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ARTICLE

Bacteroides research in Southeast Asia (1995–2025): A bibliometric analysis of trends, themes, and gaps

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ABSTRACT

Bacteroides spp. are among the most dominant members of the gut microbiota of homeothermic animals, surpassing commonly cited genera such as *Escherichia, Lactobacillus,* and *Bifidobacterium*. Their predominance supports their role as mutualists or commensals within the gastrointestinal tract. However, disruption of gut barrier integrity may allow *Bacteroides* to translocate to extraintestinal sites, where they can cause opportunistic infections. Moreover, *Bacteroides* species are notable for their high levels of clinical antimicrobial resistance and for harboring diverse resistance mechanisms among anaerobic gut bacteria. This study aimed to characterize regional research trends on *Bacteroides* through a bibliometric analysis of publications indexed in the Scopus database. All eligible original research articles on *Bacteroides* originating from Southeast Asian (SEA) countries were retrieved, and bibliographic and citation data were analyzed. Selected datasets were visualized using the CorText platform. A total of 113 *Bacteroides*-related research articles published between 1995 and 2025 were identified from SEA. Research output showed a marked increase beginning in 2019, peaking in 2023. Singapore and Thailand emerged as the leading contributors to *Bacteroides* research in the region, with Singapore also dominating in terms of productive institutions and individual authors. Moreover, the majority of the journals in which *Bacteroides* research was published were top-tier. The most highly cited article (TC = 2,375) was an international collaborative study led by a Singapore-based researcher and conducted in France. Frequently occurring keywords included "gut/fecal microbiome," "resistance gene(s)," "microbial source tracking," and "fecal pollution." Overall, this bibliometric analysis of the *Bacteroides* research landscape in SEA underscores the relatively limited volume and scope of studies in the region. The findings highlight the need to expand research efforts toward a more comprehensive understanding of *Bacteroides* epidemiology, ecology, and clinical relevance beyond the gut microbiome context.

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INTRODUCTION

Bacteroides spp. are non-spore-forming, obligately anaerobic, Gram-negative bacilli and represent the most dominant group of gut bacteria among homeothermic animals, where they reside and proliferate almost exclusively within the host gastrointestinal tract (Kabiri et al. 2013; Tamana et al. 2021; Zafar and Saier 2021). These organisms generally establish mutualistic or commensal relationships with their hosts, contributing to the maintenance of gut homeostasis, efficient digestion, and nutrient absorption, as well as the production of beneficial secondary metabolites and the modulation of host immune system development (Yanagibashi et al. 2013; Varki 2017; Landuyt et al. 2021; Li et al. 2021).

Despite their beneficial roles, *Bacteroides* spp. are also opportunistic pathogens that can cause severe infections when they spread beyond the gut. They are commonly implicated in nosocomial infections and are associated with abscess formation in the liver, lungs, and brain, as well as bacteremia (Brook 2016; Weiner et al. 2016; Majewska et al. 2021). Importantly, *Bacteroides* are regarded as the most clinically significant Gram-negative anaerobic bacilli because they exhibit high levels of antimicrobial resistance (AMR) and possess a wide array of resistance mechanisms among anaerobic gut bacteria. In human medicine, AMR patterns in *Bacteroides* infections are relatively well-documented and routinely monitored (Kierzkowska et al. 2020; Jasemi et al. 2021; Carillo Terrazas et al. 2025). Although

KEYWORDS

Bacteroides; bibliometric analysis; CorText; Southeast Asia

AMR surveillance of *Bacteroides* remains less extensive than that of major enteric pathogens, such as *E. coli*, typhoidal *Salmonella enterica,* and *Shigella* spp., it has nonetheless received increasing attention in certain regions (Karlowsky et al. 2012; Eitel et al. 2013; Merchan et al. 2016; Kajihara et al. 2023; Wu et al. 2023).

In contrast, research on AMR in *Bacteroides* within animal, agricultural, and wildlife contexts remains limited. A comprehensive review of AMR in food animals by Xu et al. (2022) identified a limited bacterial taxa and did not include *Bacteroides*. Most published studies on AMR in *Bacteroides* focus on human clinical isolates, with relatively little attention given to veterinary medicine, animal agriculture, or wildlife sciences (He et al. 2020). This gap is particularly concerning given that, unlike in humans, where antibiotics are used primarily for therapeutic purposes, antimicrobials in food-producing animals are frequently administered for non-therapeutic uses such as growth promotion and prophylaxis (Berglund 2015). Consequently, farm wastes have been shown to harbor higher concentrations of antibiotic resistance genes (ARGs) than hospital or municipal wastes (Sim et al. 2011; Ekpeghere et al. 2017; Kivits et al. 2018; Liu et al. 2018; Gao et al. 2020; Macedo et al. 2020). Although the literature on AMR in veterinary and wildlife settings is growing, specific information on AMR in *Bacteroides* in these settings remains scarce (Torres et al. 2020; Dela Rosa and Rivera 2023). Addressing this gap is critical, as *Bacteroides* constitute the dominant anaerobes in the gut of homeotherms and have been increasingly recognized as important reservoirs of ARGs (Yan et al. 2022; Yekani et al. 2022; Sood et al. 2023).

Bibliometric analysis provides a systematic and quantitative approach to mapping the structure, evolution, and accumulation of scientific knowledge. It enables the identification of research hotspots, emerging themes, and knowledge gaps by examining variables such as publication year, geographic distribution, institutional affiliations, citation patterns, keywords, and publication categories (Donthu et al. 2021; Nie et al. 2024).

In this study, bibliometric data were retrieved from the Scopus database, which is widely recognized as the largest abstract and citation database of peer-reviewed literature and offers broader subject coverage than many alternative databases (Md Khudzari et al. 2018; Ali et al. 2021; Hashem E et al. 2023; Febryanti 2025; Verma et al. 2025). By analyzing *Bacteroides*-related publications from Southeast Asia (SEA), this study aims to elucidate spatial and temporal research trends, identify thematic emphases, and highlight gaps in the regional literature. The findings are expected to provide a clearer understanding of the current research landscape on *Bacteroides* in SEA and to inform future research directions, particularly in underexplored areas such as AMR beyond the human gut microbiome.

MATERIALS AND METHODS

Software and Tools Used in the Analysis

The PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) framework guided article identification, screening, eligibility assessment, and inclusion. The sources of records and the inclusion and exclusion criteria are summarized in Figure 1 using a PRISMA-style flow diagram adapted from Torres et al. (2020).

CorText Manager (https://www.cortext.net/) was used for selected analyses, including the generation of network and contingency maps (Breucker et al. 2016). CorText Manager is a freely accessible online platform that supports both qualitative and quantitative analyses of research fields, enabling the identification of structural patterns, research status, and emerging trends (Ubando et al. 2021; Qi et al. 2025).

All bibliographic data were retrieved exclusively from Scopus (https://www.scopus.com), selected for its broad coverage of peer-reviewed literature across scientific disciplines.

Screening and Decision-Making

In accordance with PRISMA framework, the identification strategy involved searching the Scopus database for the term *Bacteroides* enclosed in quotation marks (“Bacteroides”) to retrieve records that matched the keyword exactly.

The initial search results were refined using automated filters available in Scopus. Only final, open-access research articles published in English were included. Records were further restricted to those affiliated with institutions from SEA countries, namely Brunei, Cambodia, Indonesia, Lao PDR, Malaysia, Myanmar, the Philippines, Singapore, Thailand, Timor-Leste, and Vietnam. To ensure data completeness and consistency, only articles published up to December 31, 2025, were included, and records from 2026 were excluded.

Articles that did not mention *Bacteroides* in the title, abstract, or author-provided keywords were excluded from further analysis. All retrieved articles were subsequently manually screened to confirm their contextual relevance to *Bacteroides*.

Data Analysis

All eligible records were exported in Research Information Systems (.RIS) and comma-separated values (.CSV) formats for analysis. Extracted variables included abstracts, author(s), article title, publication year, source title (journal), volume, issue, page numbers, citation count, digital object identifier (DOI), abstract, author keywords, and indexed keywords.

The finalized dataset was used to assess scientific productivity and research characteristics according to publication year, country of affiliation, journal, institution, author, citation performance, and thematic focus. Supplementary Table 1 lists all 113 journals in the dataset, along with associated metadata (e.g., contributing authors and article titles).

RESULTS AND DISCUSSION

Data Collection

The final Scopus search query used was as follows:

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TITLE-ABS-KEY("Bacteroides") AND LIMIT-TO ( AFFILCOUNTRY,"Brunei Darussalam" ) OR LIMIT-TO ( AFFILCOUNTRY,"Cambodia" ) OR LIMIT-TO ( AFFILCOUNTRY,"Indonesia" ) OR LIMIT-TO ( AFFILCOUNTRY,"Malaysia" ) OR LIMIT-TO ( AFFILCOUNTRY,"Myanmar" ) OR LIMIT-TO ( AFFILCOUNTRY,"Philippines" ) OR LIMIT-TO ( AFFILCOUNTRY,"Singapore" ) OR LIMIT-TO ( AFFILCOUNTRY,"Thailand" ) OR LIMIT-TO ( AFFILCOUNTRY,"VietNam" ) )
AND ( EXCLUDE ( PUBYEAR,2026) )
AND ( LIMIT-TO ( DOCTYPE,"ar" ) )
AND ( LIMIT-TO ( PUBSTAGE,"final" ) )
AND ( LIMIT-TO ( EXACTKEYWORD,"Bacteroides" ) )
AND ( LIMIT-TO ( SRCTYPE,"j" ) )
AND ( LIMIT-TO ( LANGUAGE,"English" ) )
AND ( LIMIT-TO ( OA,"all" ) ).
```

This query applied a series of exclusion and restriction criteria, limiting the results to final, open-access, English-language research

articles published in peer-reviewed journals, with at least one author affiliated with an institution in a SEA country. Brunei, Laos, and Timor-Leste were not included in the final query syntax because automated filtering retrieved no publications from these countries, indicating an absence of indexed research on *Bacteroides* to date. Publications from 2026 were excluded to ensure data completeness and comparability across years.

Based on these criteria, a total of 113 journal articles were retained for inclusion in the bibliometric analysis, as illustrated in the PRISMA flow diagram (Figure 1). The final dataset comprised three categories of publications:

1. Studies conducted in SEA by exclusively SEA researchers;
2. Studies conducted in SEA involving collaborations between SEA and non–SEA researchers; and
3. Studies conducted outside SEA that included at least one SEA researcher or involved collaboration with a SEA institution.

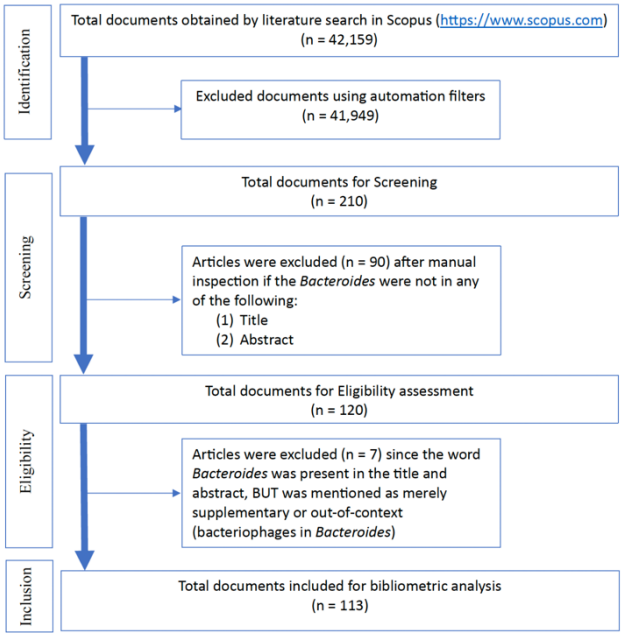

Figure 1: Preferred Reporting Items for Systematic Review and Meta-Analysis (PRISMA) flow diagram detailing the steps in identifying and screening articles for bibliometric analysis.

Publications by Year

The earliest *Bacteroides*-related article indexed in Scopus from SEA was published on April 29, 1995, and originated from Indonesia. Titled *"Microbiology of chronic suppurative otitis media in children in Surabaya, Indonesia"* (Brook and Santosa 1995), the study appeared in the *International Journal of Pediatric Otorhinolaryngology*. Following this initial publication, research output on *Bacteroides* in the SEA region remained sparse for more than two decades, as shown in Figure 2. Several years, including 1996, 1998–2000, 2003, and 2012, were recorded as having no publications. Annual publication counts did not reach double digits until 2020, when 10 studies were published. From 2023 to 2025, *Bacteroides* research in SEA showed a sustained increase, with annual outputs consistently remaining in the double digits. This upward trend culminated in 2024, when the highest number of publications was recorded, at 16 articles.

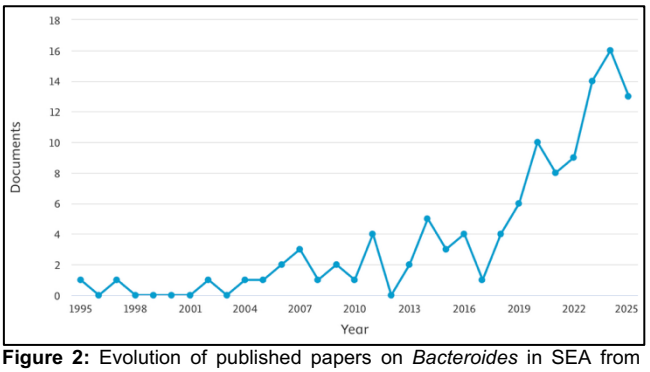

Figure 2: Evolution of published papers on *Bacteroides* in SEA from 1995 to 2025.

What does this temporal pattern imply? *Bacteroides*-related research in SEA was scarce before 2020, reflecting the region's research interests or individual government policies on scientific research. Many countries, including those in SEA, typically allocate national research and development budgets to medical research on known and common communicable diseases, vaccination, and diagnostics (Tandon et al. 2021; Lim et al. 2023; Han et al. 2025). Moreover, *Bacteroides* research is logistically demanding, as it requires an anaerobic system. Figure 2 suggests that many SEA laboratories lacked the necessary anaerobic equipment. On top of this are the expensive molecular sequencing tools that severely undermine research, especially in low-income SEA countries. The combination of a limited budget and equipment thus limits the researchers to being interested in or venturing into and specializing in *Bacteroides*.

The sharp increase in publications in 2020 may be related to the pandemic and an overall heightened attention to other health-related topics, such as the microbiome and One Health frameworks.

Publications by Country

Among SEA countries, Singapore contributed the most *Bacteroides* publications, followed by Thailand, Malaysia, Indonesia, Vietnam, the Philippines, Cambodia, and Myanmar (Figure 3). In contrast, Brunei, Laos, and Timor-Leste did not appear in the network, reflecting the absence of *Bacteroides*-related publications or author/institutional affiliations from these countries within the dataset.

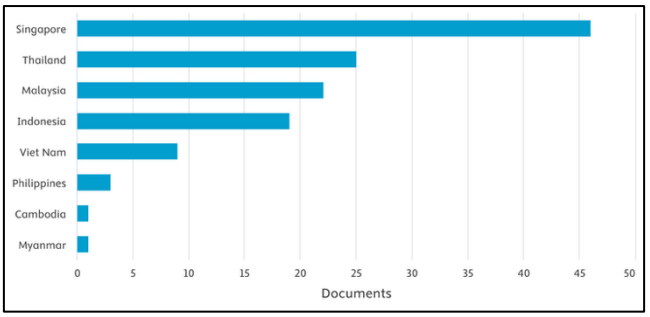

Figure 3: Number of *Bacteroides* research per SEA country from 1995 to 2025.

Singapore's dominance in *Bacteroides*-related research is driven by sustained investment in biomedical sciences and the most advanced sequencing infrastructure in SEA (Poh 2010; Economic Development Board, 2025). This contrasts with the limited representation of lower-income SEA countries, which lack adequate funding, platforms, and capacity. This is despite the higher prevalence of gut-associated diseases, AMR, and other tropical diseases (Tekola-Ayele and Rotimi 2015; Sulis et al. 2022; Woods et al. 2023). This imbalance has regional implications, such as a missing link between gut microbiome-diet-environment, a

blind spot in AMR surveillance, and all of which are underrepresented in most SEA countries. Addressing these research gaps is an opportunity to strengthen collaborative microbiome and *Bacteroides* research initiatives that support metagenomic and molecular studies in underrepresented countries.

As noted earlier, the 113 publications analyzed were not limited to studies conducted exclusively within SEA (intra-regional relationships); they also included articles that involved at least one SEA researcher or institutional affiliation, regardless of study location (global linkages). Figure 4 illustrates the global interconnectedness of *Bacteroides* research involving SEA countries using a country-level network map generated with CorText Manager.

In the network visualization, node size (represented by solid circles) is proportional to the number of *Bacteroides*-related publications per country. Clustering reflects thematic similarity among research outputs, while the distance between clusters represents the degree of relatedness between countries and their dominant research topics.

The eight contributing SEA countries were distributed across four of the six identified clusters. Research outputs from Myanmar, the Philippines, and Thailand formed a distinct cluster, indicating closely related thematic emphases, yet sufficiently differentiated from those of other countries. This cluster was positioned near Indonesia's cluster, suggesting thematic overlap and interrelated research topics between these groups. Singapore and Vietnam formed overlapping nodes, indicating highly similar, if not nearly identical, research themes. Notably, this combined cluster was also closely linked to the United States, the country with the highest overall research output on *Bacteroides*, underscoring a strong thematic alignment and international collaboration. Malaysia formed a separate cluster with a distinct thematic emphasis, while remaining closely connected to the Singapore–Vietnam cluster, suggesting partial overlap in research focus.

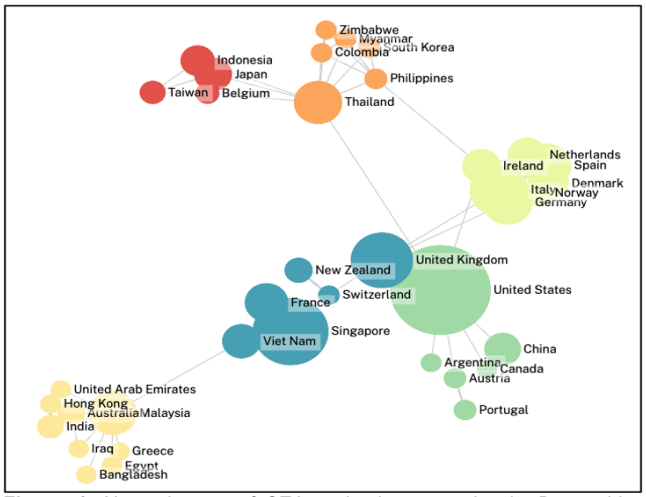

Figure 4: Network map of SEA and other countries in *Bacteroides* research.

The country-level clustering (inter-regional and global) shows how *Bacteroides* topics are distributed across. Clustering reflects drivers of research capacity, such as national research funding, overall GDP, policy priorities in science research, and even access to high-end sequencing systems. Singapore, a high-income country not only in SEA but worldwide, naturally aligns with high-research-output countries such as the US. In contrast, lower- to middle-income SEA countries tend to cluster due to common constraints, such as national funding allocation and the prioritization of more practical, immediate health solutions over long-term scientific research (Semahegn et al. 2023). These gaps point to a research direction to strengthen regional collaboration with Singapore and intra-regional collaborations with other Asian, European, and North American counterparts.

Publications by Journal

A total of 75 peer-reviewed journals published *Bacteroides*-related research associated with SEA, along with their disciplinary focus, research themes, and methodological approaches (Supplementary Table 2). Results showed that *Bacteroides* research was published across a wide range of well-ranked Scopus-indexed journals. *Bacteroides* research in SEA covers topics on general microbiology, veterinary sciences, human medicine, and many other multidisciplinary studies.

The leading journals contributing to this body of literature are summarized in Table 1.

Most studies utilized metagenomic (shotgun, metabolomics, and next-generation sequencing (NGS)) and molecular methods (PCR, qPCR, Sanger sequencing). Research themes were also very diverse, including the gut microbiome's effects on cancer, gastrointestinal, and cardiorespiratory health. Other themes include the gut microbiome and diet relations, antimicrobial resistance, and environmental and animal-associated microbiomes.

Table 1: Journals that published research on *Bacteroides* from SEA and the number of publications.

Journal	Number of *Bacteroides* research in SEA
Gut Microbes, Scientific Reports	5
Nature Communications, Veterinary World	4
BMC Microbiology, Frontiers in Cellular and Infection Microbiology, Nutrients, PLoS One	3
Animals, Applied and Environmental Microbiology, Asian Australasian Journal of Animal Sciences, British Journal of Nutrition, Frontiers in Microbiology, Frontiers in Veterinary Science, International Journal of Molecular Sciences, Journal of Applied Microbiology, Microorganisms, NPJ Biofilms and Microbiomes, Pediatric Research, PeerJ, Science	2
Others	1

The broad spread of *Bacteroides*-related research across high-impact, multidisciplinary journals demonstrates the extent to which *Bacteroides* research can reach. It also indicates that *Bacteroides* research from SEA is gaining visibility worldwide when the topics align with globally prioritized areas, such as the gut microbiome, AMR, and the One Health framework (Bertagnolio et al. 2024; Al-Khalaifah et al. 2025). Research published in *Gut Microbes, Nature Communications*, and *Scientific Reports* suggests that studies conducted in the region meet the high methodological and conceptual rigor required by these high-impact journals. However, the predominance of single-publication in journals or the recurrence of *Bacteroides* research indicates that SEA remains fragmented. This may reflect uneven access to advanced equipment, such as an anaerobic culturing facility and advanced sequencing platforms, or limitations in research funding, as some journals charge high article processing fees. Overall, Table 1 shows

that SEA researchers are capable of conducting high-impact research, but, as a region, they need better consolidation.

Publications by Institution

A total of 160 institutions worldwide contributed to *Bacteroides*-related research either conducted in SEA or involving collaboration with SEA researchers or institutions. Table 2 lists the leading institutions (Universities, Hospitals, and Research Institutes) in *Bacteroides* research, all of which are located in the SEA region. However, it is notable that there is an uneven distribution among SEA institutions, with most research concentrated in a small number of research institutions or universities, mainly from Singapore and Thailand. Among these, the three most productive SEA institutions were all based in Singapore and collectively accounted for 60 of the 113 publications, representing approximately 53% of the total *Bacteroides* research output associated with the region. It is also worth noting that only four SEA countries are highly involved in *Bacteroides* research: Singapore, Thailand, Malaysia, and Indonesia.

The two affiliate institutions of the *National University of Singapore (NUS)* (33 publications) and the *NUS Yong Loo Lin School of Medicine* (18 publications) already make a substantial contribution. There are other Singapore institutions, such as *Nanyang Technological University* (9 publications) and the *Agency for Science and Technology* (6 publications), which highlight that Singapore dominates *Bacteroides* research within SEA.

Table 2: The top leading institutions in SEA that published research on *Bacteroides*

Institution	Country	Number of publications
National University of Singapore	Singapore	33
NUS Yong Loo Lin School of Medicine	Singapore	18
Nanyang Technological University	Singapore	9
Chulalongkorn University	Thailand	7
Universiti Putra Malaysia	Malaysia	
Agency for Science and Technology and Research	Singapore	6
Universitas Indonesia	Indonesia	
Thailand National Center for Genetic Engineering and Biotechnology	Thailand	5
Mahidol University	Thailand	
Kasetsart University	Thailand	
Universiti Malaysia	Malaysia	
Universitas Gadjah Mada	Indonesia	
A*STAR Institute for Human Development and Potential	Singapore	

What does this institutional focus mean? The strong dominance of three Singaporean institutions further underscores what was discussed earlier in Figure 2, Singapore's adequate funding and policy prioritization (Economic Development Board 2025). Singapore has shown strong institutional support for the gut microbiome, with *Bacteroides* typically included (Khine et al. 2021; Cornall 2022). Regionally, this implies that the dominance of a very few institutions yields findings that are neither fully representative nor representative at all of the region's very diverse population. Thus, this gap will require expanding cross-institutional collaboration to ensure that microbiome and *Bacteroides* research become regionally relevant.

Publications by Author

A total of 160 authors contributed to SEA-related publications on *Bacteroides*. This count includes authors based within the region as well as international researchers who collaborated with SEA researchers or institutions.

The most productive authors, summarized in Table 3, were affiliated with institutions in Singapore, Thailand, and Malaysia. *Lee, Yuan Kun* of the Yong Loo Lin School of Medicine, National University of Singapore, was the leading contributor, with 10 publications, and the only author with a double-digit number of articles on *Bacteroides* in the dataset. Other highly productive Singaporean authors included *Chong, Yap Seng; Lee, Bee Wah; Kumar, Veerendra*; and *Wei Wei Thwe*. This again emphasizes Singapore's leading role in *Bacteroides* research in SEA.

Other authors within SEA, outside Singapore, include *Nitisinprasert, Sunee* (Thailand), and *Lim, Yvonne Ai Lian* (Malaysia), reflecting an emerging interest and expertise in *Bacteroides* beyond Singapore.

Table 3: Leading authors who published *Bacteroides* research in SEA or collaborated with SEA authors

Author	Record
Lee, Yuan Kun	10
Liu, Wentso; Nakayama, Jiro; Nitisinprasert, Sunee	4
Chong, Yap Seng; Clayton, Jonathan Brent; Hong, Pei-Ying; Khine, Wei Wei Thwe; Knights, Dan; Kumar, Veerendra; Lay Christophe; Lee, Bee Wah; Lim, Yvonne Ai Lian; Lu Wunwei; Wu Jerhorng Horng; Zhang, Hao	3

The concentration of highly productive authors in Singapore with high h-indices (Supplementary Table 3) suggests possible disparities in research capabilities across SEA rather than a lack of interest among researchers or the perceived relevance of *Bacteroides* in the region. This leads to limited local expertise and/or the lack of an external support system, such as the local government, that would encourage its scientists to pursue the topic. Unfortunately, the lack of, or a small pool of, prolific scientists in SEA working on *Bacteroides* would have implications for regional health, as *Bacteroides* plays a key role in overall gut-associated health and diseases that are increasingly prevalent worldwide (Tufail and Schmitz 2025; Yang et al. 2025). Thus, findings also suggest that future regional capacity-building collaborations should enable more researchers in underrepresented SEA countries. Doing so would "decentralize" expertise and generate more *Bacteroides*-specific research.

Most Cited Publications

Among the 113 articles analyzed, the ten most highly cited *Bacteroides*-related papers published between 1995 and 2025 are presented in Table 4. The most highly cited article was authored by Vétizou et al. and published in *Science*. This study was the only paper in the dataset to accumulate thousands of citations within ten years post-publication. It demonstrated the synergistic role of *Bacteroides* in enhancing the efficacy of anticancer immunotherapy.

Of the top ten papers, the first and fifth were published in *Science*, the sixth and seventh in *Scientific Reports*, and the ninth and tenth in *Gut Microbes*. Overall, the most highly cited studies focused on the role of *Bacteroides* in the gut-microbiome interactions, particularly its contributions to host health and therapeutic outcomes.

Table 4: Top paper citations, ranked by total citations.

	Paper	Total Citation (TC)
1st	Anticancer immunotherapy by CTLA-4 blockade relies on the gut microbiota (Vétizou et al. 2015) Source: *Science*	2967
2nd	Effect of tea phenolics and their aromatic fecal bacteria metabolites on intestinal microbiota (Lee et al. 2006) Source: *Research in Microbiology*	644
3rd	*Bacteroides vulgatus* and *Bacteroides dorei* reduce gut microbial lipopolysaccharide production and inhibit atherosclerosis (Yoshida et al. 2018) Source: *Circulation*	521
4th	Captivity humanizes the primate microbiome (Clayton et al. 2016) Source: *Proceedings of the National Academy of Sciences of the United States of America*	392
5th	Helminth infection promotes colonization resistance via type 2 immunity (Ramanan et al. 2016) Source: *Science*	347
6th	Intestinal microbiota distinguish gout patients from healthy humans (Guo et al. 2016) Source: *Scientific Reports*	337
7th	Diversity in gut bacterial community of school-age children in Asia (Nakayama et al. 2015) Source: *Scientific Reports*	230
8th	Bacterial population in intestines of black tiger shrimp (*Penaeus monodon*) under different growth stages (Rungrassamee et al. 2013) Source: *PLoS One*	165
9th	Probiotic-directed modulation of gut microbiota is basal microbiome dependent (Hou et al. 2020) Source: *Gut Microbes*	108
10th	A compromised development trajectory of the infant gut microbiome and metabolome in atopic eczema (Ta et al. 2020) Source: *Gut Microbes*	99

The most cited *Bacteroides* research in SEA focuses on gut microbiome-host interactions. The high citations on this topic alone are driven more by its alignment with global interest in gut microbiome research (Law et al. 2024; Sun and Zhai 2025). The high TC on *Bacteroides* in gut microbiome research reveals the citation landscape and interest in future studies on *Bacteroides,* which SEA researchers can leverage to increase global visibility. Regionally, researchers in SEA can start with gut microbiome research as a baseline for collaborations. However, this also indicates research gaps that can be exploited by SEA research. Researchers can work on ecological studies, such as *Bacteroides* in soil, sediment, wastewater, and water, and microbial/fecal source tracking, which are topics open for future study. Another underrepresented topic is *Bacteroides* in extraintestinal areas and its involvement as a commensal or pathogen. Overall, the current citation landscape highlights both research opportunities and limitations for *Bacteroides* research in SEA, as *Bacteroides* research is highly skewed towards gut microbiome. Research can be expanded towards other topics to diversify research output.

Thematic Review

Figure 5 shows that *Bacteroides* research in SEA is distributed across different subject matter. The subject ranges from biomedical topics to agricultural and multidisciplinary topics. In biomedical research, medicine accounts for the largest component (23%), followed by immunology and microbiology (19%), nursing (4%), and neuroscience (3%). In all, biomedical research accounts for 49% of the total *Bacteroides* research in SEA. Beyond biomedical topics, agricultural topics represent the second notable share, at 14%, comprising agricultural and biological sciences (10%) and veterinary science (4%). This shows the significance of *Bacteroides* research in animal sciences and food-related topics. Interdisciplinary topics accounted for 12%, including multidisciplinary research (6%), chemistry (3%), and environmental science (3%).

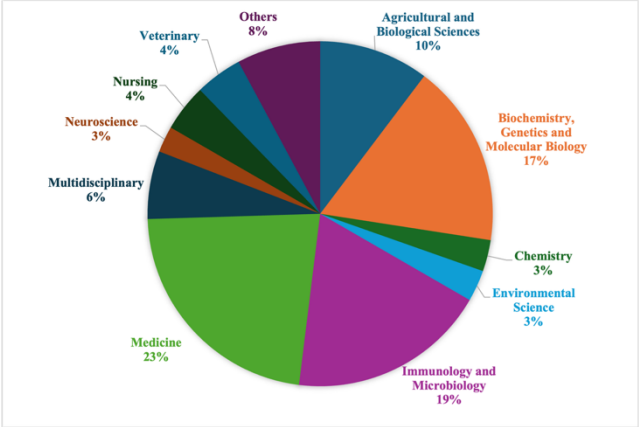

Figure 5: Subject classification of *Bacteroides* research in Southeast Asia from 1995 to 2025

The dominance of medicine-related subjects indicates that *Bacteroides* research in SEA is driven by clinical interests and government priorities. Moreover, Figure 5 and Table 4 show that SEA research on *Bacteroides* reflects both academic interest and responses to infectious diseases and AMR. Since *Bacteroides* is a frequent reservoir of antibiotic resistance genes, this research focus is significant for regional clinical guidelines and improvement of healthcare practices in the region. Additionally, the significant 10% share of *Bacteroides* research in agricultural and biological sciences in SEA suggests that *Bacteroides* is seen as a key indicator of livestock and food safety, which, in a sense, distinguishes SEA research on *Bacteroides* from the clinical/medical global trend. However, a critical gap that can be a source of innovation in SEA is the limited number of research on neurosciences and environmental sciences. Despite the global trend in the gut-brain axis (Xu and Lu 2025; Li et al. 2026), the potential for treating neurodegenerative disorders, most of SEA remains stuck in traditional microbiological topics of identification, phylogeny, and profiling. This is a missed opportunity that can be addressed through interdisciplinary collaborations across the region.

Figure 6 presents the contingency matrix generated from CorText illustrating the association between prevailing research themes and contributing countries. In the matrix, darker red intensities indicate stronger associations between specific keywords and countries.

Focusing on SEA countries, the dominant *Bacteroides*-related research themes in Singapore include resistance genes, interactions with *Escherichia coli*, microbial source tracking (MST), fecal microbiota, and gut microbiome studies. In the Philippines, research is primarily centered on 16S rDNA/rRNA gene analyses and MST. Indonesian studies predominantly focus on fecal and gut microbiomes and on 16S rDNA PCR-based approaches. In Vietnam, prevailing themes include resistance genes and 16S

rDNA–based analyses. Malaysian research emphasizes resistance genes, 16S rDNA PCR, and short-chain fatty acid production, whereas Thai studies primarily focus on resistance genes, short-chain fatty acids, and fecal microbiome composition. Notably, Singapore and Thailand exhibit the widest thematic coverage, encompassing the greatest diversity of *Bacteroides*-related research topics among SEA countries.

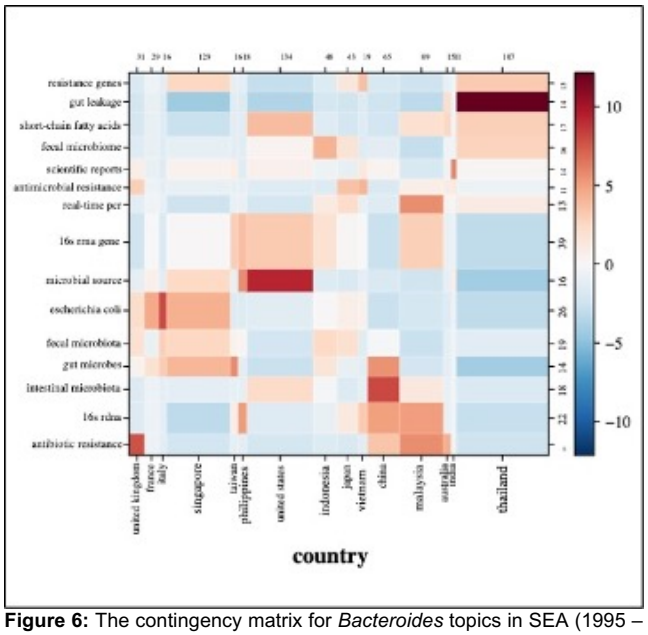

Figure 6: The contingency matrix for *Bacteroides* topics in SEA (1995 – 2025)

Singapore and Thailand exhibit high thematic diversity, spanning a broad range of topics. It also suggests more advanced research capabilities on *Bacteroides* from the classical taxonomic studies to more complex gut microbiome studies. There is also an emphasis on AMR in Malaysia, Vietnam, and Indonesia, reflecting the health priorities in those countries. The Philippines shows a strong association with MST (Malajacan et al. 2023), likely driven by concerns about local water quality. Overall, *Bacteroides* in SEA is shifting from general microbial characterization to more specialized topics.

Figure 7 illustrates the co-occurrence network generated from CorText of keywords associated with *Bacteroides* research in SEA. The most closely related themes involve other fecal-associated microorganisms such as *E. coli* and *Enterococcus*, as well as topics related to fecal pollution, water quality, MST, and gut-associated lactic acid bacteria, including *Lactobacillus* and *Bifidobacterium*. The keyword "gut microbiota" appears as the largest node in the network—larger than *Bacteroides* itself—indicating that it is the most frequently used keyword in *Bacteroides*-related studies from the region, which implies that it is the primary topic or framework of *Bacteroides* research in SEA.

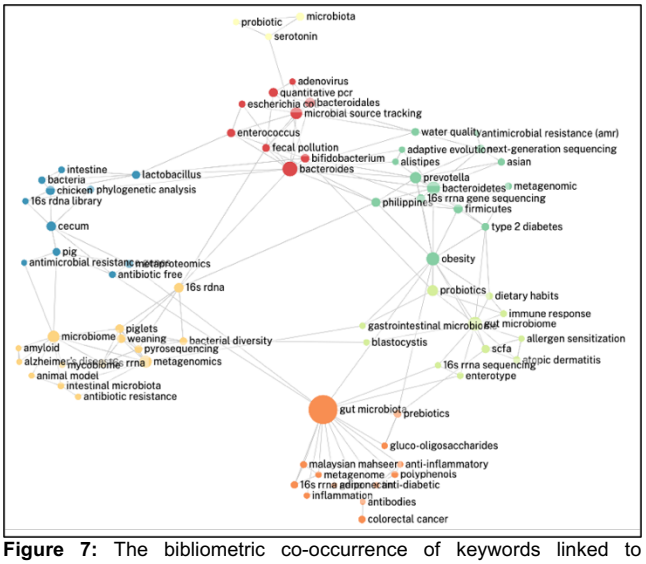

Figure 7: The bibliometric co-occurrence of keywords linked to *Bacteroides* research in SEA

The thematic keyword structure of *Bacteroides* research in SEA highlights a multidisciplinary interest within the region. Central to the network is the "gut microbiota," underscoring its major role in the region's research framework. In looking at the network, it can be seen that keywords can be categorized into four: (1) environmental, (2) clinical, (3) nutritional/probiotic, and (4) methodology. The environmental cluster, with keywords such as fecal pollution, water quality, and MST, which is closely associated with enteric microorganisms (*E. coli* and *Enterococcus*), reflects SEA's research direction towards environmental surveillance. The clinical cluster, with keywords obesity, type 2 diabetes, and interestingly, with a geographical marker, the Philippines, bridges *Bacteroides* with non-communicable diseases and their possible effect on it. The nutritional/probiotic cluster, with keywords *Lactobacillus, Bifidobacterium,* prebiotics, and probiotics, reflects the growing trend of introducing *Bacteroides* as a possible future probiotic. Moreover, it reflects a shift in perspective from viewing *Bacteroides* as an opportunistic pathogen to a focus on host health. Lastly, the consistent use of 16S rRNA gene sequencing, metagenomic, pyrosequencing, and next-generation sequencing highlights the preferred methodologies for *Bacteroides* research in SEA.

This study provides the first comprehensive bibliometric analysis of *Bacteroides* research in SEA, highlighting regional research trends, thematic emphases, collaboration patterns, and persistent knowledge gaps. By integrating citation metrics and CorText-based visualizations, the analysis highlights how SEA countries contribute to global *Bacteroides* research through both domestic outputs and international collaborations among researchers, institutions, and countries.

To date, no bibliometric study has focused exclusively on *Bacteroides*. There are bibliometric analyses publications about the gut microbiome as a whole, and they are not thematically centered on *Bacteroides.* Existing bibliometric analyses have examined broader themes, such as gut or fecal microbiota and fecal pollution, in which *Bacteroides* is treated only as one of many microbial taxa (Yue et al. 2020; Mao et al. 2022; Sun et al. 2024; Lei et al. 2025; Mo et al. 2025).

This bibliometric analysis shows that *Bacteroides* research output in SEA has increased steadily since 2019 (Figure 2), but remains modest relative to the organism's established importance in global microbiology, AMR, and One Health research. Notably, the first *Bacteroides*-related publication from SEA appeared in 1995, more

than six decades after the earliest *Bacteroides* study indexed in Scopus in 1930 (Glaser 1930). Even over the 30 years covered in this analysis, annual publication counts remained low, reaching double digits only in 2019. The delayed emergence of sustained research activity, nearly a century after *Bacteroides* was first described, suggests that scientific capacity, rather than relevance, has constrained regional productivity. While recent growth likely reflects improvements in research networking, capacity building, and access to national, regional, and international funding mechanisms, the overall pattern still underscores *Bacteroides* research in SEA.

The strong concentration of *Bacteroides*-related publications in Singapore and Thailand (Figure 3, Tables 2 and 3) mirrors disparities in research funding continuity, access to high-throughput molecular platforms, and integration into international research networks. Within SEA, Singapore and Thailand clearly emerge as focal points of *Bacteroides* research, leading in terms of publication output, institutional productivity, and author contributions. Conversely, other SEA countries have substantially fewer publications, while the absence of indexed publications from Brunei, Laos, and Timor-Leste reflects broader limitations in research infrastructure and workforce density. These three countries also rank among the lowest in nominal GDP and researcher density in the region (Tantengco et al. 2021; Tantengco and Rojo 2022), suggesting that broader structural and capacity constraints strongly influence research productivity. Moreover, these patterns indicate that *Bacteroides* research in SEA is driven primarily by institutional capacity rather than epidemiological burden, highlighting the need for coordinated regional strategies that lower entry barriers for underrepresented countries.

Thematic mapping further revealed clear research hotspots in SEA. Recent studies increasingly employ molecular approaches for *Bacteroides* identification and phylogenetic analysis using 16S rRNA gene sequencing (Dela Rosa and Rivera 2021; Vu et al. 2021; Ho et al. 2021; Diebold et al. 2023; Yingkajorn et al. 2025). However, the same thematic mapping revealed that *Bacteroides* research in SEA is dominated by descriptive studies of the gut and fecal microbiome, AMR gene prevalence, and MST. While these themes address legitimate public health and environmental concerns, their dominance has constrained the conceptual expansion of *Bacteroides* research beyond its role as a commensal indicator organism.

Notably, many AMR-focused studies (Rong et al. 2021; Dela Rosa and Rivera 2024; Yingkajorn et al. 2025) report resistance gene presence without investigating genetic context, mobility, or transmission dynamics across human, animal, and environmental reservoirs. Similarly, MST studies frequently end at detection (Zeki et al. 2021; Ruti et al. 2025), with limited integration of hydrological modeling, quantitative risk assessment, or intervention-oriented engineering approaches. This narrow thematic focus limits the research's translational impact and underscores the need for hypothesis-driven, systems-level investigations.

Although advanced -omics approaches, including metagenomics (Khan et al. 2023; Ravikrishnan et al. 2024), metaproteomics (Kingkaw et al. 2020; Chantanaskul et al. 2024), and metabolomics (Ta et al. 2020), are present in the SEA dataset, their application to *Bacteroides* remains limited. In contrast to trends in Europe and North America, where *Bacteroides* is central to mechanistic studies of host–microbe interaction (Fansler et al. 2025), immunomodulation (Roustapoor et al. 2025), and metabolic regulation (Roustapoor et al. 2025), SEA research remains largely survey-based. This is unlikely to reflect technical incapacity, as comparable methods are increasingly applied to other bacterial taxa within the region. Instead, the findings suggest a lack of strategic prioritization of *Bacteroides* as a model organism for integrative microbiome science. Thus, a strategic redirection toward strain-level, functional, and longitudinal -omics studies would enable deeper insights into *Bacteroides* ecology, pathogenic potential, and resistance evolution.

Other emerging studies from outside SEA have explored *Bacteroides* as potential probiotics (Cang et al. 2024; Peng et al. 2025) and investigated associations with colorectal cancer (Abdulamir et al. 2009; Cariño et al. 2023; Iadsee et al. 2023), obesity (Sarbini et al. 2014; Mohammad et al. 2017; Therdtatha et al. 2021; Kang et al. 2023), type 2 diabetes (Zulhaerati et al. 2019), and neurodegenerative diseases (Wanapaisan et al. 2022), consistent with growing evidence linking gut microbiome composition to systemic health outcomes.

Ecologically, *Bacteroides* research in SEA has predominantly focused on gut symbiosis and its application in water-quality assessment via MST (Nshimyimana et al. 2019; Dela Rosa and Rivera 2021; Malajacan et al. 2023). The use of *Bacteroides* as a fecal indicator for source tracking is gaining momentum, reflecting its specificity and reliability in distinguishing human and animal fecal contamination (Dela Rosa and Rivera 2023). These emerging themes provide promising directions for future *Bacteroides* research in SEA.

Lastly, from a One Health perspective, *Bacteroides* research in SEA remains compartmentalized, with limited integration across human, animal, and environmental domains. Despite growing recognition of *Bacteroides* as a robust fecal indicator and a reservoir of AMR genes, few studies have traced its movement through wastewater systems, agricultural runoff, food chains, and clinical settings.

This gap represents a significant opportunity for interdisciplinary research. Environmental engineering approaches, such as wastewater-based surveillance, treatment efficacy evaluation, and predictive modeling, could substantially enhance the translational value of *Bacteroides* research. Integrating microbiology with engineering analytics would enable *Bacteroides* to serve not only as an indicator organism but also as a sentinel for AMR dissemination and environmental health risks in SEA.

The uneven regional distribution of *Bacteroides* research highlights the importance of coordinated capacity-building initiatives. Shared biobanking facilities, standardized molecular protocols, and region-wide open-access databases would enable underrepresented countries to meaningfully engage in research. Targeted funding mechanisms that prioritize cross-country collaboration and One Health–oriented studies could accelerate the maturation of *Bacteroides* research in SEA.

CONCLUSION

This bibliometric study showed that while SEA has increased research on *Bacteroides*, it remains concentrated in one or two countries. Moreover, the focus of SEA *Bacteroides* research is largely descriptive in nature. Addressing these gaps requires collaborative capacity-building, -omics-based research approaches, hypothesis-driven studies, and the integration of One Health to unlock *Bacteroides*' full research potential in SEA.

This bibliometric study has several limitations. First, it relied exclusively on the Scopus database, potentially missing relevant publications indexed in other databases, such as Web of Science, PubMed, and Google Scholar. Second, only English-language

articles were included, potentially excluding research published in local or national languages. Despite these limitations, the dataset provides a robust overview of regional trends, major gaps, and opportunities in *Bacteroides* research across SEA.

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CONFLICT OF INTEREST

The authors declare that there is no conflict of interest.

CONTRIBUTIONS OF INDIVIDUAL AUTHORS

CJODR conceived the research idea, gathered the data, and prepared the initial and subsequent manuscript drafts. WLR contributed to study conceptualization and participated in manuscript preparation, review, and proofreading.

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