Land, Crops & Environment
Universidad Agraria del Ecuador

e-ISSN: in process / en trámite

Review Article / Artículo de revisión

Scientific Landscapes of Fusarium Wilt in Bananas: A Bibliometric Analysis of Pathogenesis, Resistance, and Control (1997–2024)

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Recibido: 08 diciembre 2025
Aceptado: 22 diciembre 2025
Publicado: 08 enero 2026

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Citación sugerida:
Culque, E.; Fey, K.; Macias, O.; Salavarria, J. and Martínez, S. (2026). Scientific Landscapes of Fusarium Wilt in Bananas: A Bibliometric Analysis of Pathogenesis, Resistance, and Control (1997–2024). *Land, Crops & Environment*, 1(1), 1–15.

Abstract

The ongoing race between banana crops and the fungal pathogen *Fusarium oxysporum* f. sp. cubense (Foc), which causes Fusarium wilt (also known as Panama disease), poses an escalating threat to global banana production. Understanding how the scientific community has responded to this pathogen–host interaction is essential for informing future control strategies. This study presents a comprehensive bibliometric analysis of research publications indexed in the Scopus database, examining publication trends, international collaboration patterns, and thematic research clusters. Results reveal a marked increase in scientific output, especially following the emergence and global spread of Tropical Race 4 (TR4). International collaboration has intensified—most notably among countries in the Northern Hemisphere, with China and the United States leading in co-authorship networks. Thematic mapping identified three major research fronts: in-depth studies on pathogen biology (e.g., virulence factors and genomics), host resistance mechanisms (e.g., defense genes and signaling pathways), and a broad spectrum of control strategies, with growing interest in biocontrol agents and advanced detection tools. Overall, the bibliometric landscape reflects the urgency of the Fusarium wilt crisis and a robust, multidisciplinary scientific response. Continued innovation, international cooperation, and integrated disease management will be key to safeguarding the sustainability of banana production worldwide.

Keywords: Fusarium wilt; Fusarium cubense; Panama disease; biocontrol.

Resumen

La actual carrera entre los cultivos de banano y el patógeno fúngico *Fusarium oxysporum* f. sp. cubense (Foc), causante del marchitamiento por Fusarium (también conocido como mal de Panamá), representa una amenaza creciente para la producción mundial de banano. Comprender cómo ha respondido la comunidad científica a esta interacción patógeno-hospedador es esencial para fundamentar futuras estrategias de control. Este estudio presenta un análisis bibliométrico exhaustivo de las publicaciones de investigación indexadas en la base de datos Scopus, examinando las tendencias de publicación, los patrones de colaboración internacional y los grupos temáticos de investigación. Los resultados revelan un marcado aumento en la producción científica, especialmente tras la aparición y propagación global de la Raza Tropical 4 (RT4). La colaboración internacional se ha intensificado, especialmente entre los países del hemisferio norte, con China y Estados Unidos a la cabeza en las redes de coautoría. El mapeo temático identificó tres líneas de investigación principales: estudios a fondo sobre la biología de los patógenos (p. ej., factores de virulencia y genómica), mecanismos de resistencia del hospedador (p. ej., genes de defensa y vías de señalización) y un amplio espectro de estrategias de control, con un creciente interés en agentes de biocontrol y herramientas de detección avanzadas. En general, el panorama bibliométrico refleja la urgencia de la crisis del marchitamiento por Fusarium y una respuesta científica sólida y multidisciplinaria. La innovación continua, la cooperación internacional y el manejo integrado de enfermedades serán clave para salvaguardar la sostenibilidad de la producción bananera a nivel mundial.

Keywords: Marchitez por fusarium; fusarium cubense; biocontrol; raza 4 tropical.

1 Introduction

Fusarium wilt of banana, commonly known as Panama disease, is a devastating vascular pathology caused by the soil-borne fungus *Fusarium oxysporum* f. sp. *cubense* (Foc) (Ploetz, 2006; Visser et al., 2004; Cong et al., 2025; Fang et al., 2024). For more than a century this disease has posed a persistent threat to global banana production (Ploetz, 2006; Daniells, 2009; Wang and Chien, 2024; Kumari et al., 2023). Early epidemics driven by Foc Race 1 led to the collapse of export systems based on the highly susceptible 'Gros Michel' cultivar (Ploetz, 2006). The subsequent emergence and rapid worldwide spread of Tropical Race 4 (TR4) has dramatically intensified the crisis, severely affecting Cavendish bananas—the backbone of both international trade and smallholder livelihoods (Dita et al., 2013; Ploetz et al., 2015; Remy et al., 2013; Arango-Palacio et al., 2024). After penetrating the roots, the pathogen colonises the rhizome and occludes the vascular tissue of the pseudostem, ultimately causing irreversible wilting and plant death (Visser et al., 2004; Ploetz, 2006; Cong et al., 2025; Fang et al., 2024). The accelerating advance of TR4 in Asia—particularly Indonesia (Hermanto et al., 2011; Wibowo et al., 2011; Kurniasari et al., 2024) and China (Bai et al., 2013; Li et al., 2013), and its confirmation in the Middle East (Ploetz et al., 2015) underscore the urgent need for robust, internationally coordinated containment strategies (Daniells, 2009; Dita et al., 2013; Arango-Palacio et al., 2024).

Effective management depends on a detailed understanding of Foc population diversity (Buddenhagen, 2009; Kumari et al., 2023), the routes and history of TR4 dissemination (Wang and Chien, 2024), and the genetic mechanisms underlying host resistance (Bai et al., 2013; Li et al., 2013; Ferreira et al., 2024; Cong et al., 2025). Recent transcriptomic and proteomic studies have revealed extensive transcriptional reprogramming and differential protein expression in resistant cultivars such as 'Yueyoukang 1' (Bai et al., 2013; Li et al., 2013). Genes involved in plant–pathogen recognition, hormone signalling (e.g. ethylene, jasmonic acid), production of pathogenesis-related proteins, and cell-wall lignification play pivotal roles in resistance (Bai et al., 2013; Li et al., 2013; Fang et al., 2024; Cong et al., 2025). Activation of salicylic-acid signalling pathways has also been linked to systemic acquired resistance induced by incompatible Foc strains (Wu et al., 2013).

Despite these advances, controlling Panama disease remains challenging (Ploetz, 2006; Daniells, 2009; Arango-Palacio et al., 2024). Current best practices rely on pathogen-free planting material and the use of clean soils (Ploetz, 2006). Breeding or selecting cultivars with full or partial resistance remains a cornerstone strategy (Bai et al., 2013; Li et al., 2013; Remy et al., 2013; Wu et al., 2013; Ferreira et al., 2024). Biological control is receiving growing attention: promising agents include non-pathogenic *Fusarium oxysporum* isolates (Ting et al., 2009) and endophytic bacteria such as *Burkholderia cenocepacia* 869T2, which reduce disease incidence while promoting vegetative growth (Ho et al., 2015). Nevertheless, large-scale efficacy and standardised application protocols still need refinement (Ting et al., 2009).

TR4 dissemination is further complicated by insect vectors such as the banana weevil *Cosmopolites sordidus* (Meldrum et al., 2013) and by weeds that can act as asymptomatic hosts (Hennessy et al., 2005). Given the looming threat to global food security and to the livelihoods of millions of farming families, internationally coordinated management—encompassing strict quarantine measures and close governmental cooperation—is imperative (Daniells, 2009; Dita et al., 2013; Wang and Chien, 2024; Arango-Palacio et al., 2024).

Against this backdrop, the present study offers a comprehensive bibliometric exploration of the scientific literature on Fusarium wilt in banana published between 1997 and 2024. By mapping publication trends, collaboration networks, and thematic clusters, we identify research patterns, emerging directions, and knowledge gaps, thereby informing the collective effort to mitigate this enduring phytosanitary threat.

2 Materials and Methods

This study used a descriptive, exploratory bibliometric approach to map the scientific landscape of the Fusarium–banana pathosystem, often described as an ongoing "arms race." Following established best practices in bibliometric research (Nasir et al., 2020), methodological guidelines for theory building (Mukherjee et al., 2022), recommendations for rigorous scientometric analysis (Haghani, 2023), and current research agendas in the field (Blümel and Schniedermann, 2020), we assessed research output, collaboration patterns, and thematic evolution within this critical area of plant pathology. Additional techniques from recent scientometric review studies were integrated to maximise completeness and analytical rigour (Shahiwala et al., 2024; Kehinde et al., 2023).

Scopus served as the sole data source because of its broad coverage in agricultural science, plant biology, and environmental research. A carefully constructed search string, combining keywords for the pathogen, the disease, and the host plant with Boolean operators (AND, OR), was executed to retrieve the most relevant records. The search period spanned 1900–2024, but only peer-reviewed journal articles were retained, excluding conference papers and book chapters to maintain data homogeneity. The initial query yielded 350 documents, which were exported in BibTeX format for further processing.

Data cleaning and normalisation were conducted in RStudio (R 4.5.0). The `bibliometrix` package (version 5.0) imported the BibTeX files into a structured data frame, after which duplicate records were identified and removed through automated routines complemented by manual checks. Inconsistencies in key fields—author names, institutional affiliations, and keywords, were resolved to ensure reliable collaboration networks, productivity metrics, and thematic analyses.

With a curated dataset in hand, we applied the analytical functions of `bibliometrix` to compute descriptive statistics (annual output, leading authors, core journals, contributing countries) and impact indicators (total citations per article, h-index). Co-authorship, co-country, and co-institution networks were visualised to reveal collaboration clusters. Keyword co-occurrence analysis, strategic diagrams, and thematic maps captured the intellectual structure and temporal evolution of research fronts, while co-citation and bibliographic-coupling analyses exposed the field's foundational literature. All graphical outputs were generated directly in R, then lightly edited with standard design software to enhance clarity.

3 Results

This bibliometric review characterises twenty-seven years of research on the Fusarium–banana pathosystem and traces its principal trends. The corpus comprises 147 sources, indicating a reasonably well-defined body of literature. Annual output has grown at 12.8 %, and the mean publication age is 5.3 years, confirming a rapidly evolving field. Each article receives, on average, 24.5 citations, a figure that points to strong scholarly visibility.

The dataset includes 1627 authors. Only nine have published single-author papers (twelve articles in total), whereas the mean of 7.3 co-authors per article attests to the prevalence of large research teams. International collaboration accounts for 35.4 % of the documents, underscoring the importance of cross-border partnerships. Most records are journal articles (272), followed by conference papers (40) and book chapters (10). Reviews (12) play a key role by synthesising existing knowledge and guiding future work. Minor label inconsistencies ("article article", "conference paper conference paper") reflect limitations in source metadata.

Work on virulence and pathogenesis has intensified, especially on Tropical Race 4 (TR4). Nitric-oxide biosynthesis genes (Zhang et al., 2024a), importin FoCKap119 (Zhang et al., 2024b), ribonuclease FoCRnt2 (He et al., 2024), and pheromone precursor FoC4-PP1 (Liu et al., 2023) are now recognised as critical virulence factors. Studies on *Fusarium odoratissimum* (an alternative name for TR4) have clarified the roles of FoSpc2 (Yang et al., 2023) and the MAT1-1-1 gene (Ang et al., 2025). Iron dependence for chlamydospore germination (Were et al., 2023) and the effector FSE1, which targets a banana MYB factor (Yang et al., 2022), further refine our understanding of infection biology. Improved phenotyping protocols—for example, the "pouring" assay in tissue-cultured plants (Koondhar et al., 2024), enhance reproducibility.

Geographical mapping in India (Thangavelu et al., 2024; Baruah et al., 2025), Colombia (Rodríguez-Yzquierdo et al., 2023), and Venezuela (Herrera et al., 2023) confirms the expanding range of TR4. Spatio-temporal analyses of Subtropical Race 4 (SR4) provide baselines for mitigation strategies. Recent reviews summarise advances in pathogenesis-related genes (Chen et al., 2024) and the regional status of TR4 (Munhoz et al., 2024). Integrated approaches include *Bacillus velezensis* EB1 with potassium sorbate (Liu et al., 2024), black-soldier-fly frass as a biofungicide (Ong et al., 2025), RNA-interference targeting FoCDCL2 (Epitawaththe Samitha Sawindri Jayasekara et al., 2025), and *Streptomyces rochei*, which provides complete greenhouse protection (Jegan et al., 2025). A major resistance QTL has been mapped in *Musa acuminata*, and the transgenic cultivar QCAV-4—now approved for commercial use—shows sharply reduced field incidence (Harding et al., 2025). Dynamic PR-1 expression during infection offers further insight into host defence (Anuradha et al., 2024).

All statistics derive from Scopus. Coverage biases, indexing policies, and disciplinary differences must be considered when interpreting citation counts or collaboration rates.

Figure 1 shows a concentration of Chinese authors linked to Fusarium-related keywords, confirming China's leading role. Other active countries include the Netherlands, the United

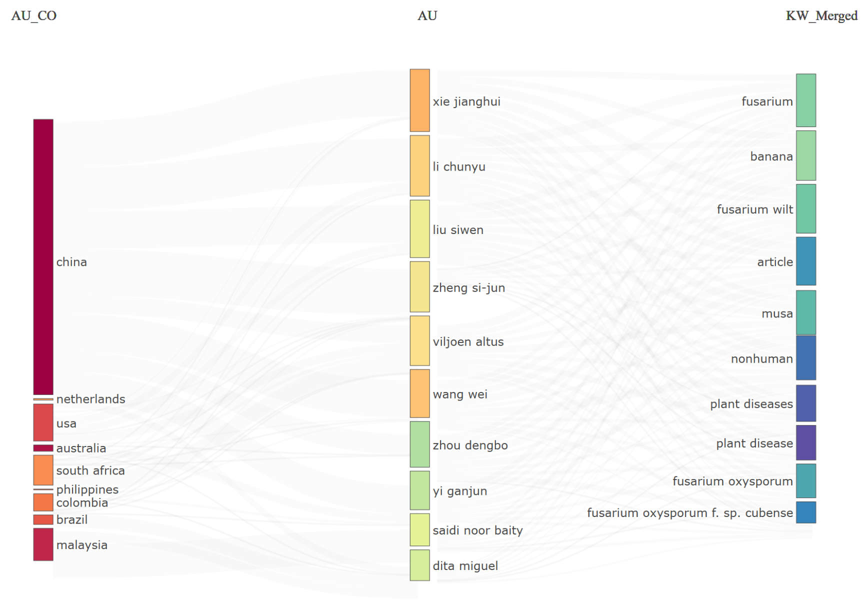

Figure 1. Tripartite relationship map (authors, countries, keywords).

States, Australia, South Africa, the Philippines, Colombia, Brazil, and Malaysia.

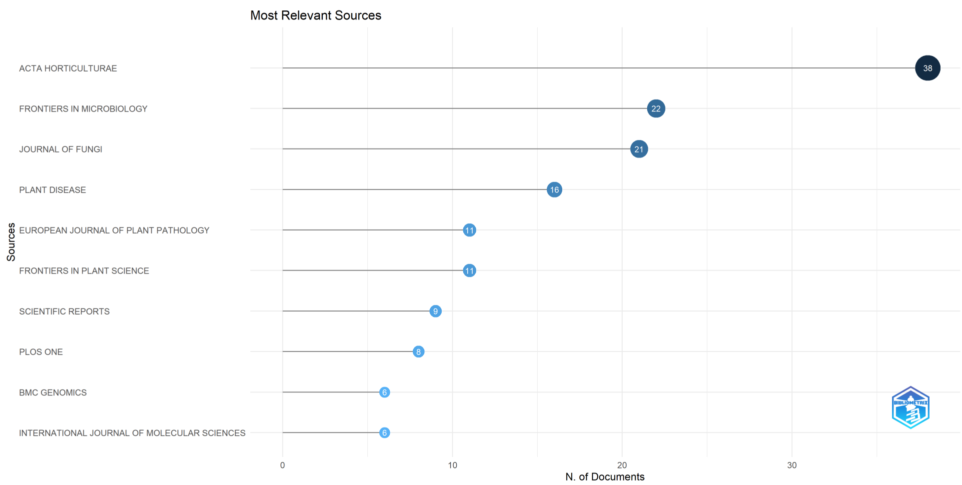

Figure 2. Core publication venues.

As Figure 2 indicates, *Acta Horticulturae* is the dominant outlet (38 articles), reflecting its role in disseminating applied horticultural research, often linked to international symposia. The remaining literature is spread across specialized and multidisciplinary journals in plant pathology, microbiology, genomics, and agronomy.

Figure 3 highlights prolific researchers—Xie Jianghui, Li Chunyu, Liu Siwen, and others—who anchor global collaboration networks. China leads in total output (134 articles) but registers only 20.9 % multi-country publications, indicating a domestic focus. By contrast, Colombia, Brazil, and Indonesia show higher proportions of international collaboration.

Figure 5 visualises publication hotspots, with Asia dominant, followed by the Americas, Europe, and Africa.

Figures 6 and 7 confirm sustained growth since 2008, punctuated by occasional peaks.

The word cloud (Figure 8), co-occurrence network (Figure 9), and MCA map (Figure 10)

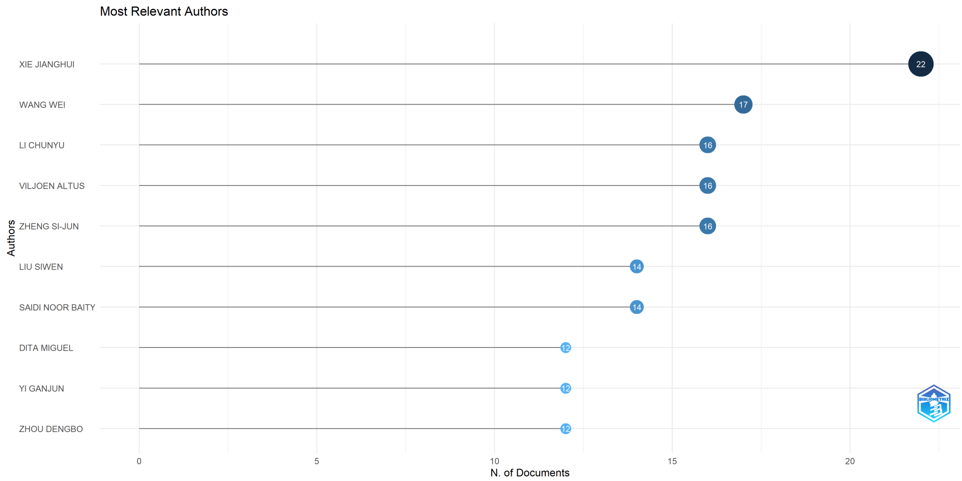

Figure 3. Leading authors and their publication counts.

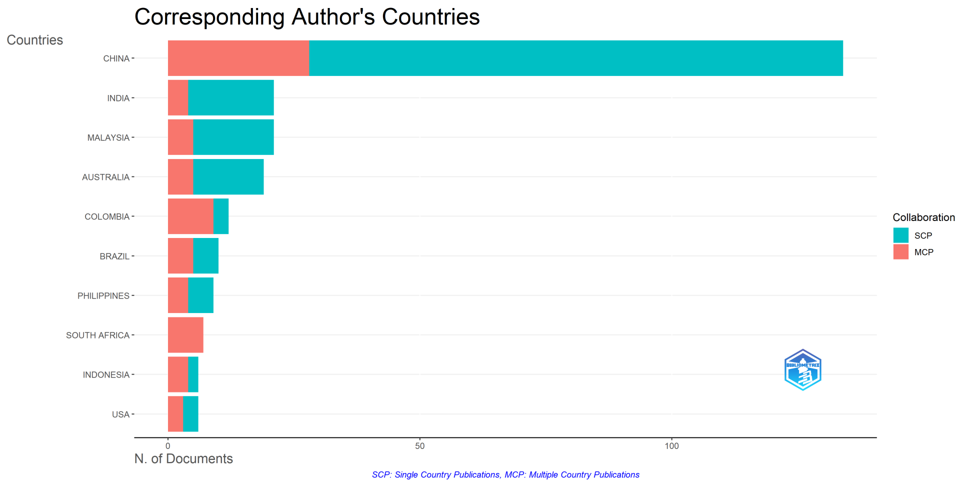

Figure 4. Single-country vs multi-country publications.

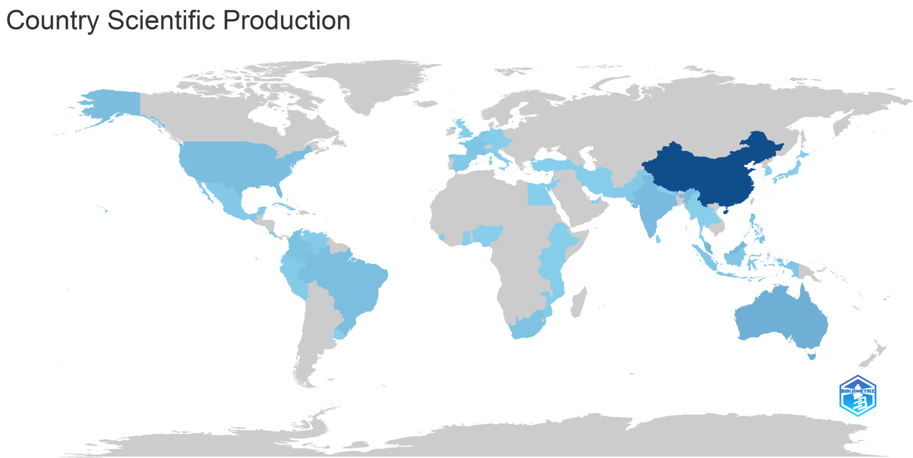

Figure 5. Global distribution of publication activity.

converge on four research fronts: molecular pathogenesis, host resistance, biological control, and biosecurity.

Finally, Figure 11 shows that the strongest ties link China with the United States, the United States with Europe, and Australia with China, underscoring the importance of Northern-Hemisphere partnerships in advancing Fusarium wilt research.

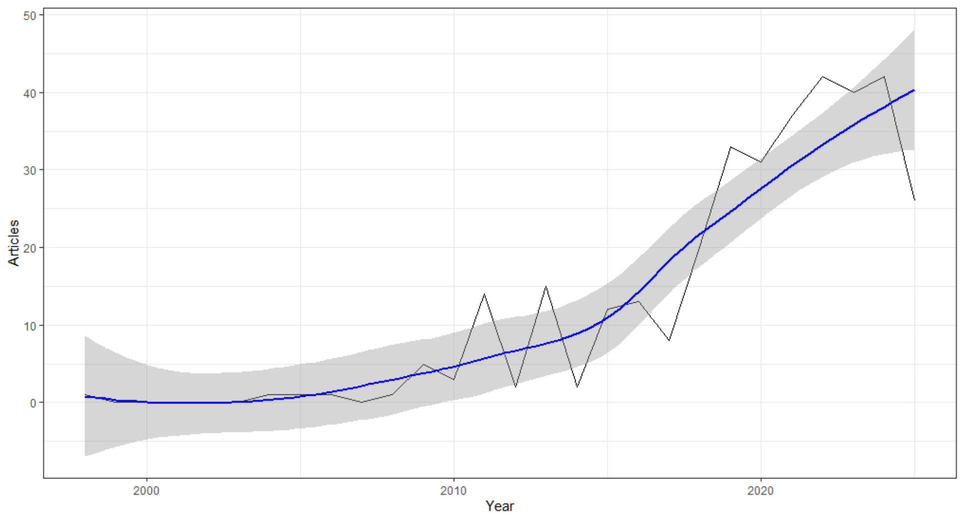

Figure 6. Annual publication trend with linear regression.

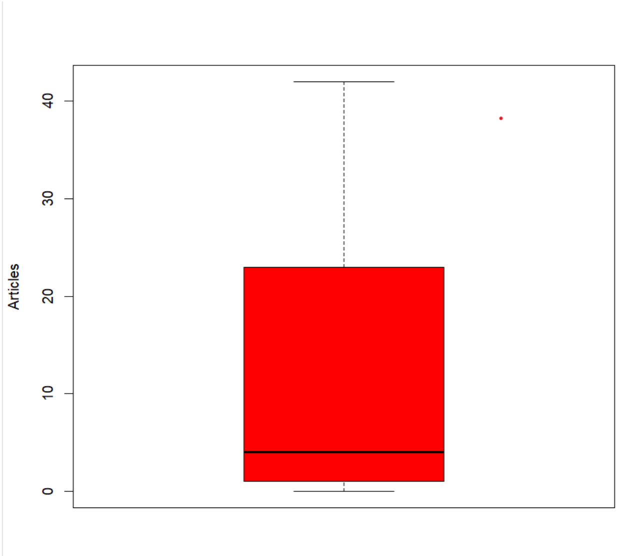

Figure 7. Distribution of annual publication counts.

4 Discussion

Our bibliometric results reveal a steady, compound growth in scholarship on the Fusarium–banana interaction (Figure 1). Peaks in annual output coincide with major epidemiological milestones—most conspicuously the first reports and subsequent global spread of Tropical Race 4 (TR4) (Roberts et al., 2024; Viljoen et al., 2020). These surges underscore how the pathogen's advance galvanises the research community. Cross-segmented tallies by document, journal, and country (Figures 2–5) confirm that the problem is global in scope. China and the United States dominate overall production and, through extensive co-authorship networks (Figure 11), drive much of the field's international integration—an essential feature when confronting a border-agnostic pathogen such as TR4. Keyword co-occurrence and thematic clustering (Figure 10) decompose this "arms race" into three interlocking fronts. The first concentrates on pathogen biology and virulence. Recent molecular studies have identified a suite of critical determinants—*foisc1*, *FocGCN5*, *FocbZIP11*, and the aminotransferase *FocAST2*, the latter chemically inhibited by albendazole (Guo et al., 2025; Xie et al., 2025; Liu et al., 2022, 2025; Thangavelu et al., 2021). Such findings expose weaknesses in the pathogen's arsenal and provide leads for new fungicidal targets.

A second research front tackles host defences. Investigators have linked lipoxygenase genes

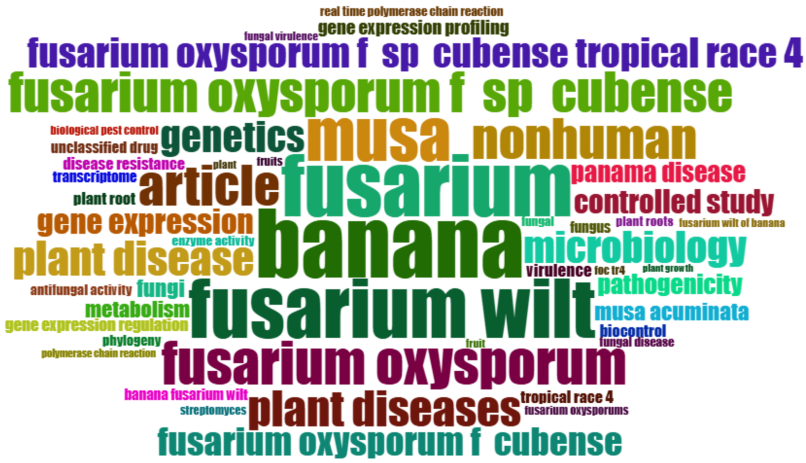

Figure 8. Keyword prominence.

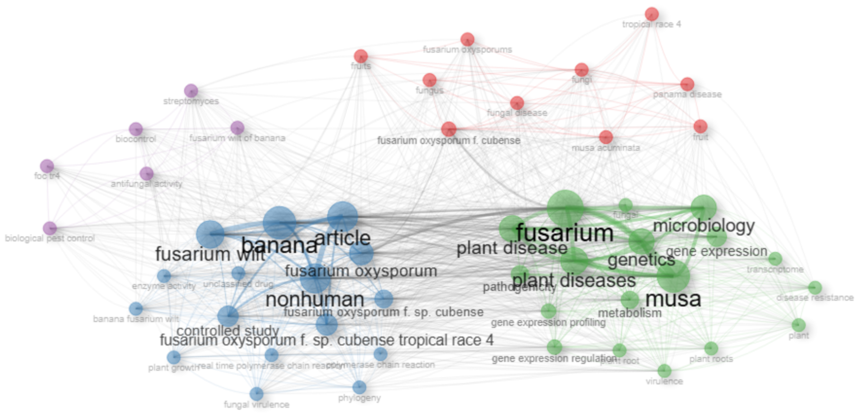

Figure 9. Keyword co-occurrence network.

(*MaLOX*) to enhanced jasmonate-mediated resistance (Liu et al., 2021); characterised vacuolar-processing enzymes (*MaVPEs*) that modulate programmed cell death; and developed rapid *in vitro* screens for resistant genotypes (Wu and Yi, 2022). Transgenic work, including CRISPR applications (Sankari et al., 2024), aims to arm Cavendish and other cultivars with durable resistance. Chemical priming with chitosan, which elevates salicylic acid and methyl-salicylate pathways, further boosts systemic immunity (Lopez-Moya et al., 2025).

The third front focuses on control technologies. Biological control has gained prominence as a sustainable alternative to synthetic fungicides. *Streptomyces* spp. produce siderophores and polyene metabolites that disrupt TR4 cell integrity and energy metabolism (Zhu et al., 2021; Cao et al., 2022; Yun et al., 2021, 2022; Duan et al., 2021). Endophytic bacteria induce systemic resistance while directly suppressing the pathogen (Nakkeeran et al., 2021; Shafi et al., 2023). Plant-derived products—lipopeptides, cinnamon extracts, legume-root phenols, and wood vine-

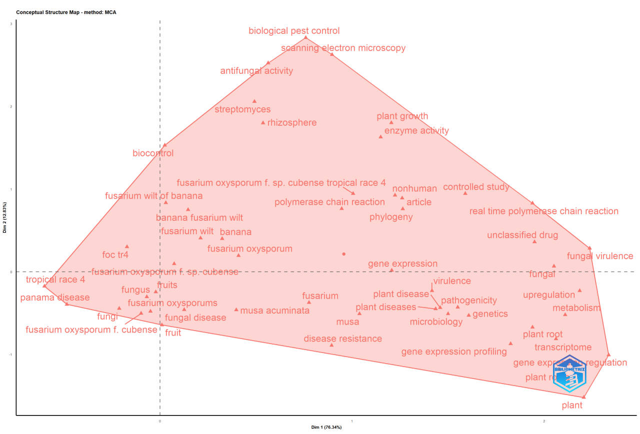

Figure 10. Conceptual structure map (MCA).

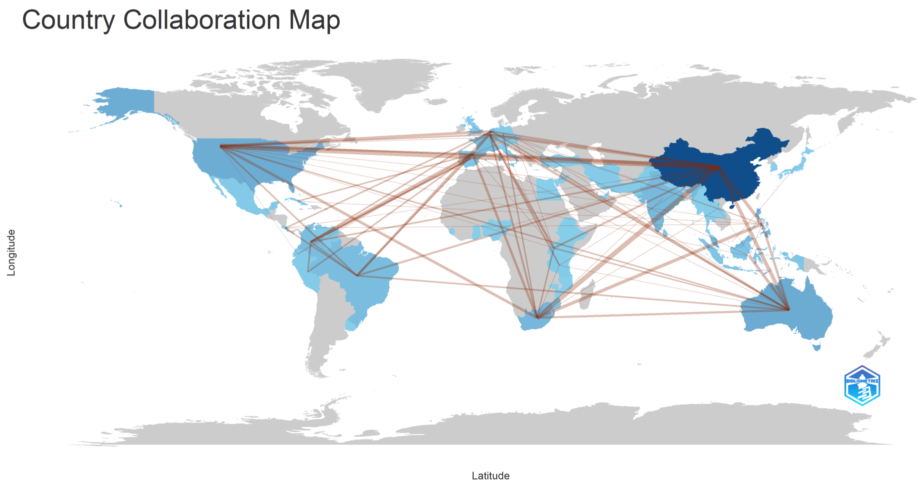

Figure 11. International collaboration network.

gar—expand the library of bio-based options (Were et al., 2022; Anggrayni et al., 2025). On the diagnostic front, AI-enabled image recognition (YOLOv4) (Ibarra et al., 2023) and micro-conidia profiling (Abigan et al., 2020) accelerate early detection, providing the "intelligence" required for timely intervention.

Together, these intertwined fronts illustrate how the scientific community is responding ,in real time, to a pathogen that continues to evolve and spread.

5 Conclusions

This bibliometric exploration of twenty-seven years of scholarship on the "arms race" between *Fusarium oxysporum* f. sp. cubense and banana reveals a vibrant, rapidly evolving discipline. The analysis documents a mounting global sense of urgency—amplified by the emergence and spread of Tropical Race 4 (TR4)—that has driven both a sharp rise in publication volume and a marked intensification of international collaboration.

Thematic mapping highlights the multifaceted nature of the struggle. One research front dissects the molecular and genetic machinery that underpins pathogen virulence, clarifying the "weapons" wielded by the fungus. A complementary line of inquiry deciphers host-defence pathways and delivers new "weapons" for the plant, including conventional breeding, genomic selection, and transgenic resistance. The most dynamic front, however, pursues sustainable control: biological agents, plant-derived compounds, and early-detection technologies together form a pipeline of environmentally compatible interventions.

The persistence of the Foc threat underscores the need for integrated solutions. Synergy between fundamental studies of pathogen–host biology and the development of practical tools is essential. Continued international collaboration, sustained technological innovation, and the deployment of bio-based strategies will be pivotal in tipping the balance of this "arms race" and safeguarding global banana production in the decades ahead.

Acknowledgments

The authors gratefully acknowledge the Escuela de Posgrado and the Universidad Agraria del Ecuador for their institutional support and for providing access to bibliographic resources essential to this research.

Conflict of interest

Authors declare no conflict of interest.

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