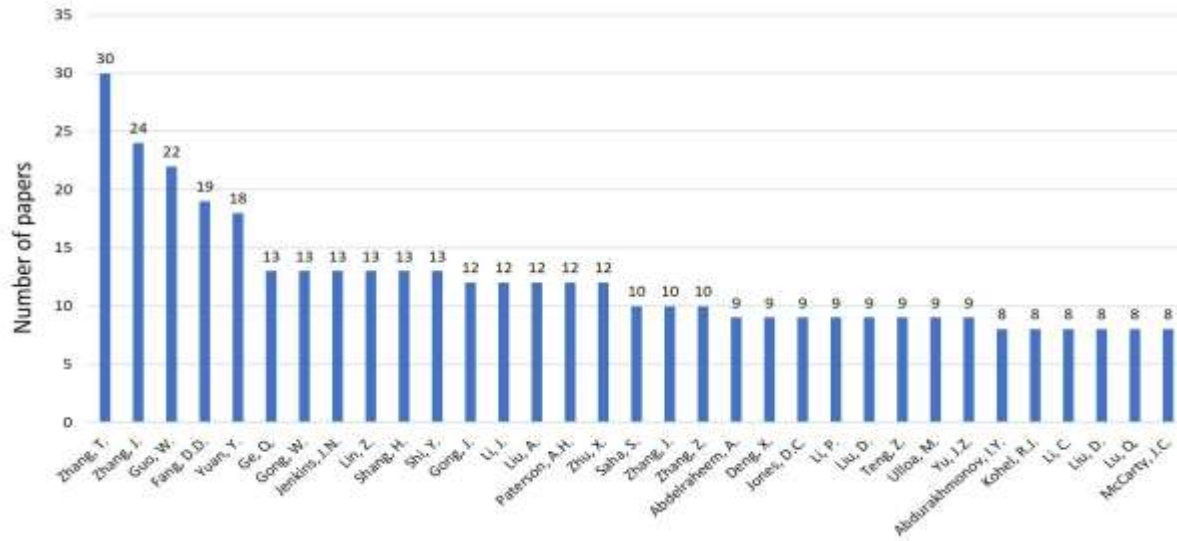


Figure 5. The highest number of articles per author published.



Figure 6. A map of the countries with the highest number of publications published in this field.

publications based on the first author of the articles, Zhang T. ranked first, with 30 articles, followed by Zhang J., with 24 articles. Other notable authors included Guo W. (22 articles), Fan D.D. (19 articles), Yuan Y. (18 articles), and others. With the top authors mostly coming from China and the USA, these countries can be the leaders in this field of study. In the country-wise analysis, Uzbekistan

ranks fifth on this list, following Pakistan and India (Figure 6).

Considering the research publications per country, all published articles have come from 27 countries in this field. Figure 6 highlights a map of the countries with the highest number of publications in marker-assisted selection in cotton. China takes first place with a share of 45% and leads other

countries conducting said research. Looking at the succeeding countries based on publication numbers, the United States takes second place with 32% (106 articles), followed by Pakistan at 7% (22 articles), India at 4% (15 articles), Uzbekistan at 3% (9 articles), Australia at 2% (7 articles), Brazil at 2% (7 articles), and Turkey at 2% (6 articles). However, the lowest indicator (1%) belongs to Israel, Egypt, and France.

Keywords are the most critical in the process of writing research articles. A maximum of 1,395 keywords reached usage in 273 articles (Figure 7). From the total, separating 82 were keywords repeated at least 10 times. For each of the 82 keywords, the total strength of the co-occurrence links with other keywords attained calculation. The process has selected keywords with the maximum total link strength. The number of lines showed the strength of the relationship between the main phrases in the publications.

The color of the points and lines following the keyword showed the chronological usage density of each clause. Each link has strength, represented by a positive numeric value, and the higher this value, the stronger the link. The visualization result showed the formation of five clusters, with 2,782 links between them and a total link strength equal to 18,325 (Figure 7). Of these, the most utilized keywords were the '*Gossypium*' occurring 111 (total link strength: 1,674), '*Gossypium hirsutum*' occurring 153 (total link strength: 1,531), 'cotton' with 126 occurrences (total link strength: 1,507), 'genetics' with 84 occurrences (total link strength: 1,477), 'quantitative trait locus' with 73 occurrences (total link strength: 1,273), 'chromosome mapping' with 60 occurrences (total link strength: 1,216), 'genetic marker' with 49 occurrences (total link strength: 908), and 'marker-assisted selection' with 44 occurrences (total link strength equal to 393).

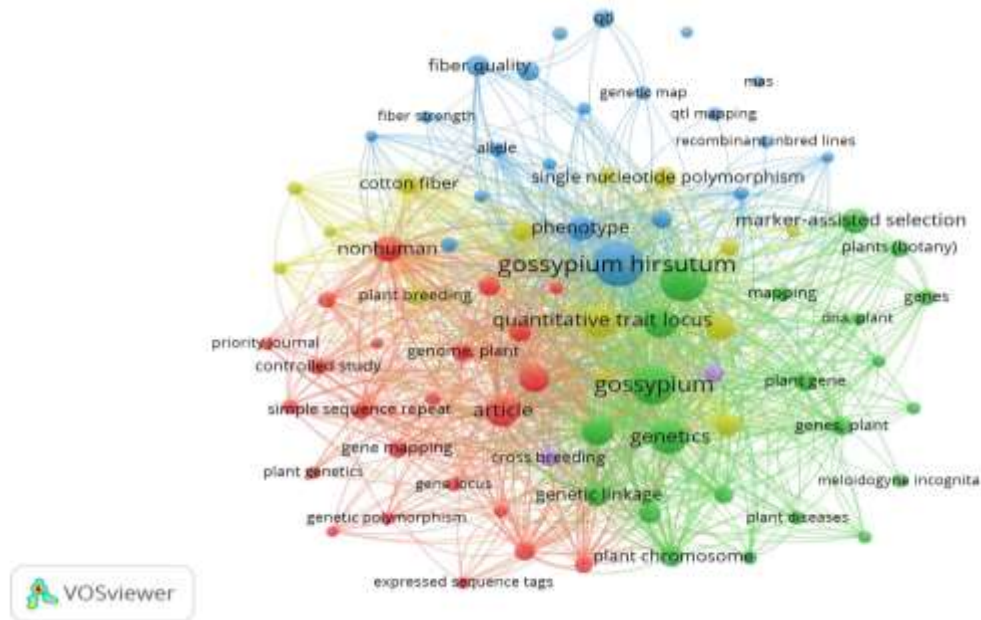


Figure 7. The most frequently used terms' temporal co-occurrence network.

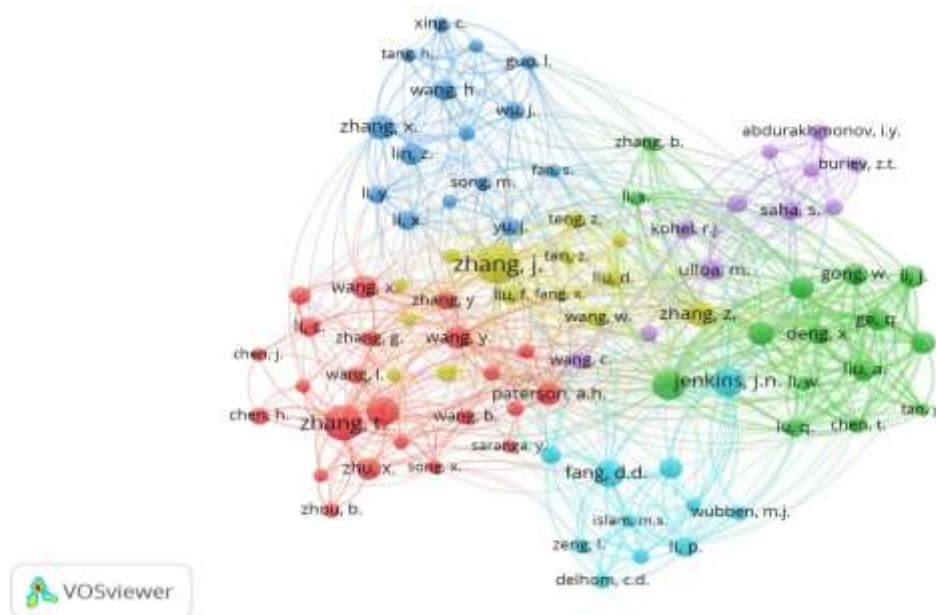


Figure 8. Most co-authored authors.

By analyzing the authors' distributions in the VOSviewer program, it was notable that 931 authors published 90 co-authored articles (Figure 8). As the number of articles increased, the connections decreased. A maximum of 30 published articles were by Zhang T., 24 by Zhang J., 22 by Guo W., 19 by Fang D.D., and 19 by Yuan Y. (Figure 8). Since not all 850 authors have linkages, the VOSviewer algorithm classified the 89 most linked authors into six clusters. Zhang J. established the most prominent cluster, with most of his research manuscripts published between 2014 and 2015. Zhang J. collaborated with four clusters. The links between them were 55, and they co-authored 38 articles. Following closely, Zhang T. organized another significant cluster, collaborating with other authors in 32 research manuscripts. However, Zhang T. published more articles in 2010. Abdelraheem A., Kuraparthy V., and Zhang M. have worked more recently on MAS in cotton. The study also observed that several clusters have communicated via Zhang J.

The most cited article was 'A microsatellite-based, gene-rich linkage map, that reveals genome structure, function, and

evolution in *Gossypium*,' published in the Journal of Genetics in 2007, with 233 citations. The paper 'Characteristics, development and mapping of *Gossypium hirsutum* derived EST-SSRs in allotetraploid cotton,' published in the Theoretical and Applied Genetics journal in 2006, has 186 citations. Furthermore, the list of the top 10 articles is available in Table 2. These articles especially highlight the importance of the MAS method in agriculture.

DISCUSSION

The results of the bibliometric analysis showed that the most cited articles had open-access publishing; however, these articles emphasized the current research. The article with the most citations was 'A microsatellite-based, gene-rich linking map of *Gossypium*, demonstrating genomic structure, function, and evolution in *Gossypium*' (Guo et al., 2007). This topic was considerably one of the most relevant issues in the research carried out by the MAS method. In addition, the article had an in-depth discussion on the SSR markers' characteristics and capabilities.

Table 2. List of the top 10 most cited articles.

Title of the article	Year	Journal name	Cited by
A microsatellite-based, gene-rich linkage map reveals genome structure, function and evolution in <i>Gossypium</i>	2007	Genetics	233
Characteristics, development and mapping of <i>Gossypium hirsutum</i> derived EST-SSRs in allotetraploid cotton	2006	Theoretical & Applied Genetics	186
Molecular mapping of QTLs for fiber qualities in three diverse lines in Upland cotton using SSR markers	2005	Molecular Breeding	178
Progress and perspective on drought and salt stress tolerance in cotton	2019	Industrial Crops & Products	158
Genetic mapping of quantitative trait loci for fiber quality and yield trait by RIL approach in Upland cotton	2007	Euphytica	158
QTL analysis of cotton fiber quality using multiple <i>Gossypium hirsutum</i> × <i>Gossypium barbadense</i> backcross generation	2005	Crop Science	158
Genetic mapping of new cotton fiber loci using EST-derived microsatellites in an interspecific recombinant inbred line cotton population	2005	Molecular Genetics & Genomics	152
Molecular diversity and association mapping of fiber quality traits in exotic <i>G. hirsutum</i> L. Germplasm	2008	Genomics	145
A comparative meta-analysis of QTL between intraspecific <i>Gossypium hirsutum</i> and interspecific <i>G. hirsutum</i> × <i>G. barbadense</i> populations	2015	Molecular Genetics & Genomics	142
Genome structure of cotton revealed by a genome-wide SSR genetic map constructed from a BC ₁ population between <i>Gossypium hirsutum</i> and <i>G. barbadense</i>	2011	BMC Genomics	137

Several scientists in this field have used this valuable information, which has led to numerous citations. The second most cited article was 'Characteristics, development, and mapping of *Gossypium hirsutum* derived EST-SSRs in allotetraploid cotton,' published in the Theoretical and Applied Genetics journal in 2006 (Han *et al.*, 2006). This article highlighted studies on applying the MAS method to plant breeding and genetic mapping. The most relevant discipline for molecular research was genetic mapping (Abdelraheem *et al.*, 2022).

In other top-cited articles, topics such as the MAS method, genetic mapping, genome-wide association mapping, QTL mapping, SSR markers, and breeding were focal (Lacape *et al.*, 2005; Shen *et al.*, 2007; Abdurakhmonov *et al.*, 2008; Yu *et al.*, 2011; Said *et al.*, 2015; Abdelraheem *et al.*, 2019). Article citations and readability were contingent upon the articles' content, quality of coverage, and the journal's Impact Factor (IF) at the time of publication. From the study, the top-cited manuscripts published were in high IF and Q1 and Q2 journals. It is worth mentioning that the Journal impact factor depended on the number of citations.

The possibility of the article gaining many citations increases when its publication is in a journal with a high IF. The more scientific research publications are published, and the more researchers are familiar with them, the more beneficial it will be to the scientists. Scientists do not waste time studying what is already proven; however, they will learn something new and work on unsolved issues.

CONCLUSIONS

In the pertinent study, the review of research manuscripts published between 1995 and 2023 could offer a thorough summary to interested scientists about the research using the MAS approach in cotton production. From the present review, China and the USA were distinct leaders in this field. The MAS methods application in growing cotton has also resulted in Pakistan, India, Uzbekistan, Australia, Brazil, and Turkey. However, other developing countries lag in MAS research and should strengthen their initiatives. The latest research findings can help scientists collaborate with chief authors and organizations.

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