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Global research landscape and trends in *Toxoplasma gondii* from 2003 to 2022: A bibliometric analysis

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ABSTRACT

Toxoplasmosis is a globally prevalent zoonotic disease with significant public health impact, yet effective prevention and control measures remain lacking. This study analyzed 10,737 publications from 2003 to 2022 in the Web of Science and Scopus databases using bibliometric methods. Key metrics, including annual publication trends, journals, core authors, contributing countries, citations, and keywords, were examined. The findings indicate that publication output in toxoplasmosis research has remained stable, with core journals predominantly in the parasitology field. The United States leads in research capacity and contributions, followed by Brazil, Germany, the United Kingdom, and France, while China shows promising potential. Epidemiological research has been a longstanding hotspot in this field, encompassing areas such as diagnosis, prevention, treatment, virulence analysis, and genotyping. The field is expanding towards mechanistic research and translational applications, shifting its emphasis from basic science to practical public health applications and disease prevention strategies. Current research frontiers and emerging trends focus on host-pathogen interactions, innovative prevention and control methods, and the global public health implications of toxoplasmosis. This study provides a comprehensive overview of the past two decades of progress in toxoplasmosis research, offering valuable insights for future studies and academic development.

1. Introduction

Toxoplasma gondii (T. gondii) has a global distribution and parasitizes the nucleated cells of humans and various animals. For immune compromised host, *T. gondii* can lead to serious consequences, making it an opportunistic pathogenic parasite (Matta et al., 2021). *T. gondii* can infect almost all warm-blooded animals, including humans, and pose a serious threat to the health of human beings and animals (Aguirre et al., 2019). In the 1970s and 1980s, the morphology, life cycle, epidemiology, pathogenic mechanisms, diagnosis, treatment, and cultivation of *T. gondii* were the main focus of Dubey et al.'s research (Webster, 2010). IFN-γ was found to be the main mediator in response *T. gondii* infection and subsequent studies related to host immune protection and the anti-*T. gondii* mechanism promoted the development of immunology in this field (Suzuki et al., 1988). In the 1990s, significant progress was made in understanding the invasion mechanisms of *T. gondii* (Carruthers and Sibley, 1997; Dobrowolski and Sibley, 1996). During this period, the application of PCR technology in the clinical diagnosis of *T. gondii* significantly accelerated genetic research, particularly in areas such as genetic diversity and population size (Holliman et al., 1990). Building on these advances, the development and implementation of genetic tools—including transfection systems, molecular markers, and gene knockout techniques—provided researchers with powerful methods to explore the parasite's biology in greater depth. These tools enabled a more comprehensive understanding of its genetic structure, pathogenic mechanisms, and host-parasite interactions. The foundational work of

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Sibley, Howe, and other scholars was crucial in shaping the direction of modern genotyping research (Howe and Sibley, 1995; Sibley and Boothroyd, 1992). As research on *T. gondii* continues to evolve, it remains an active and dynamic field, with new discoveries and publications emerging annually. Given this ongoing progress, it is important to study the research trends in *T. gondii* and understand the role that key technological innovations over the past two decades have played in shaping the field.

Bibliometrics is a statistical method that uses multiple parameters and techniques to evaluate the development of a specific field and predict its future development trend and is widely used in many fields (Sweileh et al., 2016). This method illustrates the knowledge structure and evolution of the research field through mathematical statistics and visual knowledge graphs, provides a panoramic view of the field and reveals trend topics to help establish further research directions (Miao et al., 2022). CiteSpace and VOSviewer analysis software stand out as the most commonly used tools for document information visualization. Renowned for their strong operability, effective visualization effects, and exceptional mapping abilities, these tools are instrumental in assisting researchers in identifying key information and understanding the objective landscape of scientific development within specific fields (Li et al., 2022). Compared to traditional literature metrology methods, the visual analysis of scientific knowledge graphs is more intuitive and easier to interpret.

The application of bibliometrics in the field of parasites, particularly in *T. gondii* research, remains limited, with only a few articles analyzing the evolution of *T. gondii* research in specific regions. According to the bibliometric analysis of *T. gondii* literature around the world, the current research status of *T. gondii* literature has focused mainly on a single database (Fakhar et al., 2018; Tao et al., 2023). Based on this, the present study conducted a comprehensive bibliometric analysis of *T. gondii* research literature retrieved from the Web of Science and Scopus databases spanning from 2003 to 2022. This analysis aims to unveil the shifting trends in *T. gondii* research worldwide over the past two decades, examine the distribution and research focuses of various countries, institutions, and authors, and offer insights for future research and practical applications related to *T. gondii* (Fig. 1).

2. Data and methods

2.1. Data acquisition

The Web of Science Core Collection database is recognized as the premier citation database globally, encompassing papers from highly influential journals, conference proceedings, and books. In comparison, the Scopus database currently stands as the world's largest abstract and citation database, covering approximately 15,000 scientific, technical, and medical journals (Falagas et al., 2008). To ensure the scientific rigor of this study, all data were sourced exclusively from the Web of Science Core Collection and the Scopus database. Furthermore, to comprehensively capture the core literature in the field of *T. gondii*, multiple retrieval attempts were made. The search strategy employed in the Web of Science Core Collection involved the following query: ((TI = (*Toxoplasma gondii*)) OR TI = (Toxoplasmosis)) OR TI = (Toxoplasma spp.). The Scopus database search strategy was finally determined as: (TITLE (toxoplasma AND gondii) OR TITLE (toxoplasmosis) OR TITLE (toxoplasma AND spp.)) AND PUBYEAR > 2002 AND PUBYEAR < 2023 AND (LIMIT-TO (DOCTYPE, "ar")), with all literature classified as "Article" and the time span ranging from January 2003 to December 2022.

2.2. Research methods

The primary data sources for this study were the Web of Science database supplemented with the Scopus database. The literature sourced from the Scopus database was converted into a WOS-specific TXT format and integrated with the Web of Science database using CiteSpace software. Furthermore, Excel software was employed for literature analysis, focusing on the annual fluctuations in published article counts and the distribution of periodicals.

This study used VOSviewer software to analyze the clustering co-occurrence relationships of factors such as authors and countries. Co-occurrence refers to the simultaneous appearance of specific elements in the same publication or dataset, revealing the relationships and cooperation trends between research topics, authors, or countries (co-keywords, co-authors or co-countries). Core Author Groups refer to the group of authors who have published the most papers during a specific period, commonly used to identify leading figures in the field (Liu et al., 2020). After extracting data from relevant databases, clustering maps were generated using VOSviewer to display the collaboration relationships between authors and countries. Additionally, the "Geoplot"

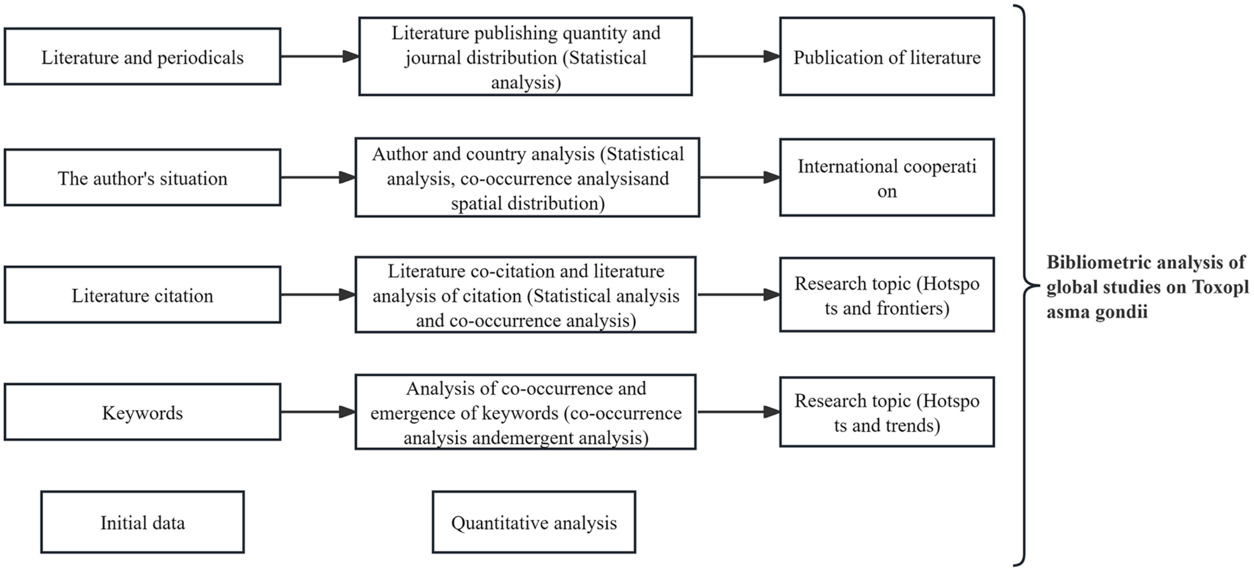


Fig. 1. Flow chart of the bibliometric analysis of *T. gondii*.

function in Scimago Graphica 1.0.36 software was used to create national cooperation networks and geographical distribution maps to show collaborations between different countries. The statistical core authors were analyzed using Price's Law. The formula for calculating core authors was as follows: M= 0.749 (Nmax)1/2, where M represents the number of papers, Nmax represents the number of papers by the most productive authors during the statistical period, and authors with M or more papers were considered core authors (Price, 1976). To ensure the representativeness of the analysis results and the readability of the images, common thresholds for cluster analysis were set: the minimum number of authors was 40, resulting in the inclusion of 41 authors, and the minimum number of published documents was 35, with 50 countries and regions ultimately selected. Analyses were conducted to generate national cooperation networks and geographical distribution maps.

The research theme involved analyzing the clustering co-occurrence of factors such as reference co-citation patterns, citation analysis of citing documents, and keywords. Reference co-citation refers to the phenomenon where two or more documents are cited together by a third document, which helps to identify the relationships and thematic connections between different references. Citing documents, on the other hand, are the works that cite the core references being analyzed, providing insights into the influence and reach of specific studies. To ensure a comprehensive and representative reference dataset, the threshold for the minimum number of citations was set to 200, resulting in the identification of 38 core references for clustering and analysis, and a visual knowledge graph of reference cocitations was constructed. The measurement function of the Web of Science and Scopus databases enables direct access to statistics regarding citation literature in related fields upon completion of retrieval. The researchers consolidated keywords with similar meanings and established a minimum threshold for keyword occurrence at 20. 121 keywords were included for co-occurrence cluster analysis and keyword emergence analysis.

3. Results

3.1. Literature quantity analysis

A total of 19,163 articles in *T. gondii* research were identified from 2003 to 2022. After excluding duplicates and articles lacking information, 10,737 articles were included in this study. The annual number of articles published increased from 289 in 2003–684 in 2022, marking a nearly 2.4-fold increase. The highest annual volume was observed in 2021, with 813 articles. An analysis of the annual publication volume and trend revealed an overall upward trajectory in the number of studies conducted in the field of *T. gondii*. From 2003 to 2007, fewer than 400 articles were published, indicating a trend toward slow growth. Subsequently, from 2007 to 2016, there was a steady increase in the number of published articles. Over the past decade, there has been a cumulative increase of more than 100 % in the number of articles about *T. gondii*. Although there was a slight decrease in the number of articles from 2016 to 2018, a steady increase was observed from 2019 to 2021, with more than 700 articles published annually (Fig. 2).

3.2. Analysis of journals published in the literature

In this study, the top 25 journals in the field of *T. gondii* research collectively published 3447 articles, accounting for 32.11 % of the total literature analyzed (Table S1). Veterinary Parasitology ranked first with 378 articles (3.52 %), followed by Journal of Parasitology (257 articles, 2.39 %) and Parasitology Research (239 articles, 2.23 %). Among these journals, 8 were from the United States, which contributed the highest number of articles (34.63 % of the top 25 total), while other key contributors included the Netherlands, the United Kingdom, and Switzerland. In terms of journal impact, 7 journals were classified in the Q1 region, with PLoS Pathogens having the highest Impact Factor (IF = 6.70), while the majority of other journals fell into the Q2 and Q3 categories. These results demonstrate that a concentrated portion of *T. gondii* research is published in a limited number of high-impact and regionally distributed journals.

3.3. Core author analysis

According to the statistical results, there were three core authors. Dubey from the USDA ARS Beltsville Agricultural Research Center ranked first according to the number of published articles, with 407 articles, accounting for 3.79 % of the total number of published articles (407/10,737). Dubey focused on genotyping, epidemiological investigation, diagnosis, and prevention and control. During the 1970s, Dubey made significant contributions to the ontogeny, morphology, and clinical diagnosis of *T. gondii*. Over the past two decades, their research has expanded globally, investigating the genetic and biological characteristics of *T. gondii*, including its population structure and virulence (Lehmann et al., 2006).

The second was Xing-Quan Zhu from Shanxi Agricultural University

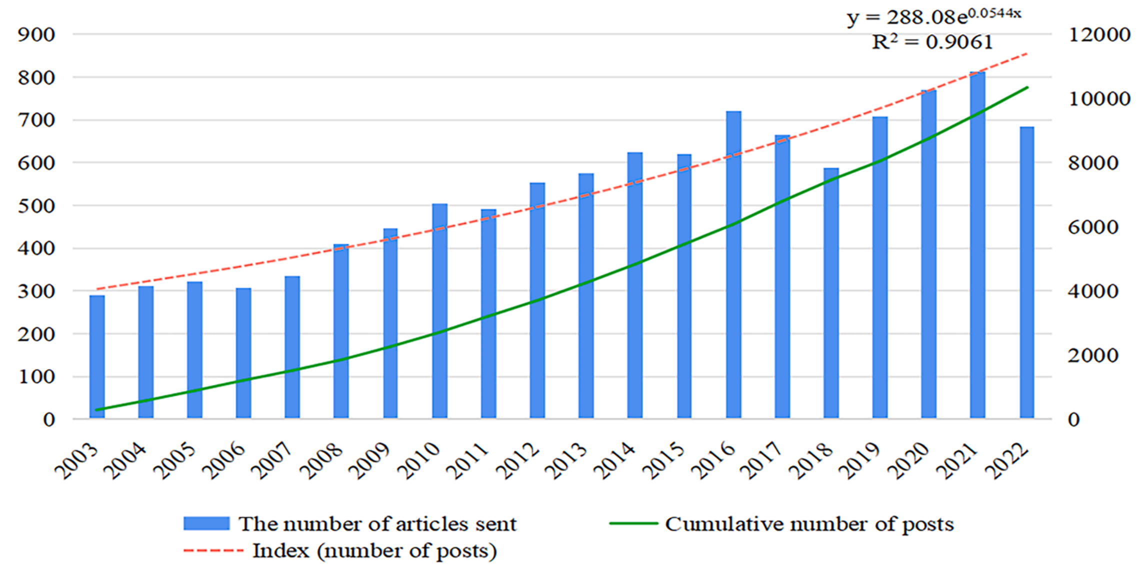


Fig. 2. The number of articles published annually in the field of *T. gondii* research in the past 20 years.

who published 230 articles, accounting for 2.14 % of the total (230/10737). Zhu focused on the epidemiology and pathogenesis of critical animal parasitic diseases, including zoonotic parasitic diseases, genomics and functional genomics, molecular vaccines, and molecular detection technology (Elsheikha et al., 2020; Huang et al., 2019; Liu et al., 2014). Zhu has significantly advanced the epidemiological understanding of *T. gondii* in China, elucidated the biological functions of numerous *T. gondii* genes, and made significant contributions to the immune prevention and control of toxoplasmosis.

Chunlei Su from Tennessee University has published 152 articles, accounting for 1.42 % (152/10,737) of the total published articles. His research primarily focused on genetic diversity, population structure, and evolution. Su has demonstrated the pivotal role of the PCR-RFLP method in identifying *T. gondii* genotypes. This method has led to the discovery of multiple distinct genotypes in South America, thereby advancing research on the diversification of *T. gondii* genotypes (Shwab et al., 2014; Su et al., 2010; Taylor et al., 2006).

The author collaboration network diagram was shown in Fig. 3. The authors who published more than 40 articles (Table S2) were composed of 6 clusters, corresponding to 6 colors, and the authors closely cooperated. Through the analysis of cooperation frequency and closeness, significant core authors were identified within the cooperation groups, with Dubey and Zhu serving as central figures. Kwok and Su were closely related to Dubey, while Zhou, Elsheikha, Huang and Zhu were closely related. Although no significant central nodes were found in the other clusters, authors both within and outside of these clusters still maintained close cooperation.

3.4. *Analysis of countries with research hotspots*

The study revealed that these literatures were originated from 153 countries and regions over the past two decades. Among them, the top 50 countries and regions (Table S3) were selected to construct a cooperative network map and depict geographical distribution (Fig. 4). Notably, the United States, China, and Brazil emerge as pivotal nations in *T. gondii* research. The participation of European countries in *T. gondii* research is generally robust, with the United Kingdom, France, and Germany leading the European endeavors. Australia stands out as the primary research hub in Oceania, while investment in this field from African countries remains relatively low, with Egypt showcasing notable achievements in *T. gondii* research in Africa. Moreover, a robust transnational cooperative research system has been established among contributing nations, with the United States spearheading global cooperation efforts, closely collaborating with countries such as China, the United Kingdom, France, Germany, and Brazil.

3.5. *Cocitation analysis of the literature*

A total of 10,737 articles were collected in this study, including 147,129 references. To obtain more extensive and representative references, 38 core references (Table S4) were clustered and analyzed, and a visual knowledge graph of the cited references was constructed (Fig. 5).

These 38 references were categorized into three clusters represented by three different colors. The red cluster encompassed the largest number of studies, all focusing on summarizing articles concerning the transmission, diagnosis, prevention, and epidemiology of toxoplasmosis. Next, the green cluster predominantly discussed genotyping and identification topics, while the blue cluster covered various aspects related to immunology, virulence factors, and the association of *T. gondii* with other diseases. Of note, the two most frequently cited articles were published by Tenter (Germany) and Montoya (USA), both of them were review articles. Tenter *et al.* provided a systematic and comprehensive examination of *T. gondii* transmission routes, significantly contributing to recent research data on transmission routes. They particularly emphasized the potential risk of oocysts as a pollution source, underscoring the necessity for enhanced research into monitoring methods for these oocysts (Tenter et al., 2000). Montoya et al. provided a comprehensive and updated summary of *T. gondii* infection and pathogenesis, diagnosis, and treatment, especially on acute infections, maternal infections, congenital infections in infants or fetuses, ocular toxoplasmosis, and infections in individuals with compromised immunity. These systematic summaries of field epidemiological studies provided crucial references for subsequent research (Montoya and Liesenfeld, 2004). The first authors of the 38 highly cited papers were from 7 countries and regions, including the United States (28), France (3), the United

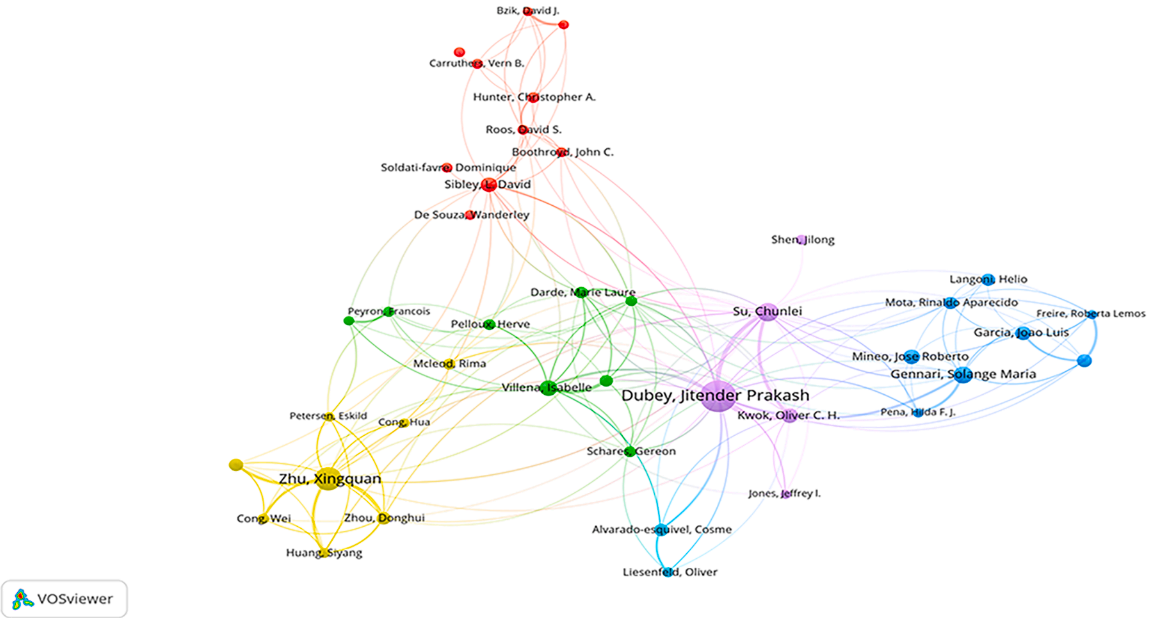


Fig. 3. Author's cooperative network graph (number of posts ≥ 40). The node in the graph corresponds to each author, the size of the node represents the frequency of occurrence of the author, the different colors represent the clustering to which they belong, the distance in front of each node represents the degree of cooperation, and the thickness of the connection between nodes represents cooperation. Author information with more than 40 articles published is shown in Table S2.

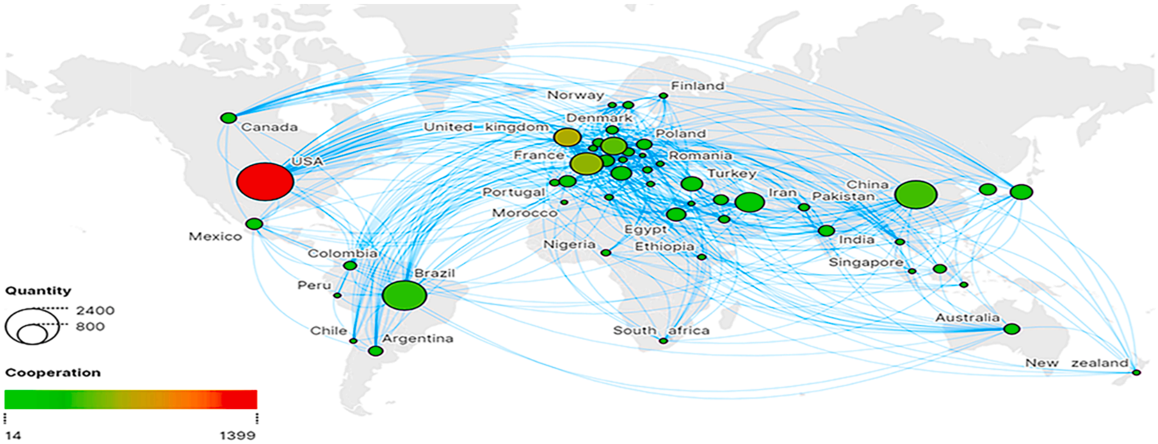


Fig. 4. National and regional cooperation network and geographical distribution map (number of publications ≥ 35). The geographical distribution map is drawn by ScimagoGraphica software. The nodes correspond to each country and region, the node size represents the occurrence frequency, and the node color change and connection represent the cooperation intensity. The analysis includes 38 core references as listed in Table S4.

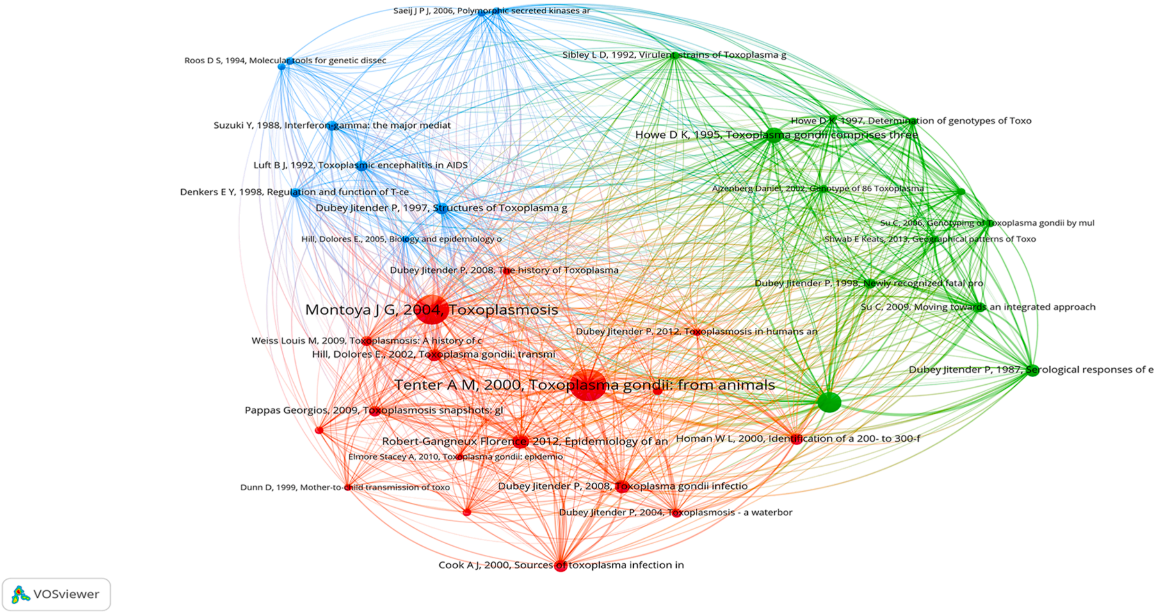


Fig. 5. Literature cocitation network (literature citation frequency ≥ 200). The nodes in the figure correspond to the literature, the node size represents the total citation frequency of the document, and the different colors represent the clustering to which it belongs.

Kingdom (3), Brazil (1), Germany (1), the Netherlands (1), and Greece (1).

3.6. *Citation literature analysis*

Analysing the changes about the annual paper volume over the past two decades, there was a significant shift before and after 2007 and 2018. Consequently, two periods of citation literature were selected for further analysis: from 2003 to 2012 and from 2013 to 2022. Twelve articles were selected to analyze the frontier changes in *T. gondii* research content (Table S5). From 2003 to 2012, a number of highly cited studies related to *T. gondii* invasion and host immune protection mechanisms emerged. In 2005, Kelly et al. first evaluated the role of IL-17 receptor (IL-17R)-mediated signal transduction in the production of protective immunity against intracellular parasites (Kelly et al., 2005). In 2006, Saeij et al. and Taylor et al. simultaneously identified the protein kinase ROP18 as the major virulence factor in the mouse model by genetic mapping using crosses among the type I, II, and III *T. gondii* lineages (Kelly et al., 2005; Montoya and Liesenfeld, 2004; Saeij et al., 2006; Taylor et al., 2006; Tenter et al., 2000). Consequently, from 2005 to 2012, research surged on the molecular basis of *T. gondii* pathogenicity, immune response, and immune evasion, focusing on secretory proteins and the interleukin family of rhoptries. Since 2013, highly cited literatures on *T. gondii* predominantly focused on the functional genomics of *T. gondii* genes. Many of these studies about research on *T. gondii* gene function by CRISPR/Cas9 which greatly enhanced research in functional genomics. This technology furnishes a technical method for a deeper understanding of *T. gondii*'s virulence, metabolism, and immunomodulatory capabilities. Furthermore, it lays the groundwork for the development of *T. gondii* vaccines and facilitates drug screening processes. The successful application of CRISPR/Cas9 technology propelled *T. gondii* research. The outstanding contributions are as follows: Shen et al. successfully applied the CRISPR/Cas9 system to the genetic manipulation of *T. gondii* in 2014, which accelerated the study of functional genes in *T. gondii* (Shen et al., 2014). Moreover, Sidik et al. used the RNA-guided Cas9 nuclease to effectively produce knockouts without selection and insert point mutations and epitope tags into the *T. gondii* genome. These methods simplified the functional analysis of parasite genes and enabled high-throughput analysis of their genomes (Sidik et al., 2014).

3.7. Keyword analysis

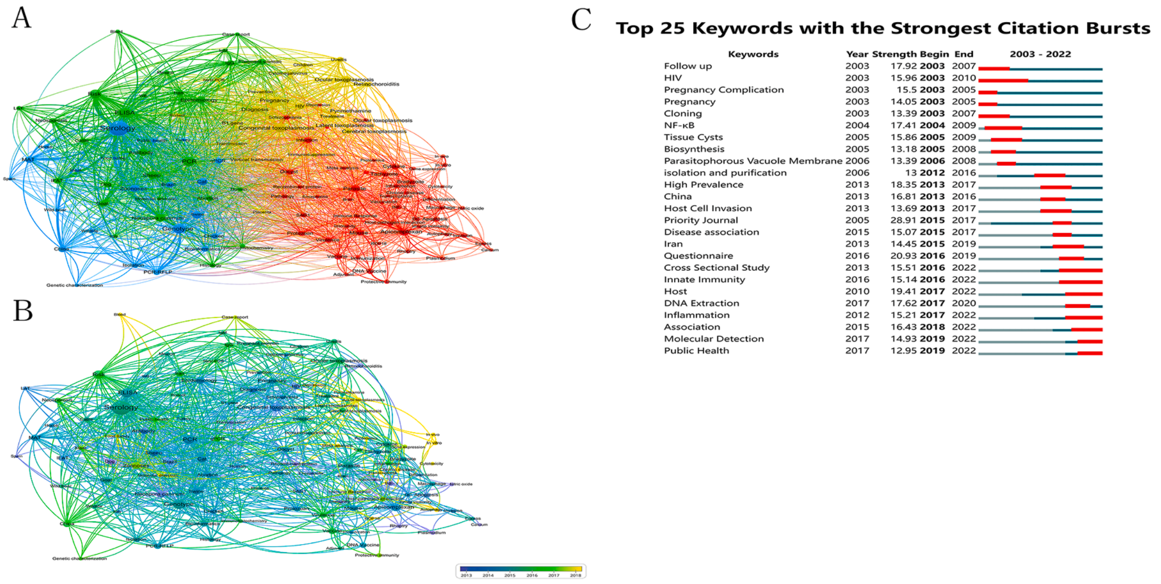
A total of 121 keywords were selected for further analysis. The keywords were generated using VOSviewer software, which extracts high-frequency terms from the titles and abstracts of the analyzed articles. These keywords were then classified into clusters, and their structural characteristics, important connections, and popularity were analyzed. Keywords were divided into four clusters: red was the most common keyword, followed by blue and green, and yellow was the least common (Fig. 6A). It was founded that the red clustering literatures focused on infection immunity and immune prevention related to control toxoplasmosis. The blue clustering predominantly explored the relationship between genotyping and virulence of *T. gondii*. The green clustering focused on the epidemiology and clinical diagnosis of toxoplasmosis, while the yellow clustering primarily addressed the diagnosis and control of human toxoplasmosis.

A visualization map of keyword co-occurrence and temporal superposition (Fig. 6B) showed that the word frequency of the keywords varied over past 20 years, but epidemiological investigations were carried out throughout these years. This phenomenon also indicated that toxoplasmosis was very important, people always pay attention to its infection. Moreover, the changes of word frequency can be divided into three stages. In the first stage (dark blue), the key words were “antibody and diagnosis”. During this period, researchers focused on the pathogen classification, and diagnosis of toxoplasmosis. With the development on technology, research entered the second stage (green), and the key words in this stage were “Serology, Genotype, ELISA, PCR, PCR-RFLP and Infection”, mainly focused on the diagnosis and prevalence of toxoplasmosis; however, more detail information was involved, such as strain isolation and strain genotypes were carried on, and lots of PCR-related techniques were gradually used for diagnosis. The third stage key words (yellow) were mainly about “Zoonoses, Food Safety, Proteomics, Chronic Disease, Acute Toxoplasmosis Cytotoxicity and Host Pathogen Interaction”, which were related to public health, disease, immune interactions between *T. gondii* and host and deeper exploration on genetic and cellular research. This also basically reflected that the research hotspots in the field of *T. gondii* had undergone several obvious changes while keeping several basic points unchanged. For the perspective of geographical distribution, from Europe to Latin America to Asia, research on *T. gondii* has been carried out in different regions; For the disease, the initial general toxoplasmosis gradually progressed to human ophthalmopathy, nervous system, acute and chronic toxoplasmosis; For the degree of concern: from the single animal or human to zoonosis and public health; For the level of diagnosis: the continuous development of diagnostic methods for initial pathogens, serology and molecular biology; For disease prevention and control, from the aspects of initial pathogen infection to proteomics, functional genomics, specific genes and immune interactions with the host, from initial humoral immunity to innate immunity.

As shown in Fig. 6C, the keyword burst analysis highlights the emerging hot spots and cutting-edge trends in *T. gondii* research. Keywords such as "Questionnaire" (strength = 20.93), "Host" (strength = 19.41), and "High Prevalence" (strength = 18.35) exhibit high burst indexes, indicating a surge of attention in these topics over a short period. Although some keywords (such as "Follow-up," "Priority Journal," "Association," and "DNA extraction") may seem unrelated to the core research areas, they represent diverse research perspectives and technical applications. For instance, "Follow-up" refers to the importance of longitudinal studies, "Priority Journal" reflects the trend of publishing in high-impact journals, "Association" highlights the links between Toxoplasma infection and other factors, and "DNA extraction," a fundamental molecular biology technique, remains crucial for experimental work in Toxoplasma research. Keywords such as "HIV," "Pregnancy," "Cloning," and "NF-κB" frequently appeared in earlier studies, underscoring the intersection of Toxoplasma research with immunology, clinical studies, and molecular biology. Between 2013 and 2015, keywords like "High Prevalence," "China," "Iran," and "Host Cell Invasion" emerged, reflecting the geographical shift in Toxoplasma epidemiology, with a particularly high focus in China and Iran. In recent years, the persistent high frequency of keywords such as "Public Health," "Innate Immunity," "Host," and "Inflammation" indicates a deepening focus on immunology, molecular diagnostics, and public health related to Toxoplasma. These findings not only reveal current research trends but also reflect the evolving direction of the field, providing valuable insights for future studies.

4. Discussion

Toxoplasmosis is a globally significant zoonotic disease, and its



Top 25 Keywords with the Strongest Citation Bursts

Keywords	Year	Strength	Begin	End	2003 - 2022
Follow up	2003	17.92	**2003**	2007	
HIV	2003	15.96	**2003**	2010	
Pregnancy Complication	2003	15.5	**2003**	2005	
Pregnancy	2003	14.05	**2003**	2005	
Cloning	2003	13.39	**2003**	2007	
NF-κB	2004	17.41	**2004**	2009	
Tissue Cysts	2005	15.86	**2005**	2009	
Biosynthesis	2005	13.18	**2005**	2008	
Parasitophorous Vacuole Membrane	2006	13.39	**2006**	2008	
isolation and purification	2006	13	**2012**	2016	
High Prevalence	2013	18.35	**2013**	2017	
China	2013	16.81	**2013**	2016	
Host Cell Invasion	2013	13.69	**2013**	2017	
Priority Journal	2005	28.91	**2015**	2017	
Disease association	2015	15.07	**2015**	2017	
Iran	2013	14.45	**2015**	2019	
Questionnaire	2016	20.93	**2016**	2019	
Cross Sectional Study	2013	15.51	**2016**	2022	
Innate Immunity	2016	15.14	**2016**	2022	
Host	2010	19.41	**2017**	2022	
DNA Extraction	2017	17.62	**2017**	2020	
Inflammation	2012	15.21	**2017**	2022	
Association	2015	16.43	**2018**	2022	
Molecular Detection	2017	14.93	**2019**	2022	
Public Health	2017	12.95	**2019**	2022	

Fig. 6. Keyword analysis of *T. gondii*. (A: co-occurrence clustering diagram; B: co-occurrence clustering and time superposition visualization map; C: *T. gondii* keyword emergence map; the blue line represents the keyword occurrence time range, and the red line represents the keyword emergence time range.).

causative agent, *T. gondii*, has emerged as a widely studied model organism, attracting considerable attention from researchers worldwide. As research on *T. gondii* continues to advance, the volume of related scientific publications has steadily grown. Therefore, a comprehensive review of existing research findings is crucial for accurately understanding the overarching trends and key focus areas in this field. This study synthesizes data on the regions, researchers, research directions, and publications related to *T. gondii*. It provides an in-depth overview of the current state of research, highlights cutting-edge developments, and identifies emerging topics within the field. By offering valuable insights for the academic community, this study aims to assist researchers in navigating the trajectory of *T. gondii* research and pinpointing future directions.

Over the past two decades, research on *T. gondii* has demonstrated a steady upward trend, with an average annual publication volume of approximately 537 papers. This underscores the sustained interest and widespread attention that this field continues to receive (Fig. 2). Research findings are predominantly published in core parasitology journals, followed by journals in related disciplines such as infectious diseases, veterinary medicine, molecular biology, and immunology. The overall distribution of journals aligns with principle of literature dispersion reflecting both the concentration effect of core journals and the diversification of research topics within the field (Table S1). In terms of academic contributions, the pioneering work by Dubey and Chun-Lei Su's et al. has laid a crucial foundation for the study of the *T. gondii* life cycle, transmission mechanisms, and diagnostic methods. Dubey's team elucidated the pathways by which *T. gondii* is transmitted to humans and animals via cat feces, advancing the epidemiological understanding of Toxoplasma infections and providing a robust scientific basis for public health prevention and control strategies (Dubey, 2004; Dubey et al., 1998; Hill and Dubey, 2002). Su's team developed a PCR-RFLP genotyping method based on nine marker loci, significantly enhancing the accuracy of *T. gondii* strain identification. Their work also unveiled the genetic diversity of Toxoplasma populations, offering powerful tools for epidemiological studies and population genetics research (Shwab et al., 2014; Su et al., 2006). More recently, the team led by Zhu highlighted the pivotal role of the PP2A holoenzyme-mediated dephosphorylation process in the growth, metabolism, and bradyzoite transformation of *T. gondii*, thereby deepening the understanding of its physiological mechanisms (Wang et al., 2022). Additionally, scholars such as David Sibley and Mineo Jose Roberto have made significant contributions to the field. Their work has expanded knowledge in areas including host-pathogen interactions, immunological and cellular responses, genetic diversity, pathogenic mechanisms, and the development of innovative therapeutic strategies (Fig. 3, Table S2) (Barbosa et al., 2012; Bernardes et al., 2006; Dunay et al., 2008; Howe and Sibley, 1995). From a regional perspective, the United States leads global research efforts on *T. gondii*, followed by France, Germany, the United Kingdom, Brazil, and China. Although research output in Africa remains comparatively limited, the high infection rates in the region emphasize the urgent need for strengthened research efforts. Such endeavors could present both significant opportunities and formidable challenges for improving prevention and control measures for *T. gondii* in the future (Fig. 4, Table S3).

In the era of information explosion, it is crucial for researchers to promptly grasp the hotspots and trends in their fields. Cited documents form the foundational knowledge base of research, while citing documents reflect its developmental dynamics. Together, they provide valuable insights into the forefront of research content (Huang et al., 2021). Keywords, as concise summaries of article topics, play an essential role in identifying hotspots and emerging trends in *T. gondii* research. Keywords co-occurrence cluster analysis can reveal hot spots in the academic field, while burst detection analysis reveals emerging trends within the discipline (Ma et al., 2022; Sun et al., 2012). This study indicates that, over the past two decades, research hotspots in the field of *T. gondii* have encompassed diagnosis, prevention and treatment, virulence analysis, and genotyping (Fig. 5, Fig. 6AB, Table S4). The interaction mechanisms between *T. gondii* and its host, advancements in disease prevention and control, and its impact on public health represent the current frontiers and emerging trends in this domain (Fig. 6BC, Table S5).

Epidemiological research on *T. gondii* has long been a prominent focus in the field, encompassing various aspects such as diagnosis, prevention, treatment, virulence analysis, and genotyping. This research has provided a crucial foundation for the scientific understanding of *T. gondii* infection. Epidemiological studies are predominantly concentrated in Brazil, China, and Iran. Host analysis indicates that human infection studies mainly focus on pregnant women, whereas animal infection studies primarily target economic animals like sheep and cattle, as well as the definitive host, the cat. *T. gondii* exhibits a broad host range, and its global infection rates vary significantly. In underdeveloped regions, infection rates can exceed 70 %, while in countries like China and Italy, the rates are notably lower, with some areas reporting rates below 1 % (Billi et al., 2016; Esubalew et al., 2020; Villar-Echarte et al., 2021; Yang et al., 2017). Major risk factors include exposure to cats, consumption of raw or undercooked food, age, and geographical location (Tegegne et al., 2016; Tian et al., 2017; Zhou et al., 2018). Diagnostic methods for *T. gondii* continue to evolve. Techniques such as enzyme-linked immunosorbent assay (ELISA), indirect hemagglutination assay (IHA), and immunocolloidal gold technology have advanced rapid detection capabilities (Robert-Gangneux and Darde, 2012). Traditional methods, including the modified agglutination test (MAT) and indirect immunofluorescence assay (IFA), remain integral to routine diagnostics. Emerging molecular biology technologies, such as real-time quantitative PCR, have further enhanced diagnostic accuracy and sensitivity (Ahmadpour et al., 2019; Wyrosdick and Schaefer, 2015). The genetic diversity of *T. gondii* reveals significant variations in its virulence and transmission patterns. Beyond the classical Types I, II, and III, numerous additional genotypes have been identified. For example, in 2020, Witter et al. conducted a genetic analysis of *T. gondii* strains in central and western Brazil, identifying 11 genotypes, which underscores the high genetic diversity of *T. gondii* in this region (Witter et al., 2020). Virulence studies have uncovered complex interactions between *T. gondii* and host cells, particularly highlighting the critical roles of ROP and GRA family proteins in immune evasion and persistent infection (Saeij et al., 2006; Taylor et al., 2006; Weeratunga et al., 2017). These findings provide fundamental insights into pathogenic mechanisms and potential therapeutic targets. Research on the prevention and control of toxoplasmosis primarily focuses on vaccine and drug development. Attenuated live vaccines have garnered attention for their robust protective efficacy, often achieved through gene knockout techniques targeting key virulence genes of *T. gondii*. While such vaccines demonstrate immunogenic potential, safety concerns regarding their residual virulence limit their application as human vaccines (Zhang et al., 2013). Genetically engineered vaccines, leveraging candidate antigens such as GRA, ROP, SAG, and MIC, offer superior immune protection compared to single-antigen vaccines (Ghaffari et al., 2021; Lu et al., 2018; Meng et al., 2012; Tian et al., 2022). Additionally, adjuvants enhance the immunogenicity of DNA vaccines, bioinformatics aids in antigen screening and vaccine design, and nanoparticles play an essential role in vaccine delivery systems (Khodadadi et al., 2021; Khorshidvand et al., 2022; Song et al., 2017). In the absence of widespread vaccine availability, the development of anti-*T. gondii* drugs has become a focal point. Current drugs, such as pyrimethamine and sulfadiazine, are primarily used to treat acute toxoplasmosis but remain inadequate for chronic infection management (Imhof et al., 2021; Wang et al., 2021). Researchers are actively exploring new drugs, including herbal medicines, natural extracts, small-molecule compounds, and nanoparticle-based therapies (Adeyemi et al., 2019; Liu et al., 2021; Saito et al., 2020; Sanfelice et al., 2019). Nanotechnology has improved drug delivery and therapeutic efficacy, while studies on small-molecule compounds have facilitated the identification of anti-*T. gondii* targets and the development of novel inhibitors. Progress has also been made with combination drug strategies, enhancing treatment outcomes (Sanfelice et al., 2019).

Research on *T. gondii* is expanding into the fields of mechanistic study and application transformation, with a gradual shift in focus from basic science to the practical implementation of public health applications, disease prevention, and control strategies. Current research frontiers are centered around three main areas: the interaction mechanisms between *T. gondii* and its host, innovative methods for disease prevention and control, and the global public health impact of *T. gondii* infection. In the study of the interaction mechanisms between *T. gondii* and its host, scientists have delved deeply into how the virulence factors of *T. gondii* regulate host immune responses and metabolic pathways (Cui et al., 2022; Li et al., 2020). *T. gondii* promotes its survival and propagation within the host by finely tuning the gene expression, signal transduction, and immune response of host cells (Gao et al., 2022; Xu et al., 2022). Gene editing technologies, such as CRISPR-Cas9, provide powerful tools for studying the functions of virulence genes. The knockout or knockout-insertion of specific genes can help unveil the pathogenic mechanisms of *T. gondii*, thereby advancing the development of anti-infective drugs and vaccines (Shen et al., 2014; Sidik et al., 2014). In the realm of disease prevention and control, research has taken on a multidisciplinary approach. The advancement of systems biology and multi-omics technologies enables researchers to conduct comprehensive analyses of multi-dimensional data during *T. gondii* infection, improving early diagnosis capabilities and providing support for predicting infection risks and intervening in high-risk groups (Kloehn et al., 2020; Nie et al., 2022). The integration of data science and artificial intelligence, particularly in drug screening and vaccine development, has greatly enhanced the efficiency of research and development efforts. Molecular simulation and high-throughput screening technologies have accelerated the discovery of novel drugs and vaccines (Deng et al., 2020; Varberg et al., 2018). As research into *T. gondii* deepens, the focus in public health has gradually shifted from addressing individual infection cases to assessing the broader impact on global health, especially in developing countries. The effects of *T. gondii* infection on pregnant women, newborns, and immunocompromised patients have become key areas of focus. Through accumulating epidemiological data, researchers have revealed the long-term health impacts of *T. gondii* infection on high-risk groups and employed health economics and social burden assessment models to quantify its social and economic costs. This research provides theoretical support for the optimization of global public health policies, with significant implications for disease prevention and control strategies, resource allocation, and international cooperation.

In the future, *T. gondii* research will continue to integrate basic research with applied transformation. As technology advances, further exploration in areas such as virulence mechanisms, vaccine and drug development, and global health impact assessments will drive the progress of this field. This will not only help uncover the core mechanisms of Toxoplasma infection but also provide new directions and strategies for global control and treatment. Ultimately, these advancements will contribute to public health and enhance disease prevention and control efforts worldwide.

5. Conclusions

This study performed a bibliometric analysis of the research status and trends in the global *T. gondii* field over the past two decades, summarized the research status and hotspots in this field, and provided data support for academic research and discipline construction. Understanding the progress and discipline development trends in this field is important for researchers.

Ethical statement

Not applicable.

Consent for publication

Not applicable.

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CRediT authorship contribution statement

Fan Shi-Jie: Writing – original draft, Visualization, Validation, Software, Methodology, Investigation, Formal analysis, Data curation. **Xia Chen-Yang:** Supervision, Project administration, Methodology. **Pan Ming:** Supervision, Investigation, Formal analysis, Data curation. **Huang Si-Yang:** Writing – review & editing, Validation, Supervision, Resources, Funding acquisition, Conceptualization. **Yang Pin:** Writing – review & editing, Validation, Supervision, Formal analysis, Conceptualization.

Declaration of Competing Interest

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

Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at doi:10.1016/j.vetpar.2025.110438.

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