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Library Knowledge Map Based on CiteSpace for Genetically Modified Soy Research

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Abstract: With the rapid development of genetically modified soybean technology, the study of genetically modified soybean has also become one of the research hotspots in plant molecular biology at home and abroad. As a new technology, genetically modified soybean has attracted wide attention from the library community at home and abroad. Many researchers have done a lot of research on various aspects of the field of genetically modified soybeans from various perspectives. These studies have played an important role in guiding the actual development of genetically modified soybean technology. Based on this, quickly and accurately grasping domestic and foreign research hotspots and cutting-edge trends in a large amount of disordered research data is a vital link in the research and development of genetically modified soybeans. This article focuses on the analysis of library knowledge maps based on CiteSpace's research on genetically modified soybeans. This article is based on the research status of GM soybeans in China and the world, and aims to address the problems existing in the development of GM soybeans in China, and draws on relevant experiences and developments in this field in the world. It provides a certain theoretical basis for Chinese scholars to grasp the scientific research dynamics of genetically modified soybeans and opens up new research fields. According to the experimental analysis in this paper, we can see that there are many institutions in China that research genetically modified soybeans, and the degree of cooperation between them is low. There are many authoritative institutions and universities in Northeast China and Beijing. Institutions in this field are closely connected worldwide, and scientific research forces have made tremendous contributions to the research of genetically modified soybeans.

1. Introduction

In recent years, genetically modified crops have developed rapidly. China has also issued safety

production certificates for genetically modified insect-resistant rice and trans-phytase corn. With the implementation of major transgenic projects in China, a number of transgenic crops with independent intellectual property rights have been developed. At present, there are more than 60 types of genetically modified crops approved in China, including genetically modified soybeans, corn and rape. The amount of literature on transgenic soybeans at home and abroad is increasing, and transgenic soybeans have gradually entered various links in the human food chain. At the same time, research on transgenic soybeans has also increased. Foreign research on genetically modified soybeans is still in a leading position in the main soybean producing countries. Compared with domestic research, foreign research on genetically modified soybeans is currently maturing. Therefore, studying the development of global genetically modified soybeans has great reference significance for the development of domestic genetically modified soybeans.

This article analyzes the research status of genetically modified soybeans from the perspective of knowledge structuring, and draws a knowledge map using CiteSpace software. Through the establishment of co-citation networks, co-authoring networks, keywords, and co-word networks, the visualization technology is used to process the knowledge structure of genetically modified soybean research; collect relevant research literature at home and abroad, and compare the similarities and differences between Chinese and foreign genetically modified soybean research in a horizontal way. Provide references and guidance [1-2]. This article builds a domestic and global research map of genetically modified soybeans, studies the volume of publications, research hotspots, authors, and institutional cooperation in the development of domestic and global genetically modified soybeans, and helps experts and scholars grasp the hotspots and development trends in the field of genetically modified soybeans. It also provides assistance in selecting cutting-edge scientific research directions, and has important academic value for the study of genetically modified soybeans [3-4].

Yonghua He believes that genetically modified crops are widely cultivated to promote global food production, alleviate environmental problems caused by the use of pesticides, reduce poverty and hunger, and bring sustained huge benefits to the global environment (especially developing countries and regions). And social benefits. Glyphosate-resistant transgenic soybean GTS 40-3-2 is currently approved as a genetically modified crop in most countries and regions. In addition to extracting soybean oil, soybean meal and other residues are also used as animal feed. In order to detect the genetically modified ingredients in the feed, 11 kinds of animal feeds in Taigu City, Shanxi Province were tested for glyphosate-resistant soybeans. The qualitative and quantitative PCR methods were used to detect the GTS 40-3-2 gene, which is related to the Ca mv35s promoter and NOS terminator, Cp4-EPSPS gene, and soybean standard lectin gene. His research provided data support for the establishment of China's genetically modified feed safety assessment system, and has important theoretical and practical significance for the rational application of genetically modified livestock and poultry products in feed production animals or raw material sources [5]. *Jia, T* studied the effect of soybean isoflavones on plant salt tolerance. He studied the transgenic soybean cotyledon hair roots expressing GmIFS1 (hrGmIFS1). Salt stress increased the content of isoflavones in hairy roots of the blank vector transgenic control, but significantly reduced root length, fresh root weight and relative water content (RWC). The content of isoflavones in hrGmIFS1 roots was significantly higher, and the above-mentioned root growth parameters decreased less. GmIFS1 gene was also transformed into tobacco plants; the plant height and leaf fresh weight of transgenic GmIFS1 tobacco plants were significantly higher than those of the control after being treated with 85 mM NaCl. The antioxidant capacity of transgenic tobacco leaves was significantly higher than the control. Our results show that the expression of GmIFS1 induced by salt stress increases the accumulation of soybean isoflavones and improves the salt tolerance of

transgenic soybean hair roots and tobacco plants [6]. *Lijun Wang* believes that NORK and soy acyl carrier protein (ACP) play important roles in nodulation. However, the relationship between Nod factor signaling and fatty acid (FA) biosynthesis during symbiotic development is unclear. His research used Agrobacterium tumefaciens-mediated transformation of hair roots to construct the gmnorkrnai plasmid and transform it into soybean roots. The number of transgenic soybean nodules was significantly reduced. In order to study the relationship between engmacp and Nod factor signal transduction, he measured the expression level of gmacp in transgenic roots of mnorkrnai soybean and found that gmacp expression was significantly reduced after inoculation with rhizobium. Therefore, during soybean root nodule development, FA biosynthesis was affected by the Nod factor signal. This finding provides valuable information for us to further understand the function of gmnorkandgmacpin symbiotic signal and nodule development [7].

The innovations of this article: (1) This article can be seen from the literature review of the current status of domestic and global research. At present, no scholars have systematically constructed a knowledge map of genetically modified soybean research based on information visualization methods. Research volume, research hotspots, author collaborations, and research institutions. (2) In this paper, a comparative study of knowledge maps is used to systematically compare domestic and global genetically modified soybeans from the perspective of knowledge maps.

2. Proposed Method

2.1. Knowledge Graph

(1) Atlas of traditional scientometrics

The most important feature of traditional scientometric maps is intuitiveness, which is displayed in the most intuitive two-dimensional and three-dimensional graphics, and under some conditions, these two-dimensional and three-dimensional graphics can be transformed into each other.

(2) Three-dimensional configuration map

The three-dimensional configuration atlas was founded by Professor Craigmer, an internationally renowned scientific metrologist. For the first time, he introduced a mathematical concept in the study of science and metrology, and described the co-authored network of scientists using the image of non-linear functions. Three-dimensional graphics. He found through research that compared with low-level talents, high-level talents are more inclined to cooperate and thus obtain better research results[8-9]. At the same time, he also summarized the general characteristics of interpersonal relationship structures in some social networks, such as conformity, authority, and collectiveness.

(3) Multidimensional scale atlas

Multidimensional scale atlas mainly uses multidimensional scale for data analysis. In multidimensional space, researchers abstract specific things or events into a point, and determine the abstract position of each point according to the relationship between these things. The closer the distance between two points of a thing, the lower the distance between two points of a thing with a lower degree of similarity. These points can be represented in two-dimensional form and three-dimensional form, as well as in multi-dimensional form. Multi-dimensional scale analysis is essentially the use of a non-linear technology to achieve data conversion. This technology can convert data in high-dimensional space to data in low-dimensional space, and maintain the data transformed into low-dimensional data still approximate the high-bit Relation mode [10].

(4) Atlas of social network analysis

The social network analysis map was first applied to the study of British anthropology in the

twentieth century. Human sociology has found that all individuals in society have more or less connections with other individuals in certain aspects. The social network atlas is based on this theory to establish a model of individual relationships and aims to describe the comprehensive structure of the overall relationship. With the continuous development of information technology, the exploration of network social relationships, the discovery of dominance types, and the tracking of information flows have been deeply integrated with social network analysis. At the same time, information behavior and information attitudes are judged and analyzed based on social network information[11]. Social network analysis has been applied to various disciplines, such as sociology, psychology, economics, information science, systems science, and computer science, etc., which has gradually transformed it from a metaphor to a realistic research paradigm .

(5) Self-mapping map

Biological research shows that although our brain has tens of thousands of cells, the functions of different groups of cell groups are different, and the performance of different organs in the human body is controlled by brain cells in different regions of the brain, for the same reason The difference in sensitivity is that brain cells in different regions respond to the same stimulus to different degrees. Some of these cells' conditioned reflexes to specific signals appear to be gradually formed by the subsequent experiments and connections. Based on these basic theories, some people have proposed artificial neural network, information visualization and its important self-organizing feature mapping model, that is, using specific analysis methods, while maintaining the basic topological structure, the The input data is accurately distributed on a one- or two-dimensional discrete grid [12].

(6) Atlas of path finding network

Path-finding network analysis uses some subjective empirical data to first evaluate the similarities and differences between many concepts or things, and then analyze some basic concepts and principles in graph theory. These concepts and their connections are used to construct Out of the mesh model. It analyzes and compares the semantic network formed based on different concepts and things, and simulates the memory model and associative thinking mode of the human brain to a certain extent. Based on this feature, path analysis network analysis in sociology and artificial intelligence has been Widely used [13]. One of the advantages of the path-finding network map is that it has certain stability. Through the analysis of the path-finding network, it is possible to achieve different concepts and layering and clustering between things.

2.2. Research Methods of Knowledge Graph

Bibliometric analysis is a kind of information statistics method with a long history. It mainly has the following types: bibliometrics by time, bibliometrics by journals, and bibliometrics by authors. In China, researchers are involved in the above types of analysis in the process of knowledge map research, but it is more common to use journals for research.

The co-citation analysis method is specifically a process of displaying co-citation network views among many documents in the form of clustering groups through clustering analysis, multi-dimensional scaling and other measurement methods. This method can be reduced by computer devices. Difficulty of analysis, visually shows a smaller number of groups. The currently widely used co-citation analysis methods are: author co-citation, journal co-citation, and subject co-citation. Author co-citation analysis is the construction and analysis of co-citation networks for authors, and then analyzes and summarizes the connections and characteristics of researchers in the field, in order to predict the evolutionary trend of research angle relationships. Journal co-citation

analysis is based on the structure of core journals in the research field of the construction of journal co-citation networks, and analyzes professional journals focusing on different professional fields. Disciplinary co-citation analysis is based on the construction of disciplinary co-citation network, showing the cross-relationships and dependencies between disciplines, and then reflecting the discipline composition and structural characteristics of the discipline system. This article mainly adopts the method of author co-citation and journal co-citation analysis.

The term frequency analysis method mainly counts the frequency of occurrence of keywords with intelligence significance and its changing rules, and then analyzes the hotspots in the research field and the cutting-edge trends.

Co-word analysis method: keywords, authors, etc. in the statistical document information are used as node types to construct a knowledge network, and then the topic structure of the research in the field, the author's cooperation network, and the source of subject knowledge structure can be visually displayed. In case studies, domestic researchers use the method of keyword co-occurrence analysis.

Multivariate statistical analysis method: Multivariate statistical analysis uses computer tools to analyze subject-related random variables. It is characterized by dimensionality reduction techniques, including factor analysis, cluster analysis, and multidimensional scale analysis.

3. Experiments

3.1. Experimental Design

In this study, CSSCI and Web of Science databases were first used to collect Chinese and foreign genetically modified soybean research literature data. After screening and filtering, CiteSpace visual analysis tools were used to construct a library of co-cited authors and core journal distribution networks to conduct research topics at home and abroad Analyze, build keywords and cluster view network to analyze mobile library research hotspots, construct emergent words and emergent word time zone views to analyze the evolution and development trends of the frontiers in the field of genetically modified soybeans.

3.2. Data Source and Processing

Before constructing a knowledge map of genetically modified soybean research, first collect and process data. In this study, in order to compare the research situation in this field at home and abroad, we need to collect Chinese and English literature data information. This paper conducts literature collection in the English Web of Science database and Chinese CSSCI database. The data is filtered by search conditions such as keywords and detailed research directions, and the filtered data is imported into CiteSpace for processing to construct a scientific knowledge map.

(1) Foreign data

The foreign data is filtered from the web of science database. Web of Science is a web-based product developed by Thomson Scientific in the United States. As a database with great international influence, it includes more than 8,000 of the most influential worldwide The database is updated weekly by peer-reviewed, high-quality journals. With its unique citation search mechanism and powerful cross-search function, Web of Science database effectively integrates important academic information resources such as academic journals, technology patents, conference proceedings, academic analysis and evaluation tools.

(2) Domestic data

The domestic data are sorted and sorted from the CSSCI database. "Chinese Social Sciences Citation Index" is called "Chinese Social Sciences Citation Index" in English, and it is abbreviated as CSSCI. The "Chinese Social Science Citation Index" (CSSCI) was developed by the China Social Science Research and Evaluation Center of Nanjing University and is a key project of the National and Ministry of Education. CSSCI follows the rules of bibliometrics, and adopts a combination of quantitative and qualitative evaluation to select academically strong and well-edited journals as the source journals from more than 2,700 Chinese humanities and social science academic journals nationwide. It currently includes more than 500 academic journals in 25 categories including law, management, economics, history, and politics.

4. Discussion

4.1. Contrast Analysis

According to the principles of bibliometrics, statistical analysis of the number of papers published in the field of genetically modified soybeans through SPSS software can visually reveal the research status and development trend in this field as a whole. Figure 1 shows the volume of GM soybeans published in major literature databases over the years.

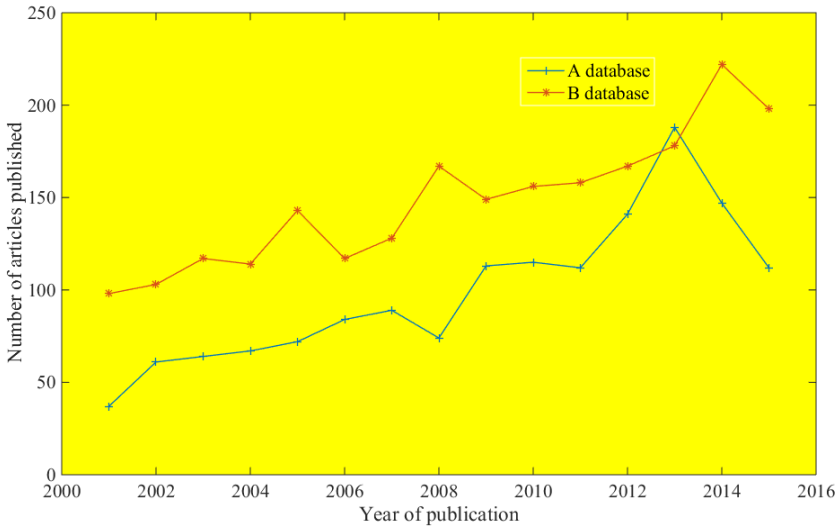

Figure 1. Statistical analysis of genetically modified soybean research papers

Paper volume is an effective proof of academic research hotspots. As shown in Figure 1, the volume of GM soybeans posted an overall upward trend, but there are differences. The number of publications of GM soybeans in the world continues to increase, and is much larger than the number of GM soybeans in China, because the global research on GM soybeans includes not only China, but also other countries such as the United States and Brazil, reflecting the trend of research in this field. Yu mature. However, the amount of GM soybeans in China showed a wavy upward trend, with large fluctuations. After reaching the peak in 2013 (193 articles), a large decline began, reflecting that China's research on GM soybeans is entering a stable development from a rapid development period. This is due to the lag of articles included in the database on the one hand, and may also be related to some policies of the Ministry of Agriculture of the other hand.

In the fifteen years from 2001 to 2015, the global GM soy has posted more papers than China ’s

GM soy, which means that the global GM soy research is generally higher than China ’s heat in this field. In 2001, China joined the WTO, and a large number of global GM soybeans flooded into China, which caused China to lose the advantage of the traditional soybean-dominated market. The research interest of GM soybeans has gradually increased, and domestic scholars have also increased their research on this. The first decline in the number of papers in 2008 was mainly due to the introduction of a large number of genetically modified soybeans from abroad, which also brought some ecological hazards to a certain extent, such as "gene drift", which caused wild soybeans to lose genetic diversity, causing Genetic pollution has weakened the enthusiasm of experts and scholars to study genetically modified soybeans. After 2009, the research literature on genetically modified soybeans in China has become increasingly hot, which cannot be separated from national policy reasons. In the No. 1 document of the central government in 2010, the issue of agriculture, rural areas and farmers was specified, and the state proposed to actively promote the "industrialization of new genetically modified varieties". This is the first time that the "industrialization of genetically modified crops" has been raised to the strategic level of national development. Many scholars in China have started a lively discussion on the topic of "industrialization of genetically modified crops". However, after 2013, the research fever of China's genetically modified soybeans gradually declined, and the industrialization debate gradually faded out of the scope of scholars' research.

Globally, the acreage of genetically modified crops is growing, including genetically modified soybeans. In 1999, the planting area of Monsanto's transgenic herbicide-resistant soybeans reached 14 million hm2. Later, it has also been widely promoted in Argentina, which has made the global research on transgenic soybeans to a certain extent. It can be seen from the figure that the global GM soybean postage has decreased by a small amount in 2006 and 2009, but this does not affect the continued increase in the heat of GM soybean. Especially in 2009, the global planting area of genetically modified soybeans reached 69.2 million hectares, an increase of 3.4 million hectares from the previous year, accounting for 52% of the total global planting area of genetically modified crops, making scholars pay more attention to the study of genetically modified soybeans, and also make the global The amount of research papers on genetically modified soybeans has been increasing, reaching a peak in 2014.

4.2. Comparative Analysis of Research Hotspot Knowledge Map

(1) Analysis of domestic research hotspots of GM soybean

After selecting "keywords" as network nodes in this article, running CiteSpace can get 376 nodes and 1,262 connections. As shown in Table 1 and Figure 2, there is a mainstream knowledge group consisting of research hotspots in the field of genetically modified soybeans. We can see that the frequency of the first 15 high-frequency words varies widely, from 221 times for GM foods to 55 times for food security. The combination of high-frequency keywords will become the research topic, which can be summarized as follows: research on whether transgenic soybeans can be commercialized, the impact of transgenic soybeans on domestic soybeans, comparative analysis of transgenic soybeans and non-transgenic soybeans, and genetics of transgenic soybeans Conversion and more. "Construction and Application of Soybean Large-scale Transgenic Technology System" summarizes the main progress made in the development of agronomic traits improved transgenic soybean materials in China over the past few years, and discusses emerging genetically modified technologies such as genome editing technology / apex integration technology in soybean. The application prospect is prospected. The "Countermeasures for the Development of China's Soybean

Industry under the Impact of Genetically Modified Soybeans" has researched the contradiction between the rigid growth of domestic soybean demand and insufficient supply so far. It is necessary to accelerate China's non-GMO to reach the independent price system and carry out the construction of soybean production bases to revitalize China's soybean industry. The content of crude fat, phenolic acid, and crude protein in transgenic soybeans is higher than that of non-transgenic soybeans. This has made a breakthrough in the research on the composition of transgenic soybeans.

Table 1. Ranking of high-frequency keywords in GM soybean literature

Frequency	Centrality	Key words
221	0.19	Genetically Modified Food
208	0.11	Soybean planting
180	0.07	Non-GMO Soy
114	0.1	Genetic transformation
107	0.08	Monsanto
102	0.02	Soybean industry
96	0.04	Non-GMO
93	0.05	Agricultural genetically modified organisms
86	0.07	Planting area
81	0.01	GMO corn
76	0.03	Commercial cultivation
69	0.04	Genetically modified ingredients
65	0.09	PCR
62	0.06	Glyphosate resistance
55	0.04	Food security

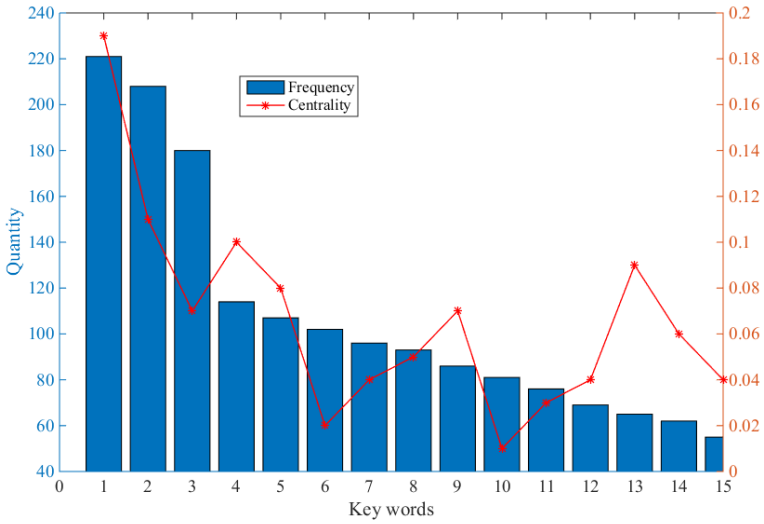

Figure 2. High-frequency keyword ranking of GM soybean literature

From this we can analyze that soybean genetically modified technology is an important means of genetic research, and China's research on genetically modified soybeans focuses on itself, including

the soybean industry and the impact of genetically modified soybeans on domestic soybeans, research on commercial cultivation, and Relatively weak in genetic transformation. Part of the reason is that at present, China does not allow the cultivation of genetically modified soybeans, and there is no research on industrialization and large-scale cultivation, which provides a reference for Chinese scholars to study the direction of genetically modified soybeans in the future.

(2) Analysis of research hotspots in the global GM soybean literature

Table 2. Ranking of high-frequency keywords in the global GM soybean literature

Frequency	Centrality	Key words
203	0.1	Expression
158	0.25	Transgenic plant
127	0.13	Arabidopsis thaliana
109	0.1	Gene
103	0.08	Protein
90	0.12	Maize
84	0.05	Transformation
84	0.03	Genetically modified organism
71	0.05	Resistance
66	0.03	Transgenic tobacco
65	0.05	DNA
63	0.04	Glyphosate
61	0.03	Identification
49	0.08	accumulation
48	0.04	Agrobacterium mediated transformation

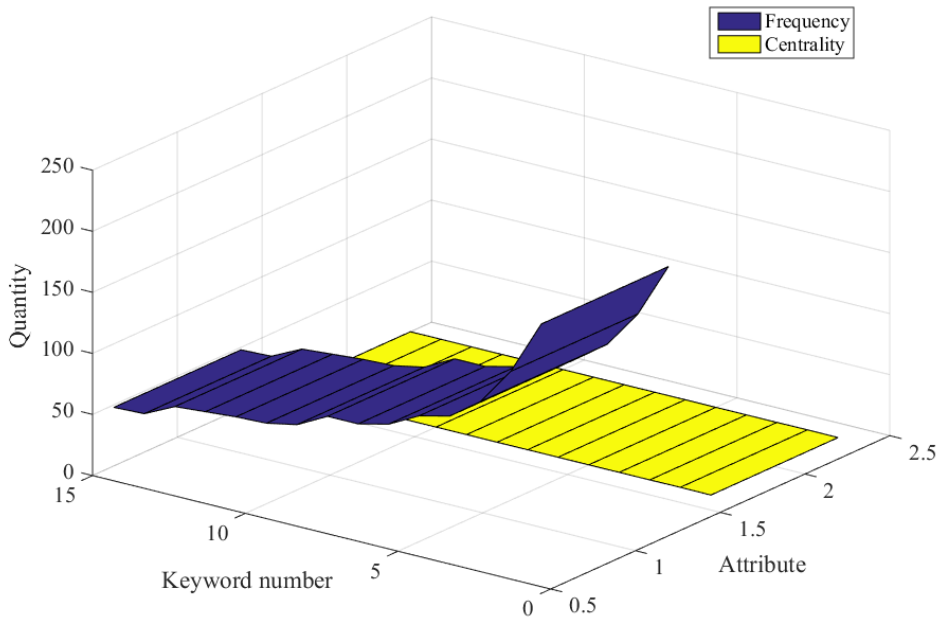

Figure 3. Global high-frequency keyword ranking of GM soybean literature

As shown in Table 2 and Figure 3, the global GM soybean literature is summarized, and the following topics are summarized: research on the GM soybean itself (including nutritional research, planting research, etc.), gene expression and genetic transformation of the GM soybean, Pros and cons of glyphosate-containing transgenic soybeans, Agrobacterium-mediated transformation methods of transgenic soybeans, and more. Since the introduction of foreign genetically modified soybeans into commercial cultivation, the United States has been a country with rapid development of biotechnology and more genetically modified soybean research and development technologies. The improvement research of -1 gene soybean and other related quality genes is in-depth, and some varieties have been promoted and large-scale planting has begun. Some people think that the transcriptome analysis of all three rows of transgenic soybean seeds found measurable changes in gene expression without modification. The difference in the transcription level may be the position of the insertion, the conversion after random mutation or directly affect the recombinant protein itself or Their combination, which indicates the gene expression effects of transgenic soybean seeds, infection time and Agrobacterium density may have some effects on transformation efficiency,

In addition, a very efficient Agrobacterium-mediated transformation system will be established for soybean callus to rely on double transformation vectors. The effects of the herbicide glyphosate and trace element foliar sprays on the two transgenic soybeans were important, and among the varieties evaluated, trace element foliar fertilizers did not increase soybean grain yield. From this, we can see that global research on planting and industrialization has matured. Some data show that in the United States, genetically modified soybeans have developed rapidly. In 1998, the planting area of genetically modified soybeans accounted for 35% of soybeans, and the proportion has been rising. The state reached 68% in 2001, and since then it has been above 91%. In Argentina, all genetically modified soybeans have been grown since 2010. In Brazil, the planting area of genetically modified soybeans in the total soybean planting area in 2013 also exceeded 90%. It can be seen that the industrialization of genetically modified soybeans has matured in most countries around the world. The current research on genetically modified soybeans focuses on the study of gene expression and Agrobacterium-mediated transformation, and the research on the composition of genetically modified soybeans is not enough, which also provides a reference for scholars to research on genetically modified soybeans in the future.

(3) Comparative analysis of research hotspots

Comparing domestic and global hot keywords, it can be seen that there is a certain similarity between the two. The same hot areas reflect the intersection of domestic and global genetically modified soybean research, and are also the mainstream areas of domestic and global research. Some of the hot keywords in the intersection set have different degrees of research interest and depth due to their different degrees of emphasis. Overall: domestic and global attention to the research of the soybean industry and the general situation of the genetically modified soybeans, the global commercialization and commercialization of genetically modified soybeans has become saturated, with emphasis on gene expression and genetic transformation, and research on the composition of genetically modified soybeans Not deep enough. In China, soybean transgenic technology is an important method for genetic research, such as the Agrobacterium-mediated transformation method, which focuses on the impact of genetically modified soybeans and non-transgenic soybeans, and is relatively weak in research and genetic transformation of commercial cultivation.

4.3. Analysis of Global Genetically Modified Soy Literature Research Institutions

Table 3. Global ranking of high-yield institutions of genetically modified soybeans

Ranking	Mechanism	Post volume
1	Chinese Acad Agr Sci	50
2	Chinese Acad Sci	47
3	USDA ARS	45
4	Univ Illinois	43
5	Monsanto Co	37
6	Univ Missouri	34
7	Iowa State Univ	28
8	Agr&Agri Food Canada	27
9	Natl Inst Agrobiol Sci	26
10	Kyoto Univ	23

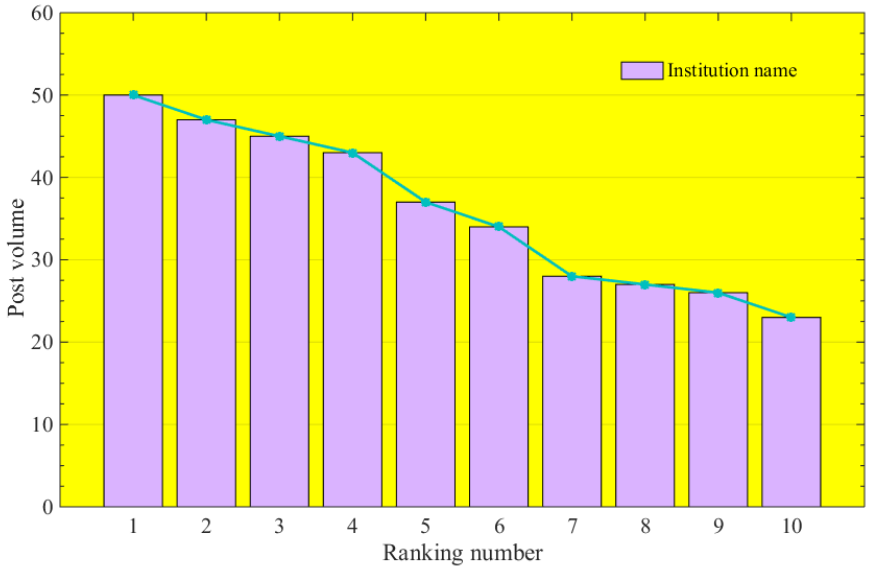

Figure 4. Global ranking of high-yield institutions of genetically modified soybeans

In CiteSpace, the node is also selected as Institution. Generate a knowledge graph in a visual form. There are 363 nodes (ie, 363 institutions) and 149 connections (ie, 149 groups of institutional partnerships) in the institutional cooperation network. As shown in Table 3 and Figure 4, we can see that the top three institutions with the highest frequency of GM soybean literature in the world are the Chinese Academy of Agricultural Sciences, the Chinese Academy of Sciences, and the United States Department of Agriculture, which shows that China's research on GM soybeans has an important position in the world . In addition, the University of Illinois, Monsanto, the University of Missouri, Kyoto University, and the University of Georgia have also posted a lot of papers. We have seen that there are connections between domestic institutions such as the Chinese Academy of Agricultural Sciences and the Chinese Academy of Sciences, and foreign institutions such as the US Department of Agriculture, the University of Missouri, and the Ohio State University have

connections, indicating that they are cooperative with each other, of which The Chinese Academy of Agricultural Sciences and the University of Missouri still have a certain connection.

The Chinese Academy of Agricultural Sciences is the highest agricultural scientific research unit in the country. The research in the agricultural field mainly covers the genetic breeding and cultivation of the main crops in China, and has established links with some universities and research institutes at home and abroad. The Chinese Academy of Sciences is a comprehensive research and development center, including China's Comprehensive Research Center for Natural Science and High Technology, and the highest academic institution in natural sciences. It has many research directions, and genetic transformation and biological research have achieved high achievements in the agricultural field. The US Department of Agriculture is mainly responsible for the planning, production, sales, and export of agricultural products and various crops. It has an important management role in the development of the US agricultural sector. We can also see that the number of Monsanto companies in the United States is relatively high, and they have good cooperation with some universities. According to data, Monsanto is a multinational agricultural company and a leading producer of genetically modified (GE) seeds. In the 1980s, Monsanto researchers developed genetically modified glyphosate-resistant soybean varieties and commercialized them earlier, which played an important role in the study of genetically modified soybeans. Institutional research ideas and methods. These institutions' research on genetically modified soybeans has had a certain impact both at home and abroad, and has also taken the lead.

5. Conclusion

From the perspective of the number of posts, the amount of posts of transgenic soybeans is generally on the rise. Among them, the global publication volume of GM soybean has continued to increase, and it is much larger than that of China's GM soybean. That is to say, the global research interest in this field is much higher than China, and it is becoming mature, especially in the United States and Brazil. Big soybean growing country. However, the amount of GM soybeans published in China showed a wavy upward trend, with large fluctuations. After reaching a peak in 2013, a large decline began, reflecting that China's research on GM soybeans is entering a stable development period from a rapid development period. On the one hand, Because of the lag of the articles included in the database, it may also be related to some policies of the Chinese Ministry of Agriculture.

From the research hotspots, domestic and global attention to the research of the soybean industry and the general situation of the GM soybean itself, the global commercialization and commercialization of the GM soybean has become saturated. Global research focuses on gene expression and genetic transformation, while the research on the composition of genetically modified soybeans is not enough. In China, genetically modified technology is an important method for research on genetically modified soybeans. It focuses on studying the effects of genetically modified soybeans and non-transgenic soybeans. It is relatively weak in genetic transformation, and the country does not allow the cultivation of genetically modified soybeans. the study.

China has made some achievements in research fields related to genetically modified soybeans, but only the Chinese Academy of Agricultural Sciences, Chinese Academy of Sciences, and Nanjing Agricultural University have entered the world's top 20 research institutions in terms of the number of published papers, and only six Chinese scholars ranked in the top 20 globally And the impact factor of articles published by Chinese researchers is relatively low. Looking at the evolution of the published disciplines, China’s GM soybean research started late in many fields. Although it

has caught up, it can basically keep the same with the global research frontier, but it cannot lead the development trend of a discipline. It should be further improved in the future. Global Impact in Genetically Modified Soy Research.

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Data Availability

Data sharing is not applicable to this article as no new data were created or analysed in this study.

Conflict of Interest

The author states that this article has no conflict of interest.

References

[1] Lu, Gui-Hua, Hua, Xiao-Mei, Cheng, Jing, Zhu, Yin-Ling, Wang, Gu-Hao, & Pang, Yan-Jun. (2018). "Impact of Glyphosate on the Rhizosphere Microbial Communities of an Epsps-transgenic Soybean Line Zuts31 by Metagenome Sequencing", Current Genomics, 19(1), pp.36-49.

[2] Hagai Cohen, Ofer M Shir, Yang Yu, Wensheng Hou, & Rachel Amir. (2016). "Genetic Background and Environmental Conditions Drive Metabolic Variation in Wild Type and Transgenic Soybean (glycine max) Seeds", Plant Cell & Environment, 39(8), pp.1805-1817. https://doi.org/10.1111/pce.12748

[3] Tengjiao Jia, Jing An, Zhen Liu, Jianjun Chen, & Bingjun Yu. (2016). "Salt Stress Induced Soybean Gmifs1 Expression and Isoflavone Accumulation and Salt Tolerance in Transgenic Soybean Cotyledon Hairy Roots and Tobacco", Plant Cell Tissue & Organ Culture, 128(2), pp.1-9.

[4] Chuanzhong Zhang, Xin Wang, Feng Zhang, Lidong Dong, & Shuzhen Zhang.(2017). "Phenylalanine Ammonia-lyase2.1 Contributes to the Soybean Response Towards Phytophthora Sojae Infection", Scientific Reports, 7(1), pp.7242.

[5] Yonghua He, Monica A. Schmidt, Christopher Erwin, Jun Guo, & Eliot M. Herman. (2016). "Transgenic Soybean Production of Bioactive Human Epidermal Growth Factor (egf)", Plos One, 11(6), pp.e0157034.

[6] Jia, T. , An, J. , Liu, Z. , Chen, J. , & Yu, B. (2016). "Salt Stress Induced Soybean Gmifs1 Expression and Isoflavone Accumulation and Salt Tolerance in Transgenic Soybean Cotyledon Hairy Roots and Tobacco", Plant Cell Tissue and Organ Culture, 128(2), pp.1-9.

[7] Lijun Wang, & Lingwei Deng. (2016). "Gmacp Expression is Decreased in Gmnork Knockdown Transgenic Soybean Roots", Crop Journal, 4(6), pp.509-516. https://doi.org/10.1016/j.cj.2016.05.005

[8] Wang Hai-long, Yang Xiang-dong, Zhang Chu, Guo Dong-quan, & Liu Fei.(2016). "Fast Identification of Transgenic Soybean Varieties Based Near Infrared Hyperspectral Imaging Technology", Spectroscopy & Spectral Analysis, 36(6), pp.1843-1847.

[9] Yan Zhao, Ying Wang, Qing Liu, Ying Zhai, Yang Zhao, & Meijuan Zhang. (2017). "Cloning of

a New Lea1 Gene Promoter from Soybean and Functional Analysis in Transgenic Tobacco", Plant Cell Tissue & Organ Culture, 130(2), pp.379-391. https://doi.org/10.1007/s11240-017-1234-3

[10] Wenli Zhu, Lifei Yang, Shouping Yang, Junyi Gai, & Yuelin Zhu. (2016). "Overexpression of Rice phosphate transporter gene ospt2, enhances nitrogen fixation and ammonium assimilation in Transgenic Soybean under Phosphorus Deficiency", Journal of Plant Biology, 59(2), pp.172-181. https://doi.org/10.1007/s12374-016-0535-0

[11] Kyong-Hee Nam, Do Young Kim, Hye Jin Kim, In-Soon Pack, & Chang-Gi Kim. (2019). "Global Metabolite Profiling Based on gc–ms and lc–ms/ms Analyses in abf3-overexpressing Soybean with Enhanced Drought Tolerance", Applied Biological Chemistry, 62(1), pp.15.

[12] Xiangdong Yang, Lu Niu, Wei Zhang, Hongli He, & Yingshan Dong.(2017). "Robust Mai-mediated Resistance to Infection of Seven Potyvirids in Soybean Expressing an Intron Hairpin nib rna", Transgenic Research, 26(9), pp.1-12.

[13] Sheng-Ling Zhou, Shi-Ping Zhu, Guang-Hao Liu, & Jie Zhu.(2017). "Rapid Detection of Transgenic Soybean Oils by Terahertz (thz) Spectroscopy", Journal of Nanoelectronics & Optoelectronics, 12(9), pp.956-960. https://doi.org/10.1166/jno.2017.2218