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Mapping the global research trends and emerging frontiers on tomato brown rugose fruit virus (ToBRFV): a bibliometric analysis (2016–2025)

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Abstract

Tomato (*Solanum lycopersicum*) is an important vegetable in diet of human population and ensuring global food security. However, the production of this crop is limited by virus diseases. Tomato brown rugose fruit virus (ToBRFV) is an emerging *Tobamovirus* threatening global tomato and other solanaceous crop production. ToBRFV has exhibited rapid transboundary dissemination, effectively circumventing established resistance genes such as *Tm-2*^{2}, and resulting in significant yield and economic losses. Although considerable studies have been conducted on biology, epidemiological patterns, and management strategies of the virus, a systematic evaluation of the research landscape remains absent. The present study addresses this gap by conducting bibliometric analysis of ToBRFV-related publications indexed in the Web of Science Core Collection. A total of 255 documents were identified across 65 peer-reviewed journals and 32 subject categories, with Plant Sciences and Virology representing the most dominant subject categories. Analysis of citation bursts and keyword evolution revealed a marked shift in research priorities—from initial efforts focused on molecular characterization and detection to more recent advances in epidemiology, disinfection strategies, and resistance breeding. Notably, transcriptomic profiling and CRISPR-based methodologies are gaining prominence as emerging frontier themes. Also, molecular breeding studies are still required since reported discovered genes fail to fully inhibit the replication of the virus in plant tissues. The major motive of this paper is to help gain insights, to inform strategic collaborations, guide funding priorities, and shape future research directions – particularly in breeding durable resistance and refining containment strategies.

Keywords ToBRFV, Plant virus, Bibliometric, VOSviewer, CiteSpace

1 Introduction

Tomato (*Solanum lycopersicum*) is among the most widely cultivated vegetables globally. The cultivation of this crop generates substantial annual revenue, which is used to support local economies. The cultivation of tomato is subject to various biotic and abiotic

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stresses, which have a considerable impact on the yield potential of various tomato varieties. Biotic stresses have been demonstrated to exert an influence on the yield of plants. Of particular concern is the Tomato brown rugose fruit virus (ToBRFV) also referred to as *Tobamovirus fructirugosum*, which was first documented in Jordan nearly a decade ago [1]. ToBRFV, classified as a member of the *Tobamovirus* genus, is a virus that has demonstrated a rapid rate of propagation and has caused significant destruction to in tomato, garden eggs and pepper. Reportedly, the virus causes approximately 55% yield losses in tomato crops irrespective of the presence or absence of the *Tm-2*^{2} gene [2]. The virus has 6.4 kb size- single-stranded positive-sense RNA genome. The genome generally has four open reading frames, two subunits of RNA-dependent RNA polymerase (RdRp) complex, a movement protein (MP), and a coat protein (CP) [3, 4].

The virus manifests symptoms such as rugose leaves and discoloration in ripened tomato fruits [5]. While resistant genes, including *Tm-1*, *Tm-2*, and *Tm-2*^{2} [6], have proven effective against most tobamoviruses, ToBRFV has been observed to circumvent the resistance mechanisms imparted by these genes, particularly overcoming the resistance conferred by the *Tm-2*^{2} gene [7]. A substantial volume of research has been dedicated to the nature, transmission mode, and virulence of various isolates of this virus [8–10]. In recent years, several high-quality research and review articles have also contributed to the growing body of knowledge on Tomato brown rugose fruit virus (ToBRFV), including those by Caruso et al. [11]. As demonstrated in the works of [12] and [13], significant advancements have been made in our understanding of the virus' nature and the research progress made to control it. Given the expanding volume of publications on this topic, bibliometric analysis serves as a valuable complementary approach, offering a macro-level, data-driven perspective on the research landscape by mapping trends, collaborative networks, and thematic evolution that are not captured in scope of canonical narrative reviews.

Bibliometric analysis is a method of evaluating published research to predict future research focus [14]. Bibliometric involves the use of systematic quantitative approach to the statistical examination of scholarly publications, facilitating the evaluation of disciplinary literature expansion, the impact of individual contributions, and temporal trends in research activity. As such, in this study we utilized bibliometric analysis to 1) to map global collaboration networks [15], to analyze publication trends and key contributors, and [16] to identify evolving and emerging research themes within the ToBRFV research area.

2 Materials and methods

2.1 Data collection

The Web of Science (WoS) core collection was chosen to gather data on ToBRFV research due to its regular data update, contains high-quality journals and has standardized citation information [16]. Data used in this study were extracted on 17th July 2025 using the advanced search "TS (topic) = ('Tomato brown rugose fruit virus*' OR 'ToBRFV*' OR 'Tomato new tobamovirus*' OR 'brown rugose virus*' OR 'novel tobamovirus on tomato*'). Documents were searched and collected based on the defined key terms in the title, keywords or abstract. The search generated 288 documents. Additionally, data was cleansed to limit the document types to research articles, meeting abstracts, review articles, editorial materials, proceeding papers, early access, and news

items with no language limitation. Documents sourced from the database were saved in the 'plain text' and 'Bibtex' format by selecting the "full records and cited references" option. A summary of the data extraction and cleansing process is summarized in Fig.S1.

2.2 Analysis methodology

2.2.1 Keywords co-occurrence analysis

The utilization of keyword co-occurrence analysis is instrumental in uncovering the core thematic structures that define a contemporary research domain. The downloaded data from WoS in 'plain text' format was inputed into the VoSviewer software. Thereafter, the fractional counting' option was selected. with "all keyword" option applied to generate terms independent of biases. The fractional counting method used generated a total of 1,022 keywords. By applying the minimum occurrences threshold of five, a total of 45 keywords met the criterion and were included in the final network visualization.

2.2.2 Co- authorship networks in ToBRFV research

Co-authorship networks serve as a valuable tool for assessing scientific collaborations among researchers. The 'plain text' file format was inputed into the VoSviewer software for analysis. In this analysis, we applied inclusion criteria based on a minimum of two publications and no citation filter. Out of the 972 authors represented in the dataset, 258 met these thresholds. These thresholds helped refine the assessment of active scholarly contributions and collaborative networks within the ToBRFV research community.

2.2.3 Document co-citation analysis

The identification of significant research clusters, mapping the evolution of scientific disciplines, and revealing the intellectual structure and thematic affinities among scholarly texts are all facilitated by document co-citation analysis. When two documents are frequently cited together in subsequent literature, it suggests a conceptual or methodological alignment between them, thereby enabling classification based on shared research themes [17]. For this analysis, VOSviewer software was employed using the 'plain text' file format with fractional counting option, with the "minimum citation of a document" threshold set at 5 to capture recently published but less cited research works. A total of 275 documents met this criterion and were included in the final co-citation network.

2.2.4 Countries analysis and subject categories

The list of top countries' contribution and subject categories were obtained from the WoS database. The database was filtered to extract records corresponding to the top ten subject categories across successive time intervals (2016–2017, 2018–2019, 2020–2021, 2022–2023, and 2024–2025), ranked by document count. The five leading countries were then identified based on publication volume, and the data were entered into Microsoft Excel, where the "insert map" function was employed to generate the geographic visualization. Similarly, the extracted data were imported into OriginPro (Version 2026, OriginLab Corporation), where a bubble chart was generated with time intervals on the X-axis and subject categories on the Y-axis, and document counts represented by both bubble size. In addition, annual publication output and mean total citations per year were visualized in OriginPro using a combined bar–line chart, with publication counts

Table 1 Types of documents published on ToBRFV from 2016 to 2025

Rank	Types	Numbers	Percentage
1	Article	194	76.1
2	Review article	17	6.7
3	Meeting abstract	16	6.2
4	Editorial material	11	4.3
5	Proceeding paper	8	3.1
6	Early access	5	2.0
7	News item	4	1.6

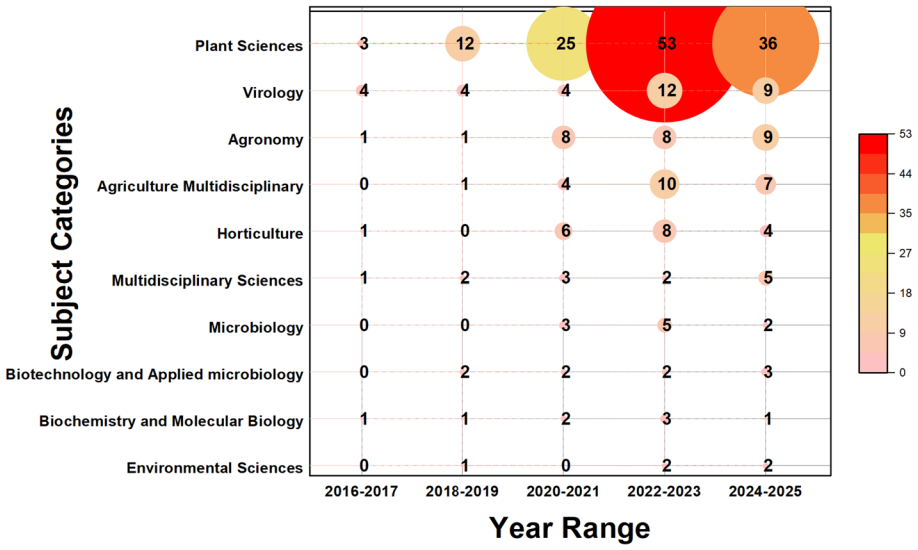


Fig. 1 Bubble chart of top 10 subject categories of ToBRFV research. The size of bubbles are proportional to the frequency of documents in a subject subject category within the corresponding year range

represented by bars and mean citations per year by an overlaid line on a secondary axis to enable concurrent trend assessment.

3 Results and discussion

3.1 Document volume

WoS subject category (hereof referred to as subject categories) refers to the disciplinary classification assigned by the database to journals indexed in its database, grouping them into specific research fields. A total of 255 records obtained from the WoS database were analyzed, and it was determined that research articles constituted a significant percentage of the total (194 records, 76.1%) (Table 1). Figure 1 illustrates the distribution of ToBRFV-related publications across subject categories and year ranges. Plant Sciences ($n = 129$) consistently dominated throughout the study period, peaking at 53 publications in 2022–2023 before declining slightly to 36 in 2024–2025. Virology maintained a stable output until 2020–2021, followed by a notable surge (12 publications) in 2022–2023 and a slight decline thereafter. Agronomy and Agriculture Multidisciplinary exhibited marked growth in 2020–2023, highlighting diversification of agricultural research. Horticulture peaked in 2022–2023, while Microbiology and Biotechnology contributions emerged strongly after 2020, reflecting growing interest in microbial and molecular approaches. Although recording fewer articles, the Multidisciplinary Sciences gained prominence in recent years. The results indicate a strong dominance of plant sciences,

with increasing integration of virology, microbiology, and multidisciplinary research, particularly during 2020–2023 interval. The Plants-Basel outlet (journal) is predominantly favored by researchers for the publication of their findings. The higher number of ToBRFV publications in Plants compared with Plant Disease can be attributed primarily to differences in journal scope, publication model, and editorial focus. The journal has a broad plant science remit and an open-access, high-throughput publishing model that accommodates diverse studies ranging from molecular characterization and genomics to biotechnology and resistance breeding, all of which constitute major themes in ToBRFV research. In contrast, Plant Disease is a more specialized, society-based journal emphasizing applied plant pathology, disease reports, and management studies, resulting in comparatively lower publication volume on topics dominated by fundamental and experimental research.

3.2 Publication output

The global distribution of scientific publications reveals a pronounced concentration of research output in specific regions, with USA [18] leading publication count. This is followed by Israel [19], Italy [20], Mexico [21], and People Republic of China [5] (Fig. 2). The USA and Mexico are great trade partners, which may have facilitated research collaboration among these countries and potentially contributing to the spike in publication volume observed in both countries. Also, Italy, USA, China is in the list of the top ten producers of tomatoes which translates to the availability of adequate funding which drives research on the pathogen. It should also be noted that disparities in research funding in developing countries constitute a significant constraint on investigations of this virus, as essential research materials are prohibitively expensive.

ToBRFV causes destructive effect on the fruits and foliar qualities of tomato and other economic crops (Fig. 3) The first detection of ToBRFV was officially reported in 2016 [1], marking the beginning of scientific report and research (Figs. 4 and 5). Correspondingly, the earliest publication on this topic appeared in the same year, as reflected in Fig. 4. A steady increase in the number of publications followed through 2018, after which an increase in trend was observed. Several early studies focused on the identification and detection of the virus in various countries, including those by [15, 22–26]. Notably, the year 2019 also recorded the first report of *Bombus terrestris* serving as a possible vector for ToBRFV transmission [27], which likely contributed to the observed increase in research output. The peak in publication volume occurred in 2022, with a total of 51

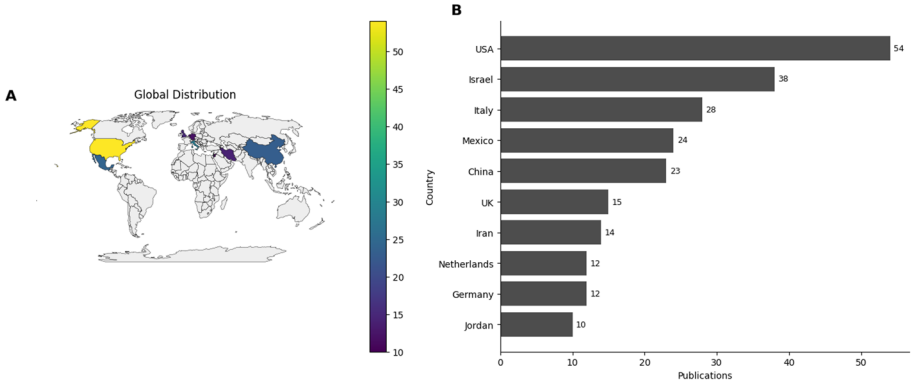


Fig. 2 Map displaying global distribution of ToBRFV research by countries (**a**) and publication numbers (**b**)



Fig. 3 Symptoms of Tomato brown rugose fruit virus (ToBRFV) infection on tomato fruit (**a**) and leaves (**b**) (Author's own source)

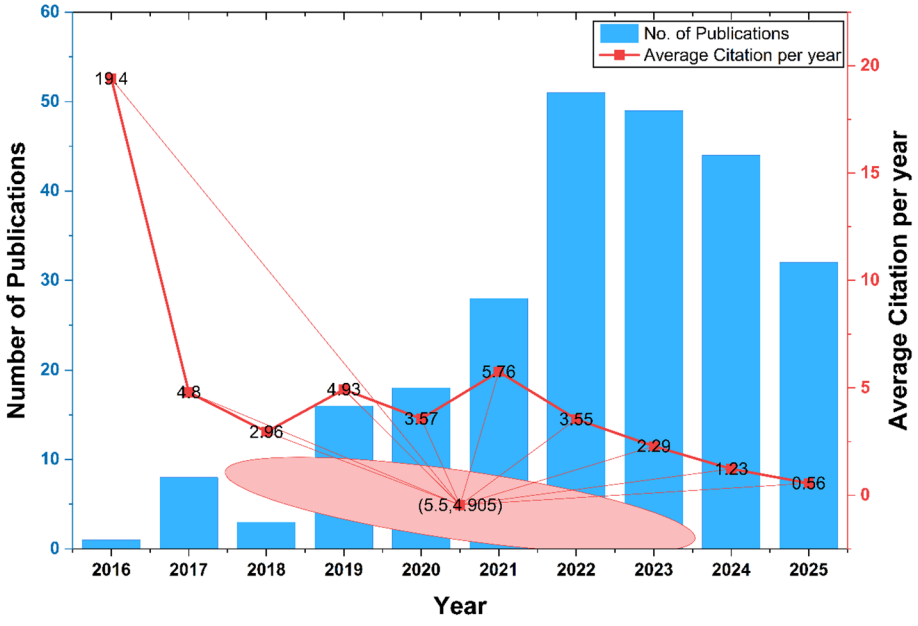


Fig. 4 Annual publications and mean total citations per year on Tomato brown rugose fruit virus (ToBRFV)

research articles published on ToBRFV. That year also recorded new reports of the virus in Syria [28], Palestine [29], Switzerland [30], Norway [20], France [31], Slovenia [32], Iran [5, 21], and Saudi Arabia [33]. Simultaneously, significant advances were made in developing robust detection methods [34–36]. Furthermore, a noble breakthrough about the development of ToBRFV-resistant tomato varieties via the knockdown of *SlTOM1a–e* homologs was also documented during this period [37]. This offered a significant contribution to the understanding of viral transmission and management strategies. These research activities, along with global economic concerns—such as seed trade embargos due to the virus' spread, as reported by the [38]—emphasized the elevated attention and urgency surrounding the virus. As expected, the year 2016 recorded a single publication output but had the highest mean citation per year in comparison to other years. This is

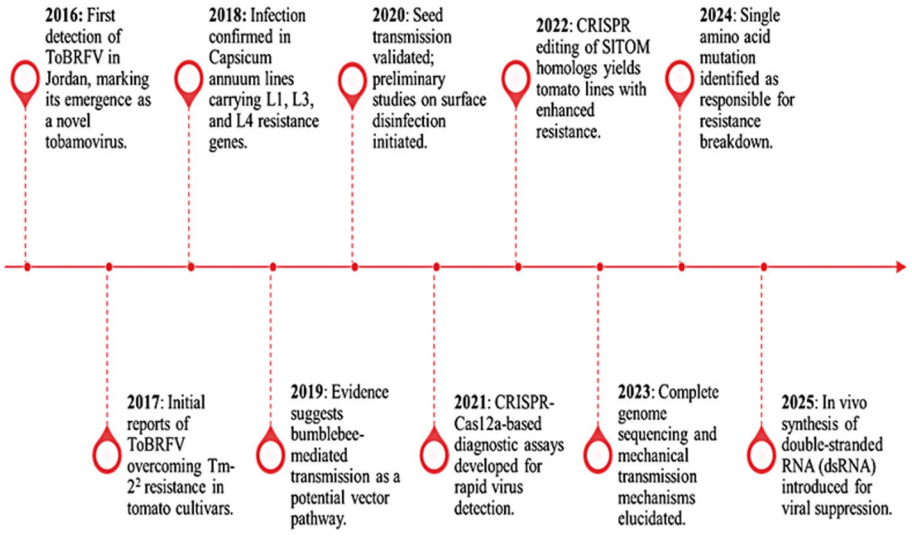


Fig. 5 Timeline of major key discoveries of Tomato brown rugose fruit virus (ToBRFV) research from 2016 to 2025

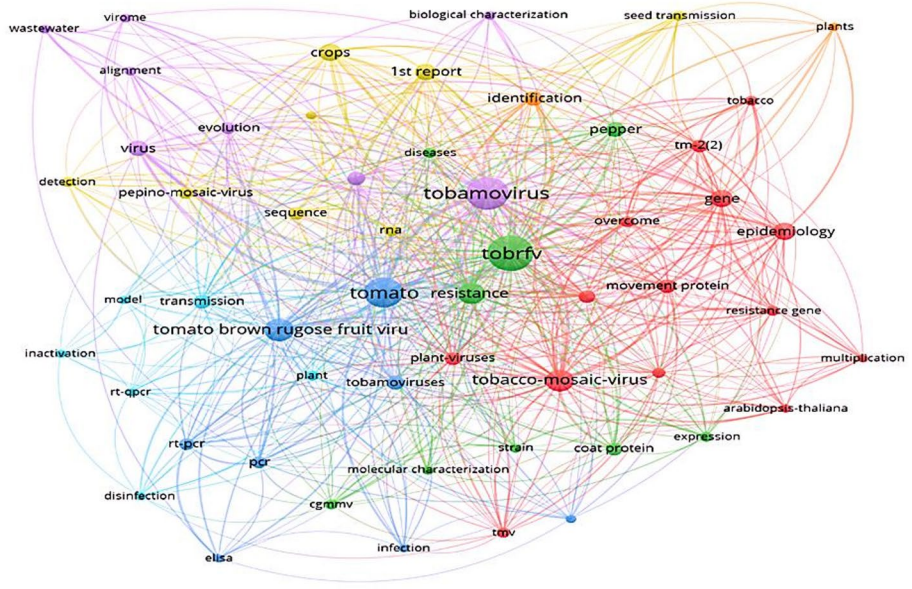


Fig. 6 A map of keyword co-occurrence analysis

understandable as subsequent research works on the field references this foundational study. In the same year, several other groundbreaking studies on the virus were reported [9, 10, 19, 35, 39–44].

3.3 Keyword co-occurrence analysis

The keyword co-occurrence map (Fig. 6) reveals four distinct clusters, each represented by a different color, illustrating the thematic relationships among frequently used terms in ToBRFV-related literature. The initial (red) and secondary (blue) clusters are predominantly comprised of keywords associated with tomato and other host plants. It is noteworthy that terms such as "coat protein" and "tobamoviruses" are also present in these clusters, reflecting the prevalent practice of targeting the coat protein and movement

protein region in RT-PCR assays to differentiate ToBRFV from other tobamoviruses. This finding serves to substantiate the presence of keywords such as 'RT-PCR' and 'PCR' within the second cluster. The third cluster (red) focuses on viral characterization, incorporating terms such as "*Tm-2*^{2}", "movement protein", and "sequence". The virus's distinctive capacity to circumvent *Tm-2*^{2}-mediated resistance trait that distinguishes it from the majority of tobamoviruses—further reinforces its unique pathogenic profile. The final cluster, designated by green, encompasses terms such as "detection", "disinfection", "resistance", and "RNA", reflecting an increased research interest on containment strategies. Recent studies have demonstrated that the virus can retain its infectivity on contaminated tools and garments [39, 45, 46]. However, these studies also demonstrated that the disinfection of seeds and agricultural equipment with suitable disinfectant concentrations can effectively eliminate the virus. Collectively, these clustering patterns underscore the evolving research priorities, particularly the shift towards mitigating viral transmission.

3.4 Keyword evolution

Figure 7 analyzes keywords and research areas on ToBRFV research. Within the niche themes, the "hts" keyword is identified. Several studies have validated the efficacy of high-throughput sequencing (HTS) technology in distinguishing and detecting ToBRFV from other viruses during mixed infections ([47]; Luigi et al., 2024). In the motor themes quadrant, transcriptomic analysis emerges as a notable keyword. This technological framework facilitates the identification of candidate genes that can be strategically modified to enhance resistance in susceptible cultivars [7, 48].

3.5 Top authors' production

The establishment of scientific relations and the acquisition of new methods can be facilitated by national and international collaboration among researchers. Regarding the subject of ToBRFV, Dombrovsky (Fig. 8) is a prominent researcher who engages in extensive research collaboration with other researchers, as evidenced by the data. As stated in the research by [41], certain peppers that possessed the L-resistance gene demonstrated

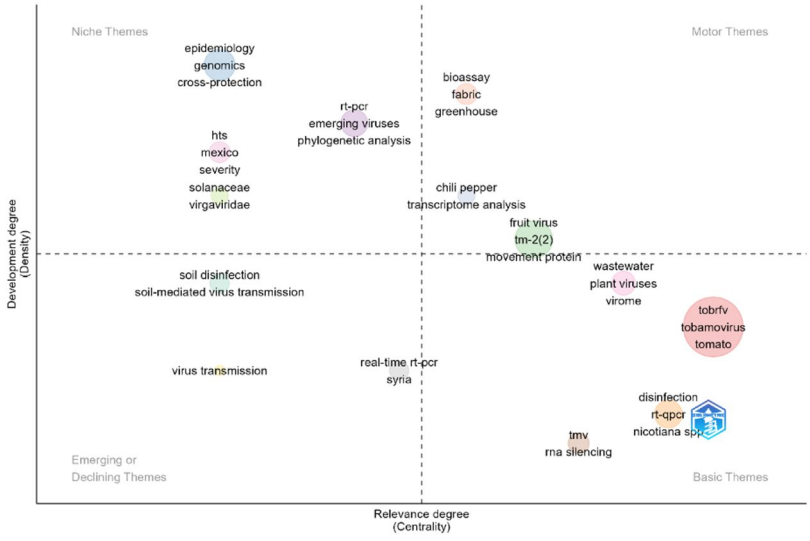


Fig. 7 A) Timeframes of research on ToBRFV

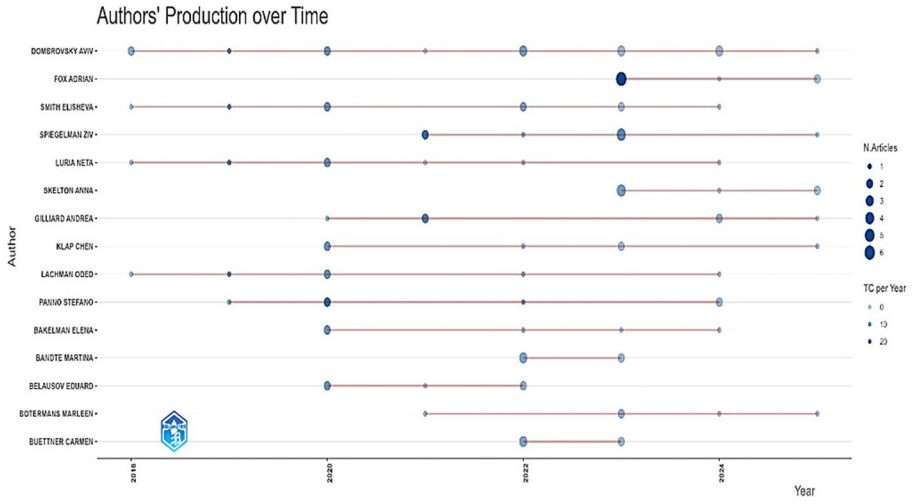


Fig. 8 A graph of top authors' production on ToBRFV research

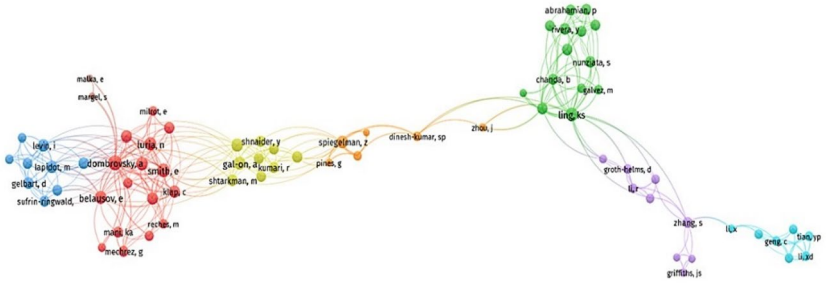


Fig. 9 A network of authors' citation analysis

a certain degree of tolerance to the virus. It is evident that this exemplary research, in conjunction with other studies [49–51], has garnered the attention of other researchers, thus prompting the proposal of collaborative endeavors on the subject. It has been demonstrated that the researcher who has collaborated most extensively may not be the one with the highest number of citations in their field of study. The publication of Salem [1] has garnered the highest number of citations, as it was the inaugural report of the virus. The article has thus far garnered 256 citations, which is the reason why its node is higher than the others.

3.6 Authors collaboration network

The co-authorship map (Fig. 9) demonstrates both collaborative concentration and structural fragmentation. A small number of highly productive authors dominate the network, while many peripheral researchers remain weakly connected. The largest cluster (red nodes) is dominated by authors such as Luria N, Smith E, Recher M,,Dombrovsky A, and others, who act as major researchers' hubs linking other researchers.It is noteworthy, that DombrovskyA, with a notable bigger node of in the cluster, has collaborated with Smith E, and Luria on reporting a new isolate of ToBRFV (A134T) which is more virulent than the wild type ToBRFV [52]. Aside, the authors has reputable collaborations with Smith of tobamovirus management [53], seed transmission of tobamoviruses [52] and report on Bumblebee to be a potent vector of the virus [27] The density of within the

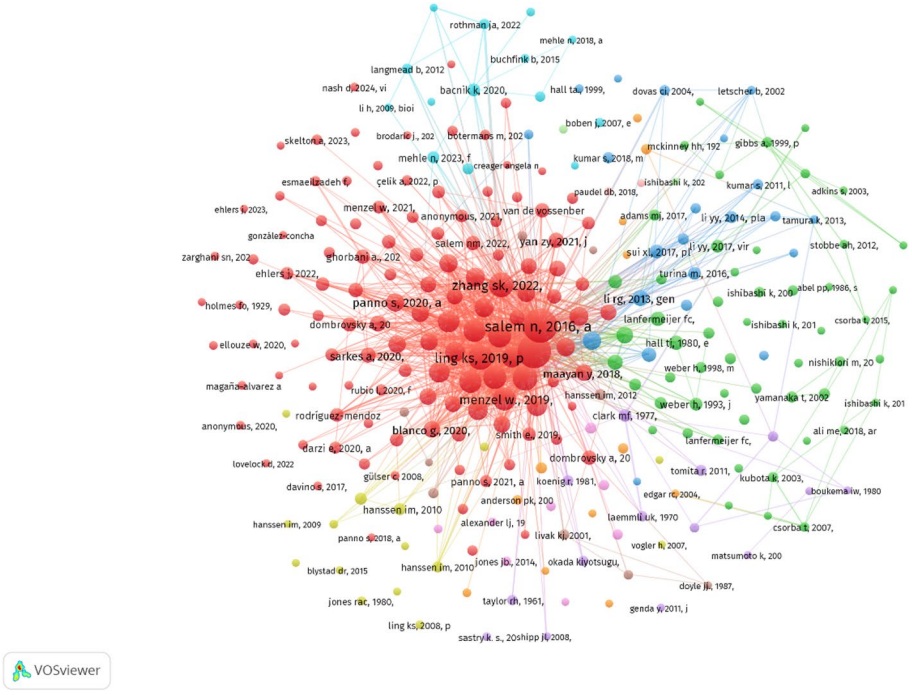


Fig. 10 A map of document co-citation analysis

cluster (intercluster) reveals connections of established and productive research community, with frequent co-authorship and shared projects.

A second significant cluster (green), centered around Rivera Y, represents another influential collaborative group. This network appears more cohesive internally but less integrated with other clusters, suggesting a or thematic specialization.

The map provides a visual representation of the citation network related to publications concerning ToBRFV since its discovery. The network under consideration consists of 50 nodes and 4 clusters, as well as 151 citation nodes. This configuration indicates that 37 authors are engaged in research cooperation through 151 links. The links represent the co-occurrence strength, with larger nodes denoting higher centrality, signifying their importance in connecting other nodes.

The document co-citation network visualization reveals a densely interconnected bibliometric landscape dominated by a salient 216 central cluster (highlighted in red) that functions as a central link to publications spanning 2002–2024. This hub, characterized by elevated node centrality and robust edge weights indicative of high co-citation frequencies, underscores the foundational influence of the 2017 publication on subsequent publications based on detection of the virus in other geographical locations, Outlying clusters in green and blue, primarily from 2022 to 2023, denote emergent subdomains originating from the core, while peripheral nodes such as Jones (2016) and Taylor (2020) highlight ancillary yet influential contributions, collectively evidencing a progressive research trajectory anchored by the pivotal 2017 work.

As illustrated in Table 2, the document with the most significant number of citations is that of Salem et al. [1], which has received 316 citations. This report constitutes the inaugural documentation of the virus. The second most-cited document (310), authored by de [54], reported that the *Tm-2*^{2} gene was not effective in protecting the plants from the virus, despite the gene's ability to confer resistance against other tobamoviruses. These,

Table 2 Top 10 most cited documents on ToBRFV

Rank	References	Total Citation	DOI	Title	Key findings	Link nodes
1	Salem et al., [1]	316	https://doi.org/10.1007/s00705-015-2677-7	A new Tobamovirus infecting tomato crops in Jordan	• A 6393-nt single-stranded new Tobamovirus isolate was sequenced and therefore named Tomato brown rugose fruit virus	157
2	Luria et al., [54]	310	https://doi.org/10.1371/journal.pone.0170429	A new Israeli Tobamovirus isolate infects tomato plants harboring *Tm-2*^{2} resistance genes	• ToBRFV was discovered to infect tomato varieties that had *Tm-2*^{2} irrespective of its resistance to other tobamoviruses	185
3	Zhang et al., [13]	172	https://doi.org/10.1111/mpp.13229	Tomato brown rugose fruit virus: An emerging and rapidly spreading plant RNA virus that threatens tomato production worldwide	• Comprehensive overview was given on the status of the virus	122
4	Levitzky et al., [27]	146	https://doi.org/10.1371/journal.pone.0210871	The bumblebee *Bombus terrestris* carries a primary inoculum of Tomato brown rugose fruit virus contributing to disease spread in tomatoes	• Bumble bees serve as primary vectors of the virus through their buzz pollination activities	74
5	Ling et al., [24]	136	https://doi.org/10.1094/PDIS-11-18-1959-PDN	First report of Tomato brown rugose fruit virus infecting greenhouse tomato in the United States	• The virus was first detected in Southern California (USA)	76

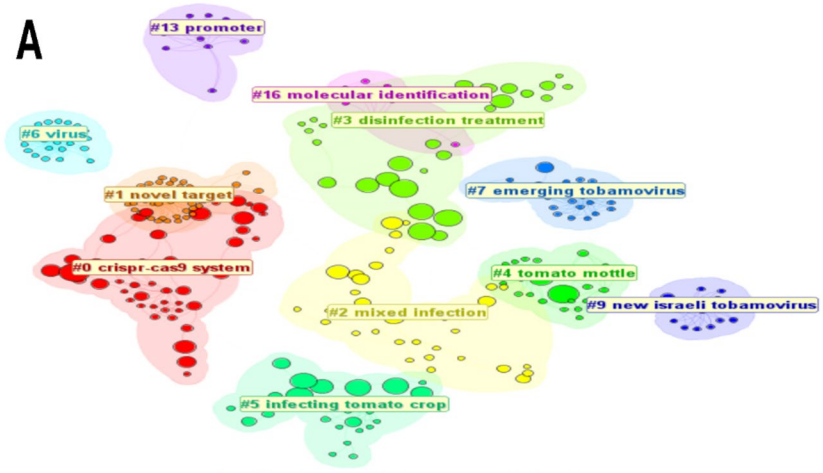
Table 2 (continued)

Rank	References	Total Citation	DOI	Title	Key findings	Link nodes
6	Oladokun et al., [55]	132	https://doi.org/10.1111/ppa.13096	Tomato brown rugose fruit disease: current distribution, knowledge and future prospects	• A review on the status of the virus was presented	54
7	Panno et al., [25]	114	https://doi.org/10.1094/PDIS-12-18-2254-PDN	First report of tomato brown rugose fruit virus on tomato crops in Italy	• The detection and presence of the virus was reported in Italy (Ragusa province)	64
8	Davino et al., [56]	111	https://doi.org/10.3390/plants9111615	Tomato brown rugose fruit virus: Seed transmission rate and efficacy of different seed disinfection treatments	• 2% hydrochloric acid + 1.5% sodium hypochlorite treatment of seeds for 24 h inactivates the virus though detectable through RT-qPCR	67
9	Alkowni et al., [15]	108	https://doi.org/10.1111/j.1461-0248.2004.00699.x	Molecular identification of tomato brown rugose fruit virus in tomato in Palestine	• The virus presence was reported in Palestine	56
10	Yan et al., [57]	100	https://doi.org/10.1094/PDIS-05-19-1045-PDN	First report of Tomato brown rugose fruit virus infecting tomato in China	• First report of the virus in China	66

in addition to other articles in the list, were instrumental in clarifying the fundamental biology and behavior of the virus during the nascent stages of research.

3.7 Citation bursts

Citation bursts are a quantitative method of identifying keywords that have been frequently cited in the literature of a given research theme or area. This analysis is especially useful in identifying subjects or topics that have experienced a surge in citations [58]. From the WoS dataset, 15 references which had the strongest citation bursts were analyzed as presented in Fig. 10B. Lines in blue represent the time interval, whereas the red lines depict the time interval in which a subject was discovered to have a burst, popularly referred to as citation burst event. The citation burst ranges from 16.57 to 3.51.



B

Top 15 References with the Strongest Citation Bursts

References	Year	Strength	Begin	End	2016 - 2025
Salem N, 2016, ARCH VIROL, V161, P503, DOI 10.1007/s00705-015-2677-7, DOI	2016	16.57	2017	2021	
Zhang SK, 2022, MOL PLANT PATHOL, V23, P1262, DOI 10.1111/mpp.13229, DOI	2022	15.29	2023	2025	
Luria N, 2017, PLOS ONE, V12, P0, DOI 10.1371/journal.pone.0170429, DOI	2017	12.44	2018	2022	
Caruso AG, 2022, ANN APPL BIOL, V181, P258, DOI 10.1111/aab.12788, DOI	2022	5.8	2023	2025	
Amer MA, 2020, NEW DISEASE REPORTS, V41, P0, DOI 10.5197/j.2044-0588.2020.041.024, DOI	2020	5.8	2021	2022	
Dombrovsky A, 2017, ADVANCES IN SEED BIOLOGY, V0, PP234, DOI 10.5772/intechopen.70244, 10.5772/INTECHOPEN.70244, DOI	2017	5	2021	2022	
Maayan Y, 2018, ARCH VIROL, V163, P1863, DOI 10.1007/s00705-018-3819-5, DOI	2018	4.73	2021	2022	
Salem NM, 2022, PLANTS-BASEL, V11, P0, DOI 10.3390/plants11172287, DOI	2022	4.69	2023	2025	
Sabra A, 2022, PLANT DIS, V106, P1310, DOI 10.1094/PDIS-05-21-1065-PDN, DOI	2022	4.36	2022	2023	
Hasan ZM, 2022, PLANT DIS, V106, P772, DOI 10.1094/PDIS-07-21-1356-PDN, DOI	2022	4.07	2022	2023	
Ehlers J, 2022, HORTICULTURAE, V8, P0, DOI 10.3390/horticulturae8080751, DOI	2022	3.94	2023	2025	
Jewehan A, 2022, J GEN PLANT PATHOL, V88, P187, DOI 10.1007/s10327-022-01055-8, DOI	2022	3.85	2023	2025	
Jewehan A, 2022, ARCH VIROL, V167, P1559, DOI 10.1007/s00705-022-05438-2, DOI	2022	3.85	2023	2025	
Samarah N, 2021, EUR J PLANT PATHOL, V159, P153, DOI 10.1007/s10658-020-02151-1, DOI	2021	3.64	2022	2025	
Chanda B, 2021, VIROL J, V18, P0, DOI 10.1186/s12985-020-01479-8, DOI	2021	3.51	2022	2025	

Fig. 10 Network visualization of reference co-citation. **A**) Clustering analysis of ToBRFV network and, **B**) Top 15 references with the strongest citation burs in the co-citation network

Overall, the top five references with the strongest citation burst was Salem [1] (burst strength,16.57; 2017–2021), [13] (burst strength, 15.9; 2023–2025), [54] (burst strength, 12.44; 2018–2022), [11] (burst strength, 5.8; 2023–2025), and [59] (burst strength, 5.8; 2021–2022). Expectedly, the first paper to report on the research topic was Salem [1] and this explains the start of citation burst from 2017 till 2021 as subsequent research on the topic references it.

Furthermore, the domain visualization depicted in Fig. 10A displays the presence of discrete thematic clusters within the domain of tobamovirus-related research. The most prominent and central cluster (#0, CRISPR-Cas9 system) underscores the growing significance of genome-editing strategies in the areas of plant virology, reflecting the field's inclination towards precision-based resistance breeding. Closely associated with this core are clusters such as novel target (#1) and molecular identification (#16), suggesting that innovations in molecular tools are strongly coupled with applied resistance strategies. This finding suggests a discernible methodological convergence in extant literature, wherein fundamental molecular insights are expeditiously translated into applied control measures. Peripheral clusters, including emerging tobamovirus (#7) and new Israeli tobamovirus (#9), signify emergent research domains with a geographic and epidemiological focus. Their peripheral positioning suggests that, while these areas are important, they have not yet attained the centrality of molecular resistance studies. Additionally, cluster light green clusters (#4- Tomato mottle mosaic virus and #5 infecting tomato

crop) due to their common host. Often, symptoms of ToMMV are difficult to distinguish them from that of ToBRFV since their symptoms are identical [60]. This may account for the presence of tomato mottle mosaic virus cluster (#) in the map. The clusters identified, namely disinfection treatment [16] and mixed infection (#2), further reflects the extensive thematic scope of tobamovirus research. This research encompasses a wide range of disciplines, from the practical applications of phytosanitary practices to the intricate dynamics of host–virus–virus interactions.

4 Conclusion

This bibliometric analysis demonstrates that ToBRFV research has expanded rapidly since 2016, with notable peaks in 2022–2023. The field is dominated by plant science and virology publications, though increasing contributions from biotechnology and microbiology reflect the adoption of molecular tools. Early research centred on detection and characterization, while recent studies emphasize resistance breeding, seed disinfection, and epidemiological monitoring. Collaboration networks reveal appreciable number of influential authors and institutions, however broader international cooperation remains can still be explored. Citation burst analyses identify foundational studies (e.g., [1, 54]) as anchors of the research landscape, while emerging hotspots point to CRISPR-mediated resistance and transcriptomic approaches. In the future, research priorities should strengthen global collaborations to help track and mitigate ToBRFV spread. By mapping the intellectual and collaborative structure of the field, this study provides a foundation for guiding future ToBRFV research and management strategies.

Supplementary Information

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Supplementary material 1.

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