

SHORT COMMUNICATION

## Research trend of bacterial leaf blight on rice in the millennium era: a bibliometric and scientometric approach for capture future insight

Syahri<sup>1</sup> & Renny Utami Somantri<sup>2</sup>

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### ABSTRACT

In the 21<sup>st</sup> century, population growth affects food demand, especially rice. *Xanthomonas oryzae* pv. *oryzae* causes bacterial leaf blight (BLB) disease, the worldwide rice production problem. As pathogen pathotypes vary, research into disease control advances rapidly. Thus, these trends must be mapped to inform future studies. This study aims to examine previous research using bibliometric and scientometric methods to inform future research. Scopus publication data was analyzed utilizing VOSviewer and CiteSpace. Research progress, popular research, productive countries, productive researchers, essential keywords, and global collaboration were explored. Analysis of recent research data predicts future trends. The findings indicate that 21<sup>st</sup>-century BLB research is advancing at an astounding rate and significantly surpasses that of previous periods, with 596 articles (91.69%) published during this era. Agricultural and Biological Sciences is the leading focus due to its substantial emphasis on genetics-related issues. A statistical analysis of the most prolific countries over the past two decades reveals that the United States, China, and India produce the highest number of articles. China and India are the two largest rice producers, respectively. Nevertheless, the most productive authors reveal that Szurek B (a French scientist) ranks first with a staggering twenty articles. Three main research clusters were found that consisted of “antibacterial agents vs. bacterial disease,” “plant resistance and immunity mechanisms,” and “pathogen virulence and pathogenicity genes.” The study about resistance genes against disease became the most cited article. We concluded that there are several future insights, including “further investigation into the alternative antibacterial agent and their formulation,” “spatial distribution, severity, and prevalence of BLB in multiple conditions,” “the microbial community on plant leaves,” and “additional research to comprehend the mechanism of the microbial community in the rice rhizosphere.” In addition, research on the stability of plant resistance genes to anticipate changes in pathogen pathotypes will be an alternative topic.

**Key words:** CiteSpace, microbial formulation, rice production, VOSviewer, *Xanthomonas oryzae* pv. *oryzae*

### INTRODUCTION

Rice stands as an essential food crop, serving as the staple food for over half of the world's population (Kong et al., 2020; Yang et al., 2021). Despite utilizing only 11% of the world's cropland, it contributes to 21% of global calorie consumption (Syahri & Somantri, 2023). With a projected 35% increase in the global population by 2050, there is a pressing need for a 70–100% rise in food production and consumption, considering expected dietary trends and economic growth (van Wart et al., 2013). According to Statista data, the world population consumed approximately

504.3 million metric tons of rice in the cropping year 2020/2021, a notable increase from 437.18 million metric tons in 2008/2009 (Cuaton & Delina, 2022).

Numerous factors pose threats to rice production, among which is disease infection, exemplified by bacterial leaf blight (BLB). BLB, a deadly bacterial disease of rice, is caused by the Gram-negative Proteobacterium *Xanthomonas oryzae* pv. *oryzae* (Sanya et al., 2022), which can manifest during various rice growth stages, with a pronounced impact observed during tillering (Sawatphanit et al., 2022). BLB has emerged as a significant challenge to rice yields in Asia, leading to substantial losses, including 50% in Malaysia, 20–80% in Indonesia, 20–40% in Bangladesh, 30–50% in the Philippines, 50–80% in Mali, 30–50% in China, and approximately 20–80% in India (Amin et al., 2023).

Research on bacterial leaf blight has advanced significantly since its initial description in Japan in 1884–1885. Disease control strategies aimed at limiting BLB damage have also evolved, beginning with the management of cultivation techniques and progressing

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Corresponding author:  
Syahri (syah026@brin.go.id)

<sup>1</sup>Research Center for Food Crops, National Research and Innovation Agency (BRIN), Cibinong Science Center, Bogor, Indonesia 16911

<sup>2</sup>Research Center for Agroindustry, National Research and Innovation Agency (BRIN), Cibinong Science Center, Bogor, Indonesia 16911

to the improvement of plant resistance. Technological advancements in the 21<sup>st</sup> century have further propelled BLB research forward. However, there is currently no comprehensive global dataset summarizing the studies conducted and how they have evolved since the turn of the millennium. Accurate literature evaluation is essential to map the focus of BLB research, understand its impact on BLB infections, and identify research gaps that need to be addressed to advance BLB research further.

This study compares BLB research before and after the 21<sup>st</sup> century to formulate future insights. The advancement of this research will have repercussions for the global development of the disease and its impact on production during that period. The research emphasis of each period can guide the formulation of future research strategies to reduce the risk of BLB. In this paper, we discuss (1) the trend of publications in BLB research; (2) the most influential research areas and their popular topics; (3) the most productive authors, countries, and their collaborations; and (4) future insights in BLB research.

Our review was based on the Scopus database, and we utilized a combination of bibliometric and scientometric techniques for analysis and visualization. Quantitative tools like bibliometric analysis can reveal valuable insights into the growth and effect of research by studying publication output and citation trends (Xu et al., 2023). Similar methods have been applied to identify factors causing the rice yield gap (Syahri & Somantri, 2023), summarize *Actinomycetes*

research (Syahri & Somantri, 2022), explore drones in agriculture (Rejeb et al., 2022), introduce microbial technology for solid-state fermentation (Yafetto, 2022), visualize Agriculture 4.0 (Mühl & de Oliveira, 2022), and so on.

On the contrary, scientometrics pertains to the quantitative examination of scientific principles, policy, and discourse (Ghaleb et al., 2022). Scientometrics is crucial in offering a visual representation and depiction of a particular research domain. It can provide an overview of the diverse aspects of the literature within a specific field of study and identify influential authors, articles, and works (Wu et al., 2022). Consequently, this paper provides a future insight of BLB research and potential issues to complement current studies.

## MATERIALS AND METHODS

**Data processing and filtering.** The approach adopted followed the protocol outline by Cuaton & Delina (2022) and Syahri & Somantri (2022; 2023). The study focused on research related to BLB in the the 21<sup>st</sup> century. We utilized Preferred Reporting Items for Systematic reviews and Meta-Analyses (PRISMA) to retrieve articles because it is a well-established method for systematic reviews and meta-analyses (Page et al., 2021; Shamseer et al., 2015), as illustrated in Figure 1. We exclusively utilized the Scopus database (<https://scopus.com>) to minimize errors and simplify data integration and analysis using various software. Scopus provides the largest peer-reviewed literature abstract

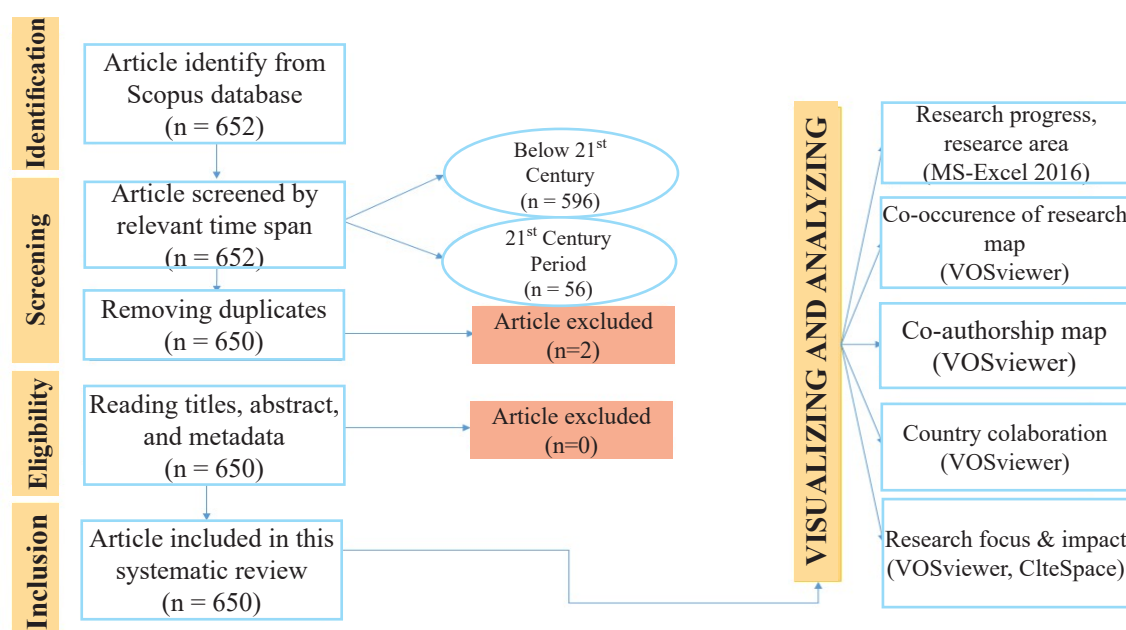


Figure 1. The PRISMA flow diagram for this systematic review. Our process resulted in 650 eligible documents (596 published in the 21<sup>st</sup> century and 54 published below the 21<sup>st</sup> century).



and citation database (Mühl & de Oliveira, 2022). Data from Scopus were retrieved using keywords to search article titles containing the terms: ((TITLE("rice") OR TITLE("paddy") AND TITLE("bacterial leaf blight") OR TITLE("*Xanthomonas oryzae*")))). Manuscript searches were conducted on 19 September 2023, at 01:00 p.m., with additional selection criteria including papers that did not match the research topic. After removing duplicate documents, we analyzed a total of 650 articles. The Systematic Review Accelerator, developed by Bond University and the Institute for Evidence-Based Healthcare, was used to screen and eliminate duplicate documents (Cleo et al., 2019).

### Analysis of the global development of research.

Data on the global evolution of research is extracted from the results of publications on Scopus. Scopus provides refined values in CSV format for this analysis. The data is then divided into two groups: data before the 21<sup>st</sup> century (1953–1999) and data after the 21<sup>st</sup> century (>2000). A bibliometric approach is employed to compare the data in these two groups. The analysis includes examining the number of articles produced throughout each period, identifying the most popular publications, determining the most productive authors and nations, and exploring the study fields associated with BLB publications. Furthermore, a correlation study is conducted to evaluate the relationship between the number of articles and citations published each year and changes in the number of publications produced. The top ten publications, authors, and countries are examined based on the highest number of papers published for each criterion. Additionally, the associated research area is determined based on the most significant coverage region in the Scopus database.

**Determine the global research focus.** BLB study topics from around the world are examined bibliometrically using VOSviewer version 1.6.19. RIS or CSV format databases from before and after the 21<sup>st</sup> century were individually read for co-occurrence, authorship, and country partnership. The main clusters in BLB studies are visualized in a VOSviewer map. The investigation was conducted using the co-occurrence method with full counting, employing a minimum keyword occurrence of 10. A thesaurus is utilized to enhance the precision of the analytic process. The linkages and impacts of each criterion are described to conclude the emphasis of BLB research worldwide.

For the scientometric mapping of keywords and determination of keyword citation bursts, especially in

the millennial era, we utilized Citespace 6.2.R4 (64-bit). The parameters set in Citespace software included time slicing from 1 January 2000 to 31 December 2023, with one slice per year. Link strength was determined using Cosine, with a k-factor set at 10. Pruning involved pruning the merged networks using pathfinder, along with other parameter settings set to default values. From this process, we summarized only the top 10 keywords with the most robust citation bursts.

**Future research trend.** Both bibliometric and scientometric studies have captured future trends in a paper published between 2022 and 2023. Unconnected and distant nodes represent the most recent research that can be conducted to enhance BLB publications.

## RESULTS AND DISCUSSION

**Rice production and their impact on research trends in the 21<sup>st</sup> century.** According to Food and Agriculture Organization (FAO) data, rice production is increasing, particularly in Asia (Figure 2). Meanwhile, the increase in rice production in Europe and the United States has been insignificant. In most regions of Asia, the rise in rice production is accompanied by increased rice demand and consumption. Compared to the period preceding the 21<sup>st</sup> century, rice production in most regions has increased dramatically. For instance, In Indonesia, rice production was below 50 million tonnes before 2000 but increased to 60 million tonnes afterward. BLB disease, estimated to cause yield losses of up to 80%, remains one of the most significant obstacles to increasing rice production. Therefore, it is essential that BLB-related research remains a priority to ensure that rice production continues to grow in tandem with rising human requirements.

The analysis results of the number of BLB-related studies, indicated by the number of published scientific articles, show a significant increase. Compared to the previous century, BLB-related research in the 21<sup>st</sup> century is advancing rapidly. Figure 3 depicts the evolution of the study during this period. The majority of the 650 publications, dating back to 1996, approximately 596 or 91.69%, have been produced within the last 20 years. This finding indicates that research on bacterial leaf blight as progressed rapidly. The increased demand for food, especially rice, and the damage caused by BLB disease have also contributed to this extensive development. This increase in the number of publications is unmistakable evidence of the determination of researchers worldwide to find

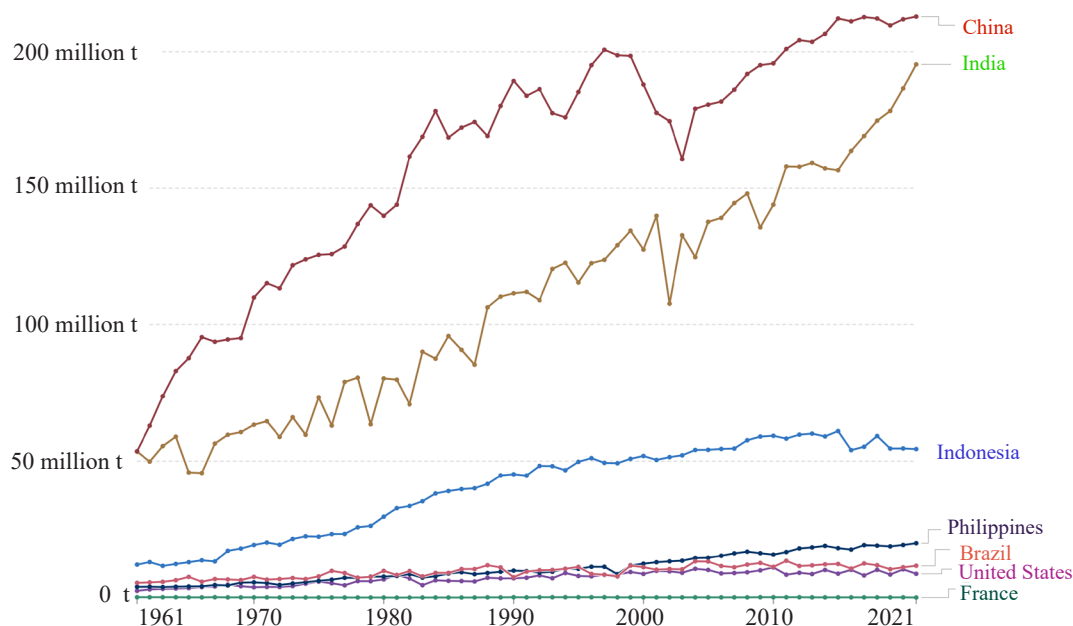


Figure 2. Rice production trend worldwide (Source: UN Food and Agriculture Organization, 2023).

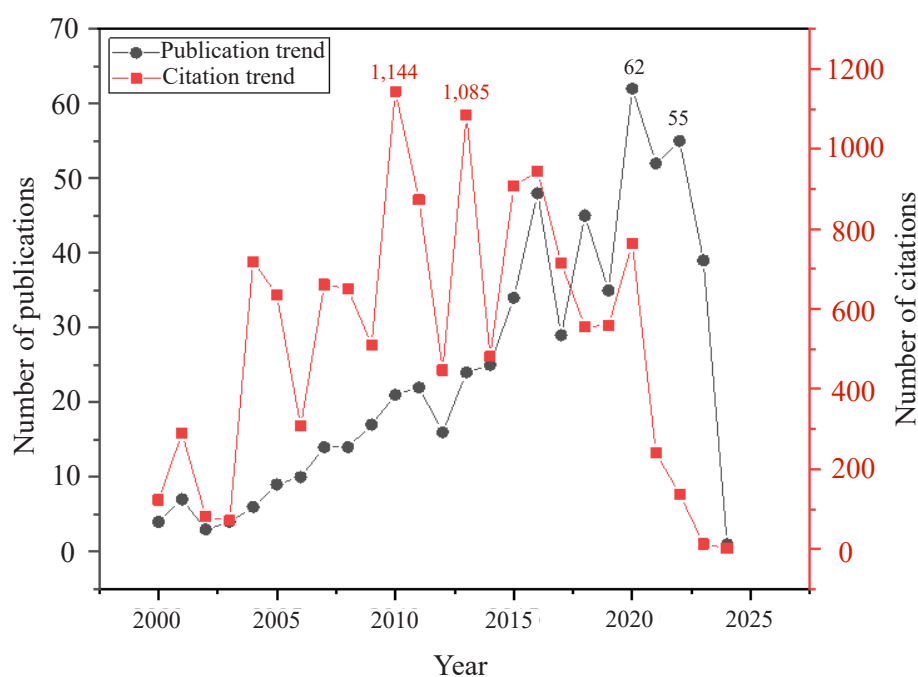


Figure 3. Development number of publications and citations of bacterial leaf blight research from 2000 to 2024.

ways to control BLB so that it has no significant effect on rice production.

According to Figure 3, research on BLB was infrequent until 2005 (ten publications) but steadily increased until reaching its apex in 2020 (62 publications). However, the annual average number of citations for publications varies. In 2010, there was the highest overall citation count, with 1,144 citations from 24 journals published that year. Conversely, in 2004, there were the most citations per publication,

with an average of 119 citations from only six Scopus publications. According to an analysis of Scopus data, Sun et al. (2004) were the most cited authors in BLB research in 2004, with 416 citations to their work. They asserted that the genetic background influences the resistance conferred by Xa26 and found that transgenic plants carrying Xa26 showed enhanced resistance compared to the donor plant. Similarly, in 2010, one of the articles published that year was among the ten most-cited publications (Table 1).

Table 1. The top ten BLB articles with the most citations

Title	Authors	NC	Source Title/Type	Q	HI	Research Insight
Xa26, a gene conferring resistance to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> in rice, encodes an LRR receptor kinase-like protein	2004 Sun et al. (2004)	416	Plant Journal/OA	Q1	300	The genetic background influences the resistance conferred by Xa26.
The genome sequence of <i>Xanthomonas oryzae</i> pathovar <i>oryzae</i> KACC10331, the bacterial blight pathogen of rice	2005 Lee et al. (2005)	352	Nucleic Acids Research/OA	Q1	607	Eight <i>Xanthomonas</i> avirulence (avr) genes, hypersensitive reaction and pathogenicity (hrp) genes, exopolysaccharide genes, and extracellular plant cell wall-degrading enzyme genes are perhaps involved in pathogenesis. These genes reveal this pathogen's interactions with its gramineous host.
Genome sequence and rapid evolution of the rice pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> PXO99A	2008 Salzberg et al. (2008)	290	BMC Genomics/OA	Q1	189	We found genome flexibility and fast evolution in Xoo. The findings suggest chromosomal variation and strain-specific adaptations can explain the enormous range of Xoo genotypes and races isolated worldwide.
Five phylogenetically close rice SWEET genes confer TAL effector-mediated susceptibility to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i>	2013 Streubel et al. (2013)	264	New Phytologist/OA	Q1	285	Five phylogenetically related SWEET proteins, likely sucrose transporters, support Xoo pathogenicity.
OsWRKY62 is a negative regulator of basal and Xa21-mediated defense against <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> in rice	2008 Peng et al. (2008)	216	Molecular Plant/OA	Q1	146	WRKY transcription factor OsWRKY62 binds XA21. OsWRKY62 negatively regulates innate immunity and mediates basal and race-specific defensive responses in rice.
The bacterial pathogen <i>Xanthomonas oryzae</i> overcomes rice defenses by regulating host copper redistribution	2010 Yuan et al. (2010)	191	Plant Cell/OA	Q1	380	Susceptibility gene XA13 works with COPT1 and COPT5 to remove copper from xylem vessels. Copper is a vital plant micronutrient that inhibits Xoo development. Xoo strain PXO99 activates XA13, COPT1, and COPT5, which regulate rice copper redistribution, making it more copper-sensitive than other strains. The role of XA13 in copper redistribution suggests a bacterial pathogenicity mechanism.
A paralog of the MtN3/saliva family recessively confers race-specific resistance to <i>Xanthomonas oryzae</i> in rice	2011 Liu et al. (2011)	184	Plant, Cell and Environment/OA	Q1	225	We characterize the Xoo resistance recessive gene xa25 here. Transforming the dominant Xa25 into a resistant rice line with the recessive Xa25 eliminated Xoo PXO339 resistance. PXO339 rapidly produced dominant Xa25 but not recessive or other Xoo strain infections. Compared to its susceptible allele in rice-Xoo interaction, the xa25-encoding protein and its expression pattern suggest that xa25-mediated resistance differs from most R proteins.
Antimicrobial activity and induction of systemic resistance in rice by leaf extract of <i>Datura metel</i> against <i>Rhizoctonia solani</i> and <i>Xanthomonas oryzae</i> pv. <i>oryzae</i>	2004 Kagale et al. (2004)	175	Physiological and Molecular Plant Pathology/Purchase	Q2	84	Rice plants treated with <i>D. metel</i> leaf extract showed a higher accumulation of pathogenesis-related (PR) proteins and other defense-related chemicals, indicating systemic resistance. The mass spectrometry matches daturin's published mass spectra, a <i>D. metel</i> withanolide molecule.
Difficidin and bacilysin from <i>Bacillus amyloliquefaciens</i> FZB42 have antibacterial activity against <i>Xanthomonas oryzae</i> rice pathogens	2015 Wu et al. (2015)	172	Scientific Reports/OA	Q1	282	Difficidin and bacilysin caused downregulated gene expression in <i>Xanthomonas</i> virulence, cell division, and protein and cell wall synthesis.
Two type III effector genes of <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> control the induction of the host genes OsTFIIAγ1 and OsTFX1 during bacterial blight of rice	2007 Sugio et al. (2007)	169	Proceedings of the National Academy of Sciences of the United States of America/OA	Q1	838	OsTFX1 and OsTFIIAγ1 were induced by type III effector genes pthXo6 and pthXo7, newly discovered transcription activator-like (TAL) effector family members.

NC= number of citation, Q= journal quartile, HI= h-index, OA=open access.

According to Table 1, most papers from the 21<sup>st</sup> century with the maximum number of citations were in the field of genetics research. Research focusing on plant resistance, susceptibility, and pathogen virulence genes have become prominent, resulting in numerous citations. Addressing the mitigation of damage caused by bacterial leaf blight is a crucial issue in this regard. Furthermore, 90% of the most cited articles were published in prestigious journals (Q1) or proceedings and had a high h-index. These results underscore the importance of a journal's reputation for researchers when citing articles. Another determining factor is the classification of the journal as open access, facilitating unrestricted accessibility for all individuals. The study findings indicate that up to 90% of the top 10 articles belong to the open-access journal category. Higher citation numbers for an article make it easier for search engines to locate it. Finally, the increase in rice production has led to higher researcher output, especially in BLB research and publications. Increased citations consequently enhance researchers' reputations.

**Most popular authors.** An examination of the number of scholars with the most publications over the last two decades reveals that only three countries dominate, notably France, the United States, and China. Szurek B (Scopus ID: 6506404936), a French researcher, leads the field in BLB papers (Figure 4). Meanwhile, Sonti RV (Scopus ID: 6701649749) and Verdier V (Scopus ID: 7004263804) are in second and third place. However, this top ten category is based solely

on the number of articles published by the primary author. This finding suggests that the author with the most publications may still be a member of the same research team with the same publications as the other authors in the top ten. As a result, co-authorship analysis was performed using VOSviewer to examine the authors' relationships. This study indicates that the five most popular researchers are not from main rice-producing nations. This finding suggests that BLB is a significant disease attracting the interest of European and American countries for further study. This is also based on rice being one of the significant agricultural commodities that affect the global economy. Rice is the primary food crop in developing countries (Jamal et al., 2023) and contributes to about 20% of daily calorie intake worldwide (Durand-Morat & Chavez, 2020). Asia accounts for approximately 90% of rice production and consumption worldwide (Mohanty et al., 2010). However, the demand for rice on a global scale is expected to rise due to the growing global population and the increasing per capita consumption in Sub-Saharan Africa, the Middle East, and South America (Jamal et al., 2023). According to Durand-Morat & Chavez (2020), total consumption in Africa increased by 1.16%, in America by around 0.90%, and in Europe by 0.87%. Meanwhile, the yearly drop in per-capita consumption of Asian rice is estimated to be 0.28%. This enhances comprehension of the geographical dynamics and the relative significance of each region's participation in the global rice economy. Ensuring the health and productivity of rice crops is necessary for worldwide food security. Additionally,

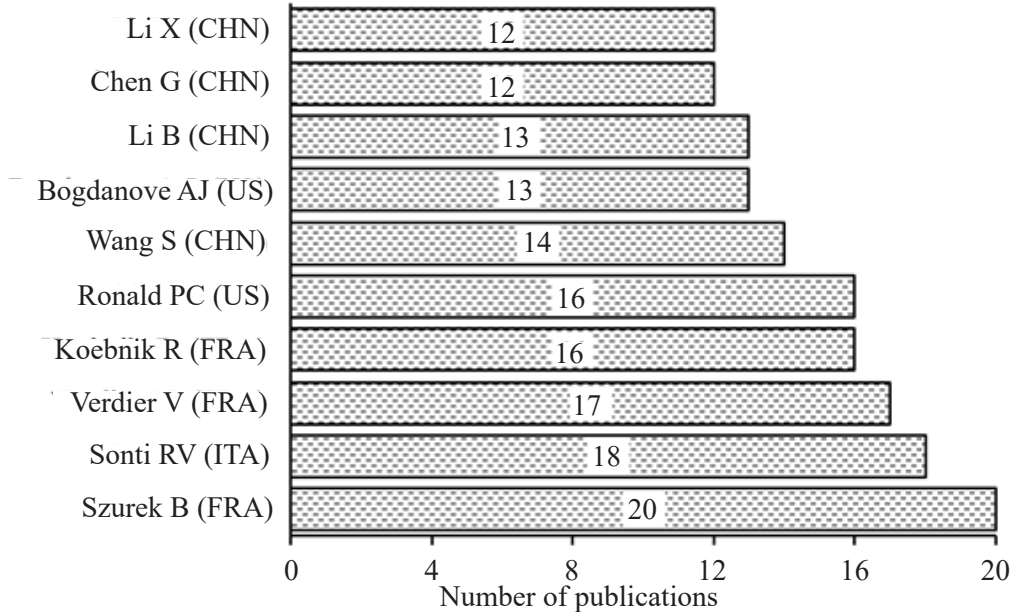


Figure 4. Top 10 most productive author and their nations.



occurrences of diseases such as BLB have the potential to destabilize global rice markets, impacting both prices and trading trends. Another rationale is that experts from nations that do not mainly produce rice can contribute to worldwide initiatives aimed at understanding and eliminating bacterial leaf blight. Collaborative research facilitates the establishment of a shared repository of knowledge and has the potential to result in the creation of more efficient approaches for disease control. This knowledge will be the foundation for developed countries to advance technological solutions to control BLB, such as developing resistant varieties and pesticides. Besides, global collaboration between researchers encourages them to conduct BLB-related research, even if this disease is not necessarily prevalent in their region. Therefore, the greater the number of established research collaborations, the greater the researcher's productivity.

The author cluster map is depicted in Figure 5. Chen G (Scopus ID: 34967917200) and Sonti RV (Scopus ID: 6701649749) appear unrelated to the other authors, as evidenced by the author clustering results. Szurek B and Koebnik R (Scopus ID: 6604067727) are in the same cluster (green) as Wang L et al. (Scopus ID: 57191616709) and are closely related. Similarly, Ronald PC (Scopus ID: 7005957829) and Li B (Scopus ID 57109502100) form distinct but interconnected groups. Bibliometric evidence also indicates that authors from the United States, China, and France

have contributed to BLB-related works. This contrasts with the Italian author (Sonti RV) who lacks connections with authors from these three countries. The similarity of their research topics and whether or not their respective research institutions collaborate are among the factors that influence the relationships between authors. Generally, the number of citations obtained will correlate positively with the number of published documents and author relationships. This is exemplified by Szurek, who has the most publications and can generate many citations. His collaborations with Salzberg et al. (2008) and Streubel et al. (2013) are among the ten most-cited papers. Similarly, Sonti RV also appears to have numerous citations. The results indicate that research on the Xoo resistance gene corresponds to Scopus publication topics.

**Most productive country.** According to a bibliometric study, Asian countries dominate BLB-related publications (Figure 6). Over half of the world's population consumes rice as a staple food, with Asia, Sub-Saharan Africa, and South America being the primary consumers. Therefore, it is logical that BLB research in Asia is accelerating. China has the most relevant publications, with 194 articles, followed by India (138) and the United States (87). This is far higher than the country that initially reported BLB, Japan. Farmers in the Fukuoka area of Japan first reported bacterial leaf blight disease in 1884 (Gnanamanickam

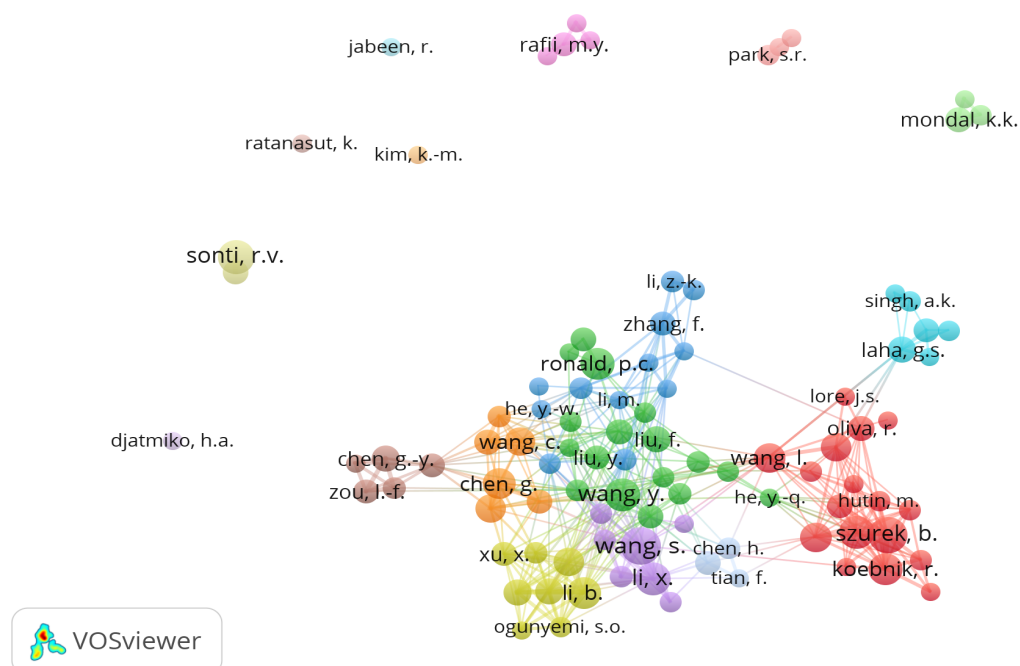


Figure 5. Author collaboration worldwide in BLB research (lines illustrate interconnection between author, same color of nodes describe same cluster).

et al., 1999).

France is the only country in the top ten from the European continent. Even Szurek B, a researcher from this country, is the world's most prolific BLB researcher. Szurek's research accounts for 62.5% of French publications. These findings demonstrate that the world's major rice-producing countries, such as China and India, continue to dominate BLB research and publishing. Meanwhile, other countries in the world's top ten rice producers, including Indonesia, Pakistan, and the Philippines, are highly productive in BLB research. This finding also suggests that BLB disease is a severe problem that the world's major rice-producing countries should be aware of. This condition has prompted other affluent countries, including France, the United States, South Korea, and Japan, to

begin studying it. The number of publications and rice yield produced by the top ten countries have a high positive correlation ( $r=0.93$ ). The study suggests that BLB is a significant disease that requires investigation, particularly in rice-producing countries worldwide. In addition, these results indicate that increasing rice production cannot be a part of the numerous studies conducted.

Figure 7 depicts the collaboration between authors from each country. Researchers require global network collaborations to strengthen their skills and address research gaps. We found seven interconnected country clusters, but four dominate in BLB research. Cluster #1 includes China, South Korea, Singapore, and Australia; Cluster #2 has India, the United States, and Brazil; Cluster #3 includes Indonesia and Taiwan;

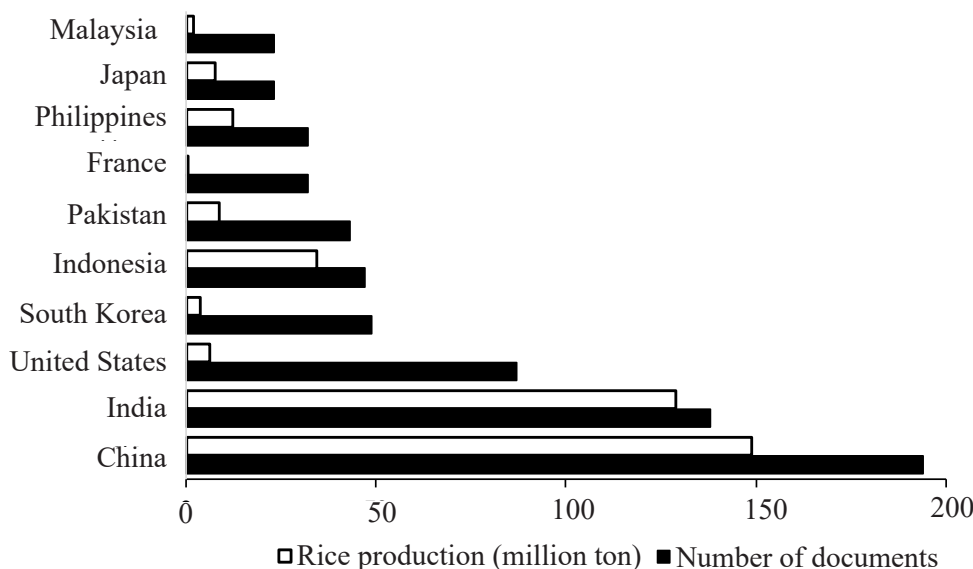


Figure 6. The most productive countries in BLB research and their rice production.

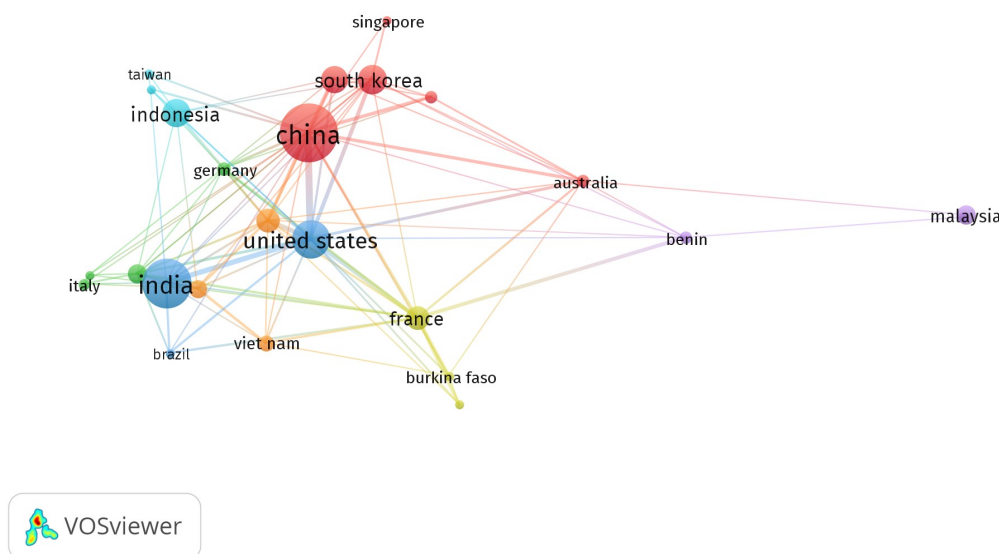


Figure 7. Global collaboration network (larger nodes indicate more articles, lines connecting nodes show country link research).

and Cluster #4 includes France and Burkina Faso. China, India, and the United States have numerous collaborations in BLB research. There are 19 documented linkages between Chinese scholars and other countries, making China a country with global connections (Asia, America, Africa, Europe, and Australia).

Meanwhile, Indonesia has only eight connections to countries in Asia, Europe, and America. Even within regions of Southeast Asia, Indonesia, Malaysia, or Singapore has no direct link. Meanwhile, France has demonstrated the ability to construct an extensive network (14 linkages) with fewer periodicals. The more extensive network formed among researchers will ensure the quality of the research and have the potential to be acknowledged by other researchers. As a result, it is logical that no Indonesian authors are among the top ten most productive authors.

**Popular research areas.** Figure 8 depicts ten of 21 significant study areas usually connected with BLB research worldwide. BLB research touches practically every existing scientific topic. Agricultural and Biological Sciences dominate BLB research subjects (42.14%). It is natural given that BLB is a rice pathogenic bacteria, and rice is the main diet for most of the world's population. Notably, Biochemistry, Genetics, and Molecular Biology are ranked second in research subjects, with a rate of 25.73%. This finding signifies that the study relating to this discipline is a well-researched topic. The main ones in this domain are control efforts that involve genetically enhancing

varieties or reducing disease virulence by changing their DNA. Meanwhile, various other low-category subjects, such as engineering, veterinary science, materials science, physics, astronomy, and so on, will become new issues for future BLB studies.

At the very least, research in this field will make it easier for researchers to innovate and boost prospects for collaboration among researchers with diverse expertise. The subject of computer science, which is gaining popularity in the 21<sup>st</sup> century, can inspire the identification of computerization-based BLBs. discussing this topic is due to article analysis in the 21<sup>st</sup> century. Razali et al. (2022) conducted research named “Development of an electrochemical immuno-sensor strip for early detection of rice bacterial leaf blight (BLB) disease and its application on a portable device.” However, no bibliometric or scientometric research on computer science has been covered. Therefore, research related to this topic has an excellent opportunity to complement research areas associated with BLB.

**Research comparison between before and after the 21<sup>st</sup> century.** Before the turn of the 21<sup>st</sup> century, the research foci of the world were still quite diverse and divided into four clusters (Figure 9), including: “Cluster I (●) Biological investigation of *X. oryzae* as the cause of BLB,” “Cluster II (●) Disease management,” “Cluster III (●) Influence of BLB on rice growth,” and “Cluster IV (●) Management of plant resistance.” Research on plant resistance and development was uncommon during this time. Its small size and remote location

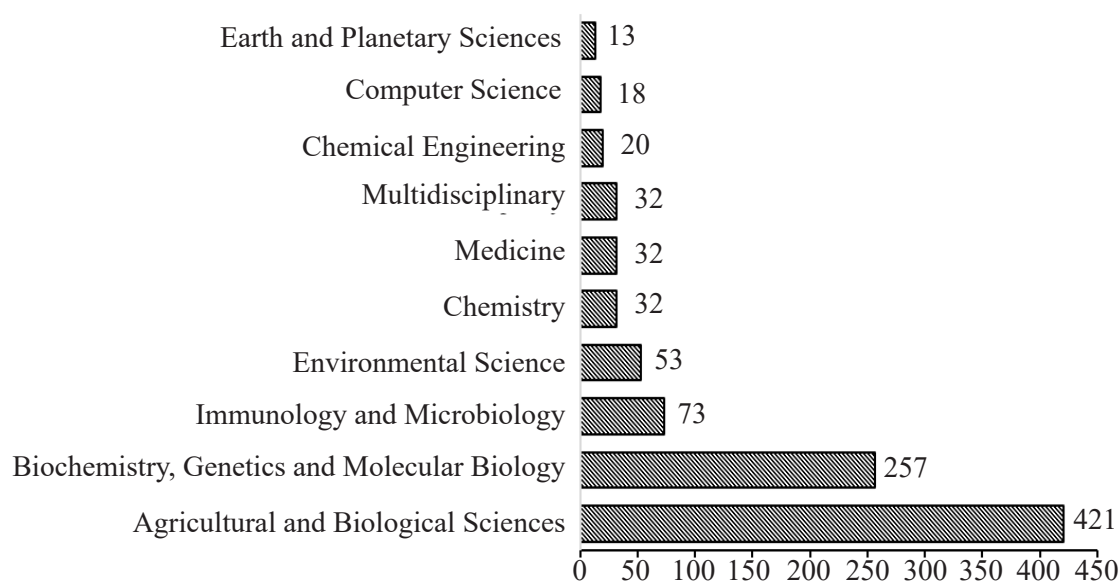


Figure 8. Ten most popular research fields of BLB study.

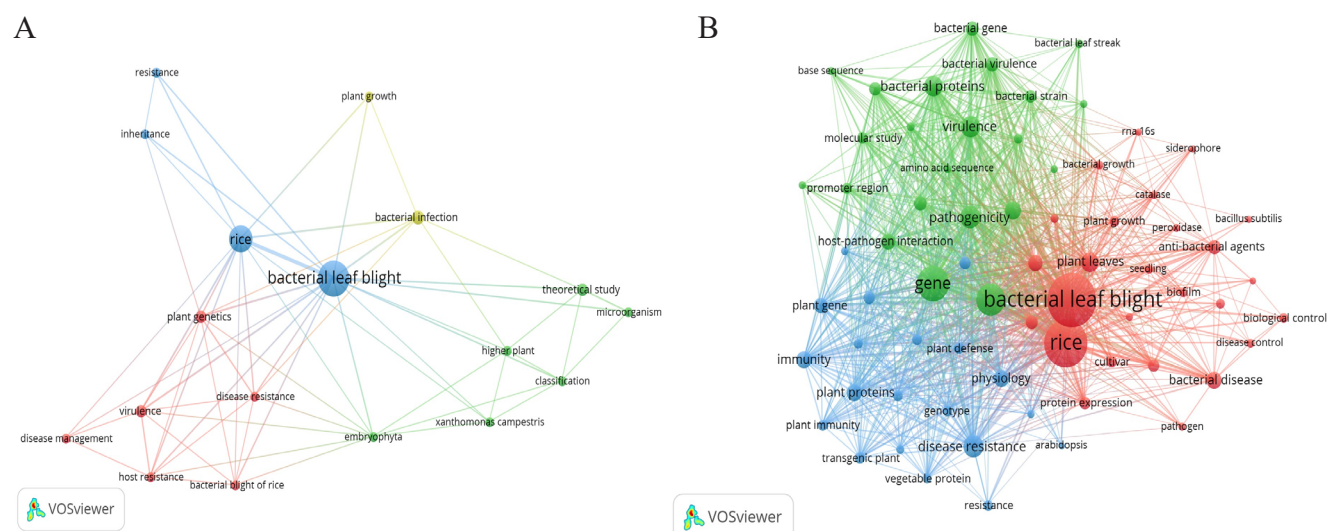


Figure 9. Comparison of BLB research maps. A. Before the 21<sup>st</sup> century; B. After the 21<sup>st</sup> century.

from the central node (BLB) confirm this conclusion. This finding is significant given that BLB is a novel rice-infecting pathogen. Consequently, investigation into the pathogen's bioecology and the implementation of early control measures are essential.

Research in the 21<sup>st</sup> century is more diverse and complex than before that period. Only three clusters were formed in this era. However, so many nodes are arranged in the cluster. Nearly 92% of BLB research was published during this time, making this reasonable. Cluster I (●) is associated with antibacterial agents vs bacterial disease, cluster II (●) is associated with plant resistance and immunity mechanisms, and cluster III (●) is associated with pathogen virulence and pathogenicity genes. Numerous connections between nodes demonstrate that the three clusters are extraordinarily well interconnected. Aside from this, science focused during this period on BLB control technology, whether through biological control, enhanced plant resilience, or efforts to disrupt the virulent genes of *Xoo*. In response to rising demand from population growth, rice production is anticipated to grow during this period.

The small size of the nodes indicates that the number of publications associated with the topic is still less, whereas the lines on the map depict the relationship between issues. The greater the number of lines connecting nodes, the greater the number of research connections relating to that subject. We can locate novel BLB-related topics using this map and these criteria. For instance, “the impact of siderophores on plant immunity,” as well as “the virulence and pathogenicity of BLB,” “the effect of genotype and plant immunity on the formation of bacterial biofilms,” “the impact of transgenic plants on bacterial disease,”

and other “antimicrobial agents.”

On the other hand, scientometric analysis identifies five dominant BLB research clusters in the 21<sup>st</sup> century (Figure 10). Similar to bibliometric study, “promoting virulence,” “specific virulence factor,” “comparative transcriptome profiling,” “novel insight (BLB disease),” and “silver nanoparticles” are the primary clusters. Scientometric analysis yielded a cluster map with a modularity (Q) of 0.3164 and a mean silhouette (S) of 0.6842. Modularity and mean silhouette values were used to evaluate clustering results' confidence. Q-values larger than 0.3 indicated significant clustering, S-values >0.5 suggested believable clustering, and S-values >0.7 indicated powerful clustering (Ye et al., 2023). Further examination of the top terms cited by researchers worldwide provides similar results (Table 2).

The results of identifying ten keywords with the most robust citation bursts are presented in Table 2. The burst analysis of BLB research reveals that in the period 2000 and 2023, the keywords “molecular sequence data,” “nucleotide sequence,” “genes,” and “plant protein” have gained significant attention. These keywords reflect the growing interest and importance attributed to their respective areas of study. Notably, “molecular sequence data” holds a strength value of 10.08, “nucleotide sequence” has a strength value of 9.66, and “genes” is at 5.71. However, these terms were popular in the early and middle periods. The keyword “plant protein,” with a strength value of 5.23, has become popular after 2015. These findings demonstrate that genetics research is the most important topic. The interesting insight from the analysis results is that “*Xanthomonas oryzae* pv. *oryzicola* (Xoc)” is one of the strongest citation burst keywords with a strength



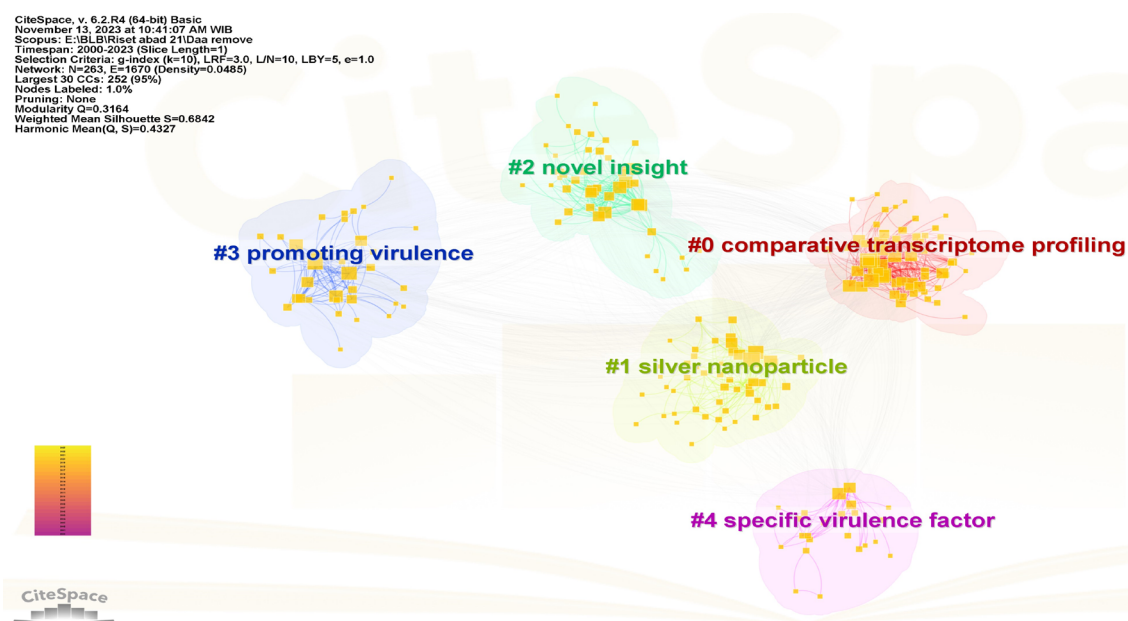


Figure 10. A scientometric map that visualizes the central cluster of BLB research in the 21<sup>st</sup> Century. The cluster numbers are designated in ascending order from zero, while the cluster names are denoted in color. A reduced number of clusters means an increased number of articles.

Table 2. Top ten keywords with the strongest citation bursts

Keywords	Year	Strength	Begin	End	2000 - 2023
bacteria (microorganisms)	2000	27.53	2000	2012	<div><div></div></div>
<i>Oryza sativa</i>	2001	22.56	2001	2014	<div><div></div></div>
<i>Oryza</i>	2015	10.80	2015	2023	<div><div></div></div>
molecular sequence data	2004	10.08	2004	2008	<div><div></div></div>
nucleotide sequence	2004	9.66	2004	2012	<div><div></div></div>
<i>Xanthomonas oryzae</i> pv. <i>oryzicola</i>	2004	5.95	2011	2014	<div><div></div></div>
genes	2001	5.71	2001	2011	<div><div></div></div>
growth	2015	5.55	2015	2021	<div><div></div></div>
plant leaves	2007	5.45	2013	2018	<div><div></div></div>
plant protein	2016	5.23	2016	2023	<div><div></div></div>

of 5.95. This finding is reasonable because Xoc often causes symptoms similar to those caused by Xoo. Moreover, African Xoo strains are more closely related to the Asian Xoc (Soto-Suárez et al., 2010).

Our scientometric study correlates systematic reviews with the articles with the most citations, demonstrating that approximately ninety percent are related to genetic research (as shown in Table 1). Keywords with the strongest citation bursts provide systematic and visual analysis of keyword-related citation bursts. This incisive analysis helps scientists understand their areas' focus points, rising patterns, and significant relevance (Xu et al., 2023). By studying these keywords' strength values, one can have a

comprehensive insight into their research prominence and influence, enabling deliberate selection of critical terms for subsequent study. An exhaustive assessment educates academics about the present research climate and guides them to areas of scholarly investigation with tremendous potential for growth and discovery.

**Research trends in the future.** The research requirements for BLB control can be determined by analyzing recent research published in Scopus. Scientometric analysis was conducted using CiteSpace and VOSviewer to assess their relationships. Figure 11 demonstrates that, of the total of nine clusters of BLB-related articles published, the terms “responsive

CiteSpace, v. 6.2.R4 (64-bit) Basic  
 November 14, 2023 at 9:13:52 AM WIB  
 Scopus: E:\BLB\Iriset abad 21\Daar remove  
 Timespan: 2022-2023 (Slice Length=1)  
 Selection Criteria: g-index (k=25), LRF=3.0, L/N=10, LB=5, e=1.0  
 Network: N=148, E=283 (Density=0.026)  
 Largest 30 CCs: 148 (100%)  
 Nodes Labeled: 1.0%  
 Pruning: Pathfinder  
 Modularity Q=0.777  
 Weighted Mean Silhouette S=0.8129  
 Harmonic Mean(Q, S)=0.7945

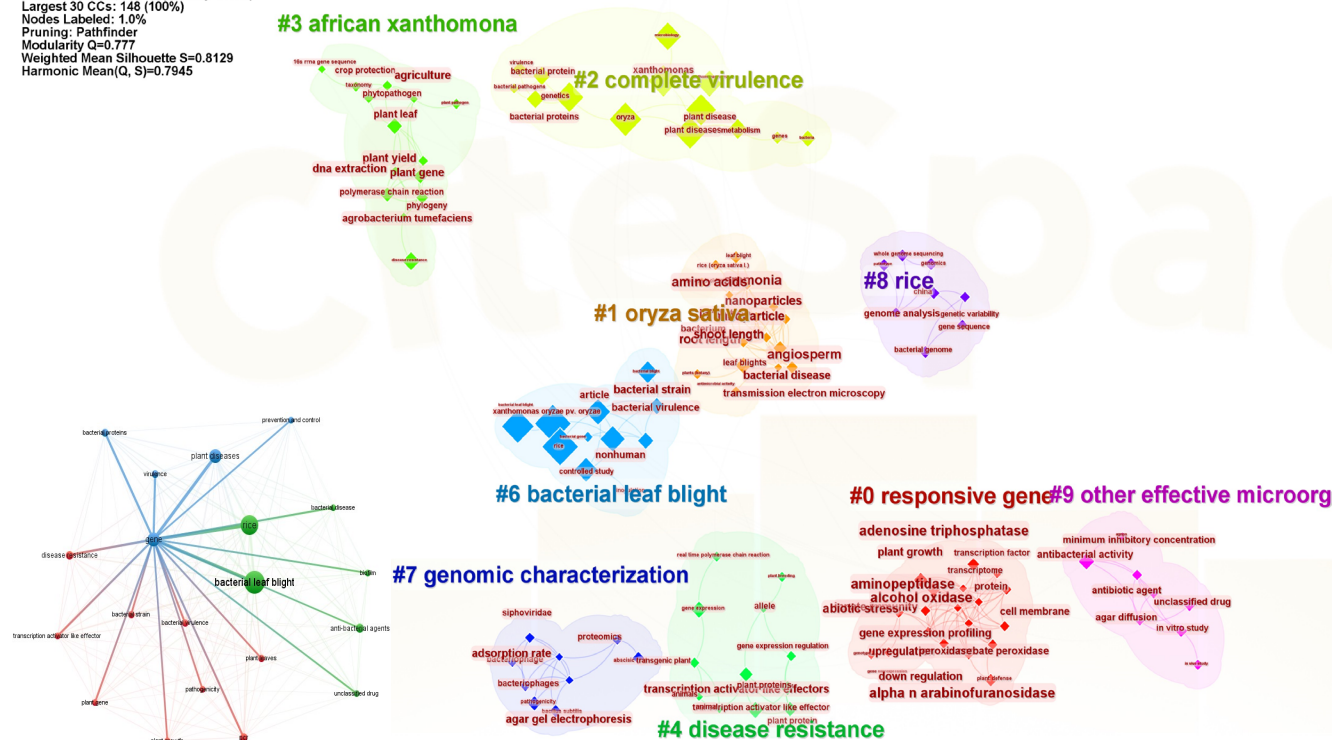


Figure 11. Visualization of future research trends based on cluster map of a recent study in 2022-2023 (Inset: capture of bibliometric analyses research map related to genetic topics).

genes,” “complete virulence,” “disease resistance,” and “genomic characterization” continue to dominate the research. This topic is essential due to the close relationship between resistance genes and plant resistance to BLB, which can affect the growth of rice plants. The findings of this cluster analysis are exceedingly good, as evidenced by the weighted mean silhouette (S) of 0.8129 and the modularity (Q) value of 0.7777.

Multiple studies demonstrate that increasing plant resistance through genetic modifications can result in the downregulation of other genes, including those that control plant growth and yield. It is prudent and straightforward for farmers to employ resistant varieties to reduce the risk of damage from BLB. Additionally, research related to “other effective microorganisms” will continue to be a significant and valued subject. It is critical to conduct additional research on producing nano-formulations from effective microorganisms to improve their field-level efficacy and efficiency. Out of the total articles examined, only two pertained to the formulation of beneficial microbes, including “bioformulation and delivery system of *Pseudomonas fluorescens* (Jambhulkar & Sharma, 2014)” and “bioformulation development of strain N1 (Sawatphanit et al., 2022)”.

The bibliometric analysis depicted in the inset photograph demonstrates the close relationship between gene research and other studies, including virulence, pathogenicity, disease resistance, plant growth, antibacterial agents, and disease control. Based on these findings, it can be concluded that research trends about genes that regulate plant resistance and growth when infected by BLB will continue to be an essential theme for future research. The stability of plant resistance genes to anticipate changes in pathogen pathotypes and their effect on boosting plant growth could be an alternative area for future study. In addition to this, investigations pertaining to the control and prevention of Xoo biofilm formation are crucial. Collaboration between breeders and researchers in BLB disease is essential to developing superior rice varieties with sustained resistance and high production capacity.

Based on these findings, several future insights to minimize the impact of bacterial leaf blight on rice production are recommended, including: a) Further investigation is warranted to probe the viability of alternative antibacterial agents as biocontrol agents against rice bacterial leaf blight, as exemplified in the inquiry utilizing the *Bacillus* strain; b) Understanding the spatial distribution, severity, and prevalence of

bacterial leaf blight in various rice-growing regions and the environmental factors that contribute to the disease requires additional research; c) Additional investigation is warranted regarding the plant leaves microbial community and their mechanism of action in controlling phyllosphere bacterial diseases; d) Further research may be warranted to investigate the shelf life and long-term storage stability of bioformulations incorporating beneficial bacteria designed to prevent rice bacterial leaf blight; e) There is a need for additional research to comprehend the response mechanism of the microbial community in the rice rhizosphere to bacterial leaf blight infection; f) Enhanced investigation in the subject of computer science to enhance studies relevant to BLB disease.

### CONCLUSION

In the millennium era, the number of publications related to BLB research continues to increase along with the increasing need for rice. Of the 650 articles indexed by Scopus, around 91.69% of them were published in this period. Genetics, including research in “Agricultural and Biological Sciences,” dominates publications and citations for this disease. The world’s largest rice producers—China and India—still dominate this field’s journals. However, European researchers (Szurek B, Sonti RV) and American researchers (Ronald PC) still dominate publishing productivity. Global collaboration improves publication quality and researcher capability. In conclusion, enriching studies related to antibacterial agents and their formulations, understanding the spatial distribution of the disease in multiple conditions, investigating the microbial community in the phyllosphere/rhizosphere and its impact on disease progression, and rapid identification based on computer sciences are needed to complete existing research. Finally, research on the stability of plant resistance genes to anticipate changes in pathogen pathotypes must continue.

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### AUTHORS’ CONTRIBUTIONS

Syahri (SYA) and Renny Utami Somantri (RUS) considered, planned, and arranged the manuscript. RUS collecting, filtering and interpreting data. SYA performed scientometric and bibliometric analysis. SYA and RUS discussing the results and writing the manuscript. The authors provided response and comments on the research flow, data analysis and interpretation as well as shape of the manuscript. All the authors have read and approved the final manuscript.

### COMPETING INTEREST

The authors declare that they have no known competing financial interest or personal relationship that could have appeared to influence the work reported in this paper.

### REFERENCES

- Amin T, Gupta V, Sharma A, Rai PK, Razdan VK, Sharma SK, Singh SK, Lone JA, Yaqoob M, Singh B, & Gupta SK. 2023. Distribution of *Xanthomonas oryzae* pv. *oryzae* pathotypes in basmati-rice-growing areas of Jammu and Kashmir, India. *Agronomy*. 13(3): 713. <https://doi.org/10.3390/agronomy13030713>
- Cleo G, Scott AM, Islam F, Julien B, & Beller E. 2019. Usability and acceptability of four systematic review automation software packages: a mixed method design. *Syst. Rev.* 8: 145. <https://doi.org/10.1186/s13643-019-1069-6>
- Cuatón GP & Delina LL. 2022. Two decades of rice research in Indonesia and the Philippines: a systematic review and research agenda for the social sciences. *Humanit. Soc. Sci. Commun.* 9: 372. <https://doi.org/10.1057/s41599-022-01394-z>
- Durand-Morat A & Chavez EC. 2020. *International Rice Outlook-International Rice Baseline Projections, 2019-2029*. University of Arkansas. Fayetteville.
- Ghaleb H, Alhajlah HH, Abdullah AAB, Kassem MA, & Al-Sharafi MA. 2022. A scientometric analysis and systematic literature review for construction project complexity. *Buildings*. 12(4): 482. <https://doi.org/10.3390/buildings12040482>
- Gnanamanickam SS, Priyadarisini VB, Narayanan NN, Vasudevan P, & Kavitha S. 1999. An

- overview of bacterial blight disease of rice and strategies for its management. *Curr. Sci.* 77(11): 1435–1444.
- Jamal MR, Kristiansen P, Kabir MJ, & de Bruyn LL. 2023. Challenges and adaptations for resilient rice production under changing environments in Bangladesh. *Land*. 12(6): 1217. <https://doi.org/10.3390/land12061217>
- Jambhulkar PP & Sharma P. 2014. Development of bioformulation and delivery system of *Pseudomonas fluorescens* against bacterial leaf blight of rice (*Xanthomonas oryzae* pv. *oryzae*). *J. Environ. Biol.* 35(5): 843–849.
- Kagale S, Marimuthu T, Thayumanavan B, Nandakumar R, & Samiyappan R. 2004. Antimicrobial activity and induction of systemic resistance in rice by leaf extract of *Datura metel* against *Rhizoctonia solani* and *Xanthomonas oryzae* pv. *oryzae*. *Physiol. Mol. Plant Pathol.* 65(2): 91–100. <https://doi.org/10.1016/j.pmpp.2004.11.008>
- Kong W, Ding L, & Xia X. 2020. Identification and characterization of genes frequently responsive to *Xanthomonas oryzae* pv. *oryzae* and *Magnaporthe oryzae* infections in rice. *BMC Genomics*. 21: 21. <https://doi.org/10.1186/s12864-019-6438-y>
- Lee BM, Park YJ, Park DS, Kang HW, Kim JG, Song ES, Park IC, Yoon UH, Hahn JH, Koo BS, Lee GB, Kim H, Park HS, Yoon KO, Kim JH, Jung CH, Koh NH, Seo JS, & Go SJ. 2005. The genome sequence of *Xanthomonas oryzae* pathovar *oryzae* KACC10331, the bacterial blight pathogen of rice. *Nucleic Acids Res.* 33(2): 577–586. <https://doi.org/10.1093/nar/gki206>
- Liu Q, Yuan M, Zhou Y, Li X, Xiao J, & Wang S. 2011. A paralog of the MtN3/saliva family recessively confers race-specific resistance to *Xanthomonas oryzae* in rice. *Plant Cell Environ.* 34(11): 1958–1969. <https://doi.org/10.1111/j.1365-3040.2011.02391.x>
- Mohanty S, Wailes E, & Chavez E. 2010. The global rice supply and demand outlook: the need for greater productivity growth to keep rice affordable. In: Pandey S, Byerlee D, Dawe D, Dobermann A, Mohanty S, Rozelle S, & Hardy B (eds.). *Rice in the Global Economy: Strategic Research and Policy Issues for Food Security*. pp. 175–87. International Rice Research Institute. Los Banos, Philippines.
- Mühl DD & de Oliveira L. 2022. A bibliometric and thematic approach to agriculture 4.0. *Heliyon*. 8(5): E09369. <https://doi.org/10.1016/j.heliyon.2022.e09369>
- Page MJ, McKenzie JE, Bossuyt PM, Boutron I, Hoffmann TC, Mulrow CD, Shamseer L, Tetzlaff JM, Akl EA, Brennan SE, Chou R, Glanville J, Grimshaw JM, Hróbjartsson A, Lalu MM, Li T, Loder EW, Mayo-Wilson E, McDonald S, McGuinness LA, Thomas J, Tricco AC, Welch VA, Whiting P, & Moher D. 2021. The PRISMA 2020 statement: an updated guideline for reporting systematic reviews. *BMJ* 372: n71. <https://doi.org/10.1136/bmj.n71>
- Peng Y, Bartley LE, Chen X, Dardick C, Chern M, Ruan R, Canlas PE, & Ronald PC. 2008. OsWRKY62 is a negative regulator of basal and *Xa21*-mediated defense against *Xanthomonas oryzae* pv. *oryzae* in rice. *Mol. Plant*. 1(3): 446–458. <https://doi.org/10.1093/mp/ssn024>
- Razali H, Awaludin N, Husin NH, Zulkepli SA, Rahman RA, Ismail MR, Ramachandran K, Salam F, & Said NAM. 2022. Development of an electrochemical immunosensor strip for early detection of rice bacterial leaf blight (BLB) disease and its application on a portable device. *MJAS*. 26(6): 1191–1204.
- Rejeb A, Abdollahi A, Rejeb K, & Treiblmaier H. 2022. Drones in agriculture: A review and bibliometric analysis. *Comput. Electron. Agric.* 198: 107017. <https://doi.org/10.1016/j.compag.2022.107017>
- Salzberg SL, Sommer DD, Schatz MC, Phillippy AM, Rabinowicz PD, Tsuge S, Furutani A, Ochiai H, Delcher AL, Kelley D, Madupu R, Puiu D, Radune D, Shumway M, Trapnell C, Aparna G, Jha G, Pandey A, Patil PB, Ishihara H, Meyer DF, Szurek B, Verdier V, Koebnik R, & Bogdanove AJ. 2008. Erratum to: Genome sequence and rapid evolution of the rice pathogen *Xanthomonas oryzae* pv. *oryzae* PXO99A. *BMC Genomics*. 9: 534. <https://doi.org/10.1186/1471-2164-9-534>
- Sanya DRA, Syed-Ab-Rahman SF, Jia A, Onésime D, Kim KM, Ahohuendo BC, & Rohr JR. 2022. A review of approaches to control bacterial leaf blight in rice. *World J. Microbiol. Biotechnol.* 38: 113. <https://doi.org/10.1007/s11274-022->



03298-1

- Sawatphanit N, Sutthisa W, & Kumlung T. 2022. Bioformulation Development of *Bacillus velezensis* strain N1 to control rice bacterial leaf blight. *Trends Sci.* 19(21): 6315. <https://doi.org/10.48048/tis.2022.6315>
- Shamseer L, Moher D, Clarke M, Gherzi D, Liberati A, Petticrew M, Shekelle P, Stewart LA, & the PRISMA-P Group. 2015. Preferred reporting items for systematic review and meta-analysis protocols (PRISMA-P) 2015: elaboration and explanation. *BMJ.* 350: g7647. <https://doi.org/10.1136/bmj.g7647>
- Soto-Suárez M, González C, Piégu B, Tohme J, & Verdier V. 2010. Genomic comparison between *Xanthomonas oryzae* pv. *oryzae* and *Xanthomonas oryzae* pv. *oryzicola*, using suppression-subtractive hybridization. *FEMS Microbiol. Lett.* 308(1): 16–23. <https://doi.org/10.1111/j.1574-6968.2010.01985.x>
- Streubel J, Pesce C, Hutin M, Koebnik R, Boch J, & Szurek B. 2013. Five phylogenetically close rice SWEET genes confer TAL effector-mediated susceptibility to *Xanthomonas oryzae* pv. *oryzae*. *New Phytologist.* 200(3): 808–819. <https://doi.org/10.1111/nph.12411>
- Sugio A, Yang B, Zhu T, & White FF. 2007. Two type III effector genes of *Xanthomonas oryzae* pv. *oryzae* control the induction of the host genes OsTFIIAγ1 and OsTFX1 during bacterial blight of rice. *PNAS.* 104(25): 10720–10725. <https://doi.org/10.1073/pnas.0701742104>
- Sun X, Cao Y, Yang Z, Xu C, Li X, Wang S, & Zhang Q. 2004. Xa26, a gene conferring resistance to *Xanthomonas oryzae* pv. *oryzae* in rice, encodes an LRR receptor kinase-like protein. *TPJ.* 37(4): 517–527. <https://doi.org/10.1046/j.1365-3113X.2003.01976.x>
- Syahri & Somantri RU. 2022. A scientometric and bibliometric analysis for actinomycetes research-current status and future trends. *Jurnal Perlindungan Tanaman Indonesia.* 26(2): 93–106. <https://doi.org/10.22146/jpti.77558>
- Syahri & Somantri RU. 2023. Learning from global research to analyze contributing factors in rice yield gap : bibliometric approach towards Indonesia's self-sufficiency. *Agric. Nat. Resour.* 57(3): 479–490. <https://doi.org/https://doi.org/10.34044/j.anres.2023.57.3.12>
- van Wart J, Kersebaum KC, Peng S, Milner M, & Cassman KG. 2013. Estimating crop yield potential at regional to national scales. *Field Crops Res.* 143: 34–43. <https://doi.org/10.1016/j.fcr.2012.11.018>
- Wu L, Wu H, Chen L, Yu X, Borriss R, & Gao X. 2015. Difficidin and bacilysin from *Bacillus amyloliquefaciens* FZB42 have antibacterial activity against *Xanthomonas oryzae* rice pathogens. *Sci. Rep.* 5: 12975. <https://doi.org/10.1038/srep12975>
- Wu L, Danko Y, Chen F, Yao X, & Zhang F. 2022. Mapping the literature of integrated marketing communications: a scientometric analysis using citespace. *Innov. Mark.* 18(1): 152–167. [https://doi.org/10.21511/im.18\(1\).2022.13](https://doi.org/10.21511/im.18(1).2022.13)
- Xu J, Zeng Y, Yu C, Xu S, Tang L, Zeng X, Huang Y, Sun Z, Xu B, & Yu T. 2023. Visualization of the relationship between fungi and cancer from the perspective of bibliometric analysis. *Heliyon.* 9(8): e18592. <https://doi.org/10.1016/j.heliyon.2023.e18592>
- Yafetto L. 2022. Application of solid-state fermentation by microbial biotechnology for bioprocessing of agro-industrial wastes from 1970 to 2020: a review and bibliometric analysis. *Heliyon.* 8(3): e09173. <https://doi.org/10.1016/j.heliyon.2022.e09173>
- Yang J, Dai Z, Wan X, Munir S, Wang X, Wei L, & Ji G. 2021. Insights into the relevance between bacterial endophytic communities and resistance of rice cultivars infected by *Xanthomonas oryzae* pv. *oryzicola*. *3 Biotech.* 11: 434. <https://doi.org/10.1007/s13205-021-02979-2>
- Ye H, Du Y, Jin Y, Liu F, He S, & Guo Y. 2023. Articles on hemorrhagic shock published between 2000 and 2021: A CiteSpace-Based bibliometric analysis. *Heliyon.* 9(8): e18840. <https://doi.org/10.1016/j.heliyon.2023.e18840>
- Yuan M, Chu Z, Li X, Xu C, & Wang S. 2010. The bacterial pathogen *Xanthomonas oryzae* overcomes rice defenses by regulating host copper redistribution. *Plant Cell.* 22(9): 3164–3176. <https://doi.org/10.1105/tpc.110.078022>