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Bacteroides thetaiotaomicron and Human Health: A Bibliometric Analysis of Global Research Trends

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ABSTRACT

Bacteroides thetaiotaomicron is a highly abundant Gram-negative anaerobic bacterium that plays a crucial role in maintaining intestinal homeostasis and modulating intestinal diseases. A bibliometric study was conducted to examine global publication trends on *B. thetaiotaomicron*, using the Scopus database and scientific metrics software over the period 1965-2024. The study investigated variables such as publication year, reference numbers, article type, country, language, and author affiliation. Among the 2,510 articles reviewed on *B. thetaiotaomicron*, findings indicated that inflammatory bowel disease was the most frequently studied condition. The journal "Anaerobe" published the highest number of articles (n = 68). The United States ranked as the leading country, contributing 969 publications. A total of 14 languages were used in the publications, with 96% written in English. Given the increasing prevalence of digestive diseases and the need for more effective treatments than conventional therapies, *B. thetaiotaomicron* could be considered a promising therapeutic candidate.

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1. INTRODUCTION

The genomes and biochemical reactions of intestinal microbes are more important than those of their hosts, making them essential for host metabolism, immunology, development, and behavior[1]. The profound impact of intestinal microbes on host metabolism is evident in their capacity to break down dietary components, extract energy from food, and modulate nutrient absorption. In addition, these microbes interact with the host immune system, influencing immune development, pathogen response, and the regulation of inflammation. Recent research has emphasized the role of gut microbiota in neurodevelopment and behavior, with emerging evidence linking microbial composition to conditions such as anxiety, depression, and neurodevelopmental disorders[2]. The gut microbiome can influence host metabolism and homeostasis through its metabolites, secretions, and cellular constituents. With the advancement of microbiome science, the complex relationships among gut microbiota, human health, and disease are gradually being elucidated[3]. More than 25 years ago, *Bacteroides* were recognized as significant organisms capable of colonizing plant polysaccharides and host-derived products. This ability is essential for meeting the organism's needs and provides critical digestive functions for the host[4].

Considering that traditional probiotics have generally demonstrated only marginal healing effects, bacteria such as *Bacteroides thetaiotaomicron* play a vital role in controlling insulin resistance, reducing intestinal inflammatory effects, and maintaining the integrity of the intestinal surface. Hence, *B. thetaiotaomicron* is regarded as a new preventive and therapeutic agent, representing the next generation of probiotics[5].

In the human gastrointestinal tract, *B. thetaiotaomicron*, a Gram-negative anaerobic bacterium, constitutes approximately 6% of the total bacterial population and 12% of the genus *Bacteroides*[6]. The genome of *B. thetaiotaomicron* encodes a total of 230 glycoside hydrolases. Its proteome includes 20 sugar-specific transporters, 163 outer membrane proteins that bind polysaccharides, and 172 enzymes classified as glycoside hydrolases[7]. This bacterium influences the amount of energy extracted from food, as well as impacts insulin sensitivity and lipid metabolism. Dysbiosis of *B. thetaiotaomicron* could contribute to metabolic disorders, colitis, and inflammatory bowel disease[8]. Prior research, particularly on gut bacteria, indicated a potential dual role in enhancing mucosal immunity and regulating immune homeostasis[9-11]. Collectively, the aforementioned studies highlight the critical role of *B. thetaiotaomicron* in various diseases.

Despite the extensive research on *B. thetaiotaomicron*, a comprehensive bibliometric analysis specifically focusing on this bacterium has not yet been conducted, particularly in recent years during which the field has experienced substantial growth and diversification. The present review sought to fill this important gap by providing a systematic analysis of global research trends, key contributors, and emerging focus areas. The bibliometric analysis mapped the research landscape of *B. thetaiotaomicron* by offering an overview of recent developments and identifying major trends, geographic and institutional contributions, and seminal works that have shaped the field. All literature on *B. thetaiotaomicron* was thoroughly evaluated based on article type, publication year, citation count, country of origin, institutional affiliation, author information, funding sponsors, journal distribution, co-authorship networks, international collaborations, indexed terms, and author keyword co-occurrences. The current study addresses the absence of comprehensive, and quantitative analyses in this rapidly evolving area of microbiota research.

2. MATERIALS AND METHODS

2.1. Search strategy

This bibliometric review employed the Scopus database to retrieve all documents related to *B. thetaiotaomicron*. Scopus was selected for its extensive resource coverage, superior comprehensiveness, and high accuracy compared to other bibliographic databases such as PubMed, Web of Science, and Google Scholar. As a source-neutral abstract and citation database curated by independent subject matter experts, Scopus provides researchers, librarians, research managers, and funders with robust discovery and analytics tools that support the advancement of ideas, individuals, and institutions[12]. The search was conducted using the TITLE-ABS-KEY fields with the keyword “thetaiotaomicron”, covering all records from 1965 (the inception of the database) through 2024. To ensure the inclusion of all relevant citations and bibliometric indicators, the entire dataset was retrieved on the search date. The extracted data were subsequently imported into spreadsheet software, such as Microsoft Excel, to facilitate statistical analysis of bibliometric information. This process enabled the identification and ranking of key bibliometric elements, including frequently cited publications, leading journals, well-regarded institutions, major funding agencies, prominent authors, and countries with the highest research output. No restrictions were applied regarding language or document type, ensuring maximum global coverage.

2.2. Selection criteria

The inclusion criteria included articles that provided empirical data or reviews related to *B. thetaiotaomicron*, while the exclusion criteria were limited to errata and editorial commentaries. The selection process involved a systematic review of titles, abstracts, and, where necessary, full texts to assess their relevance and alignment with the thematic scope of the study. To comprehensively map the literature landscape of *B. thetaiotaomicron*, we employed a multifaceted bibliometric approach. First, we characterized all retrieved articles by subject area and document type to evaluate thematic breadth and heterogeneity. Next, we analyzed original research articles to identify the prevailing methodologies, target populations, and the conditions or diseases under investigation. Finally, we collected a dataset of both original and review articles to explore distribution of publication year and citation counts to identify the most productive journals, institutions, funding agencies, authors, and countries of origin. Additionally, we visualized collaborative networks to highlight relationships among keywords, thematic terms, authors, and countries.

2.3. Data extraction

Following the selection of articles, all relevant bibliometric data were downloaded in comma-separated values format to ensure the accuracy of citations, bibliographic details, abstracts, keywords, and funding information. The data extraction was meticulously

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conducted, capturing key indicators such as publication year, citation metrics, author information, and institutional affiliations.

2.4. Data analysis

VOSviewer (version 1.6.16, Centre for Science and Technology Studies, Leiden University, the Netherland) was employed for data visualization. The software was used for the construction and exploration of scientific networks within the research landscape of *B. thetaiotaomicron*. These networks included connections among authors, institutions, countries, keywords, and thematic terms. Relationships within these networks were established based on co-occurrence (keywords and terms appearing together), co-authorship (authors collaborating on publications), co-citation (articles citing one another), bibliographic coupling (articles referencing similar works), and citation patterns. VOSviewer was particularly effective in identifying densely interconnected networks of co-occurring author keywords and terms, as well as the most frequent co-authorships among authors and their affiliated institutions[13].

3. RESULTS

3.1. Number of publications, subject area, and article types

A total of 2,510 documents were retrieved from the Scopus database and categorized by publication type. Original research articles represented the predominant category, comprising 1,977 (78.76%) documents. This trend was followed by 330 (13.14%) review articles, 60 (2.39%) notes, 47 (1.78%) short surveys, 28 (1.11%) conference papers, 22 (0.87%) letters, and 20 (0.79%) book chapters. Additional document types included 13 (0.51%) editorials, 11 (0.43%) errata, 1 (0.03%) retraction notice, and 1 (0.03%) conference review (Fig. 1A).

3.2. Classification based on article language

Using the defined search strategy, articles were identified in different languages. The majority of the articles were published in English (2,413 articles), followed by German (n = 33), Japanese (n = 16), Russian (n = 11), and Chinese (n = 10). Additional languages included Polish (9 articles), French (n = 7), Spanish (n = 4), Czech (n = 3), and Ukrainian (n = 2). There was also one article each in Italian, Korean, Slovenian, and Turkish (Fig. 1B).

3.3 Analysis based on the subject category

An analysis of the retrieved articles showed that 527 articles were classified under the subject area of medicine, followed by immunology and microbiology, biochemistry, genetics, and molecular biology. Additional subject areas with fewer contributions included pharmacology, toxicology and pharmaceutics (n = 264), agricultural and biological sciences (n = 216), multidisciplinary (n = 128), environmental sciences (n = 128), chemistry (n=123), chemical engineering (n = 77), nursing (n = 52), computer sciences (n = 49), engineering (n = 41), physics and astronomy (n = 40), mathematics (n = 34), neurosciences (n = 31), veterinary (n = 18), materials science (n = 16), health professions (n = 15), dentistry (n = 8), social sciences (n = 7), energy (n = 6), and psychology, economics, econometrics, finance, earth, and planetary sciences" (n = 1) (Fig. 1C).

3.4. Distribution of *B. thetaiotaomicron* articles based on the study design and disease

The titles and abstracts of all 1,977 original articles were reviewed to determine the study population addressed in each publication. The majority of studies (n = 992) involved human subjects, while fewer studies (n = 361) utilized animal models. Figure 1D presents the most common medical conditions associated with *B. thetaiotaomicron*, along with the number of corresponding publications. Colitis was the most commonly studied disease, followed by obesity, diabetes, Crohn's disease, ulcerative colitis, and inflammatory bowel disease.

3.5 Years of article distribution

Figure 2A illustrates the global scientific output on *B. thetaiotaomicron* indexed in Scopus from 1965 through 2024, highlighting a clear upward trend in publication volume. The first article indexed in Scopus was published in 1965, followed by a consistent publication rate over 30 years. By 2005, the annual number of articles had increased to 35. In 2024, there was a significant increase in the number of studies, reaching a peak of 229 publications.

3.6 Top-cited articles and citation metrics

Articles published in 1966, 1967, 1968, and 1972 received the fewest citations, whereas those published in 2013 in "Nature" received the highest citation count, totaling 3,935. Table 1 summarizes the key characteristics of the 10 most-cited articles on *B. thetaiotaomicron*. Overall, the number of publications on this bacterium has steadily increased over the past 60 years, with a significant rise in recent years. This trend highlights the growing scientific interest in its biological and clinical significance.

3.7. Leading journals in *B. thetaiotaomicron* research

Table 2 presents the number of articles published by the top-ranking journals on *B. thetaiotaomicron*. The five most active journals—"Anaerobe", "Frontiers in

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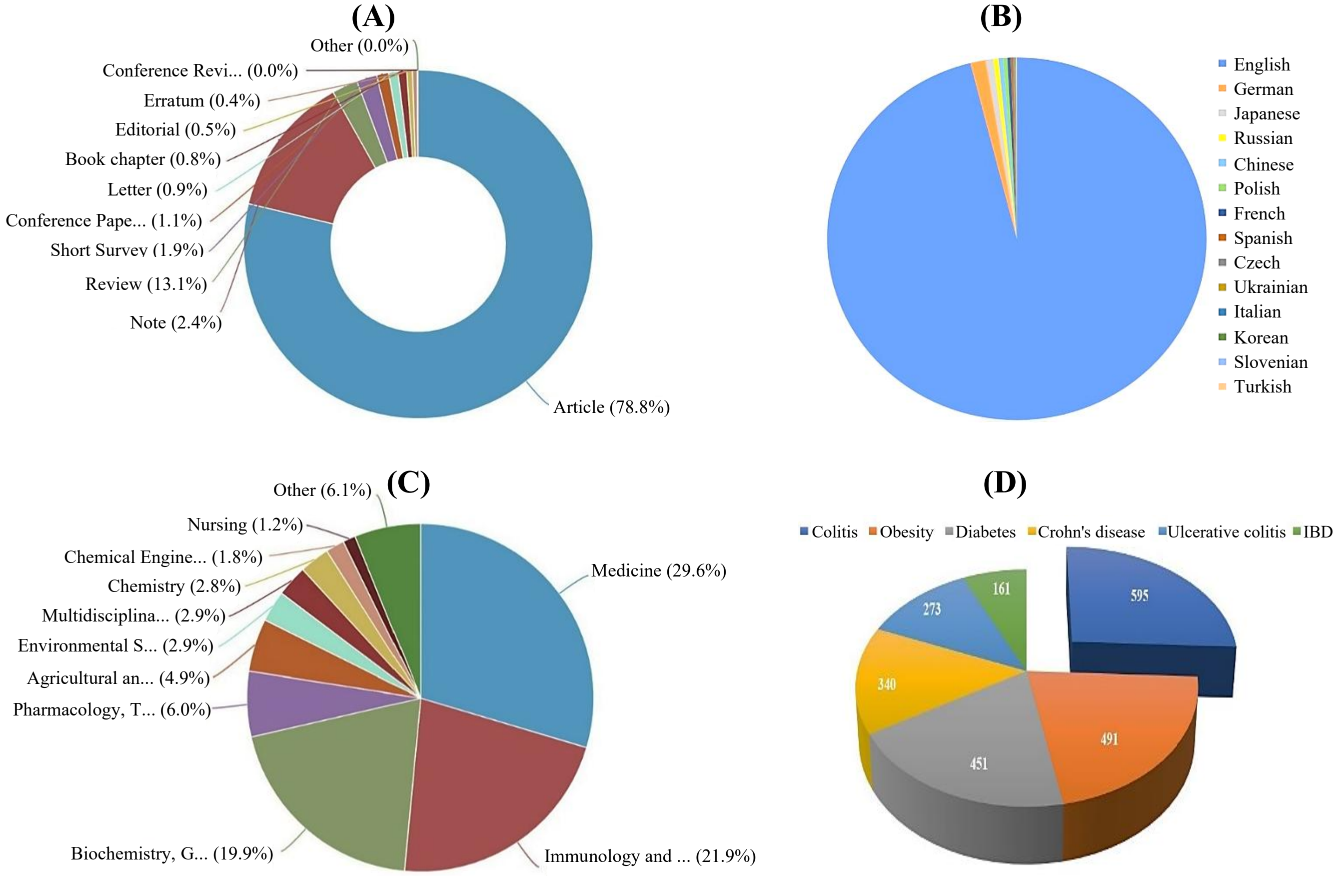

Fig. 1. (A) Distribution of *B. thetaiotaomicron*-related publications by articles type; (B) language classification of articles published on *B. thetaiotaomicron*; (C) subject area categorization of retrieved articles; (D) major diseases associated with *B. thetaiotaomicron* and the number of corresponding publications.

Microbiology", "Antimicrobial Agents and Chemotherapy", "Journal of Bacteriology", and "Cell Host and Microbe"—have collectively contributed to a significant number of articles on *B. thetaiotaomicron*, with 68, 68, 65, 62, and 51 articles published, respectively. Their consistent output demonstrated their prominence and expertise in this research area. Table 3 depicts the most highly cited article on *B. thetaiotaomicron* published in the journal "Anaerobe", showing the impact of the journal on advancing research in this field. "Anaerobe" published its first articles on *B. thetaiotaomicron* in 1995, which received 182 citations.

3.8. Analysis of *B. thetaiotaomicron* publications based on country

As depicted in Figure 2B, the United States leads in publishing articles on *B. thetaiotaomicron*, with a total of 969 publications, most of which resulted from international collaborations. China ranks second with 286 publications, followed by the United Kingdom (n = 236), Japan (n = 198), and France (n = 166).

3.9. Top productive institutions in the publication

Figure 2C presents the most productive institutions publishing articles on *B. thetaiotaomicron*. The University of Illinois Urbana–Champaign ranked first with 75 publications, followed by Washington University School of Medicine in St. Louis (n = 72), INRAE (n = 68), the School of Molecular and Cellular Biology (n = 62), and the University of Michigan Medical School (n = 61).

3.10. Major sponsors driving research on *B. thetaiotaomicron*

Figure 2D illustrates the most active sponsors supporting research on *B. thetaiotaomicron*. The National Institutes of Health (NIH) is the leading sponsor, contributing to 269 publications. Following NIH, the National Natural Science Foundation of China (NSFC), the National Institute of General Medical Sciences (NIGMS), the National Institute of Allergy and Infectious Diseases, and the National Institutes of Diabetes and Digestive and Kidney Disease have supported 144, 126, 122, and 118 articles, respectively.

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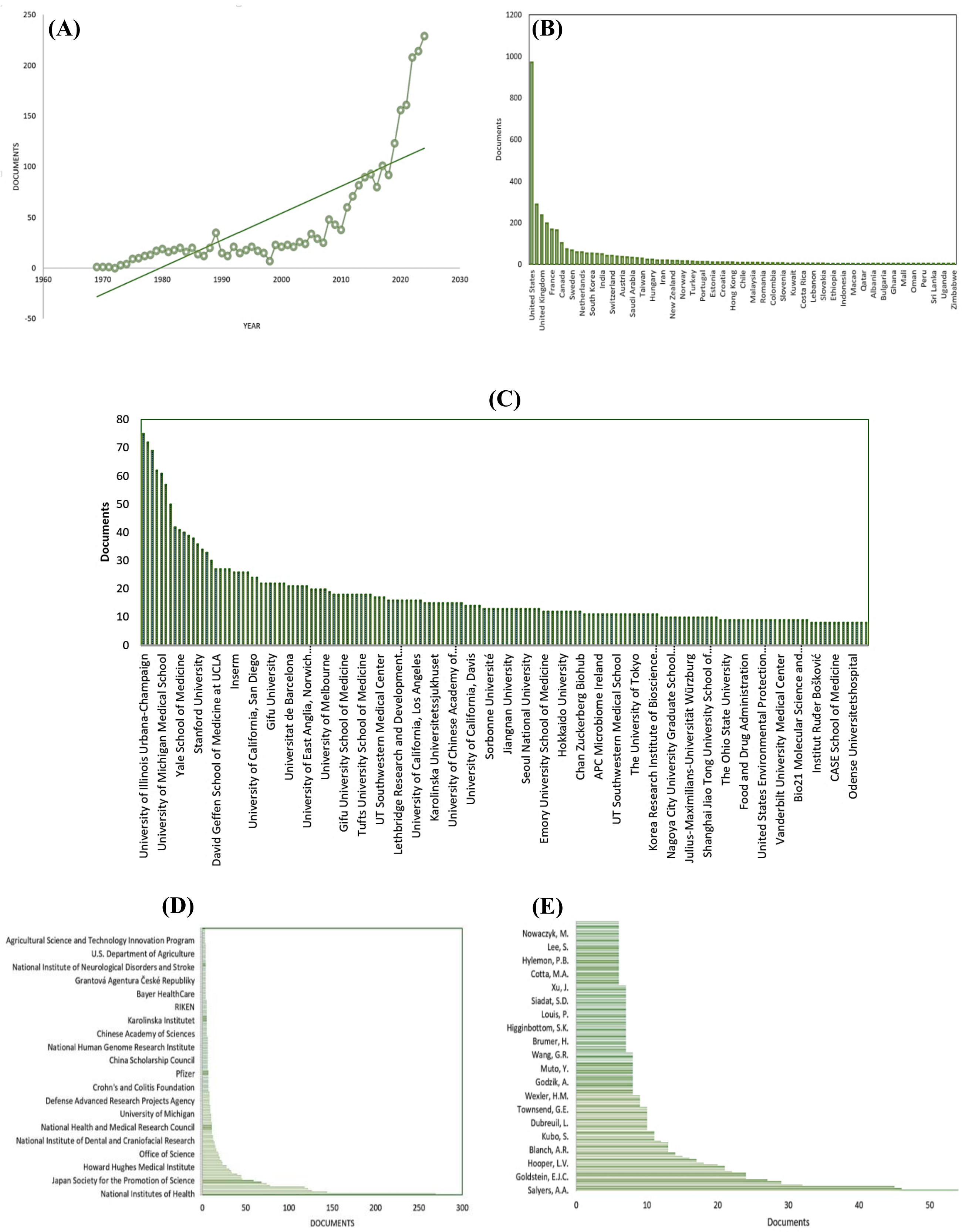

Fig. 2. (A) Annual trends in publications related to *B. thetaiotaomicron*; (B) the leading countries contributing to *B. thetaiotaomicron* research; (C) the most productive situations in the publication of *B. thetaiotaomicron* studies; (D) the major funding sponsors supporting *B. thetaiotaomicron* research; (E) the most prominent authors in the field of *B. thetaiotaomicron*.

Table 1. List of top-cited articles on *B. thetaiotaomicron*

Citation	Title	Source	Type	Year	Authors
3935	Commensal microbe-derived butyrate induces the differentiation of colonic regulatory T cells	Nature	Research article	2013	Furusawa et al.[38]
2632	Anticancer immunotherapy by CTLA-4 blockade relies on the gut microbiota	Science	Research article	2015	Vétizou et al.[39]
1855	Molecular analysis of commensal host-microbial relationships in the intestine	Science	Research article	2001	Hooper et al.[40]
1750	Role of the gut microbiota in immunity and inflammatory disease	Nature Reviews Immunology	Review article	2013	Kamada et al.[41]
1714	Gut biogeography of the bacterial microbiota	Nature Reviews Immunology	Review article	2015	Donaldson et al.[42]
1583	Bacteroides: The good, the bad, and the nitty-gritty	Clinical Microbiology Reviews	Review article	2007	Wexler et al.[43]
1577	Intestinal short-chain fatty acids and their link with diet and human health	Frontiers in Microbiology	Short communication	2016	Ríos-Covián et al.[44]
1565	The long-term stability of the human gut microbiota	Science	Research article	2013	Faith et al.[45]
1558	Microbial degradation of complex carbohydrates in the gut	Gut Microbes	Review article	2012	Flint et al.[46]
1225	Polysaccharide utilization by gut bacteria: Potential for new insights from genomic analysis	Nature Reviews Microbiology	Review article	2008	Flint, H.J et al.[47]

Table 2. Contributions of journals to publication on *B. thetaiotaomicron*

Score	Journal	Number of publications
1	Anaerobe	68
2	Frontiers In Microbiology	68
3	Antimicrobial Agents and Chemotherapy	65
4	Journal Of Bacteriology	62
5	Cell Host and Microbe	51

Table 3. Most highly cited articles on *B. thetaiotaomicron* published in the journal "Anaerobe"

Title	No. of citations
A dynamic partnership: Celebrating our gut flora	313
Chemical communication in the gut: Effects of microbiota-generated metabolites on gastrointestinal bacterial pathogens	105
Recent evolution of antibiotic resistance in the anaerobes as compared to previous decades	98
In vitro fermentation of alginate and its derivatives by human gut microbiota	92
Sphingolipid composition in Bacteroides species	75

3.11. Publications based on authors

As shown in Figure 2E, the most active authors in the research on *B. thetaiotaomicron* were: (1) Salyers, A.A. (54 publications); (2) Gordon, J.I. (46 publications); (3) Martens, E.C. (45 publications); (4) Watanabe, K. (32 publications); (5) Sonnenburg, J.L. (29 publications). These authors have made significant contributions to the literature on *B. thetaiotaomicron*.

3.12. The most co-occurrences author's keywords

Figure 3A presents the most commonly used keywords by the author based on a minimum occurrence threshold of 10. The most frequent terms included "*B. thetaiotaomicron*" (n = 162 co-occurrences), "Bacteroides" (n = 155), "microbiota" (n = 124), "microbiome" (n = 126), "anaerobes" (n = 36), "anaerobic bacteria" (n = 31), "probiotics" (n = 39), "inflammatory bowel disease" (n = 38), "diet" (n = 22), and "prebiotics" (n = 21). These patterns indicate a strong research focus on gut microbiota and its related health implications (Fig. 3A).

3.13. Frequently co-occurring terms in *B. thetaiotaomicron* research

A review of publications on *B. thetaiotaomicron* exhibited several frequently co-occurring terms. The most prominent keywords included "*B. thetaiotaomicron*" (n = 2,035), "nonhuman" (n = 1,727), "article" (n = 1,557), "humans" (n = 1,409), "Bacteroides" (n = 1,021), "intestinal flora" (n = 974), and "microbiology" (n = 532). These terms were identified using a minimum occurrence threshold of 20. Of a total of 18,997 words analyzed, 3,113 met this criterion. The identified keywords were classified into three distinct clusters (Fig. 3B).

3.14. Relationship between authors and countries

Figure 3C illustrates the network of co-authorship among researchers who studied on *B. thetaiotaomicron*. To be included in the analysis, authors needed to publish at least one paper, resulting in a total of 54 qualifying individuals out of 1,965. Figure 3D depicts international research collaborations by mapping connections between countries involved in *B. thetaiotaomicron* publications. This analysis set a minimum threshold of 10 documents per country, with 52 out of the 121 countries meeting the inclusion criterion.

3.15. Qualitative analysis based on the significance of our findings

The bibliometric analysis highlighted a dynamic progression in the study of *B. thetaiotaomicron* over several decades. Initial research during the 1960s and 1970s focused on its taxonomic classification and its role within the gut microbiota. These early efforts laid the groundwork for more detailed investigations into the functional behavior of *B. thetaiotaomicron*, particularly its interactions within the intestinal environment and its influence on host physiology. From the early 2000s onward, there was a significant increase in scholarly output, coinciding with major technological advancements in genomics and proteomics. These innovations enabled researchers to explore the molecular pathways through which *B. thetaiotaomicron* modulates metabolic activity and immune function. This shift in focus is reflected in the rising citation rates of studies published in high-impact journals, with a notable 2013 article in "Nature" being cited over 3,000 times, indicating the microbe's growing importance in biomedical research. As research advanced, *B. thetaiotaomicron* has been recognized not only as a passive resident of the human gut but also as a promising candidate for therapeutic interventions in gastrointestinal diseases. The United States has become a central hub for this research, leading in both publication volume and citation impact. This geographic concentration highlights a broader trend toward specialization and collaborative scholarship, as evidenced by the increasing prevalence of multi-author and multi-institutional studies. These developments reflect the complexity of the field and the interdisciplinary approaches necessary to fully understand the health-related implications of *B. thetaiotaomicron* on human health.

4. DISCUSSION

This study employed bibliometric data to assess research patterns on *B. thetaiotaomicron*. The analyzed documents spanned from the earliest report in 1965 through 2024. The findings indicated that *B. thetaiotaomicron* has become a prominent focus on contemporary scholarly research. Over the past two decades, its visibility has steadily increased, reaching a peak in 2024. Researchers have increasingly sought to elucidate the correlation between gut microbiota and various health conditions using emerging and advanced methodologies[14-16]. Numerous diseases have been linked to changes in gut microbiota composition, including colitis and obesity[17,18]. When the composition of intestinal microbiota alters due to disease, the abundance of the *Proteobacteria* phylum tends to increase, while anti-inflammatory bacteria, including *B. thetaiotaomicron*, decreases[19]. *B. thetaiotaomicron* plays a central role in this microbial population, as mucin-degrading bacteria can significantly influence microbiome composition and host physiology. Several dietary interventions have been

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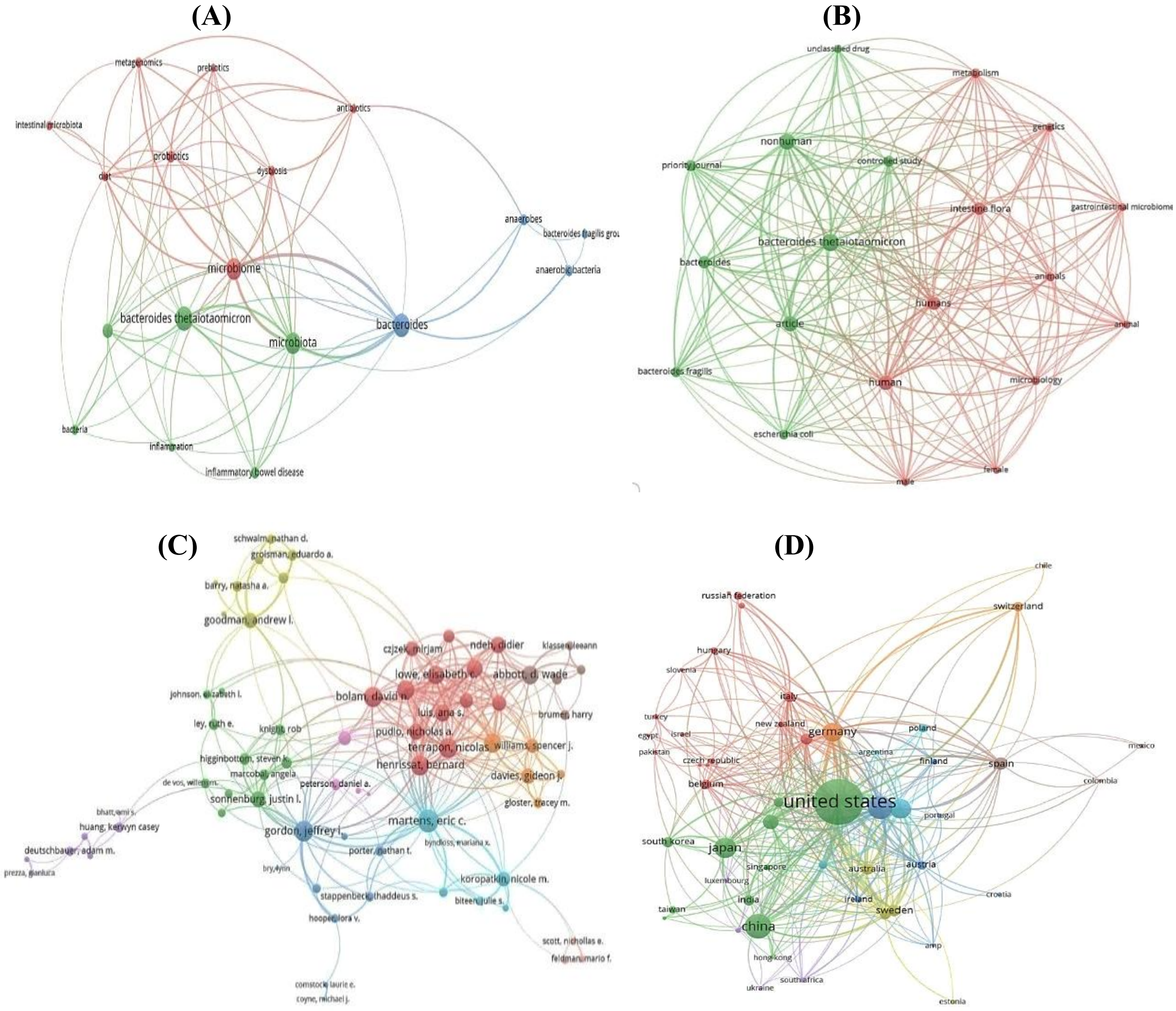

Fig. 3. (A) The most commonly used keywords by authors; (B) a cluster map showing the frequency of terms; (C) a profile illustrating co-authorship among authors who publish articles on *B. thetaiotaomicron*; (D) a visual representation of international collaboration networks in the research field related to *B. thetaiotaomicron*.

reported to impact *B. thetaiotaomicron*[20]. In animal studies, it has been observed that administering substances that increase *B. thetaiotaomicron* could improve the host's physiological condition[21].

Our research revealed a growing global interest in microbiota. Industrialized nations such as the United States, the United Kingdom, Japan, China, and France have demonstrated significant engagement in this field due to its profound implications. Institutions in the United Kingdom, France, and the United States were identified as the most productive in this area. Terms like "*Bacteroides thetaiotaomicron*", "*Bacteroides*", "gut microbiota", and "microbiota" have recently gained attention due to the critical role of gut microbiota composition in various diseases, leading to the emergence of a new field of study known as "microbiota". Additionally, the most popular terms included "*Bacteroides thetaiotaomicron*", "nonhuman", "article", "humans", "*Bacteroides*", "peer-reviewed journal", "intestine flora", and "*Bacteroides fragilis*". Our study also demonstrated that a significant portion of current research investigates the effects of *B. thetaiotaomicron* in animal studies, in addition to its role in human investigations. This increasing focus on the metabolic and immunological interactions of *B. thetaiotaomicron* within the human gut microbiota suggests a potential shift toward personalized microbiome-based therapies.

Historical research trends have emphasized the critical role of *B. thetaiotaomicron* in maintaining gut

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homeostasis and modulating host metabolic pathways, as reflected by the increase in publications examining its enzymatic and genetic contributions to digestion and immune regulation. While gut homeostasis has long been linked to *B. thetaiotaomicron*, earlier investigations have been primarily concentrated on mechanistic insights into mucin degradation, host immunity, and metabolic activity[22,23]. What has been lacked is a consolidated perspective that situates these biological findings within a structured overview, in which scholarly attention to *B. thetaiotaomicron* has expanded and shifted over time. Likewise, although the immunological and metabolic effects of *B. thetaiotaomicron* have been thoroughly described[24], relatively few studies have systematically connected these functions across disciplines, bridging microbial biology with broader host physiology and disease outcomes. Attention to the geographic and institutional dynamics of this research has also been limited, despite their significance in recognizing scientific leadership and fostering translational collaborations[25-27].

By applying bibliometric tools to nearly six decades of literature (1965–2024), our study provides this structured perspective, similar to previous bibliometric efforts in related fields. Luo et al. explored global trends in the gut microbiota–osteoporosis interface to identify dominant themes and future directions[28]. Wang et al. emphasized how bibliometric analyses deepen the understanding of emerging perspectives[29]. Similarly, Zyoud's assessment of microbiota and nonalcoholic fatty liver disease research demonstrated the value of mapping research activity over time and regions[30]. Also this study supplies a quantitative synthesis of publication trends and institutional contributions. It highlights dominant themes while revealing the imbalance between studies using animal models and those focused on human or translational research. This analytical framework exposes underexplored areas and establishes a structured foundation for future interdisciplinary. Our analysis quantified publication growth, highlighted contributions from leading institutions, and traced thematic concentrations, such as colitis, while also addressing the imbalance between animal-based investigations and human studies. This integrative framework situates *B. thetaiotaomicron* research within a broader scientific context, identifies areas that warrant further exploration, and establishes a foundation for more interdisciplinary and clinically oriented work.

One of the key findings of this study is the prominence of colitis in research related to *B. thetaiotaomicron*, underscoring the bacterium's importance in gastrointestinal health and disease. This finding necessitates further exploration into the mechanisms underlying its interactions with the host and their potential implications for the pathogenesis and management of colitis. Two significant developments contribute to this emphasis. First, inflammatory bowel diseases have increasingly been recognized as a global health concern, extending beyond their traditional prevalence in Western countries and drawing sustained scientific interest[31,32]. Second, a growing body of experimental work demonstrates that *B. thetaiotaomicron* has protective effects in models of intestinal inflammation through mechanisms such as aryl hydrocarbon receptor activation and vesicle-mediated immune modulation[10,33-35] . The convergence of these clinical and biological factors provides a clear rationale for the rising research activity focused on colitis and related inflammatory pathways. Additionally, the clustering of terms related to mucin utilization and polysaccharide metabolism reflects the well-documented enzymatic capabilities of this bacterium, which includes an extensive set of glycoside hydrolases and transporters[36,37]. This alignment of bibliometric signals and functional studies indicates that research on *B. thetaiotaomicron* has progressed from descriptive reports to targeted investigations of nits' metabolic specialization and clinical relevance.

Looking forward, these foundational insights pave the way for translational research targeting *B. thetaiotaomicro*n for therapeutic interventions. The growing sophistication in genomics and microbiome engineering offers promising avenues to manipulate this bacterium, potentially leading to breakthroughs in the treatment of inflammatory bowel disease, obesity, and other metabolic disorders.

5. CONCLUSION

The present study assessed the key bibliometric features of all publications related to *B. thetaiotaomicron* that are indexed in Scopus, providing a comprehensive overview of the development of research in this area over time. The findings indicate a growing scholarly interest in *B. thetaiotaomicron*, and future research is expected to increasingly explore its association with various host health conditions, as well as its potential therapeutic and preventive applications. This study represents the first comprehensive bibliometric analysis of *B. thetaiotaomicron*, focusing on study design, target populations, and disease contexts involved. While alternative databases, such as Web of Science and Google Scholar, could have been considered, Scopus was selected for its broad coverage and high citation rates. It is important to note that the scope of this analysis was limited to publications indexed in Scopus, which may have excluded relevant studies from non-Scopus journals that could further enhance the bibliometric landscape.

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DECLARATION

Acknowledgments

Not applicable.

Generative AI and AI-assisted technologies

ChatGPT (OpenAI) was used for language editing and grammatical refinement. All study design, data analysis, and scientific interpretations were conducted exclusively by the authors.

Ethical approval

The research complied with all applicable institutional and national guidelines for the handling of bibliographic data.

Consent to participate

Not applicable.

Consent for publication

All authors reviewed the results and approved the final version of the manuscript.

Authors' contributions

FHL: conceptualization, methodology, writing–original draft, data curation, resources; MH: writing–review & editing, supervision and validation; FE: writing–original draft, investigation; MT: writing–review & editing and validation; SDS: conceptualization, methodology, supervision, and validation.

Data availability

Data available on request from the authors.

Competing interests

The authors declare that they have no competing interests.

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Supplementary information

The online version does not contain supplementary material.

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