



Research on the global development trend of biological breeding

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Abstract. [Objective] Through the study of the global development trend of bio-breeding, we can find global research hotspots, major research institutions, collaborations, etc., and provide decision-making support for organizations in the field of bio-breeding. [Methods] International high-level papers are an important source of information to characterize basic research, and the papers in the core database of Web of Science were used as the data source, and the analysis was conducted using the CiteSpace bibliometric analysis tool. [Re-sults] The analysis results show that the global biological breeding research shows a year-on-year growth trend; China, the United States, India, France, and Germany are the main issuing countries, of which China and the United States are the fastest-growing countries, and the advantage of issuing papers relative to other countries is constantly expanding. The major issuing organizations of global biological breeding are the Chinese Academy of Sciences (CAS), the US Department of Agriculture (USDA), the Chinese Academy of Agricultural Sciences (CAAS), the University of California (UC), and the French National Center for Scientific Research (CNRS). Although the Chinese Academy of Sciences and the Chinese Academy of Agricultural Sciences ranked first and third in terms of the number of publications among the world's major publishers, there is still a big gap between their influence and that of the major publishers in the United States and France.

Keywords: Biological Breeding, Seed Industry, Literature Analysis, The Global Situation.

1 Foreword

Biological breeding refers to the process of using whole genome selection, gene editing technology, synthetic biotechnology, and other cutting-edge biotechnology to breed new varieties of organisms, including transgenic breeding, molecularly assisted labeling, molecular design breeding, genomics breeding, and gene editing breeding [1]. Breeding development can be roughly divided into four categories: the choice of farmers, phenotype, molecular breeding, and intelligent design breeding four times [2]. As the current international has entered the intelligent design breeding age, the development of the seed industry field has become various countries' attention hot spots. Journal articles are an important source of information characterizing basic

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research. Therefore, based on the bibliometric analysis, we carried out the research on the global development trend of biological breeding, found the global research hotspots, major research institutions, and cooperation, and provided decision-making support for institutions in the field of biological breeding.

At present, there have been some scholars based on literature analysis methods to carry out research fields related to crop trend analysis. Giraldo P, using the Scopus database for wheat and barley relevant scientific literature and patents, has carried on the evaluation of literature metrology, discovered the developing trend of both is different, and analyzed the reasons behind the [3]. Yan Z. H. et al. conducted a literature analysis of SCI papers in the field of crop transgenic breeding based on the Science Citation Index Expanded (SCIE) database and found that China ranked first in the number of publications, and the Chinese Academy of Sciences was the most publishing institution [4]. Lu Yao, based on the Web of Science database, such as the selection of plant molecular biology 50 copies of journals and with the research object as keywords retrieval, was analyzed by using the method of literature metrology paper output quantity and influence in China, revealing the research hotspot in the field of plant molecular biology research [5]. Qi S. J., etc. Based on the ESI data platform, because of "crop biotechnology breeding," five research front 103 paper cores are analyzed in the literature [1]. The research of scholars, explained based on the literature analysis method to carry out the trend of research as feasible [6–8], laid the foundation for this study. However, as a rapidly developing discipline, there is still a lack of comparative studies on the global development trend and key countries of biological breeding. This study is based on the Web of Science database, using the method of periodical literature, analysis of a single expansion of the crops in the field of biological breeding, to publish a trend annual global biological breeding research focus, dispatch agency distribution, analysis, determine the research direction for research in the field of biological breeding institutions, and provide decision support.

2 Data sources and research methods

2.1 Data Sources

The Web of Science (WoS) Core Collection is a database of more than 12,000 authoritative academic journals in the world, with comprehensive and high-quality literature. In this paper, the WoS core collection is used as the data source; the search scope includes papers and review papers; and the search period is from January 2012 to June 30, 2019. Because the concept of biological breeding is too broad, the construction of retrieval is the difficulty of this study. After reading the literature, consulting experts, and repeated testing, the search results were preliminary analyzed, and the search strategy was optimized step by step. The final search strategy covers the key technologies involved in traditional biological breeding, design breeding, and wisdom breeding. After data cleaning, a total of 85,503 pieces of literature were obtained.

2.2 Research Methods

CiteSpace is an information visualization software developed by Chen Chaomei's team in the United States to effectively draw the map of scientific knowledge, which can clearly show the core authors and institutions in a certain knowledge field, the evolution process of keywords, citation nodes, kinds of literature, and other contents on the map [9, 10]. At present, it has been widely used by scholars in the bibliometric analysis of medicine, biology, agronomy, and other fields [6–8]. Therefore, visualization analysis of biological breeding literature by CiteSpace is feasible. In this study, literature preservation and data format conversion were carried out according to software requirements, and CiteSpace was used to generate charts related to the number of publications, publication institutions, and high-frequency keywords, so as to carry out research on the development trend of global biological breeding and provide decision support for biological breeding research institutions and management departments.

3 Literature Overview

3.1 Annual publication trends

In the past decade, the number of annual publications in the field of biobreeding has been increasing year by year, and the specific data are shown in Fig. 1, indicating that the research on biological breeding has been continuously strengthened. In terms of the trend of publications by countries, China and the United States ranked the top two countries in terms of the number of publications, followed by India, Germany, and France, but none of these three countries had more than 1,000 publications, and the growth trend was slow. Since 2012, China has achieved rapid development in the field of biological breeding, and its advantage over other countries in terms of the annual number of publications has been gradually expanding, and it surpassed the United States and ranked first in 2019. Although China has already ranked first in terms of the number of publications, the number of citations per paper, which characterizes the quality of papers, is much lower than the number of publications. In the first half of 2022, for example, China ranked 26th with an average of 0.89 citations per paper, indicating that China is a biological breeding research country, but has not yet become a research power.

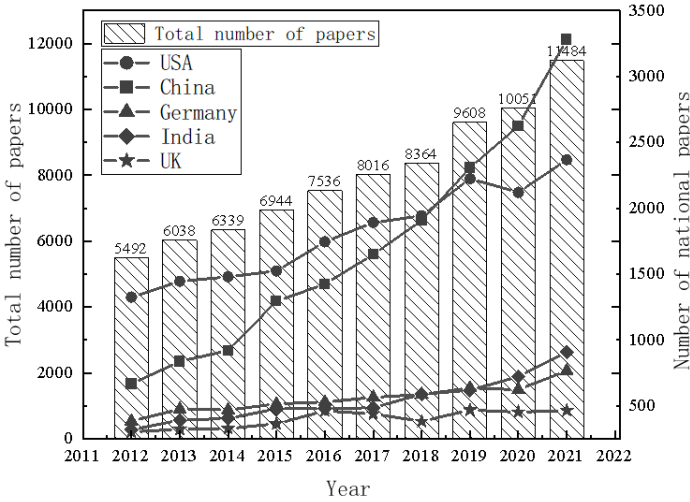


Fig. 1. Trend of publications in the field of biological breeding

3.2 Distribution of issuing institutions

The number of publications can reflect the scientific research activity of the institution. Table 1 lists the top ten institutions in the field of biological breeding with the number of publications, including 5 research institutes, 2 agricultural functional departments, 2 universities (alliances), and 1 international strategic consortium. Chinese Academy of Sciences (CAS) and Chinese Academy of Agricultural Sciences (CAAS) are the major publishing institutions in China, with CAS ranking at the top with 3,136 publications.

The importance of a node is represented by the number of shortest paths passing through a node, and the size of the intermediary centrality is proportional to its importance. In CiteSpace, nodes with intermediation centrality greater than 0.1 are considered critical nodes. From Table 1, the French National Center for Scientific Research and the US Department of Agriculture rank first and second respectively, while the Chinese Academy of Sciences and the Chinese Academy of Agricultural Sciences are significantly lower than these two institutions, indicating that Chinese top scientific research institutions still have great room for improvement in this field.

Table 1. Top 10 institutions and related information

No.	Organization	Country	Organization Type	Lit er- ature No.	Centrality
1	CAS	China	Research Institute	3136	0.02

2	USDA	USA	Function departments	2 358	0.29
3	CAAS	China	Research Institute	2 221	0.06
4	University of California	USA	University	2 200	/
5	CNRS	France	Research Institute	2 119	0.31
6	Udice French Research Universities	France	University	2 096	/
7	INRAE	France	Research Institute	1 778	0.14
8	ICAR	India	Research Institute	1,7 28	0.02
9	Ministry of Agriculture and Rural Affairs of China	China	Function departments	1 577	0.14
10	CGIAR	/	League of strategy	1 503	/

Note: The reason why the Ministry of Agriculture and Rural Affairs of China appears in the issuing institutions is that the key laboratories established by the Ministry of Agriculture relying on universities have marked the words of the Ministry of Agriculture and Rural Affairs of China when issuing papers.

3.3 The analysis of the keywords

The keyword timeline expands each cluster keyword according to its first appearance year in the timeline, which reflects the formation and evolution of research hotspots to a certain extent. The keyword timeline from 2012 to 2022 is drawn, as shown in Figure 2, where the diamond node size on the timeline represents the frequency of keyword occurrence in this cluster. The keywords with larger nodes in the figure were mainly clustered in 2012, indicating that these high-frequency keywords had appeared in 2012 or even earlier, and these research hotspots had been in the field of biological breeding for a long time. Especially clustering # 0 (deoxyribonucleic acid), # 2(abiotic stress with the highest heat), # 3 (expression). The cluster words were roughly divided into three categories: ① research objects, including *Pseudomonas aeruginosa* and deoxyribonucleic acid; ② breeding technology, including genomic selection and genome editing; ③ functional properties, mainly related to grain yield, abiotic stress, diseases, to hold. According to the keyword analysis, researchers pay more attention to *Pseudomonas aeruginosa* and DNA, and mainly use genome selection, gene editing, and other technologies to solve problems such as abiotic stress and improve yield and disease resistance.

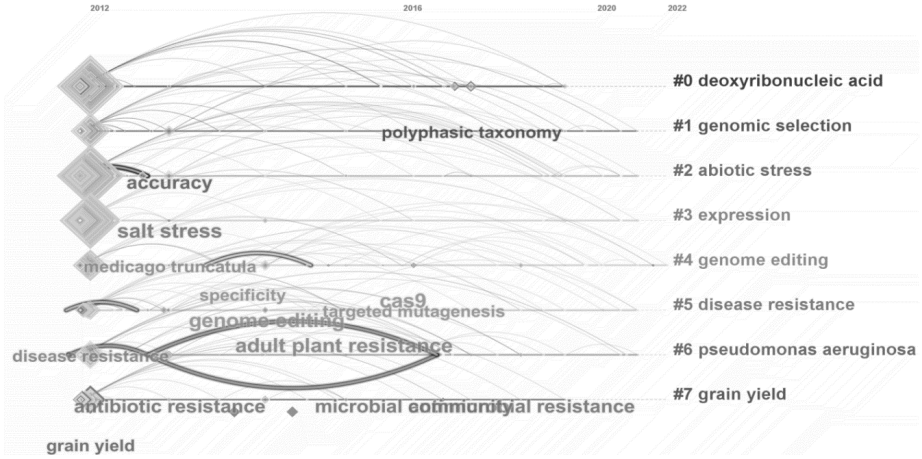


Fig. 2. Keyword Clustering Timeline

Keyword emergence detection can find keywords with large changes in citation in a certain period of time. Combined with burst detection and betweenness centrality index, it is beneficial to find emerging hotspots in the research field. Screening of betweenness centrality is greater than 0.1 and the emergent period until 2022 keywords, table 2. Genome-wide association study has the strongest emergence intensity and the highest betweenness centrality, which has attracted more attention in the field and has a high influence. The emergence intensity of antimicrobial resistance follows closely, and the reason may be due to the enhancement of the ability of parasites, bacteria, and viruses to resist microbial drugs [11], which will lead to drug failure, not only affecting the survival of plants and animals, but also endangering human life and health. Therefore, research attention has been rapidly increasing in recent years. Chloroplast genome burst detection and betweenness centrality are higher, but the lowest frequency shows that although the study is relatively small, but has strong development potential, and is worthy of attention. Targeted mutagenesis is one of the important tools of reverse genetics, burst detection with the betweenness centrality is relatively high, but the frequency is higher, showing that the influence is limited but still has some heat. Biogeography mainly explores the temporal and spatial distribution of organisms, which is closely related to the genetic evolution of organisms. The intensity and frequency of emergence are low, but the centrality of the intermediary is high, which indicates that the related studies are rare but have important research value. Research on osmotic stress, freezing tolerance, salinity tolerance, and leaf rust, which are related to biotic and abiotic stresses, have also received attention from scholars, especially salt tolerance, which has the highest frequency and outstanding performance.

Table 2. High Burst Detection keywords

No.	Keywords	Burst Detection	Betweenness Centrality	Frequency
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1	genome-wide association study	26.94	0.46	168
2	antimicrobial resistance	26.34	0.15	154
3	chloroplast genome	25.86	0.26	103
4	targeted mutagenesis	8.11	0.1	162
5	osmotic stress	7.51	0.3	115
6	biogeography	6.94	0.24	111
7	freezing tolerance	6.47	0.13	139
8	salinity tolerance	6.35	0.42	237
9	leaf rust	2.48	0.3	204

4 Analysis of Chinese and American studies

4.1 Research hot spot analysis

With the help of a clustering algorithm, keywords can be grouped according to their closeness, which is more conducive to the analysis of research hotspots in the field. The module value (Q) and the average contour value (S) of the cluster reflect the significance and homogeneity of the cluster map, respectively. When $Q > 0.3$, it means that the community structure of the division is significant. When $S > 0.7$, it indicates that the clustering is convincing [9]. Based on the cluster analysis of Chinese and American literature, 27 clusters of Chinese biological breeding research and 26 clusters of American biological breeding research were identified by consensus. The Q value of the US study cluster was 0.8743 and the S value was 0.959 2, while the Q value of the Chinese study cluster was 0.8847 and the S value was 0.966 1, indicating that the clusters were reasonable and effective. After sorting out the keyword clusters in China and the USA, we eliminated the repetitive cluster #18 (genetic parameter) in China and cluster #21 (United States) which is not highly correlated with breeding, and finally got Table 3.

Table 3. Clustering of Keywords for Biological Breeding Research in China and the U.S.

Serial Number	Clustering Cluster		Serial Number	Clustering Cluster	
	China	USA		China	USA
# 0	molecular mapping ^{②③}	genome editing ^⑤	# 14	rhizosphere soil ^①	expression ^①
# 1	genetic parameter ^①	drought tolerance ^{①②}	# 15	recent advance	hybridization ^③
# 2	malignant phenotype ^②	pseudomonas aeruginosa ^④	# 16	genome editing ^③	growth ^①
# 3	seed development ^④	genomic selection ^③	# 17	genetic diversity ^③	drug delivery

# 4	nitrogen metabolism ^①	dynamics ^①	# 18	/	genetic diversity ^①
# 5	genomic prediction ^③	phenotypic plasticity ^①	# 19	mesenchymal stem cell ^④	derivative ^③
# 6	wild chinese vitis pseudoreticulata ^④	population structure ^①	# 20	gene expression analysis ^①	signal transduction ^①
# 7	drought response ^①	genomic selection ^③	# 21	phenotypic plasticity ^①	/
# 8	novel actinobacterium ^④	cell wall ^④	# 22	genome-wide association study ^{②③}	dna methylation ^①
# 9	grain size ^{①②}	homologous recombination ^③	# 23	drought tolerance ^{①②}	quantitative trait loci ^{②③}
# 10	genetic map ^②	synthetic biology ^③	# 24	acyl-homoserine lactone ^④	grain yield ^{①②④}
# 11	sterile wheat ^④	genome ^{①②}	# 25	total synthesis ^③	virulence ^①
# 12	facile synthesis ^③	conservation ^①	# 26	endophytic actinobacterium ^④	
# 13	salt tolerance ^{①②}	genetic parameters ^①			

Note: The superlabeled numbers are the corresponding categories of this cluster: ① studies on the influence of environment on genes and phenotypes, ② gene-phenotype association study ③ breeding techniques and methods, ④ biological breeding objects.

According to the clustering statistics in Table 3, keyword clustering in China and the United States is divided into four categories: (1) Studies on the influence of environment on genes and phenotypes, including studies on tolerance to biological and abiotic stresses, phenotypic plasticity, genetic diversity, etc.; (2) Gene and phenotypic association studies, aiming at understanding gene sequence information, and the organic relationship between genome sequence information, gene function, and phenotype; (3) Breeding techniques and methods, including quantitative trait loci (QTL) mapping, genome-wide association study, (GWAS), genomic selection, genome editing, facile synthesis, total synthesis, etc.(4) Biological breeding research objects, including sterile wheat, *Pseudomonas aeruginosa*, Chinese Wild Grapes. The smaller the cluster number, the larger the cluster scale. From the top 10 clusters, the interaction between genes, phenotype, and environment is a common concern in China and the United States. In addition, the United States also focuses on breeding technology and methods.

In order to further compare and analyze the studies between China and the United States, the keywords of biological breeding research in China and the United States were classified and sorted according to the results of cluster analysis, as shown in Table 4. There are similarities between Chinese and American studies in three re-

search directions, but each has its own emphasis. The following is based on a keyword cluster graph and high-frequency keywords, and a specific analysis is carried out on the basis of a literature review.

Table 4. Categorization of keywords for biological breeding research in China and the United States

Main research directions		Keywords and frequency	
		China	USA
The first direction: Gene-phenotype association study		identification (1,878 reps) gene expression (956 reps) sequence (981 reps) quantitative trait loci (538 reps) genome-wide association (205 reps) agronomic trait (238reps)	identification (1,164 reps) gene expression (828 reps) sequence (491 reps) quantitative trait loci (412 reps) genome-wide association (184 reps) agronomic trait (69 reps)
	Studies on tolerance to biological and abiotic stresses	biosynthesis (531 reps) abscisic acid (434 reps) response (464 reps) disease resistance (274 reps) abiotic stress (250 reps)	biosynthesis (319 reps) abscisic acid (159 reps) response (464 reps) disease resistance (238 reps) abiotic stress (127 reps)
Studies on the influence of environment on genes and phenotypes	Phenotypic plasticity	phenotypic plasticity (340 reps) natural selection (62 reps)	plasticity phenotypic (929 reps) natural selection (321 reps)
	Genetic diversity study	evolution (903 reps) genetic diversity (543 reps) population structure (245 reps) genetic variation (117 reps) natural selection (62 reps) conservation (48 reps) genetic parameter (49 reps)	evolution (1,562 reps) genetic diversity (456 reps) population structure (378 reps) genetic variation (248 reps) natural selection (321 reps) conservation (232 reps) genetic parameter (108 reps)
The third research direction: breeding technology and method research	QTL mapping and genome-wide association analysis	quantitative trait loci (538 reps) genome-wide association (205 reps)	quantitative trait loci (412 reps) genome-wide association (184 reps)
	Marker-assisted selection and genomic selection	Marker-assisted selection (67 reps) genomic selection (29 reps)	Marker-assisted selection (94 reps) genomic selection (191 reps)

Gene editing technology and biosynthetic technology	biosynthesis (531 reps) derivative (286 reps) genome editing (113 reps)	biosynthesis (319 reps) derivative (95 reps) genome editing (99 reps)
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Research commonalities. China and the United States have more about gene expression, and genotype identification research literature, the important keywords gene expression and identification have a very high frequency: ① gene expression research. Gene expression synthesizes the genetic information of genes into functional gene products through transcription, translation, and processing, which are closely related to the growth and development of organisms. Epigenetic modification affects gene expression to a certain extent, Jeffrey (2015) pointed out that epigenetic modification can change homologous gene expression and reprogram the gene expression network, thus promoting polyploid adaptation to the local environment, and gene expression varies under different environmental stresses, Dong Xuan (2022) et al. found that under drought stress and salt stress in tea tree, the gene expression of CsTLP1 to CsTLP43, 43 sweet protein genes were differentially expressed under drought stress and salt stress in tea tree. In addition, a number of related highly cited literature in the United States also discussed the CRISPR/Cas system, which can be applied to gene expression enhancement and gene expression reduction to realize the precise regulation of gene expression, which is of great significance to the improvement of crop traits. 2021, American scholars such as Chi Yi-Ping and other scholars have developed the third-generation CRISPR system that can activate the expression of multiple genes at once. CRISPR-Act3.0 [12], the level of gene activation increased dramatically. ② Genotype identification. Currently, scholars have genotyped the barley kinesin family [13], the OTU DUB family in rice [14], and the cucumber PP2C gene family [15], and identified a large number of candidate genes with relevant molecular markers through a series of functional genomics and trait localization methods [16]. With the rapid development of high-throughput gene sequencing technology, precise identification of genotypes has become possible. American scholars Hiroki Takagi et al. (2013) proposed a QTL-seq method for rapid identification of plant QTL by whole-genome resequencing of DNA from two large populations and successfully identified QTL for important agronomic traits in rice by the QTL-seq method. Domestic scholars Dong Wei et al. (2018) identified watermelon genes based on high-throughput sequencing of BSA analysis. dwarf genes and found that Cla010726 might be a candidate dwarf gene. From the point of view of sequencing technology development, the United States has an early start in sequencing technology relative to China's research and occupies a leading position in sequencing technology. Walter Gilbert and Frederick Sanger took the lead in developing the first gene sequencing technology and the first-generation sequencer in the United States in 1977 [17], and after that, the United States Illumina and ABI developed the second-generation sequencing technology (also known as the next-generation sequencing technology), and the sequencing throughput was dramatically increased [18]. Currently, Oxford Nanopore Technologies (USA) has developed the fourth-generation nanopore sequencing technology and the corresponding nano sequencer, which further accelerates the accurate identification of genotypes and gene mining.

According to the comparison of the above studies between China and the United States, it is found that there are three significant differences in biological breeding research between China and the United States: (1) In the study of environment, gene, phenotype, and the relationship among the three, the United States focuses more on the plasticity of phenotype and the related research of genetic variation. In addition, it pays more attention to the collection and protection of wild relatives; China pays more attention to the correlation analysis between genes and phenotypes and the study of tolerance to environmental stress. Therefore, China should strengthen the collection and protection of wild germplasm resources, the plasticity of phenotype, and the related research of genetic variation, so as to provide a strong germplasm resource base for biological breeding. (2) In terms of breeding technology, China lags behind in the development and optimization of genome selection breeding technology and gene editing technology as a whole, and it is necessary to strengthen the independent development of chassis technology to overcome the core key technologies. (3) In breeding methods, the United States mainly focuses on molecular breeding research, and has a leading advantage in genome selection breeding research and application. China urgently needs to strengthen the research of molecular breeding, and the combination of molecular breeding with machine learning, artificial intelligence, and other information technologies.

4.2 Research Institutions in China and the US

Using the 18,713 domestic and 19,094 U.S. documents searched in the WOS core database as the data, we generated the cooperative network maps of Chinese and U.S. biobreeding research institutions (Figs. 3 and 4), in which the size of the nodes indicates the number of documents issued by the research institutions, and the thickness of the lines between the nodes represents the intensity of cooperation between the research institutions. The top 3 institutions in China in terms of publication volume are the Chinese Academy of Sciences (2,733 articles), the Chinese Academy of Agricultural Sciences (1,714 articles), and the University of Chinese Academy of Sciences (947 articles). In the United States, the Agricultural Research Service of the United States Department of Agriculture (1,756 articles), the University of California, Davis (749 articles), and the University of Florida (745 articles) had the highest number of publications. The overall number of publications in the United States was lower than that in China, indicating that China had an advantage in terms of research publications. However, the density of institutional cooperation network in China is 0.0165, which is lower than that in the United States (0.021, 4), indicating that the degree of cooperative research on biological breeding in China is relatively low, and there is still a large room for cooperation among institutions.

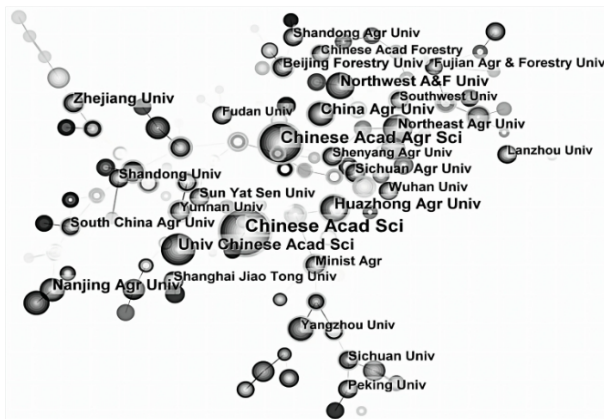


Fig. 3. Cooperative network of Chinese Biological breeding research institutions

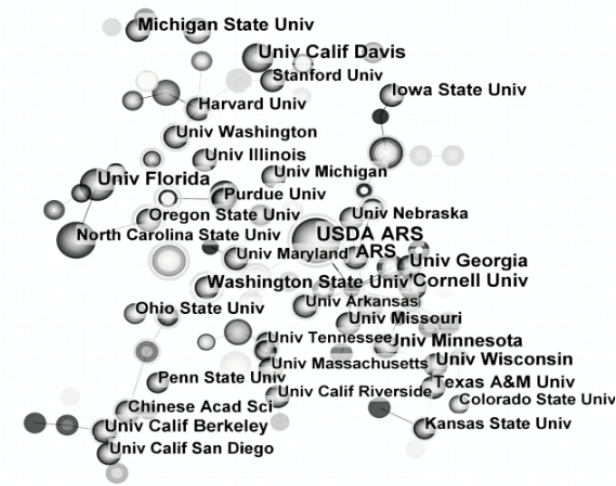


Fig. 4. Cooperative network of American Biological breeding research institutions

By analyzing the cooperative research of high-impact institutions in China and the United States, it is found that most of the research in China and the United States is cooperative research, in which the cooperation between universities and scientific research institutions and the cooperation between universities and universities are the mainstream of cooperative research. In terms of the participation of enterprises in research, there are few literatures in both China and the United States. Further analysis of the participation of Chinese and American enterprises in research shows that in terms of cooperation between enterprises and research institutions, domestic enterprises mainly cooperate with the Chinese Academy of Sciences, Chinese Academy of Agricultural Sciences, and their affiliated units, such as China Rice Research Institute, Shenzhen Institute of Agricultural Genetics, and Institute of Agricultural Resources and Agricultural Regionalization, but lack cooperation with foreign research institu-

tions. American enterprises mainly cooperate with the Agricultural Research Service of the US Department of Agriculture, followed by the Chinese Academy of Agricultural Sciences, Pakistan's Institute of Engineering and Applied Sciences, Riken Research Institute, and other foreign research institutions, and frequent cooperation with foreign research institutions. In terms of cooperation between enterprises and universities, most of the American cooperative enterprises are seed giants, while most of the Chinese cooperative enterprises are tobacco companies. The domestic cooperative research between seed enterprises and universities is relatively insufficient. Further analysis of the situation of industry-university-research cooperation found that Chinese enterprises published very few cooperative documents, the domestic enterprises involved in the cooperation are mainly China Construction Bank, China Tobacco Yunnan Industrial Co., LTD., and China National Tobacco Corporation. In the United States, the cooperative enterprises include not only Monsanto, DuPont, Cargill, and other leading agricultural companies in the world but also other industry giants such as Miayou Medical International, Nestle, and Mars. In comparison, the participation of domestic breeding companies in the basic research of breeding innovation is obviously insufficient. Monsanto (formerly an American multinational agricultural company, acquired by Bayer in Germany in June 2018) has frequent cooperation between industry, academia, and research. Statistics show that more than 80% of the documents published by Monsanto are published in cooperation with universities or scientific research institutions, many of which are multinational institutions. The cooperation objects include the US Department of Agriculture, the French National Center for Scientific Research, the Chinese Academy of Sciences, the Gregor Mendel Institute of the Austrian Academy of Sciences, and other important research forces in various countries.

5 Epilogue

5.1 Research Conclusions

Global biological breeding research has shown a year-on-year growth trend, with China, the United States, India, France, and Germany as the major issuing countries, of which China and the United States are the fastest growing, with an expanding advantage over other countries in terms of the number of articles issued. The major issuing organizations of global biological breeding are the Chinese Academy of Sciences (CAS), the US Department of Agriculture (USDA), the Chinese Academy of Agricultural Sciences (CAAS), the University of California (UC), and the French National Center for Scientific Research (CNRS). Although the Chinese Academy of Sciences and the Chinese Academy of Agricultural Sciences rank first and third in terms of the number of publications among the world's major publishers, there is still a large gap between their influence and that of the major publishers in the United States and France.

Both China and the U.S. have focused on gene expression and genotype identification, while U.S. scholars have paid more attention to phenotypic plasticity, genetic

variation, and the collection and conservation of wild germplasm resources. Both China and the U.S. have adopted cooperative research in biological breeding, and it is worth mentioning that the cooperation between U.S. seed enterprises and academic and research institutes is more frequent, which reflects the insufficiency of China's seed enterprises to participate in basic research of biological breeding from another side.

5.2 Research Implications

First, to promote cooperation between industry, academia, and research. Strong enterprises, strong seed industry. We should focus on encouraging enterprises to strengthen cooperation with universities and institutes to jointly promote core technology breakthroughs in the field of biological breeding. Taking the global pig breeding giant PIC enterprise as an example, it relied on the technical advantages of the veterinary discipline of the University of Cambridge and the animal genetic discipline of the University of Edinburgh to achieve rapid development at the beginning of its establishment. Breeding enterprises can also make full use of the national research power and the research power of the region, so as to rapidly obtain the technical advantage and thus form the market competitiveness.

Second, encourage interdisciplinary cooperation. Currently, research in the field of breeding presents the development trend of multi-disciplinary cross, multi-technology cross-border fusion, and the cross of computational science, life sciences, engineering, and other disciplines have already formed a biosynthesis, so only around the common goal of establishing an interdisciplinary long-term cooperation mechanism is more conducive to breakthrough results.

Thirdly, we will vigorously strengthen international cooperation. International cooperative research can quickly achieve the effect of taking advantage of strengths and complementing weaknesses. The frequent cooperative research between large enterprises such as Monsanto and the world's top scientific research institutions has shown that international cooperative research can quickly promote biological breeding research.

5.3 Research Prospects

In this study, the literature obtained from the search was used as the basis of analysis. Although the search formula was corrected in several rounds before the analysis, which can reflect the general trend to a certain extent, the data for specific institutions may be biased due to the fact that it is difficult to optimize both the detection rate and the accuracy rate at the same time. As a next step, when the analysis is conducted for specific organizations, the search strategy will be adjusted using the organization as the search element to ensure the accuracy of the analysis results.

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