

## **A COMPREHENSIVE BIBLIOMETRIC ANALYSIS OF GENE FAMILY RESEARCH ON ABIOTIC OR BIOTIC STRESS**

Yuhe Kan<sup>1</sup>, Dan Xi<sup>1</sup>, Huilian Liu<sup>1</sup>, Kunhao Yang<sup>2</sup>, Liang Yan<sup>3</sup>, and Ruirui Xu<sup>1\*</sup>

<sup>1</sup> College of Biology and Oceanography, Weifang University, Weifang, Shandong, 261061 P.R. China

<sup>2</sup> Lunan Pharmaceutical Group Co., Ltd, Linyi, Shandong, 276000 P.R. China

<sup>3</sup> School of Chemical Sciences, University of Chinese Academy of Sciences, Beijing, 100000 P.R. China

Corresponding author's E-mail: xuruirui2006@163.com

### **ABSTRACT**

The research of gene families on abiotic or biotic stress has been extensively studied for nearly 30 years, but the developments, emerging areas of growth, or new insight in the field haven't been reported until now. This study was aimed to analyze the developments in the field of gene families related to abiotic or biotic stress. Thus, we conducted a bibliometric analysis utilizing the Bibliometrix R package to examine publications obtained from the WoS database. The findings indicate a significant annual rise in scientific production. Notably, China and Japan emerge as impactful contributors to this field. BMC Genomics is the most influential source, and Yong Zhou is the most influential author. The publication by Cantero *et al.*, (2006) is recognized as the most influential in this context. *Arabidopsis* is still a popular model organism for gene family study under abiotic stress. The keywords **expression**, **identification**, **tolerance**, and **gene family** are the most discussed. The **database**, **heat**, and **tolerance** are trending topics in the future. These findings can guide researchers to search for intended information rapidly, find new topics and collaboration opportunities, and provide comprehensive bibliometric analysis in the research field of gene families related to abiotic or biotic stress.

**Keywords:** bibliometrics, gene family, abiotic or biotic stress, publication growth, trend topic

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### **INTRODUCTION**

Gene families consist of DNA segments that have undergone repeated duplication and divergence over time through common descent, originating from a shared ancestral DNA sequence that has been replicated and modified extensively (Liberles and Dittmar, 2008; Fang *et al.*, 2022). It plays an ever-growing, crucial role in regulating genes and facilitating vital biological functions during both normal development and the progression of diseases (Grinberg and Millen, 2005; Ahmed *et al.*, 2014). Recently, several gene families have been widely recognized, such as the homeobox gene family, the myosin gene family, and the heat shock protein family. The homeobox gene A10 (HOXA10) maintains embryonic development (Zanatta *et al.*, 2010). The regulation of cell elasticity, cell migration, exocytosis, and endocytosis in B-lymphocytes can be attributed to the myosin gene family, including myosin 1 G (Myo1g) (Olety *et al.*, 2010; López-Ortega *et al.*, 2016). Heat-shock transcription factors (HSFs) regulate the heat-shock response and some crucial developmental processes in plants (Almoguera *et al.*, 2020). In recent years, advancements in sequencing technology have led to an accumulation of scientific knowledge from gene

family research, surpassing the information collected in previous years. For example, the genome-wide sequencing of 500 plant species has been completed (Antonelli *et al.*, 2020), promoting research on plant genomics at the molecular level. Plant whole genome sequencing allows researchers to identify and classify new gene families based on sequence similarity and functional characteristics, trace the origin and evolution of gene families by comparing the genomes of different species, facilitates the functional annotation of gene families based on homology with well-characterized genes in other organisms. For example, Single Molecule Real Time (SMRT) sequencing platform can overcome some obstacles including repeats and GC rich regions in genome and was used to sequence and assemble gluten gene families from different cultivars of wheat (Zhang and Messing, 2017). For the rapid analysis of plant gene families, many gene family databases, including the Gene Family Database in Poplar (GFDP) (Wang *et al.*, 2018), PlantGF (Li *et al.*, 2022), GenFam (Bedre and Mandadi, 2019), and the Apple Gene Function & Gene Family DataBase (AppleGFDB) (Zhang *et al.*, 2013), have been constructed. Those gene family databases can provide valuable resource for collecting gene family members and providing comprehensive annotations. For example,

AppleGFDB can help collecting, storing, arranging, and integrating functional genomics information of the apple. It was estimated that the publications related to gene families may have exponential growth in the future.

The knowledge of the impact of abiotic or biotic stress on biology is essential for understanding ecosystem dynamics (Garchitorena *et al.*, 2015), informing conservation and management practices (Hernández-Lambraño *et al.*, 2019), safeguarding plants against biotic pests (Anuar *et al.*, 2023), improving agricultural productivity (Calanca, 2017), and unraveling evolutionary processes (Balbinott and Margis, 2022). Recently, researchers have focused attention on studying the relationships between gene families and abiotic or biotic stress. For example, the WRKY gene family in plants plays a crucial role in mediating responses to both abiotic and biotic stresses, such as drought, salinity, and pathogen attacks (Bai *et al.*, 2018). Understanding the functional roles of specific gene families, like WRKY, in stress responses provides valuable insights into the molecular mechanisms involved.

In order to examine and condense empirical studies on gene families related to research on abiotic or biotic stress, a conventional systematic literature review can establish connections or correlations among objectives, methodologies, outcomes, and variables found in existing literature (Uluhan *et al.*, 2019; Aksu and Memon, 2023). This approach helps to generate generalizable knowledge and identify new avenues for further research. However, systematic literature reviews carry the potential for bias, encompassing factors such as selection bias, insufficient blinding, attrition bias, selective outcome reporting, and publication bias, among others (Owens, 2021). Hence, a quantitative bibliometric analysis is urgent to summarize global progress and trends.

Bibliometric analysis is a quantitative method used to evaluate and analyze scientific literature. It involves examining patterns and trends within bibliographic data to gain insights into the publication output, leading sources, most relevant authors, most productive countries, institutions, authors and their collaborations, top keywords, trend topics, and so on in this field (Aria and Cuccurullo, 2017). Overall, bibliometric analysis provides a systematic approach to understanding the structure, dynamics, and impact of scientific literature, offering valuable insights for researchers, funding agencies, and policymakers in making informed decisions regarding research priorities, collaborations, and resource allocation. Some bibliographic databases, such as WoS and Scopus, can help to find some basic information, including article type, publication per year, most cited authors, and most popular sources, but some data analysis, including bibliometric networks, emerging trends, citation networks of scientific publications and citation counts of research

output, *et al.*, must be conducted by using different types of software tools, such as VOSviewer (Van Eck and Waltman, 2010), CiteSpace (Chen, 2006), Publish or Perish (Harzing, 2007), and CitNetExplorer (Van Eck and Waltman, 2014). However, they are not flexible, and the result analysis is not comprehensive. Bibliomertix, based on the R language, is an extensive and powerful software tool for conducting bibliometric analysis in science (Moral-Munoz *et al.*, 2020). In this paper, we perform bibliometric analyses using the Bibliomertix R package, which is flexible, quickly upgraded, and seamlessly integrated with other statistical R packages. This enables us to conduct a thorough analysis of current academic literature on gene families related to abiotic or biotic stress. The aim is to provide some vital information including annual scientific production, the influence ranking and network of countries, journals, authors, documents and trend topics in this field.

## MATERIALS AND METHODS

The methodological framework of the bibliometric study was established according to a report by Aria and Cuccurullo (2017), which was first published in 2017. Within this section, the conventional workflow for bibliometrics is outlined, encompassing aspects such as study design, data collection, and data analysis, referencing the study conducted by Omotehinwa (2022) was in **Figure 1**.

**Study design.** The aim is to identify the knowledge base of study on gene families in abiotic or biotic stress. In addition, the study limitations should be considered or selected. To clarify our research objectives, the specific questions answered by this study are enumerated as follows:

- i. What is the annual scientific production in this field?
- ii. What are the most influential countries and countries that collaborate?
- iii. What is the most popular source and its network of co-citations?
- iv. What are the most influential authors, authors' co-citations and institutional collaborations?
- v. What are the most cited document and its networks of co-citation?
- vi. What are the top keywords, networks of co-occurrences and trending topics among the keywords?

**Data collection.** The primary approach employed in this study is bibliometric research methodology to address the research problem. The experimental dataset is sourced from the abstract and citation database of WoS (Web of Science) (<https://www.webofscience.com>), which is the most common, well-known, and characterized by a higher-quality data source suggested by the official website for bibliometric studies. As an illustration, the

WoS offers the "Keyword Plus" (ID tag), recommended by many publications as the optimal content field for conducting topic analysis, whereas Scopus lacks this metadata. We obtained 3520 documents in WoS core collection database when it involved defining search strings as follows: topic ("gene family" OR "gene families") AND topic ("abiotic stress" OR "biotic stress"). All records were exported to plaintext documents in batches via the WoS document search interface since 500 records at a time are limited in the database. The publication type only with "J" (articles) and language with "ENGLISH" were filtered, and documents of type "Letter", "Note", "Editorial", "Retracted", and author with "NA" were removed. The filtering returned 3176 documents analyzed in this study.

**Data analysis and visualization.** The filtered file was converted into bibliographic data frames for analysis after uploading. In this study, data analysis was carried out to determine the growth rate of publications, the basic information of countries, authors, institutions, sources, documents, keywords and their collaborations, co-citations, and co-occurrences as presented by networks, as well as trending topics. We use the command-based Bibliometrics package (v4.2.1) in R Studio to visualize the analysis. The analysis was performed on January 7, 2024.

## RESULTS

**Main information:** The main information about the data collected was summarized in **Table 1**. 3176 articles published in 296 scientific journals between 1997 and 2023 from the WoS database were obtained through our filtering process. The usage of the author's Keywords (DE) or Keywords Plus (ID) is approximately double the number of relevant items. On average, there are five authors (4.67) per article. Other information includes the total number of authors and references, the author's collaboration, and more information about the entire document in this dataset.

**Annual scientific production:** **Figure 2** presents the annual scientific productions covering the period 1997-2023. This curve is divided into three phases, which are characterized by the years 1997-2013, 2014-2019, and 2020-2022. In 1997-2013, the number of publications was slightly increased, but it suddenly climbed to 113 papers in 2014, which was about two times that in 2013. The number of papers between 2014 and 2019 increased largely and kept about 100~250 each year. After 2019, it began to accelerate significantly until 2022, which has been the highest and most significant year regarding scientific output (570 publications). In 2023, the number of publications was slightly lower than in 2022.

**The most productive, cited countries and their**

**collaboration:** We showed the top 10 countries with scientific contributions to this field (**Figure 3a and Table S1**). China was the most publication-productive country, which is about ten times more than India, which ranked in second place. The citation impact metrics (total citations and average article citations) were commonly used to measure the academic influence of countries. Total citations are a reflection of the overall impact and productivity of a country's research output, indicating a substantial body of influential research produced by its academics. On the other hand, average article citations serve as a metric to gauge the average impact of individual articles, suggesting that the country's research holds greater influence on a per-article basis. **Figure 3b** presents the most top 10 cited countries based on the number of single-country total citations. China is the first cited country. Somehow, the dispersion between China and India (the second ranked country) is quite noticeable in total citations (more than six times). For analysis of average article citations, the top 3 countries are Japan, the USA, and Germany. Noticeably, China is in first place with total citations, but it has relatively low average article citations and is in last place.

The most productive countries worked collaboratively (**Figure 3c and Table S1**). China has significantly contributed to the collaboration network, with every network member having collaborated with both China and the United States in some capacity. The collaboration between the United States and China is particularly noteworthy among these interactions.

**The most popular sources and their co-citation network:** It is crucial to comprehend journals that concentrate on publishing papers and assess their impact according to numbers of publications, total citations, and academic divisions of the Chinese Academy of Sciences (CASAD, a widely used ranking system in China) (Shen *et al.*, 2020) (<http://www.fenqubiao.com/>). This information on publication sources will guide researchers to read or submit papers to those journals. The top 10 journals with the highest number of articles published were listed in **Figure 4a and Table S2**. In terms of numbers of publications, the most productive journals were Int. J. Mol. Sci. (291), Front. Plant Sci. (288), and BMC Genomics (180). However, BMC Genomics, with amazingly 6144 total citations, is the most leading journal, followed by Front. Plant Sci. (TC = 5496) and BMC Plant Bio. (TC = 4507). The co-citation network of top 10 sources with high total link strength in the database is presented in **Figure 4b**. Interestingly, all sources had almost same link numbers and same total link strength, meaning that they focus on the same research field.

**The most relevant authors, author's collaborations and their institutional collaborations:** The current paragraph highlights the most prolific researchers,

authors' productions over the years, authors' collaborations, and institutional collaborations in this field. **Table 2** provides a summary of the top 10 influential authors ranked by DF (dominance factor) with their number of publications, total citations, and corresponding h-index *et al.* The h-index, proposed by J.E. Hirsch in 2005, quantifies an author's cumulative impact and performance by assessing the relationship between publications and citations, effectively measuring the fusion of quantity and quality in their scholarly output (Hirsch, 2005). Several bibliometric studies use the DF factor to filter influential authors (Gatto and Drago, 2020; Campira *et al.*, 2022), since DF gives priority to the first author of multi-authored articles compared with h-index or total citation. Wei Hu has the highest h-index and total citations among top 10 authors. It was also highlighted that Yong Zhou was the first author in publications with multi-author articles. **Figure 5a** illustrates top 10 authors' production over time. Wei Hu and Yan Yan had more total citations in 2017 than in other years, as indicated by the darker circles.

The network of authors' collaborations showed eight clusters in **Figure 5b**. The blue cluster revealed that Yan Li (Nanjing Agricultural University), Jun Wang (Shanghai Jiao Tong University), and Jian Wang (Zhoukou Normal University) have well-established collaborations. A well-established collaboration (green cluster) can also be seen between Jing Wang from the Chinese Academy of Agricultural Sciences, China, Chao Chen from Northeast Agricultural University, China, and Hui Wang from Southwest Minzu University, China. Yan Yan had the most authors' collaborations with a high total link strength. In addition, it can be inferred that all authors in the cluster were Chinese, meaning that the Chinese authors largely facilitate collaborations.

**Figure 5c** shows the network of institutional collaborations. All the institutions clustered in blue and red were based in China except the National Research Institute for Agriculture, Food, and Environment (INRAE), the green cluster is institutions in the USA. Connections are largely between institutions within the same country. The Chinese Academy of Agricultural Science and the Ministry of Agriculture and Rural Affairs, both in China, have well-established collaborations. One of the most collaborative institutions in this field was the Ministry of Agriculture and Rural Affairs.

**The most cited documents and document's co-citations:** **Table 3** lists the top 10 articles including authors' information, publication year, publication sources (journal), digital object identifier (DOI), global citation score (GCS), local citation score (LCS), and research area. The publications were ranked by LCS since it is reasonable and popular to measure the number of times each publication has been cited by other publications within the dataset analyzed in this study

rather than GCS in the entire WoS database. The most influential publication with high LCS was Cantero *et al.*, (2006).

The network of co-citations showed a relationship between two documents. As shown in **Figure 6**, we can observe that the research papers by Livak (2001) and Chen (2020) *et al.* have been co-cited by other documents. The color of the nodes in the co-citation network indicated different research fields. The blue nodes depict tools or web servers for method development focusing on bioinformation, and the red nodes relate to databases or protein evolution analysis of new functions.

**The most relevant words, keyword co-occurrence assessments, and trend topics:** The author's keywords and keyword plus were retrieved from publications to show the relative keywords in these fields. The most significant keyword in the word cloud generated from keyword plus (ID) is *arabidopsis*, which encompasses other frequent keywords such as *expression*, *tolerance*, *identification*, and *gene family* (**Figure 7a**). The authors' keywords in Table S3 were *abiotic stress*, *gene expression*, *phylogenetic analysis*, *evolution*, *genome-wide analysis*, and so on.

**Table 1. Main information and summary of the dataset.**

Description	
Period	1997-2023
Sources (journals)	296
Annual growth rate %	24.21
Document average Age	5.08
Average citations per doc	23.49
Average citations per year per doc	2.829
References	81428
Document Type	
Articles	3176
Document Contents	
Keywords plus (ID)	4893
Author's keywords (DE)	5423
Authors	
Authors	14819
Author appearances	22925
Authors of single-authored docs documents	11
Authors of multi-authored docs documents	14808
Authors Collaboration	
Single-authored docs	12
Docs per Author	0.214
Authors per docs	4.67
Co-Authors per docs	7.22
International co-authorships (%)	16.28

The Keywords Co-occurrence Network (KCN) (**Figure 7b**) was constructed using the top 50 keywords,

which include both keyword plus and author's keywords. This approach aims to gain new insights into a field by examining the co-occurring keywords in the analyzed literature (Radhakrishnan *et al.*, 2017). The blue and red clusters represent distinct research topics. Specifically, the blue cluster contains the most frequently occurring keyword, *arabidopsis*. The keywords in the red cluster had lower overall frequencies compared to the red cluster. However, they provided valuable information related to subjects of abiotic and biotic stress, including *oxidative stress*, *salt tolerance (stress)*, *disease resistance*, *abscisic acid (ABA)*, and *salicylic acid (SA)*, as well as *stress*

*tolerance*.

The trend topic plot is shown in Figure 7c. The trending topics before 2017 related to the keywords *disease resistance*, *signaling pathways*, *cDNAs*, *key enzyme*, and so on may involve research in the field of plant biology on plant signaling, disease resistance mechanisms, and related gene expression and metabolic pathways. The *heat*, *tolerance* and *database* were the most discussed and trend topic in 2019 and 2023, indicating that genome evolution and function in the field of biology may be trending topics.

**Table 2. The top10 most influential authors.**

Rank by DF	Author	Dominance Factor	Tot Articles	Single-Authored	Multi-Authored	First-Authored	Rank by Articles	H-in dex	Total citations
1	Yong Zhou	0.48148148	27	0	27	13	1	12	349
2	Wei Wang	0.35294118	17	0	17	6	7	9	500
3	Wei Hu	0.32000000	25	0	25	8	3	19	1046
4	Yapeng Fan	0.18750000	16	0	16	3	9	5	65
5	Yan Li	0.11111111	18	0	18	2	6	7	319
6	Yan Wang	0.10000000	20	0	20	2	5	11	444
7	Jing Wang	0.07692308	26	0	26	2	2	9	195
8	Yu Wang	0.06250000	16	0	16	1	9	8	244
9	Juan Wang	0.05882353	17	0	17	1	7	6	131
10	Yan Yan	0.04545455	22	0	22	1	4	15	851

**Table 3. The top10 cited documents.**

Paper	DOI	LCS	GCS	Research area
Cantero, 2006, Plant Physiol. Biochem.	10.1016/j.plaphy.2006.02.002	19	124	rabidopsis annexin gene family
Hegedus, 2003, Plant Mol. Biol.	10.1023/B:PLAN.0000006944.61384.11	17	240	BnNAC gene family
Reyna, 2006, Mol. Plant-Microbe Interact	10.1094/MPMI-19-0530	17	146	MAPK gene family
Jang, 2004, Plant Mol. Biol.	10.1023/B:PLAN.0000040900.61345.a6	16	368	PIP gene family
Wagner, 2002, Plant Mol. Biol.	10.1023/A:1015557300450	15	401	GST super-family
Maskin, 2001, Plant Sci.	10.1016/S0168-9452(01)00464-2	9	77	Asr gene family
Kaplan, 2004, Plant Physiol.	10.1104/pp.104.040808	9	328	BMV gene family
Schultz, 2002, Plant Physiol.	10.1104/pp.003459	7	186	AGP gene family
Skinner, 2005, Plant Mol. Biol.	10.1007/s11103-005-2498-2	7	199	CBF gene family
Sánchez, 2006, Planta	10.1007/s00425-005-0144-5	6	71	PEPC gene family

**Table S1. Top countries' scientific production.**

#	Country	Articles	Freq	SCP	MCP	MCP Ratio
1	China	2293	0.72426	2044	249	0.109
2	India	238	0.07517	208	30	0.126
3	USA	111	0.03506	74	37	0.333
4	Korea	83	0.02622	60	23	0.277
5	Brazil	33	0.01042	21	12	0.364
6	Italy	32	0.01011	15	17	0.531
7	Germany	28	0.00884	13	15	0.536
8	Spain	27	0.00853	17	10	0.370
9	Australia	24	0.00758	13	11	0.458
10	Canada	21	0.00663	17	4	0.190

Note: SCP: Single Country Publications; MCP: Multiple Country Publications

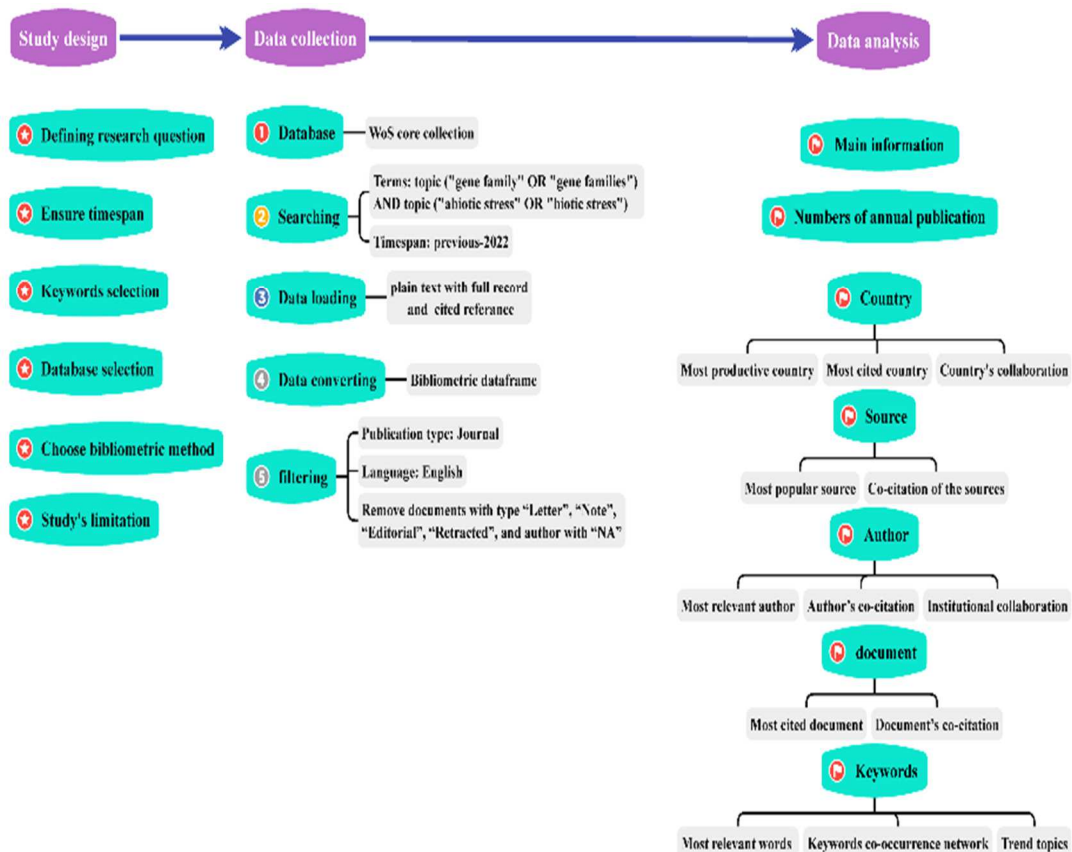
**Table S2. Top10 preferred periodicals.**

Sources	Articles	Total citations	CASAD
Int. J. Mol. Sci.	291	2585	Q2
Front. Plant Sci.	288	5496	Q2
BMC Genomics	180	6144	Q2
BMC Plant Bio.	162	4507	Q2
Plants	131	617	Q2
PLoS One	111	4129	Q3
Genes	98	1071	Q3
PeerJ	92	733	Q3
Plant Physiol. Biochem.	92	1993	Q2
Gene	80	1566	Q3

Note: The journals are ranked based on the numbers of articles. CASAD: Academic Divisions of the Chinese Academy of Sciences.

**Table S3. Most significant words from author’s keywords and keyword plus.**

#	Author Keywords (DE)	Articles	Keywords-Plus (ID)	Articles
1	abiotic stress	1120	<i>arabidopsis</i>	1210
2	gene expression	378	expression	844
3	gene family	222	tolerance	662
4	phylogenetic analysis	212	identification	486
5	expression analysis	203	gene family	479
6	expression pattern	164	protein	445
7	genome-wide analysis	117	evolution	440
8	drought stress	116	Rice	408
9	salt stress	112	abiotic stress	360
10	Evolution	110	drought	358



**Figure 1** The workflow including study design, data collecting and data analysis in this study.

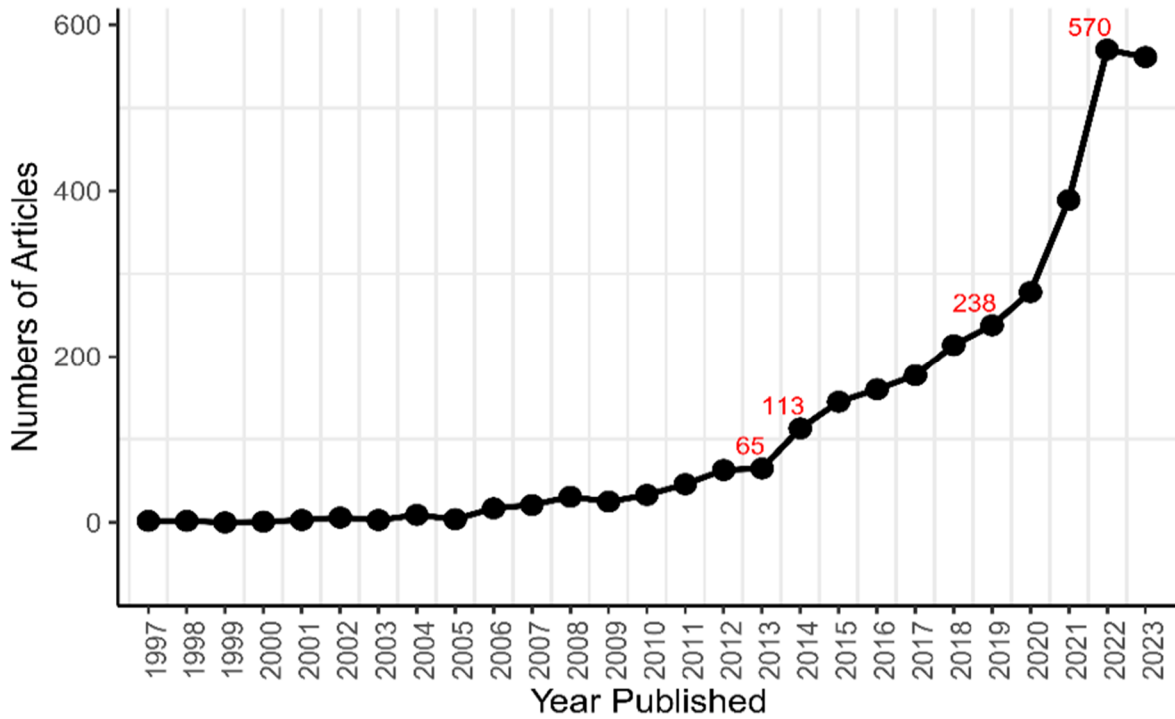


Figure 2 The publication growth.

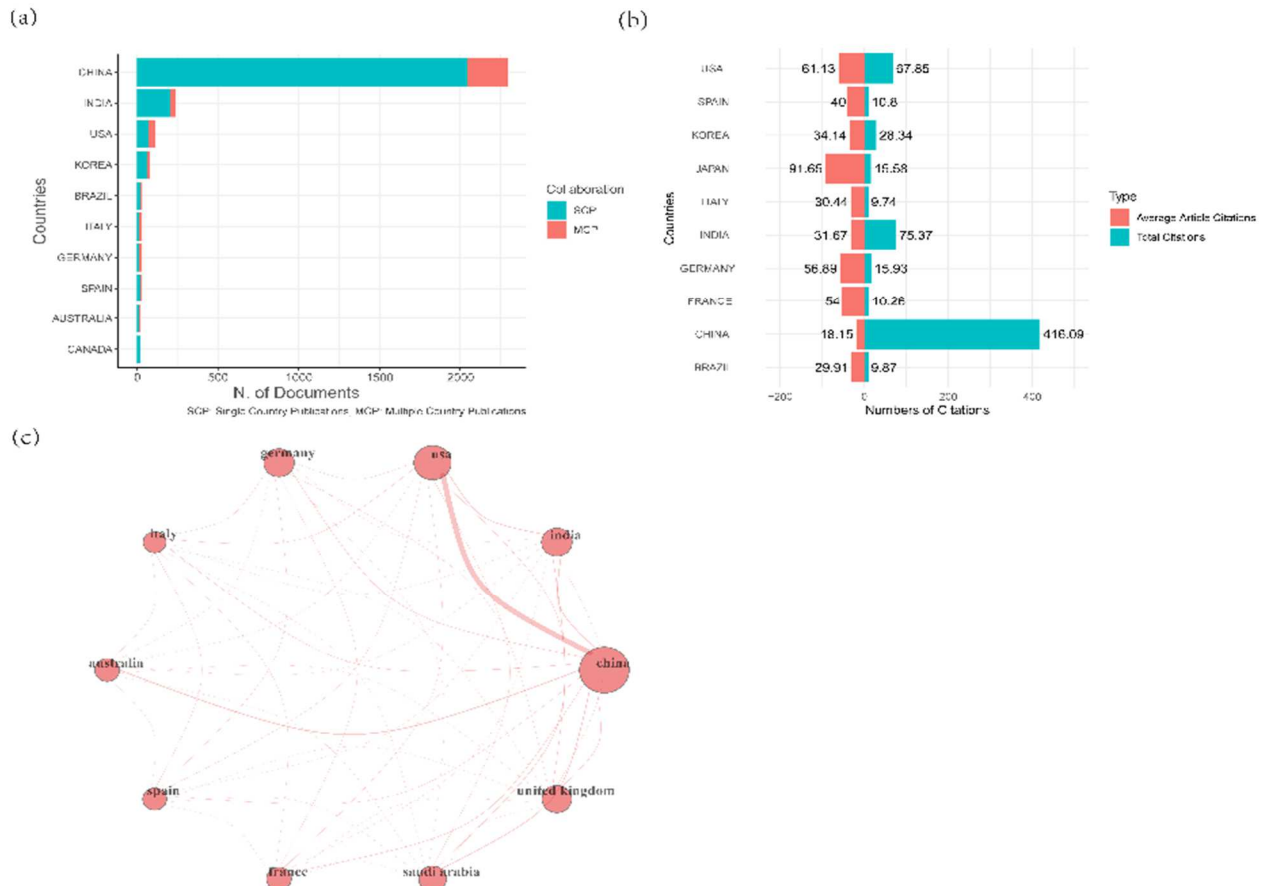


Figure 3 (a) Most productive countries; (b) Citations per country; (c) Networks of countries collaboration. Note: SCP: Single country publications; MCP: Multiple country publications.



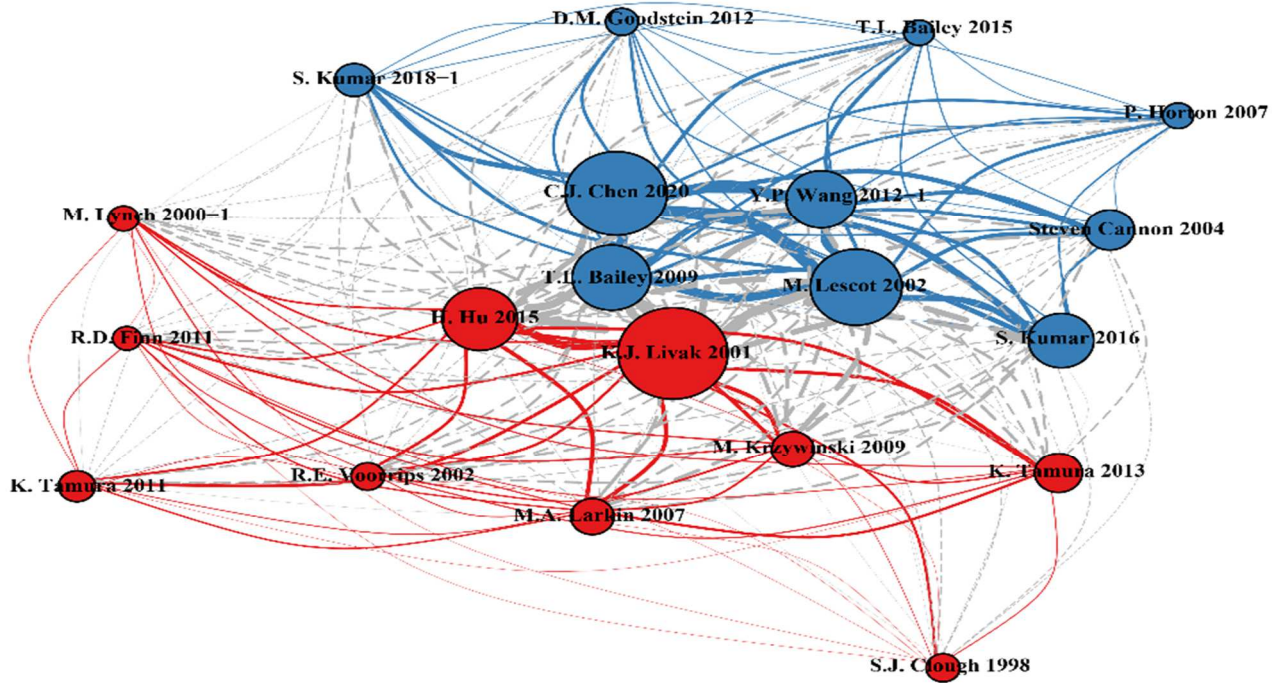
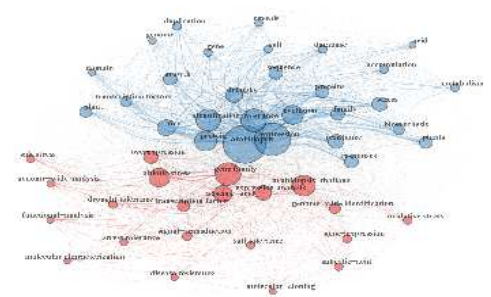


Figure 6 A co-citation network graph of documents.

(a)

(b)



(c)

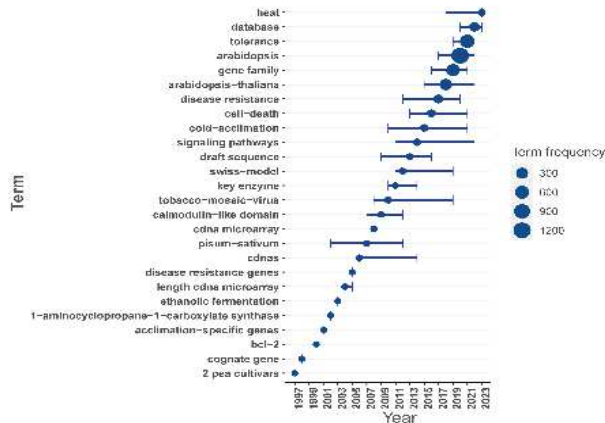


Figure 7 (a) Word cloud generated from keyword plus (ID); (b) Keywords co-occurrence network (KCN); (c) Trend topics.

## DISCUSSION

Abiotic stresses such as drought, salinity, heat, and cold, as well as biotic stresses such as diseases and pests, pose significant threats to global food security. Understanding the gene families involved in stress response can help in developing stress-tolerant crop varieties through genetic engineering or breeding programs. This bibliometric analysis that focuses on gene family research on abiotic or biotic stress tries to establish the study trend in terms of authors, citations, journals, country, and also topics.

The number of articles still increases, largely with an annual scientific production growth rate of 24.21% from 1997 to 2023 (**Table 1**). The reason behind the significant increase was that sequencing has been a mature and advanced technology to study the whole genome since 2014. After that, the progress in sequencing methods pioneered by Illumina, GenapSys, PacBio, and Nanopore, some has significantly increased sequencing volume to several billion nucleotides within a brief period and at a low cost (Satam *et al.*, 2023), which also helped to establish gene family databases in recent years, such as GenFam (Bedre and Mandadi, 2019) (<https://www.mandadilab.com/genfam/>, 2018), PlantGF (Li *et al.*, 2022) (<http://biodb.sdau.edu.cn/PGF/index.html>, 2022), GFDP (Wang *et al.*, 2018) (<http://gfdp.ahau-edu.cn/>, 2018), and TAIR (Garcia-Hernandez *et al.*, 2002) (<https://www.arabidopsis.org/index.jsp>, 2007). Hence, the inexpensive, high-throughput sequencing technology will greatly accelerate the exploration of the gene family involved in plants' responses to environmental stress. In 2023, scientific production suddenly declined, largely due to the impact of COVID-19.

The countries' academic influence was assessed by using the index of total citations and average citations. In terms of the number of publications and total citations, China stands out as the most productive in publishing research articles. Japan holds the most substantial global influence based on average total citation indicators, despite having a relatively smaller number of articles. So, the quality of publications from China still needs to be improved. Furthermore, China plays a crucial role in the collaborative network among the top countries and maintains strong collaboration with the USA. The increasing collaboration between China and the U.S. in the field of science can be attributed to several factors, such as the rise in Chinese research funding, a higher number of internationally educated Chinese scientists and engineers, and modifications to the databases that track China's contributions to science (Wagner *et al.*, 2015).

The analysis finds that the Int. J. Mol. Sci. is the most preferred periodical for researchers publishing articles on gene families with research on abiotic and biotic stress between the years 1997 and 2023 because it

has broad interest in biology (<https://www.mdpi.com/journal/ijms/about>). However, the journal "BMC Genomics" is the most influential in this field. In addition, six and four journals fall into Q2 and Q3, according to CASAD in 2022. 60% of journals based on gene families have relatively high quality (top 25% journals, Q2), indicated by CASAD, which was in accordance with the h-index.

The study reveals that Yong Zhou and Hu Wei are the most influential authors on the topic. In terms of dominance ranking, Zhou Yong emerges as the primary author. Their contributions primarily revolve around analysis, with a similar focus. Yong Zhou is an associate professor at the Key Laboratory of Crop Physiology, Ecology, and Genetic Breeding, Ministry of Education, Jiangxi Agricultural University, China. He has carried out various research, taught, and presented his results in biological functions, and expression regulation of plant leaf development, and stress associated with genes. Wei Hu is an associate researcher at the Institute of Tropical Bioscience and Biotechnology, Chinese Academy of Tropical Agricultural Sciences, China. Through his studies, he mainly engaged in research on the molecular mechanisms of plant responses to stress, plant genetic engineering, and plant genomics. In terms of author's production over time, the publication by Wei Hu with the most total citations per year in 2017 reported that the *PYL-PP2C-SnRK2* genes in bananas play a role in tissue development, fruit development, and ripening, as well as responding to abiotic stress (Hu *et al.*, 2017). In addition, the regional cooperation among authors from China was obvious, as illustrated by the network of author collaborations. The institutional collaborations tend to have geographical boundaries, and Chinese institutions have strong cooperation.

The publications with high LCS mean high relativity in the field of plants' responses to environmental stress. The authors in those publications all focus on gene family research with abiotic stress. As to the publications with high LCS, the most co-cited publication is Cantero *et al.*, (2006), real-time quantitative PCR was employed to monitor changes in annexin expression in response to various abiotic stresses, including salt, drought, and high- and low-temperature conditions (Cantero *et al.*, 2006). But, Nakashima *et al.*, (2007) should pay more attention because of the high GCS. Nakashima proposed that *OsNAC6*, as a transcriptional activator in response to abiotic and biotic stresses in plants, activates the expression of peroxidase (Nakashima *et al.*, 2007). The network of co-citations showed two clades, including developmental tools for evolution analysis and databases or web servers with sequence alignment analysis. Overall, the results indicate that the study of gene families in plants' responses to environmental stress involves two main aspects, including the use of developmental tools including

databases and network servers, reflecting the diversity and complexity of the field of plant gene family research.

The keywords in a publication indicate the primary research areas of focus, and the frequency of keyword occurrence indicates the topics emphasized in that specific research area. As per our analysis, *Arabidopsis*, *gene expression*, *tolerance*, and *gene family* are the most commonly recurring keywords. *Arabidopsis*, as a commonly used model plant, has significantly advanced our comprehension of gene family studies, aided by its comprehensively annotated genome and related databases like TAIR. Utilizing *A. thaliana* as a primary reference, researchers have unveiled a series of transcription factors in plants that exert a pivotal role in plant growth, stress responses, and metabolite synthesis. For example, a study focused on GbWRKY20 derived from *Ginkgo biloba*, recognized as a vital transcription factor in various plant processes, by performing phylogenetic analysis using *Arabidopsis* as a model. Expression analysis has elucidated that GbWRKY20 exhibits distinct responses to heat, drought, NaCl, cold, and methyl jasmonate treatments, implying its potential involvement in plant growth and responses to abiotic stresses and hormonal treatments (Zhou *et al.*, 2021). Abscisic acid (ABA) is a phytohormone that plays a pivotal role in plant responses to various environmental stresses, particularly drought. In response to drought conditions, ABA initiates a range of physiological processes, including stomatal closure, modulation of the root system, organization of soil microbial communities, activation of transcriptional and post-transcriptional gene expression, and metabolic adjustments (Muhammad Aslam *et al.*, 2022). SA, a naturally occurring plant hormone, holds a central role in facilitating stress tolerance among plants. It is notably recognized for its contribution to the plant defense response against a broad spectrum of biotic and abiotic stresses. The mechanisms governing SA's actions in stress tolerance can be intricate and continue to be an active area of research. Potential mechanisms underlying SA-mediated plant stress tolerance include: (1) SA's interaction with osmolytes; (2) engagement with mineral nutrients; (3) participation in ROS signaling and the modulation of antioxidants; (4) interplay with major secondary metabolites; and (5) interactions with other hormones (Khan *et al.*, 2015). The trend topic, including *heat*, *tolerance*, and *databases* may involve the study of how plants evolve adaptive mechanisms to combat abiotic stresses, including adaptive strategies at the genetic and ecological levels. Last but not least, the database for gene function or evolution analysis is urgently needed to be developed for studying plants without a referenced genome.

**Limitation:** Our bibliometric review has some limitations. First, the publications available only in the English language were collected by us. Secondly, we

only collected publications in the Web of Science core collection database rather than all databases. Hence, several publications related to gene families in abiotic or biotic stress research may be skipped; nevertheless, these electronic preprints in the preprint citation index database are not peer-reviewed articles.

**Perspective:** Future research referring to gene families and abiotic or biotic stress is expected to advance our understanding of the molecular mechanisms underlying stress responses and enable the development of innovative strategies for stress tolerance in organisms. Several key research directions are anticipated to shape this field in the coming years.

- i. Elucidating the epigenetic mechanisms is vital for underlying the stress response in plants. Multiple studies show that epigenetic modifications help plants rapidly adapt to aggressive biotic and abiotic stresses by activating or silencing gene expression (Ashapkin *et al.*, 2020). In a recent report, Lin-Lin Hu proposed that histone modification (HM) genes in allotetraploid rapeseed could play a role in ammonium, salt, boron, cadmium, nitrate, and potassium stress responses by co-expression network analysis, suggesting the significance of BnaHMs in regulating stress adaptation in rapeseed (Hu *et al.*, 2023). Additional epigenetic modifications, such as DNA methylation and acetylation, play a crucial role in regulating the expression of plant genes under diverse abiotic stress conditions (Roychowdhury *et al.*, 2023).
- ii. By integrating high-throughput sequencing data, researchers can identify key genes involved in stress responses, providing a comprehensive view of the regulatory mechanisms underlying gene family dynamics. For example, Qi Xie's group has made breakthrough progress in understanding the molecular mechanism of plant alkali tolerance (Zhang *et al.*, 2023). They detected a negative regulation of the alkaline tolerance major gene *ATI* (Alkaline tolerance 1) in sorghum through genome-wide association study analysis. Knockout of *ATI* and its homologous genes enhanced alkali tolerance in sorghum, rice (*Oryza sativa*), foxtail millet (*Setaria italica*), and maize (*Zea mays*), and increased yield under alkaline stress. Hence, high-throughput sequencing technology could help reveal new mechanisms for crop adaptation to environmental stress by identifying key genes.
- iii. Applying the panomics pipeline or an omics-integration approach to decode a plant's responses to abiotic stress tolerance is instrumental in comprehending the molecular mechanisms underlying the plant's reactions to abiotic stress. This comprehensive analysis sheds light on the interplay of genes, transcripts, proteins, epigenomes,

cellular metabolic circuits, and the resulting phenotype (Roychowdhury *et al.*, 2023). For instance, both single-omics analysis (SOA) and multi-omics integration (MOI) studies have yielded novel insights into the early response of oil palm plants to salinity stress. This study identified specific genes, proteins, metabolites, and pathways directly impacted by this stress (Bittencourt *et al.*, 2022). In the future, leveraging extensive data gathered from multi-omics layers, coupled with advanced bioinformatics and computational tools, will offer valuable insights into the mechanisms governing stress responses. This approach will facilitate the development of targeted strategies for enhancing stress tolerance.

- iv. Exploiting the full potential of crop wild relatives (CWRs) can reveal unique alleles, gene family configurations, and regulatory elements associated with stress tolerance. By screening Asian Vigna wild types, Naito *et al.* identified genes associated with salt stress response, including sodium and potassium transporters (Naito *et al.*, 2022). Utilizing CWRs as a source of crucial abiotic traits for developing well-adapted and climate-smart varieties will significantly contribute to sustainable agricultural production.

In summary, future research in the field of gene families and abiotic or biotic stress will leverage multidisciplinary approaches, advanced technologies, and comprehensive data integration to unravel the molecular mechanisms underlying stress responses and develop strategies for stress tolerance improvement. These research directions hold great potential for enhancing the resilience of organisms to environmental stressors and promoting sustainable agriculture and ecosystem management.

**Conclusion:** Abiotic stresses, including drought, salinity, heat, and cold, as well as biotic stresses such as diseases and pests, pose significant threats to global food security (Teshome *et al.*, 2020; Zhang *et al.*, 2022). Understanding the gene families involved in stress response can help in developing stress-tolerant crop varieties through genetic engineering or breeding programs (Bhatnagar-Mathur *et al.*, 2008). Considering the expansion of sequencing data, systematic literature reviews are limited for researchers to get comprehensive knowledge of interesting objects. Hence, a quantitative bibliometric analysis is urgent to summarize global progress and trends.

The results revealed that annual scientific production has largely increased. China and Japan are impactful countries in this field. BMC Genomics is the most influential source, and Yong Zhou is the most influential author. The institutional collaborations have geographical proximity. The publication of Cantero *et al.*

(2006) is considered the most influential publication. Whether *Arabidopsis* is still a popular model organism for gene family study with abiotic stress, the researchers may be likely to pay more attention to gene family research for exploring the response of abiotic stress based on *Arabidopsis* in the future. The keywords **expression**, **identification**, **tolerance**, and **gene family** are the most discussed. The **database**, **heat**, and **tolerance** are trending topics in the future. Our study offered valuable insights for researchers to identify new areas of research, relevant sources, and potential collaborations, enabling them to make informed decisions while studying the gene family for stress response research and its applications.

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**Conflict of Interest:** The authors declare that they have no conflicts of interest.

**Additional Information:** The scripts used are saved in GitHub [https://github.com/Yuhe-Kan/scripts\\_of\\_bibliometric\\_for\\_gene\\_family\\_of-stress\\_2023\\_12-main](https://github.com/Yuhe-Kan/scripts_of_bibliometric_for_gene_family_of-stress_2023_12-main).

**Supplementary Material:** Supplementary material is available on

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## REFERENCES

- Ahmed, A.M., M.M. Pinheiro, P.C. Divis, A. Siner, R. Zainudin, I.T. Wong, C.W. Lu, S.K. Singh-Khaira, S.B. Millar, S. Lynch, M. Willmann, B. Singh, S. Krishna and J. Cox-Singh (2014). Disease progression in *plasmodium knowlesi* malaria is linked to variation in invasion gene family members. PLoS Neglected. Trop. Dis. 8(8): e3086. doi: 10.1371/journal.pntd.0003086
- Aksu, D.A. and A. Memon (2023). Identification of drought-responsive genes in Turkish Bread Wheat (*T. aestivum* L.) Cultivar Gerek 79 by mRNA differential display analysis. Int. J. Life Sci. Biotechnol. 6(3): 322-334. doi: 10.38001/ijlsb.1302905
- Almoguera, C., P. Prieto-Dapena, R. Carranco, J.L. Ruiz

- and J. Jordano (2020). Heat stress factors expressed during seed maturation differentially regulate seed longevity and seedling greening. *Plants* 9(3): 335. doi: 10.3390/plants9030335
- Antonelli, A., C. Fry, R.J. Smith, M.S.J. Simmonds, P.J. Kersey, H.W. Pritchard, M.S. Abbo, C. Acedo, J. Adams, A.M. Ainsworth, B. Allkin, W. Annecke, S.P. Bachman, K. Bacon, S. Bárrios, C. Barstow, A. Battison, E. Bell, K. Bensusan, M.I. Bidartondo, R.J. Blackhall-Miles, J.S. Borrell, F.Q. Brearley, E. Breman, R.F.A. Brewer, J. Brodie, R. Cámara-Leret, R. Campostrini Forzza, P. Cannon, M. Carine, J. Carretero, T.R. Cavagnaro, M.E. Cazar, T. Chapman, M. Cheek, C. Clubbe, C. Cockel, J. Collemare, A. Cooper, A.I. Copeland, M. Corcoran, C. Couch, C. Cowell, P. Crous, M. da Silva, G. Dalle, D. Das, J.C. David, L. Davies, N. Davies, M.N. De Canha, E.J. de Lirio, S. Demissew, M. Diazgranados, J. Dickie, T. Dines, B. Douglas, G. Dröge, M.E. Dulloo, R. Fang, A. Farlow, K. Farrar, M.F. Fay, J. Felix, F. Forest, L.L. Forrest, T. Fulcher, Y. Gafforov, L.M. Gardiner, G. Gâteblé, E. Gaya, B. Geslin, S.C. Gonçalves, C.J.N. Gore, R. Govaerts, B. Gowda, O.M. Grace, A. Grall, D. Haelewaters, J.M. Halley, M.A. Hamilton, A. Hazra, T. Heller, P.M. Hollingsworth, N. Holstein, M.J.R. Howes, M. Hughes, D. Hunter, N. Hutchinson, K. Hyde, J. Iganci, M. Jones, L.J. Kelly, P. Kirk, H. Koch, I. Grisai-Greilhuber, N. Lall, M.K. Langat, D.J. Leaman, T.C. Leão, M.A. Lee, I.J. Leitch, C. Leon, E. Lettice, G.P. Lewis, L. Li, H. Lindon, J.S. Liu, U. Liu, T. Llewellyn, B. Looney, J.C. Lovett, L. Luczaj, E. Lulekal, S. Magassouba, V. Malécot, C. Martin, O.R. Masera, E. Mattana, N. Maxted, C. Mba, K.J. McGinn, C. Metheringham, S. Miles, J. Miller, W. Milliken, J. Moat, P.G.P. Moore, M.P. Morim, G.M. Mueller, H. Muminjanov, R. Negrão, E. Nic Lughadha, N. Nicolson, T. Niskanen, R. Nono Womdim, A. Noorani, M. Obreza, K. O'Donnell, R. O'Hanlon, J.M. Onana, I. Ondo, S. Padulosi, A. Paton, T. Pearce, O.A. Pérez Escobar, A. Pieroni, S. Pironon, T.A.K. Prescott, Y.D. Qi, H. Qin, C.L. Quave, L. Rajaovelona, H. Razanajatovo, P.B. Reich, E. Rianawati, T.C.G. Rich, S.L. Richards, M.C. Rivers, A. Ross, F. Rumsey, M. Ryan, P. Ryan, S. Sagala, M.D. Sanchez, S. Sharrock, K.K. Shrestha, J. Sim, A. Sirakaya, H. Sjöman, E.C. Smidt, D. Smith, P. Smith, S.R. Smith, A. Sofo, N. Spence, A. Stanworth, K. Stara, P.C. Stevenson, P. Stroh, L.M. Suz, B.B. Tambam, E.C. Tatsis, I. Taylor, B. Thiers, I. Thormann, V. Vaglica, C. Vásquez-Londoño, J. Victor, J. Viruel, B.E. Walker, K. Walker, A. Walsh, M. Way, J. Wilbraham, P. Wilkin, T. Wilkinson, C. Williams, D. Winterton, K.M. Wong, N. Woodfield-Pascoe, J. Woodman, L. Wyatt, R. Wynberg, B.G. Zhang and T. Ulian (2020) *State of the world's plants and fungi 2020*. Royal Botanic Gardens, Kew.
- Anuar, M.S.K., A.M. Hashim, C.L. Ho, M.Y. Wong, S. Sundram, N.B. Saidi and M.T. Yusof (2023). Synergism: Biocontrol agents and biostimulants in reducing abiotic and biotic stresses in crop. *World J. Microbiol. Biotechnol.* 39(5): 123. doi: 10.1007/s11274-023-03579-3
- Aria, M. and C. Cuccurullo (2017). Bibliometrix: An R-tool for comprehensive science mapping analysis. *J. Informetr* 11(4): 959-975. doi: 10.1016/j.joi.2017.08.007
- Ashapkin, V.V., L.I. Kutueva, N.I. Aleksandrushkina and B.F. Vanyushin (2020). Epigenetic mechanisms of plant adaptation to biotic and abiotic stresses. *Int. J. Mol. Sci.* 21(20): 7457. doi: 10.3390/ijms21207457
- Bai, Y., S. Sunarti, C. Kissoudis, R.G.F. Visser and C.G. van der Linden (2018). The role of tomato WRKY genes in plant responses to combined abiotic and biotic stresses. *Front. Plant Sci.* 9: 801. doi: 10.3389/fpls.2018.00801
- Balbinott, N. and R. Margis (2022). Review: Unraveling the origin of the structural and functional diversity of plant cystatins. *Plant Sci.* 321: 111342. doi: 10.1016/j.plantsci.2022.111342
- Bedre, R. and K. Mandadi (2019). GenFam: A web application and database for gene family-based classification and functional enrichment analysis. *Plant Direct.* 3(12): e00191. doi: 10.1002/pld3.191
- Bhatnagar-Mathur, P., V. Vadez and K.K. Sharma (2008). Transgenic approaches for abiotic stress tolerance in plants: Retrospect and prospects. *Plant Cell Rep.* 27(3): 411-424. doi: 10.1007/s00299-007-0474-9
- Bittencourt, C.B., T.L. Carvalho da Silva, J.C. Rodrigues Neto, L.R. Vieira, A.P. Leão, J.A. de Aquino Ribeiro, P.V. Abdelnur, C.A.F. de Sousa and M.T. Souza (2022). Insights from a multi-omics integration (MOI) study in oil palm (*Elaeis guineensis* Jacq.) response to abiotic stresses: Part one-salinity. *Plants (Basel)* 11(13): 1755. doi: 10.3390/plants11131755
- Calanca, P.P. (2017). Effects of abiotic stress in crop production. In: Ahmed M., and Stockle C., editors. Quantification of climate variability, adaptation and mitigation for agricultural sustainability. Cham: Springer International Publishing. doi: 10.1007/978-3-319-32059-5\_8
- Campra, M., P. Riva, G. Oricchio and V. Brescia (2022).

- Bibliometrix analysis of medical tourism. *Health Serv. Manage Res.* 35(3): 172-188. doi: 10.1177/09514848211011738
- Cantero, A., S. Barthakur, T.J. Bushart, S. Chou, R.O. Morgan, M.P. Fernandez, G.B. Clark and S.J. Roux (2006). Expression profiling of the *Arabidopsis* annexin gene family during germination, de-etiolation and abiotic stress. *Plant Physiol. Biochem.* 44(1): 13-24. doi: 10.1016/j.plaphy.2006.02.002
- Chen, C. (2006). CiteSpace II: Detecting and visualizing emerging trends and transient patterns in scientific literature. *J. Am. Soc. Inf. Sci. Technol.* 57(3): 359-377. doi: 10.1002/asi.20317
- Chen, C., H. Chen, Y. Zhang, H.R. Thomas, M.H. Frank, Y. He and R. Xia (2020). TBtools: An Integrative toolkit developed for interactive analyses of big biological data. *Mol. Plant* 13(8): 1194-1202. doi: 10.1016/j.molp.2020.06.009
- Fang, Y., J. Jiang, X. Hou, J. Guo, X. Li, D. Zhao and X. Xie (2022). Plant protein-coding gene families: Their origin and evolution. *Front. Plant Sci.* 13: 995746. doi: 10.3389/fpls.2022.995746
- Garchitorena, A., J.F. Guégan, L. Léger, S. Eyangoh, L. Marsollier and B. Roche (2015). *Mycobacterium ulcerans* dynamics in aquatic ecosystems are driven by a complex interplay of abiotic and biotic factors. *eLife* 4: e07616. doi: 10.7554/eLife.07616
- Garcia-Hernandez, M., T.Z. Berardini, G. Chen, D. Crist, A. Doyle, E. Huala, E. Knee, M. Lambrecht, N. Miller, L.A. Mueller, S. Mundodi, L. Reiser, S.Y. Rhee, R. Scholl, J. Tacklind, D.C. Weems, Y. Wu, I. Xu, D. Yoo, J. Yoon and P. Zhang (2002). TAIR: A resource for integrated *Arabidopsis* data. *Funct. Integr. Genomics* 2(6): 239-253. doi: 10.1007/s10142-002-0077-z
- Gatto, A. and C. Drago (2020). A taxonomy of energy resilience. *Energy Policy* 136: 111007. doi: 10.1016/j.enpol.2019.111007
- Grinberg, I. and K. Millen (2005). The *ZIC* gene family in development and disease. *Clin. Genet.* 67(4): 290-296. doi: 10.1111/j.1399-0004.2005.00418.x
- Harzing, A.W. (2007) Publish or Perish. Available at <https://harzing.com/resources/publish-or-perish> [Accessed 30 August 2024].
- Hernández-Lambrano, R.E., D.R. de la Cruz and J.Á. Sánchez-Agudo (2019). Spatial oak decline models to inform conservation planning in the Central-Western Iberian Peninsula. *For. Ecol. Manage.* 441: 115-126. doi: 10.1016/j.foreco.2019.03.028
- Hirsch, J.E. (2005). An index to quantify an individual's scientific research output. *Proc. Natl. Acad. Sci. U. S. A.* 102(46): 16569-16572. doi: 10.1073/pnas.0507655102
- Hu, L.L., L.W. Zheng, X.L. Zhu, S.J. Ma, K.Y. Zhang, Y.P. Hua and J.Y. Huang (2023). Genome-wide identification of Brassicaceae histone modification genes and their responses to abiotic stresses in allotetraploid rapeseed. *BMC Plant Biol.* 23(1): 248. doi: 10.1186/s12870-023-04256-1
- Hu, W., Y. Yan, H. Shi, J. Liu, H. Miao, W. Tie, Z. Ding, X. Ding, C. Wu, Y. Liu, J. Wang, B. Xu and Z. Jin (2017). The core regulatory network of the abscisic acid pathway in banana: Genome-wide identification and expression analyses during development, ripening, and abiotic stress. *BMC Plant Biol.* 17(1): 145. doi: 10.1186/s12870-017-1093-4
- Khan, M.I., M. Fatma, T.S. Per, N.A. Anjum and N.A. Khan (2015). Salicylic acid-induced abiotic stress tolerance and underlying mechanisms in plants. *Front. Plant Sci.* 6: 462. doi: 10.3389/fpls.2015.00462
- Li, J., S. Yang, X. Yang, H. Wu, H. Tang and L. Yang (2022). PlantGF: An analysis and annotation platform for plant gene families. *Database (Oxford)* 2022: baab088. doi: 10.1093/database/baab088
- Liberles, D.A. and K. Dittmar (2008). Characterizing gene family evolution. *Biol. Proced. Online* 10: 66-73. doi: 10.1251/bpo144
- Livak K.J. and T.D Schmittgen (2001). Analysis of relative gene expression data using real-time quantitative PCR and the  $2^{-\Delta\Delta C_T}$  method. *Methods* 25(4):402-408. doi: 10.1006/meth.2001.1262
- López-Ortega, O., E. Ovalle-García, I. Ortega-Blake, A. Antillón, B. Chávez-Munguía, G. Patiño-López, R. Fragozo-Soriano and L. Santos-Argumedo (2016). Myo1g is an active player in maintaining cell stiffness in B-lymphocytes. *Cytoskeleton (Hoboken)* 73(5): 258-268. doi: 10.1002/cm.21299
- Moral-Munoz, J.A., E.E. Herrera-Viedma, A. Santisteban-Espejo and M.J. Cobo (2020). Software tools for conducting bibliometric analysis in science: An up-to-date review. *El Profesional de la Información* 29(1): e290103. doi: 10.3145/epi.2020.ene.03
- Muhammad Aslam, M., M. Waseem, B.H. Jakada, E.J. Okal, Z. Lei, H.S.A. Saqib, W. Yuan, W. Xu and Q. Zhang (2022). Mechanisms of abscisic acid-mediated drought stress responses in plants. *Int. J. Mol. Sci.* 23(3): 1084. doi: 10.3390/ijms23031084
- Naito, K., T. Wakatake, T.F. Shibata, K. Iseki, S. Shigenobu, Y. Takahashi, E. Ogiso-Tanaka, C. Muto, K. Teruya, A. Shiroma, M. Shimoji, K.

- Satou, T. Hirano, A.J. Nagano, N. Tomooka, M. Hasebe, K. Fukushima and H. Sakai (2022). Genome sequence of 12 *Vigna* species as a knowledge base of stress tolerance and resistance. *BioRxiv*. doi: 10.1101/2022.03.28.486085
- Nakashima, K., L.S. Tran, D. Van Nguyen, M. Fujita, K. Maruyama, D. Todaka, Y. Ito, N. Hayashi, K. Shinozaki and K. Yamaguchi-Shinozaki (2007). Functional analysis of a NAC-type transcription factor OsNAC6 involved in abiotic and biotic stress-responsive gene expression in rice. *Plant J*. 51(4): 617-630. doi: 10.1111/j.1365-3113X.2007.03168.x
- Olety, B., M. Wälte, U. Honnert, H. Schillers and M. Bähler (2010). Myosin 1G (Myo1G) is a haematopoietic specific myosin that localises to the plasma membrane and regulates cell elasticity. *FEBS Lett*. 584(3): 493-499. doi: 10.1016/j.febslet.2009.11.096
- Omotehinwa, T.O. (2022). Examining the developments in scheduling algorithms research: A bibliometric approach. *Heliyon* 8(5): e09510. doi: 10.1016/j.heliyon.2022.e09510
- Owens, J.K. (2021). Systematic reviews: Brief overview of methods, limitations, and resources. *Nurse Author & Ed*. 31(3-4): 69-72. doi: 10.1111/nae2.28
- Satam, H., K. Joshi, U. Mangrolia, S. Waghoo, G. Zaidi, S. Rawool, R.P. Thakare, S. Banday, A.K. Mishra, G. Das and S.K. Malonia (2023). Next-generation sequencing technology: Current trends and advancements. *Biology* 12: 997. doi: 10.3390/biology12070997
- Radhakrishnan, S., S. Erbis, J.A. Isaacs and S. Kamarthi (2017). Novel keyword co-occurrence network-based methods to foster systematic reviews of scientific literature. *PLoS One* 12(3): e0172778. doi: 10.1371/journal.pone.0172778
- Roychowdhury, R., S.P. Das, A. Gupta, P. Parihar, K. Chandrasekhar, U. Sarker, A. Kumar, D.P. Ramrao and C. Sudhakar (2023). Multi-omics pipeline and omics-integration approach to decipher plant's abiotic stress tolerance responses. *Genes (Basel)* 14(6): 1281. doi: 10.3390/genes14061281
- Shen, Z., S. Tong, F. Chen and L. Yang (2020). Novel utilization of a paper-level classification system for the evaluation of journal impact: An update of the CAS J. Ranking. *ArXiv*: 2006.05047. doi: 10.48550/arXiv.2006.05047
- Teshome, D.T., G.E. Zharare and S. Naidoo (2020). The threat of the combined effect of biotic and abiotic stress factors in forestry under a changing climate. *Front. Plant Sci*. 11: 601009. doi: 10.3389/fpls.2020.601009
- Uluhan, E., E.N. Keleş and F. Tufan (2019). Analysis of WRKY transcription factors in barley cultivars infected with *Fusarium culmorum*. *Int. J. Life Sci. Biotechnol.* 2(3): 165-174. doi: 10.38001/ijlsb.588730
- Van Eck, N.J. and L. Waltman (2010). Software survey: VOSviewer, a computer program for bibliometric mapping. *Scientometrics* 84(2): 523-538. doi: 10.1007/s11192-009-0146-3
- Van Eck, N.J. and L. Waltman (2014). CitNetExplorer: A new software tool for analyzing and visualizing citation networks. *J. Informetr.* 8(4): 802-823. doi: 10.1016/j.joi.2014.07.006
- Wagner, C.S., L. Bornmann and L. Leydesdorff (2015). Recent developments in China–U.S. cooperation in science. *Minerva* 53(3): 199-214. doi: 10.1007/s11024-015-9273-6
- Wang, H., H. Yan, H. Liu, R. Liu, J. Chen and Y. Xiang (2018). GFDP: The gene family database in poplar. *Database (Oxford)* 2018: bay107. doi: 10.1093/database/bay107
- Zanatta, A., A.M. Rocha, F.M. Carvalho, R.M.A. Pereira, H.S. Taylor, E.L. Motta, E.C. Baracat and P.C. Serafini (2010). The role of the *Hoxa10/HOXA10* gene in the etiology of endometriosis and its related infertility: A review. *J. Assist. Reprod. Genet.* 27(12): 701-710. doi: 10.1007/s10815-010-9471-y
- Zhang, S., G.H. Chen, Y. Liu, H. Chen, G. Yang, X. Yuan, Z. Jiang and H. Shu (2013). Apple gene function and gene family database: An integrated bioinformatics database for apple research. *Plant Growth Regul.* 70: 199-206. doi: 10.1007/s10725-013-9787-6
- Zhang, H., F. Yu, P. Xie, S. Sun, X. Qiao, S. Tang, C. Chen, S. Yang, C. Mei, D. Yang, Y. Wu, R. Xia, X. Li, J. Lu, Y. Liu, X. Xie, D. Ma, X. Xu, Z. Liang, Z. Feng, X. Huang, H. Yu, G. Liu, Y. Wang, J. Li, Q. Zhang, C. Chen, Y. Ouyang and Q. Xie (2023). A Gγ protein regulates alkaline sensitivity in crops. *Science* 379(6638): eade8416. doi: 10.1126/science.ade8416
- Zhang, H., J. Zhu, Z. Gong and J.K. Zhu (2022). Abiotic stress responses in plants. *Nat. Rev. Genet.* 23(2): 104-119. doi: 10.1038/s41576-021-00413-0
- Zhang, W. and J. Messing (2017). PacBio for haplotyping in gene families. *Methods Mol. Biol.* 1151: 61-71. doi: 10.1007/978-1-4939-6750-6\_3
- Zhou, T., X. Yang, G. Wang and F. Cao (2021). Molecular cloning and expression analysis of a WRKY transcription factor gene, *GbWRKY20*, from *Ginkgo biloba*. *Plant Signal. Behav.* 16(10): 1930442. doi: 10.1080/15592324.2021.1930442.