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Global advances in research on plant resistance genes: an updated compilation and bibliometric analysis

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Abstract

Plant resistance genes play a critical role in enhancing crop immunity against various biotic stresses, such as pathogens, nematodes, and insects, safeguarding global agricultural productivity. A collection of plant resistance genes identified between 1992 and 2017 has been reported previously. To provide an updated overview of advances in research on plant resistance genes, we sorted out the mapped, identified, and cloned plant resistance genes reported from 2018 to the present. Data analyses revealed a total of 101 plant resistance genes reported since 2018, mainly from economically important crops (rice and wheat) and the model plant *Arabidopsis thaliana*, with a main focus on fungi, bacteria, and viruses. We subsequently conducted a bibliometric analysis of 9533 publications on plant resistance genes from the Web of Science core collection between 2007 and 2024. The number of publications increased from 334 in 2007 to 937 in 2024, significantly contributed by the institutions of the United States and China. Both the United States Department of Agriculture and the Chinese Academy of Agricultural Sciences are the top two institutions contributing to these publications. The top three journals in terms of publication volume are The Plant Cell, Journal of Integrative Plant Biology, and Plant Science. In addition, the leading journals Nature and Science published approximately 5% and 9% of these publications, respectively. Keywords analysis identified four primary research clusters: molecular mechanisms of plant resistance genes, plant immunity, wheat-specific resistance, and rice disease management. This study provides valuable insights into research trends, collaboration, and high-impact areas, serving as a resource for advancing plant resistance strategies to ensure global food security.

Keywords Plant disease-resistance genes, Bibliometric analysis, NLR, Pathogen, VOSviewer

Background

Global agriculture constantly faces threats from pathogens and pests, with estimates indicating that diseases alone cause 10–20% losses in major crops every year (Savary et al. 2019). These losses are exacerbated by climate change, which often intensifies the spread and severity of disease (Chaloner et al. 2021). The economic impact of these losses is profound, not only reducing food

availability but also increasing production costs. Thus, enhancing disease resistance in crops through deploying the plant immune system is urgent and important for controlling many crop diseases (Jones et al. 2024).

Plants possess a sophisticated immune system to resist a wide range of pathogens, consisting of two primary layers: pathogen-associated molecular pattern (PAMP)-triggered immunity (PTI) and effector-triggered immunity (ETI) (Jones and Dangl 2006; Ngou et al 2022a). The first layer, PTI, is activated when pattern recognition receptors (PRRs) located on the plant cell surface detecting conserved PAMPs, such as flagellin or chitin (Boller and Felix 2009). PTI usually contributes to halting pathogen

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invasion at an early stage. However, successful pathogens have evolved to overcome PTI by secreting effector-specialized proteins that interfere with host PTI defense. To counteract these effectors, plants have evolved a second layer of immunity, known as ETI. This involves the recognition of specific pathogen effectors by intracellular resistance proteins (Cui et al. 2015). ETI is generally more robust than PTI, often leading to localized cell death known as the hypersensitive response (HR), which restricts pathogen spread (Coll et al. 2011). PTI and ETI work synergistically, where they do not function separately but rather tightly interlinked and mutually potentiating (Ngou et al. 2022b, 2022c; Yu et al. 2024). Recent research also demonstrates that NLR-mediated immune response is bolstered by the PRR activation (Ngou et al. 2021).

As reviewed previously (Kourelis and van Der Hoorn 2018), plant resistance (*R*) genes can be classified into nine functional mechanisms that fall broadly into two categories: pathogen perception and loss of susceptibility. In brief, perception mechanisms involve either extracellular or intracellular recognition. Cell-surface receptor-like proteins/kinases (RLPs/RLKs) detect pathogen signals directly or indirectly via host factor modification. Intracellular nucleotide-binding leucine-rich repeat receptors (NLRs) recognize pathogenic effectors directly, or indirectly through guard/decoy mechanisms, or via integrated domains. Additionally, transcription activator-like effectors can trigger the expression of executor genes. Loss-of-susceptibility mechanisms include active disarming of pathogens, passive resistance due to disrupted host–pathogen interactions, or host reprogramming that reduces compatibility. A detailed introduction to the molecular mechanism of plant *R* gene-mediated resistance can be found in previously published review articles (Kourelis & van Der Hoorn 2018; Jones et al. 2024; Gu et al. 2025).

Among the cloned *R* genes, the majority encode NLRs, followed by RLPs/RLKs, with fewer executor genes and loss-of-susceptibility cases (Kourelis and van Der Hoorn 2018). Canonical plant NLR proteins are composed of multiple domains, including the central nucleotide-binding domain (NB) and C-terminal leucine-rich repeat domain (LRR). NLR proteins are further subdivided into CNLs (CC-NLRs) and TNLs (TIR-NLRs) on the basis of their N-terminal coiled-coil (CC) or Toll/interleukin-1 receptor (TIR) domain (Faris and Friesen 2020). The NB domain binds ATP and undergoes conformational changes upon pathogen recognition (Young and Innes 2006). The LRR domain is involved in the recognition of pathogen-derived effector proteins (Kobe and Kajava 2001). In some cases, atypical integrated domains (ID) are embedded in

NLRs (NLR-ID), functioning as a “decoy” to recognize and trigger defense responses against pathogen effectors (Kroj et al. 2016; Zhu et al. 2025).

The first *R* gene, *Hm1*, cloned from maize was reported in 1992 (Johal and Briggs 1992). Over the past three decades, significant progress has been made in the identification and cloning of plant *R* genes. Kourelis and van Der Hoorn (2018) organized the cloned 314 *R* genes through a comprehensive review of related publications over 25 years spanning from 1992 to 2017. With the input of advanced biotechnologies and numerous efforts, the number of cloned *R* genes has steadily increased, accompanied with several milestone achievements in research on plant *R* genes. One of the achievements is the structural resolution of the CNL protein ZAR1 along with the PBL2 kinase sensor and pseudokinase RKS1 (Wang et al. 2019). Soon after the ZAR1 resistosome was structurally elucidated, the structures of several other resistosomes, such as Sr35, RPP1, ROQ1, and NRC4, were rapidly determined (Martin et al. 2020; Ma et al. 2020; Zhao et al. 2022; Liu et al. Cell 2024). Another achievement is the recent studies on the tandem kinase, as an important class of plant *R* genes, which were determined to interact with NLR to form hetero-oligomer that confers resistance to multiple fungal pathogens (Chen et al. 2025; Lu et al. 2025). All advances, which are not limited to the aforementioned, offer a rational framework for engineering disease resistance, enabling the design of NLRs with broadened or novel recognition specificity for durable crop protection.

Bibliometric analysis is a powerful method, which is used to extract valuable information from a great number of publications, such as research trends, contributions of institutions and scholars, and their collaboration. Bibliometric analysis has been used to assess the landscape of various academic studies. For instance, Tang and colleagues conducted a bibliometric analysis of publications about plant resistance to fungal pathogens (Tang et al. 2022). In this study, we collected over 9000 publications on plant *R* genes in the Web of Science core database between 2007 and 2024. Following the collection of the cloned plant *R* genes previously organized by Kourelis and van Der Hoorn (2018), we updated all the cloned, mapped, and identified plant *R* genes published by the end of 2024 and classified them into different categories in terms of their host origins or targets. We subsequently conducted bibliometric analyses of these publications in terms of multiple aspects, such as countries, institutions, and authors, as well as their networks. Our findings could provide valuable resources for researchers, funding agencies, agricultural policymakers, and educators by offering a comprehensive view of the progress, challenges, and opportunities in this field.

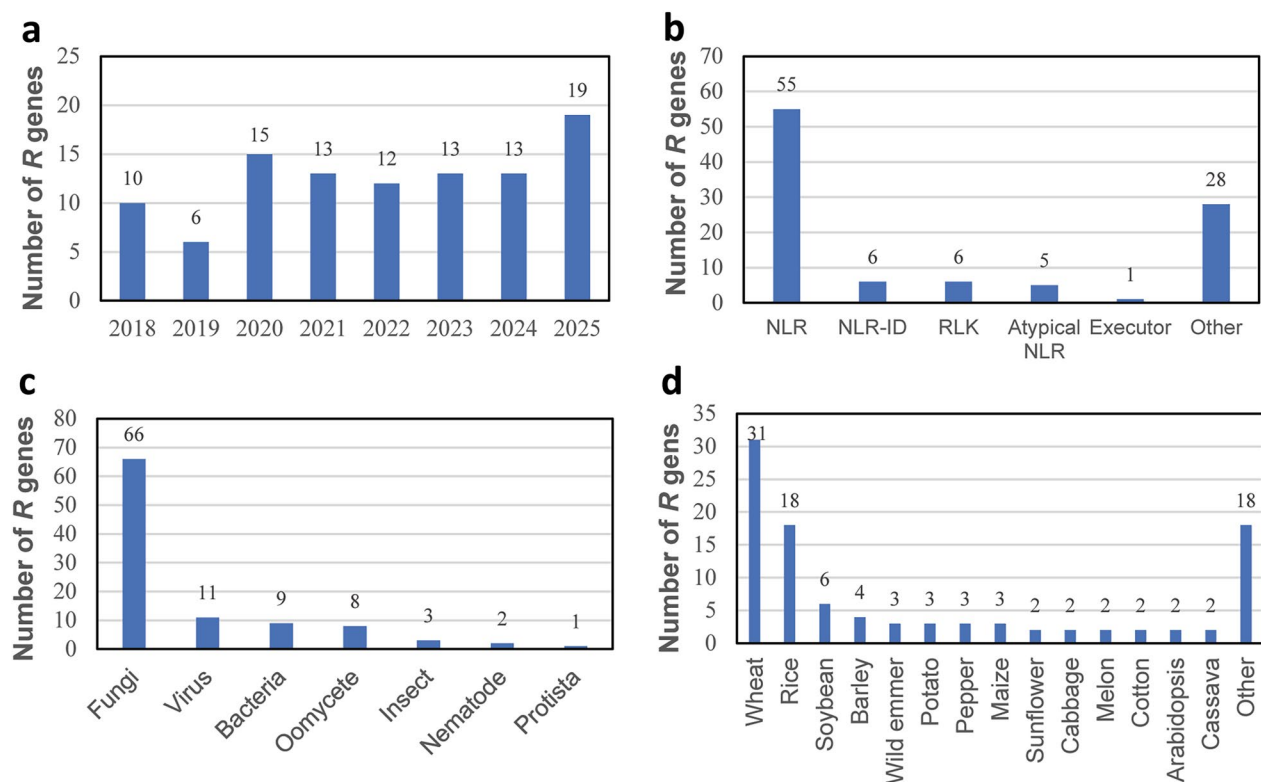


Fig. 1 The number of plant *R* genes reported from 2018 to the present. **a** The number of plant *R* genes reported annually. **b** The classification of plant *R* genes. **c** The plant *R* genes were grouped according to the pathogens against which they act. **d** The plant *R* genes were grouped by the host species carrying them

Results

Trends in the discovery of plant *R* genes since 2018

Over the past three decades, extensive research has been conducted to discover plant *R* genes. Kourelis and van Der Hoorn (2018) summarized plant *R* genes cloned between 1992 and 2017. To provide the latest research progress, we followed their work to collect all plant *R* genes reported since 2018, which included identified and cloned genes (Fig. 1). Identified *R* genes refer to those that have been fine-mapped to a specific gene associated with resistance traits. Cloned *R* genes refer to those that have been isolated, sequenced, and characterized, and with their functions confirmed. Since 2018, a total of 101 *R* genes have been reported, with 81 cloned and 20 identified (Additional file 1: Table S1). The number of *R* genes reported annually ranges from 10 to 15, except for the years 2019 and 2025 with remarkable variations. Obviously, the number of *R* genes increases substantially in 2025, as of which 18 *R* genes have been reported to date (Fig. 1a), indicating the significant progress has been made in the identification of plant *R* genes in 2025.

Among the reported *R* genes, typical NLRs constitute the largest group, with 55 members accounting for approximately 55% of the total (Fig. 1b). Non-canonical

NLRs, including NLR-IDs and atypical NLRs, comprise 6 and 5 genes, respectively, together representing about 11%. RLK-type *R* genes are represented by 6 members. In addition, 28 *R* genes belong to other categories, second only to NLRs. Collectively, these observations indicate that NLRs represent the predominant class of *R* genes, while non-canonical NLRs and other *R* gene types contribute substantially to the overall diversity of the *R* gene repertoire.

We subsequently classified the reported plant *R* genes according to the types of target pathogen (Fig. 1c). *R* genes against fungal pathogens are the most abundant, with 66 genes accounting for 66% of the total. This is followed by the *R* genes which target viruses and bacteria, with 11 and 9 genes, respectively. In contrast, *R* genes against oomycete, protist, insect, and nematode are relatively rare. Overall, these data strongly correlate with the severity of damage caused by different types of pathogens in plants.

Finally, we analyzed the plant sources of these *R* genes (Fig. 1d). Data analysis revealed that wheat and rice are the predominant sources, contributing approximately 30% and 18% of the total *R* genes, respectively, highlighting the strong research focus on staple crops in

combating pathogens and pests. Other notable sources include soybean (6%), barley (3%), wild emmer (3%), pepper (3%), and maize (3%). The “Other” category comprises 18 *R* genes, each isolated from a different plant species. Together, these results indicate that *R* gene discovery has been strongly shaped by both agricultural importance and species diversity.

Overall views of articles on plant *R* genes published between 2007 and 2024

To comprehensively analyze recent research progress on the plant *R* gene, we screened a total of 9533 scientific publications on this subject from the Web of Science core collection from 2007 to 2024. This extensive collection underscores the significant interest and progress in understanding the action mechanisms and applications of plant *R* genes. Among these publications, approximately 87% are original research articles, reflecting the active and continuous efforts of scientists to uncover new insights and data. The remaining 13% are review articles, which serve as valuable summaries and syntheses of the existing knowledge, providing a broader perspective on the advancements in this field. During this period, the number of publications increased from 344 in 2007 to 937 in 2024 (Fig. 2). There was a sharp increase in 2020 compared with the previous year, 2019. The number of publications continues to grow, suggesting that research on plant *R* genes has been a hotspot in recent years. These findings will help scientists explore new frontiers and deepen their understanding of these critical genetic elements.

Global development of plant *R* gene research topics and their citation impacts

By analyzing bibliometric data, we revealed the distribution of 27,612 unique keywords from those screened publications. To pinpoint the most significant research hotspots, a co-occurrence threshold of 30 was applied, resulting in a VOSviewer visualization featuring 445 items (Fig. 3). Each item is depicted by a label and a circle, with their sizes reflecting the item's weight—larger labels and circles indicate higher weights, whereas smaller ones signify lower weights. The color of each item denotes its cluster affiliation, and top 1000 strong co-occurrence connections are illustrated with linking lines.

Within this network, all the keywords are categorized into 4 clusters, which are displayed with different colors. These clusters are led by the most frequent keywords “disease resistance”, “genes”, “identification”, and “rice”, respectively. Each cluster represents distinct subdomains of plant *R* genes.

Red cluster (Cluster 1): This cluster encompasses 166 items, which include genes related to expression, resistance, defense, salicylic acid, and plants. These terms shed light on the expression of plant *R* genes involved in plant defense and activated by salicylic acid in plants. Green cluster (Cluster 2): This cluster contains 121 items focusing on sophisticated and tightly regulated plant resistance. This cluster includes terms such as *Arabidopsis thaliana*, disease resistance, cell death, plant immunity, effectors, recognition, and defense responses, reflecting the molecular mechanism of plant immunity in the model plant *A. thaliana*. The blue cluster (Cluster 3) encompasses 115 items, such as identification, wheat, quantitative trait locus, markers, pathogens, genome, diversity, adult plant resistance, durable resistance,

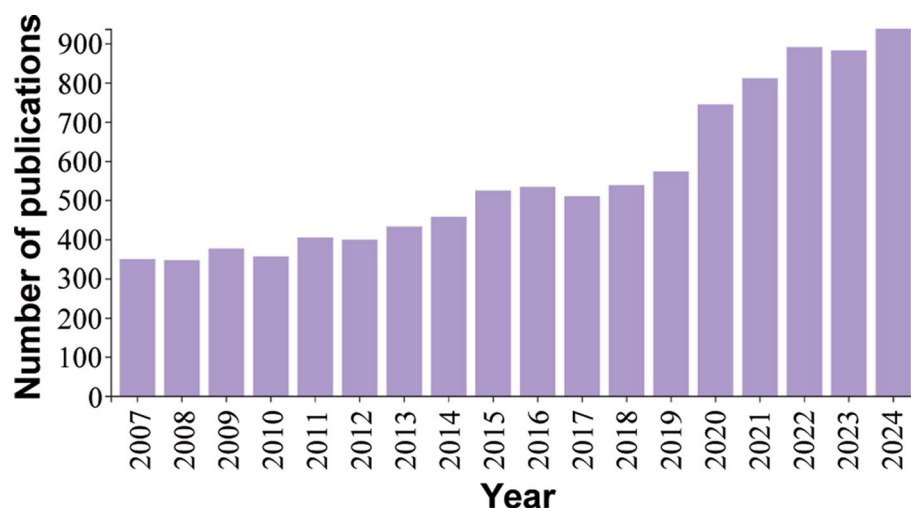
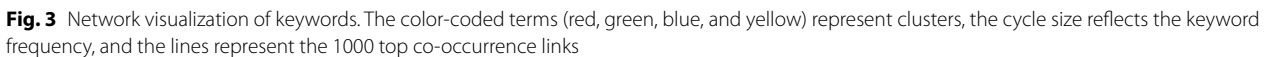


Fig. 2 The number of articles on plant *R* genes published annually between 2007 and 2024



In another way, we presented the keywords with a density (Fig. 4). In this visualization, each term is represented on a color gradient, which indicates the density of keywords in different areas of the map. The color scheme ranges from blue (indicating low density) to yellow (indicating high density). High-density areas include keywords such as disease resistance, genes, identification, *A. thaliana*, rice, wheat, potato, and tomato, indicating a strong emphasis on the identification of *R* genes in these plants. Conversely, areas with lower density (blue)

By analyzing bibliometric data from those publications, a collaborative clustering map was constructed to reveal patterns of international cooperation, key contributing countries, and temporal dynamics within this research domain (Fig. 5). The United States and China have produced the greatest number of publications in this field, indicating their leading roles and the presence of well-established research programs focused on plant *R* genes. Temporal clustering of the collaboration map shows that the United States, Japan, and several European countries (e.g., Netherlands, Switzerland, and France) were among the earliest and most prolific contributors (white cluster). Countries such as Romania, Germany, South Korea, and Thailand joined the collaborative network at a later stage (yellow cluster), reflecting their growing engagement during the middle phase of this research area. More recently, China, Pakistan,



We subsequently analyzed the temporal evolution and institutional distribution of research on plant *R* genes (Fig. 6). Temporal patterns indicated by color coding distinguish the contributions of different institutions. Organizations involved in earlier stages of research are associated primarily with the blue cluster, which includes prominent institutions such as INRA (France), Max Plant Institute for Plant Breeding Research (Germany), and Wageningen University (Netherlands). In contrast, nearly all institutes from China clustered together at the right

Among the most prolific institutions, the United States Department of Agriculture (USDA) ranks number 1 in terms of 619 publications, followed by the Chinese Academy of Agricultural Sciences with 367 publications (Additional file 1: Table S2). However, the Chinese Academy of Sciences distinguishes itself by achieving a markedly higher total citation score, suggesting that its contributions are not only quantitatively significant but also of particularly high scientific impact. Notably, of the top 9 institutions by publication output, four are based in the United States, four in China, and one in France (Additional file 1: Table S2). This distribution highlights the predominant role of these countries, especially China and the United States, in shaping the global research agenda on plant *R* genes.

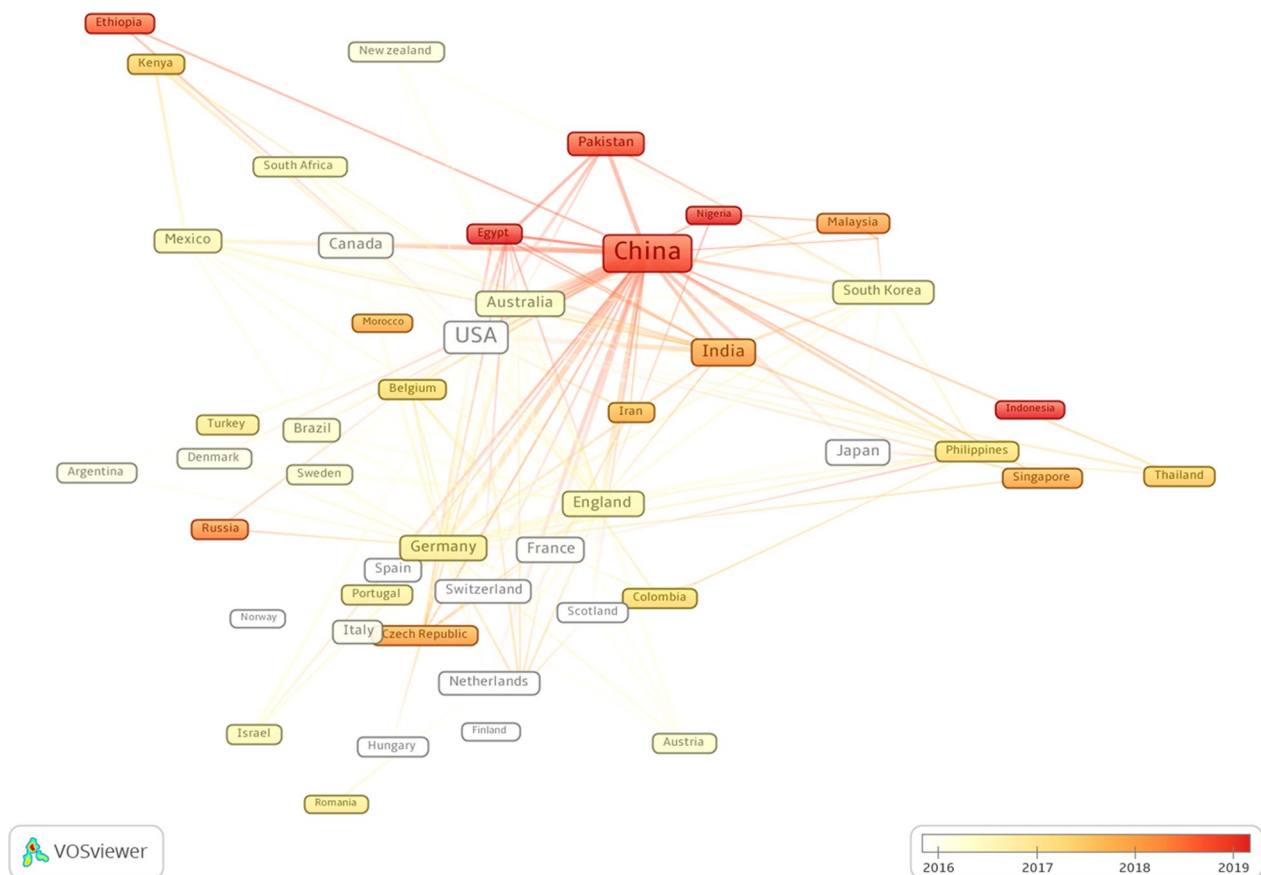


Fig. 5 Time-indexed collaborative map of countries indexed by year. The color of the scale bar indicates the collaboration occurrence early (white) to recent (red). Frame size reflects the number of publications from that country. Lines show the 200 strongest co-occurrence links

Key authors contributing to plant *R* gene research

To assess the contributions of scientists to research on plant *R* genes, we analyzed the authors with the top 10 citations from these screened publications (Table 1). The data reveal that Jonathan Jones leads the list, with a total of 5627 citations from 59 publications, indicating both high productivity and sustained influence in this research field. Sophien Kamoun, Jeffery Dangl, and Jane Parker have similarly high citations of approximately 4600, with substantial publications. Notably, Jian-Min Zhou, despite having only 21 publications, amassed 3501 citations, showing the highest average number of citations per publication. Additionally, the contributions of Yuelin Zhang, Richard Visser, Jijie Chai, and Ravi Singh are notable, with these four authors collectively accounting for a total of 11,725 citations. This analysis highlights the diverse citation profiles among leading authors in plant *R* gene studies, reflecting varying balances between research productivity and per-publication impact.

Journals associated with publications related to plant *R* genes

A total of 207 different journals are engaged in these publications, highlighting the interdisciplinary nature of the research and its relevance to various scientific communities. This widespread publication pattern also highlights the importance of plant *R* genes in multiple fields, including plant biology, genetics, and agricultural sciences. The significance of this topic is evident in its contributions to leading journals, such as *Nature* and *Science*. We analyzed publication volume across the top 8 journals, ranked by the number of publications (Fig. 7). Among the top 8 journals, both *Nature* and *Science* journals published 14 and 26 papers during this period, respectively, reflecting the broad scientific significance and visibility of plant *R* gene research. The *Plant Cell*, *Plant Science*, and the *Journal of Integrative Plant Biology* were the three leading journals publishing the largest number of articles between 2007 and 2024. Additionally, *Nature Plants* and *Plant Communications* also published a substantial number of articles, highlighting their sustained dedication to advancing this research area.

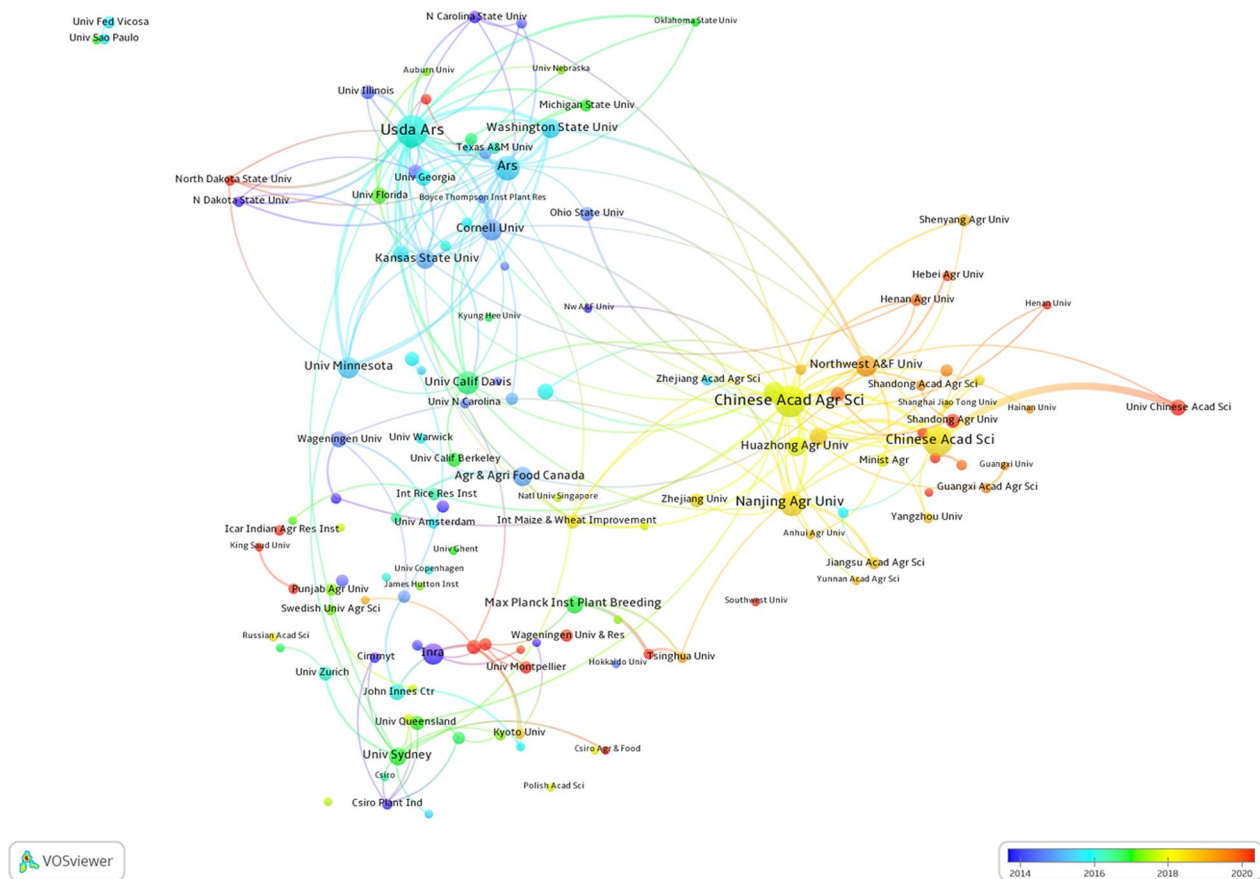


Fig. 6 Collaborative clustering map of the organizations indexed by time. The scale represents the earlier (blue) or more recent (red) year when the authors of each organization published their papers. Each node's size corresponds to the publication output of the respective organization. The connecting lines indicate the 200 strongest co-occurrence links between organizations

Table 1 The authors with the top 10 citations from publications in plant *R* gene research

Name of author	Number of total citations	Number of documents	Citation number per document
Jonathan Jones	5627	59	95
Sophien Kamoun	4627	65	71
Jeffery Dangl	4577	40	114
Jane Parker	4450	54	82
Xin Li	3526	84	42
Jian-Min Zhou	3501	21	167
Yuelin Zhang	3149	33	95
Richard Visser	2977	44	68
Jijie Chai	2943	29	101
Ravi Singh	2656	53	50

Among the leading journals, the top 20 most-cited articles underscored the importance of these influential studies on plant *R* genes. These articles have received a

total of 9692 citations. This significant citation count highlights their substantial impact on the field. The distribution of these top articles further illustrates their prominence: five and four articles are published in *Science* and *Nature*, respectively; nine are published in the *Plant Cell*, one in the *Plant Biotechnology Journal* or *Nature Plant*. This distribution not only reflects the high level of research in these prominent journals but also emphasizes the considerable impact and relevance of the research conducted in this area.

Discussion

In this research, we summarized the plant *R* genes identified and cloned from 2018 to the present, providing the latest research progress in the identification of plant *R* genes. Moreover, we conducted bibliometric analyses of publications on plant *R* genes from multiple aspects, including keywords, contributions of countries, organizations, and authors, and journals and most-cited articles. Bibliometric analyses present a global view of the dynamic changes in plant *R* gene research and the

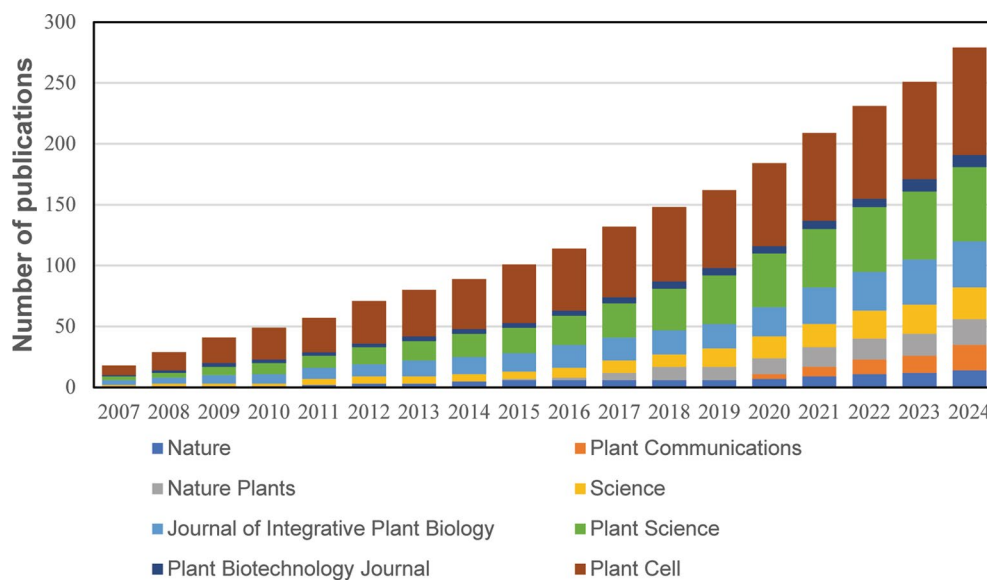


Fig. 7 High-impact journals with their respective numbers of publications on plant *R* gene research from 2007 to 2024

academic connections among countries, organizations, and authors. This study provides valuable insights into research trends, collaboration, and high-impact areas, serving as a resource for advancing plant resistance strategies to ensure global food security.

Over the past thirty years, there has been significant progress in the analysis and discovery of plant *R* genes. The comprehensive analysis of plant *R* genes has revealed a number of plant *R* genes discovered since 2018. The advent of advanced genomic technologies and bioinformatics tools in the 2010s led to a rapid increase in gene discoveries (Da Silva et al. 2019; Joshi et al. 2023) as well as the impact of new technologies such as CRISPR/Cas genome editing and high-throughput sequencing. These advancements have resulted in a surge of reports on cloned genes and enhanced methods for creating lasting resistance in crops (Fernandez-Gutierrez and Gutierrez-Gonzalez 2021; Joshi et al. 2023; Kumar and Nikhil 2023).

A total of 101 plant *R* genes have been identified and cloned from various plants in the past eight years (Fig. 1). Approximately 66% of the plant *R* genes target fungal pathogens. This finding is consistent with the economic importance of fungal diseases. Relatively few *R* genes have been discovered for oomycetes, protists, nematodes, and insects. These findings may reflect several factors, including research priorities, the varying complexities in identifying effective resistance against different pathogens, and the accessibility of pathogen targets in the research process. This suggests that there may be untapped opportunities for researchers to expand their

efforts into these less-explored areas, potentially leading to breakthroughs in crop protection strategies.

The observed distribution of identified and cloned plant *R* genes in plant species reflects both strategic research priorities and the practical demands of global agriculture. The predominance of rice (18%) and wheat (30%) among the collected *R* genes underscores the central role of these staple crops in food security and the considerable investment in improving their resistance to pathogens (Kourelis and van Der Hoorn 2018). Cloning efforts have focused on economically important fungal diseases, such as rice blast and wheat powdery mildew (Moytri et al. 2012; Kumar and Nikhil 2023). The significant representation of pepper (3%), barley (3%), and cabbage (3%) further illustrates a tendency to focus on crops of high economic importance and those with established genomic resources. This skew in *R* gene discovery suggests both a knowledge gap and an opportunity: diversifying *R* gene research to include underexplored crops could yield novel *R* gene variants and expand the genetic toolkit for disease resistance. Furthermore, as climate change and pathogen evolution continue to threaten diverse cropping systems, broadening the phylogenetic scope of *R* gene studies will be essential for future agricultural protection.

Overall, publications in the field of plant *R* genes are increasing, objectively indicating good development momentum in this field. China and the United States have relatively greater numbers of publications; however, China has caught up in more recent publications. In recent years, China has achieved considerable

advancements in understanding plant innate immunity and identifying *R* genes, acknowledging their crucial role in sustainable agriculture (Deng et al. 2021). Among the top 15 countries with a high number of publications, developing countries have the least number of publications and few collaborations with developed countries. However, many developing countries still lack sufficient collaboration in this area, as they face challenges in terms of policy, public awareness, and investment environments that hinder technology diffusion and innovation (Spielman et al. 2007). Strengthening partnerships with China and these developed nations could enhance the research and application of plant *R* genes.

In the field of plant *R* gene research, highly cited articles published in top-tier journals play a crucial role in shaping the research agenda and accelerating advancements. These articles are often visionary, providing insights that set the direction for future studies and applications. A prime example is *The Plant Cell* journal, which has emerged as a leading platform for communication among plant *R* gene researchers. Among the top 20 most cited articles in plant *R* gene research, nearly half have been published in *The Plant Cell* (Additional file 1: Table S3). This statistic underscores this journal's critical influence in driving the field forward. Moreover, the leading journals *Nature* and *Science* contributed substantially in the field. The high-quality research published in these leading journals not only provides essential references for researchers but also helps guide future studies, foster academic exchange, and promote collaboration, thereby facilitating the continuous development of plant *R* gene research.

Despite its relatively late start compared with several other countries/regions, China has made remarkable strides in the field of plant *R* gene research, demonstrating a strong commitment to advancing this field of science (Ming et al. 2014). Several research institutions in China have emerged as highly competitive and significant, such as the Chinese Academy of Sciences and the Chinese Academy of Agricultural Sciences, both of which have established strong collaborations with domestic and foreign institutions (Fig. 6). Chinese researchers have achieved significant breakthroughs in this field, such as the resolution of the resistosomes ZAR1 and ROQ1 structures (Wang et al. 2019; Ma et al. 2022). Undoubtedly, the collective efforts of key projects, specialized laboratories, and university partnerships have played a pivotal role in bolstering innovative research capacity in this field.

Despite remarkable progress in the study of plant *R* genes, significant challenges remain and call for broader exploration. Future research should extend beyond classical NLR-mediated mechanisms to include novel

resistance pathways such as non-host resistance and unconventional immune modules. High-resolution structural studies and comparative genomics will continue to uncover the molecular basis of resistosome assembly, effector recognition, and host–pathogen co-evolution, providing valuable templates for rational engineering. Equally important is a deeper understanding of sensor-helper NLR networks, which underpin immune robustness and redundancy. Artificial intelligence, particularly machine learning, will accelerate discovery by predicting NLR-effector interactions, simulating evolutionary dynamics, and guiding the design of broad-spectrum and durable *R* genes. From an applied perspective, integrating genome-wide association studies (GWAS) with precision genome editing technologies such as CRISPR will enable multi-gene pyramiding strategies to improve resistance durability while reducing the risk of pathogen adaptation. Field-level validation under diverse environments, coupled with the integration of NLR-mediated immunity with other defense layers such as PRR signaling and hormonal pathways, will be essential to translate these advances into resilient agricultural systems.

In the context of escalating global trade tensions and the rise of technological protectionism, plant *R* gene research, a strategic frontier closely tied to agricultural security, food sovereignty, and biological resource governance—must be pursued with greater strategic foresight and prudence. While strengthening intellectual property rights and achieving key technological breakthroughs, it is equally important to focus on the local discovery and conservation of genetic resources. Meanwhile, selective and strategic engagement in international scientific collaboration is necessary. A balanced approach that integrates open cooperation with protective safeguards will help achieve mutual benefit, drive scientific innovation, and support broader societal advancement.

Although this study presents a comprehensive summary of cloned and identified plant resistance genes reported to date, we acknowledge that newly reported genes or unindexed publications may not have been captured. In addition, the bibliometric analysis is based solely on records from the Web of Science Core Collection, which may not reflect all global research outputs.

Methods

Database search

On January 11, 2025, a search was conducted in the Web of Science (WoS) core collection database to retrieve bibliographic records related to plant *R* gene research from 2007 to 2024. To pinpoint relevant publications on plant *R* genes, the following keyword logic was employed in a combined search of the title, abstract, and keyword fields (per publication): (TS=(Plant*)) AND TS=(“resistance

gene*” OR “R gene*” OR “*NB-LRR*” OR “NLR*” OR “TNL*” OR “CNL*”) NOT TS=(“antibiotic resistance gene*” OR “arg”). The records were manually cleaned to exclude unrelated publications used for bibliometric analyses. The publications published from 2018 to 2024 were then analyzed to summarize newly discovered *R* genes within this period. We counted plant *R* genes following a previously described method (Kourelis and van Der Hoorn 2018). The Excel files containing the *R* genes are provided in Additional file 1: Table S1. The plain text files containing the publication records are attached in Additional file 2.

Bibliometric mapping and clustering

The retrieved publications from 2007 to 2024 were used to create bibliometric maps via the VOSviewer software version 1.6.20 (van Eck and Waltman 2010), which is freely available at www.vosviewer.com. The software was specifically designed to build, visualize, and investigate bibliometric maps in the scientific domain (Van Eck and Waltman 2010). The term maps were generated using VOSviewer. A term map, alternatively known as a co-word map, offers a two-dimensional visualization of a research domain. In this representation, terms with stronger associations are positioned closer together, whereas those with weaker connections are spaced farther apart. Consequently, term maps serve as valuable overviews for discerning the underlying structure of a research topic. Only terms occurring a minimum of 30 times were selected from the retrieved publications. To display the elements on the maps, the software employs the VOS (visualization of similarities) mapping technique, which is closely associated with the multidimensional scaling method. The method can be further explained in the previous publications (van Eck and Waltman 2010; Nardi et al. 2016). Additionally, we conducted term density visualization of the keywords, following a previously described method (van Eck and Waltman 2010). In brief, in the item density visualization, items are displayed with their labels, much like in the network, and overlay visualizations are presented. Each point's color here shows the item density at that spot. The color typically ranges from blue to green to yellow. Points with more neighboring items and higher-weight neighbors appear more yellow. Conversely, those with fewer or lower-weight neighbors appear more blue.

We also generated a collaborative clustering map indexed by time on countries and organizations related to plant *R* gene research. In the collaborative clustering map, the size of the frame or circle represents the number of publications, and the color indicates the time. For the collaboration of countries, we used a color scale ranging from white (terms predominantly appearing from 2016 or earlier), yellow (2017–2018) to red (2019 or later). Thus, white terms were mainly found in older collaborations, whereas red terms

were predominantly present in more recent collaborations. The same approach was used for organization collaborations.

Before commencing the analysis in VOSviewer, a thesaurus file (Additional file 3) was generated to ensure consistency in handling different spellings and synonyms of the same term, and to exclude irrelevant terms.

Importantly, while a term map offers a simplified representation of reality, it may result in information loss and partial representation of the investigated field (van Raan 2014). It is important to take this limitation into account when interpreting the results.

In addition, we evaluated the number of publications in prominent journals and identified the top twenty most-cited documents published in these journals. The data were collected from the WoS core collection, which allows the selection of top journals, as we refined the data to focus on these top journals. The Web of Science database also provides an option to sort publications by citation count. Therefore, we organized the documents according to their citation numbers to determine the top twenty most-cited documents.

Abbreviations

CC	Coiled-coil
CNL	CC-NB-LRR
CRISPR	Clustered regularly interspaced short palindromic repeats
ETI	Effector-triggered immunity
GWAS	Genome-wide association studies
HR	Hypersensitive response
ID	Integrated domain
LRR	Leucine-rich repeat
MAPK	Mitogen-activated protein kinase
NB	Nucleotide-binding
NLR	Nucleotide-binding leucine-rich repeat
PAMP	Pathogen-associated molecular pattern
PRR	Pattern recognition receptor
PTI	PAMP-triggered immunity
R	Resistance
RLK	Receptor-like kinase
RLP	Receptor-like protein
TIR	Toll/Interleukin-1 receptor
TNL	TIR-NB-LRR
USDA	United states department of agriculture
VOS	Visualization of similarities
WoS	Web of science

Supplementary Information

The online version contains supplementary material available at <https://doi.org/10.1186/s42483-025-00399-1>.

Additional file 1: Table S1. Summary of plant disease resistance genes: cloning, identification, and mapping status (2018–2024). **Table S2.** The top 9 organizations ranked by the number of articles on plant *R* genes. **Table S3.** High-impact articles and their distribution in plant *R* gene research.

Additional file 2: The plain text files containing the publication records.

Additional file 3: Ten source files containing the topic information of publications on plant resistance genes.

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Author contributions

JK performed methodology, data analysis, and original writing, ZD conducted conceptualization and revision.

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Data availability

All relevant data are within the manuscript and its additional files.

Declarations

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

The authors declare no competing interests.

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