

CONTEMPLATING THE BIBLIOMETRIC DATA ONTO SEPSIS AND GUT MICROBIOME: MAPPING TRENDS, COLLABORATIONS, AND GLOBAL CONTRIBUTIONS

Li Zhang¹, Yi Wang², Ping Li¹, Xiang Li², Xiangyou Yu^{1,2*}

¹Department of Nursing, Xinjiang Medical University, Xinjiang Uygur Autonomous Region, 830001, China

²Critical Medicine Center, The First Affiliated Hospital of Xinjiang Medical University, Urumqi 830054, Xinjiang Uygur Autonomous Region, China

Submitted in July 2024, accepted in November 2024

Abstract. Sepsis is a leading cause of hospital mortality, closely linked to gut dysfunction and dysbiosis. The gut microbiome's role in sepsis pathogenesis and progression necessitates a comprehensive bibliometric analysis to elucidate current research trends. Utilizing the Science Citation Index Expanded (SCI-E) database, literature was systematically retrieved using the terms: sepsis AND (“gut” OR “gastrointestinal”) AND (“microbiome” OR “microbiota” OR “microflora” OR “bacillus”). After data refinement and duplicate removal, 2485 articles were included for statistical analysis using R software's bibliometric package, with Excel used to visualize publication trends. Findings demonstrate a progressive annual increase in published studies and citations. The United States and France emerged as primary contributors, exhibiting extensive international collaboration. Among leading institutions, the University of California ranked highest in research output, while Wiersinga WJ from the University of Amsterdam led in publication volume and collaborative networks. Research predominantly focuses on critical care medicine, immunology, and microbiology, with keywords such as sepsis, microbiome, microbiota, and microflora recurring. Current trends indicate a growing focus on the relationship between sepsis and gut microbiome dynamics, with a notable gap in evidence-based clinical applications. The prominence of the United States in the field underscores the need for well-designed clinical trials and prospective cohort studies to advance therapeutic strategies. Strengthening global collaboration, particularly through increased involvement of Chinese researchers, is crucial for a comprehensive understanding and future advancements in this complex and evolving field.

1. Introduction. 2. Material and Methods. 2.1. Data Source. 2.2. Search Strategy. 2.3. Analysis. 2.4. Statistical Analysis. 3. Results. 3.1. General Information. 3.2. Analysis of Countries and Institutions. 3.3. Author's Analysis. 3.4. Journals Analysis. 3.5. Keywords Analysis. 4. Discussion. 5. Conclusion.

Keywords: bibliometrics study, gut microbiome, sepsis

1. Introduction

Sepsis, a life-threatening condition resulting from the body's dysregulated response to infection (Singer *et al.* 2016), is a significant contributor to mortality in severe patients, with a mortality rate of up to 29.0%. Septic shock is a severe form of sepsis and is by the means of serious, circulatory, cellular, and metabolic abnormality, because of the hypotension, which is not corrected by the fluid resuscitation, that accounts for the increase in the death rate (Liu *et al.* 2022). The pathogenesis of sepsis involves a complex interplay of infection, inflammation, immunity, coagulation,

and, notably, intestinal dysfunction and flora imbalance (Haak and Wiersinga 2017, Adelman *et al.* 2020). Among critically ill patients, the gut microbiome has gained prominence in sepsis research, drawing increasing attention from intensive care unit (ICU) physicians seeking ways to enhance gut microbiome health for improved survival in patients with sepsis.

The gut microbiome comprises the interaction between intestinal flora and the host, encompassing the intestine, intestinal epithelial cells, secretions, ingested food, and nutrients (Cresci and Bawden 2015, Heintz-Buschart and Wilmes 2018). Of particular significance is the role of intestinal flora, which plays a crucial role

* Corresponding Author: Xiangyou Yu, Department of nursing, Xinjiang Medical University, Xinjiang Uygur Autonomous Region, 830001, China; Critical Medicine Center, The First Affiliated Hospital of Xinjiang Medical University, Urumqi 830054, Xinjiang Uygur Autonomous Region, China, email: yuxiangyou2023@sina.com

© 2024 Li Zhang *et al.*

This is an open access article licensed under the Creative Commons Attribution-NonCommercial-NoDerivs License (<http://creativecommons.org/licenses/by-nc-nd/4.0/>)

Cite as:

Contemplating the bibliometric data onto sepsis and gut microbiome: mapping trends, collaborations, and global contributions. Zhang L. *et al.*, ADV MICROBIOL-NY, 2024, 63, 4, 191–198, <https://doi.org/10.2478/am-2024-0016>

in nutrient metabolism, digestion, absorption, resistance to external bacterial colonization, anti-tumor activities, and maintenance of the intestinal barrier and immune function (Jandhyala *et al.* 2015, Hills *et al.* 2019). The pathogenesis of sepsis involves the interaction of infection, inflammation, immune dysfunction, coagulation defect, and the disrupted blood-gut barrier is the central part of it. In sepsis, gut permeability increases and the gut bacteria and endotoxins can migrate out of the gut into the bloodstream, which sparks the body's inflammatory reaction and organ dysfunction. The blood-gut barrier's impairment gives rise to the difficult immune system situation, moreover, the vicious cycle of inflammation – bacterial multiplication – and the further endotoxin that is added into the bloodstream. Thus, the restoration of the blood-gut barrier is being the key issue in treating sepsis as well as the gastrointestinal microbiome as a component that participates in this process providing the default barrier and the health of the mucosal wall (Dubin 2018). Consequently, investigating the relationship between sepsis and the gut microbiome has become a key focus of numerous studies.

Current research on sepsis and the gut microbiome takes various angles, with some studies examining microbiome composition (Miller *et al.* 2021), others exploring microbiota dynamics (Kullberg *et al.* 2021), and additional investigations considering broader aspects of flora involvement. While reviews provide comprehensive summaries and analyses of the interplay between sepsis and the gut microbiome (Tourelle *et al.* 2021, Zanza *et al.* 2022), a macroscopic analysis of the overall research landscape in this field is lacking.

To address this gap, our study utilizes bibliometric methods in literature research to systematically analyze published works. Through retrieval, statistical processing, and comprehensive analysis of relevant literature, we aim to unveil the current state of research on the gut microbiome of sepsis patients. Bibliometric enables exploration of key aspects such as geographic distribution of research, institutional affiliations, prominent researchers, favored journals, and prevalent keywords within the literature corpus (Brandt *et al.* 2019). This methodological approach aims to provide an in-depth understanding of the current focus and developmental trajectory in the expansive field of sepsis and gut microbiome research.

2. Material and Methods

2.1. Data Source

The Science Citation Index Expanded (SCI-E) database in the Web of Science Core Collection (WOSCC) was utilized as the primary data source for retrieval.

SCI-E is a leading and the most common used database for bibliometric research (Wu *et al.* 2022, Wu *et al.* 2024), encompassing English literature and, to some extent, literature in other languages with English abstracts, providing a comprehensive representation of global scientific research.

2.2. Search Strategy

A “subject” retrieval method was employed for this study, using the retrieval formula: sepsis AND (“gut” OR “gastrointestinal”) AND (“microbiome” OR “microbiota” OR “flora” OR “bacillus”). The search was restricted to publications from 2004 onwards. This search strategy included sepsis broadly without differentiating between bacterial and fungal origins. Therefore, the results reflect a general analysis of sepsis cases that may include studies on both bacterial and fungal sepsis, depending on the scope of individual articles.

2.3. Analysis

All records and references from the search results were exported in plain text format and analyzed using the bibliometric software package in R. The analysis included; number of documents published by each country in the field, cooperative relationships between countries, number of documents published by institutions, cooperative relationships between institutions, number of documents published by researchers, cooperative relationships between researchers, citation status of researchers, number of documents published in journals, utilization of keywords.

2.4. Statistical Analysis

Trend charts illustrating the annual number of published documents and the number of cited documents were generated using Excel software. Qualitative data were presented quantitatively and as percentages, facilitating a rigorous statistical exploration of the bibliometric landscape. This methodology provides insights onto the global distribution, collaborative networks, institutional contributions, researcher engagement, citation impact, and journal dissemination within the field of sepsis and gut microbiome research.

3. Results

3.1. General Information

A meticulous examination of relevant research literature resulted in the retrieval of 2558 records. Post-duplicate removal, 2485 articles were considered

Table I
Type of publications on sepsis and gut microbiome.

Type	Publications	Percentage (%)*
Original articles	1671	67.24
Reviews	279	11.23
Clinical trial	105	4.23
Meeting	228	9.18
Editorials	72	2.90
Abstract	63	2.54
Online first	27	1.09
Case Report	40	1.61

Note: *percentage of 2485

for detailed analysis (Table I). This diverse dataset comprised 1671 original treatises, 279 review papers, 105 clinical studies (distinctly separated from the original treatises), 72 editorial materials, 228 conference proceedings papers, 63 conference abstracts, 27 advanced online publications, and 40 case reports. Analysis of the dataset revealed a discernible temporal pattern, illustrating a consistent year-on-year increase in the number of published documents (Fig. 1). Concurrently, the citation frequency of this literature exhibited a parallel upward trend, indicating a growing impact within the scientific community over time (Fig. 1). The cumulative citations for these documents reached an impressive 62247, with an average citation frequency of 25.05 times per document. A thorough examination of research directions, as depicted in Table II, illuminated the primary thematic concentrations within the dataset. Predominantly, the studies were centered on Infectious Diseases, Gastroenterology, Hepatology, Biochemistry and Molecular Biology. Additionally, substantial engagement was observed in the domains of Immunology, Pathology, and Microbiology, signifying the interdisciplinary nature of research exploring the intricate dynamics between sepsis and the gut microbiome. These results collectively contribute to a comprehensive understanding of the study landscape,

Table II
Research directions of publications on sepsis and gut microbiome.

Directions	Publications	Percentage (%)*
Infectious diseases	1657	66.68
Gastroenterology hepatology	1428	57.46
Biochemistry molecular biology	1074	43.22
Immunology	1039	41.81
Pathology	956	38.49
Microbiology	931	37.46
Nutrition dietetics	914	36.78
Pharmacology pharmacy	879	35.37
Food Science technology	708	28.49
Genetics heredity	703	28.29

Note: *percentage of 2485

delineating the composition of the literature corpus, temporal dynamics, and thematic concentrations. Such insights are instrumental in appreciating the evolving trends and scientific contributions within the realm of sepsis and gut microbiome research.

3.2. Analysis of Countries and Institutions

The examination of source countries within the literature corpus reveals substantial contributions from the United States, France, and the United Kingdom, displaying a marked prominence over other nations (Fig. 2). Notably, the United States exhibits a noteworthy lead, surpassing the combined literature output of the third to seventh-ranked countries. This underscores the significant influence wielded by these leading nations in shaping discourse on sepsis and the gut microbiome. An assessment of international collaboration scores, serving as an indicator of research cooperation enthusiasm, discloses the collaborative nature inherent in the field. The United States emerges as a key collaborator, boasting the highest cooperation score, followed by France, Germany, and other European

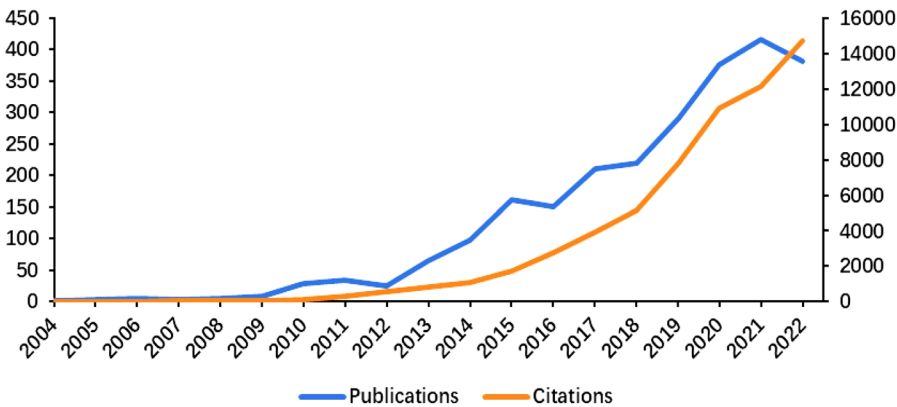


Fig. 1. Annual trends of publications and citations.

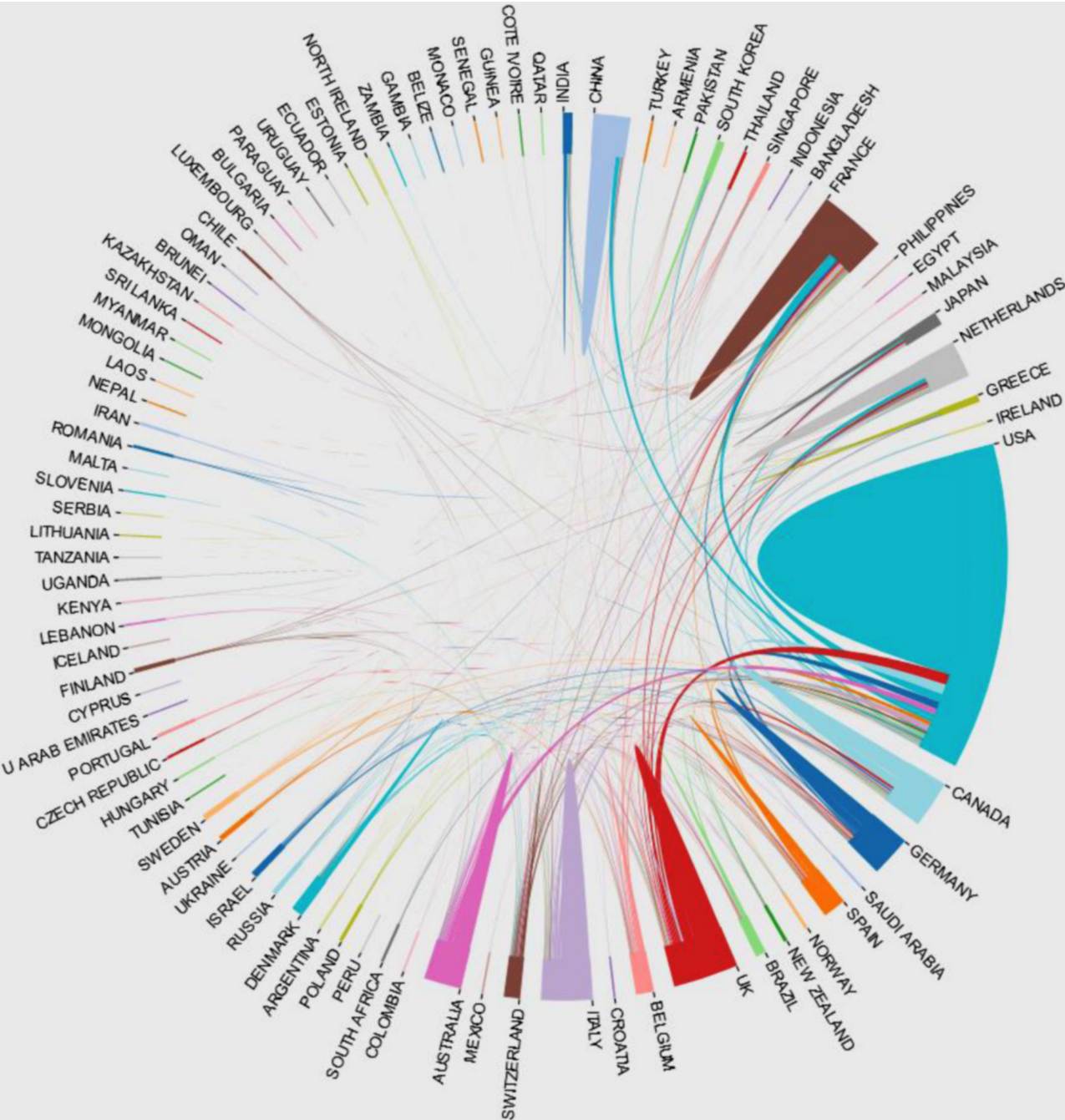


Fig. 2. Countries in publications and cooperations.

nations (Table III). Importantly, despite China holding the eighth position in total publications, its cooperation enthusiasm ranks tenth, indicative of a more reserved engagement in collaborative research initiatives within this scientific domain. Upon analyzing the institutions contributing to the published literature (Table IV), five of the top ten research institutions are situated in the United States, with the University of California leading the cohort. France is represented by two institutions in the top ten, while the Netherlands, the United Kingdom, and China each have one institution. The central cooperation score unveils the collaborative dynamics among these institutions, with the University of Cali-

fornia demonstrating the highest enthusiasm for collaboration, followed by the University of Amsterdam and the University of Chicago. Noteworthy is the independent research stance of Southern Medical University China, ranking ninth in the number of published documents. This institution stands out for its self-reliant research endeavors, displaying limited collaboration with external entities, marking a distinctive scholarly approach to sepsis and gut microbiome research. These findings provide a grounded and professionally articulated insight into global contributions, international collaboration dynamics, and institutional engagements within the expansive field of sepsis and gut microbiome

Table III
Centrality of countries in the studies on sepsis and gut microbiome.

Ranks	Countries	Centrality
1	USA	0.36
2	France	0.24
3	Germany	0.21
4	England	0.20
5	Italy	0.17
6	Netherlands	0.16
7	Spain	0.15
8	Australia	0.13
9	Canada	0.12
10	China	0.11

Table IV
Top 10 institutes by number of publications on sepsis and gut microbiome.

Institutions	Publications	Percentage (%)*
University of California	88	3.54
University of Amsterdam	85	3.42
Udice French Research Universities	63	2.54
University of Chicago	60	2.41
Institute National De La Sante	50	2.01
University of Michigan	45	1.81
Harvard University	39	1.57
Newcastle University UK	35	1.41
Southern Medical University China	34	1.37
University of Minnesota	30	1.21

Note: *percentage of 2485

literature. Such insights enrich our understanding of the collaborative and independent scientific pursuits instrumental in advancing knowledge within this domain (Table V).

Table V
Top 10 institutes by centrality on sepsis and gut microbiome.

Ranks	Institutions	Centrality
1	University of California	0.24
2	University of Amsterdam	0.23
3	University of Chicago	0.18
4	Udice French Research Universities	0.17
5	Institut National De La Sante	0.15
6	University of Michigan	0.14
7	University of Florida	0.13
8	Chulalongkorn University	0.12
9	Northumbria University	0.11
10	Universidade De Sao Paulo	0.11

3.3. Author’s Analysis

Wiersinga WJ from the University of Amsterdam in the Netherlands was identified as the most productive author in this field, as evident in the analysis results (Table VI). Professor Wiersinga also holds the highest centrality score (Table VII), highlighting the extensive impact of their contributions within the scholarly network. Further scrutiny reveals that Professor Wiersinga has authored a substantial number of articles on sepsis and gut microbiome, with over half published in prestigious journals such as JAMA, Lancet sub-journal, Gut, and other top-tier publications. Notably, collaborative associations among the top 10 authors include Wiersinga WJ and van der Poll T from the University of Amsterdam, and Berrington JE and Stewart CJ from Newcastle University, UK.

Table VI
Top 10 authors by number of publications on sepsis and gut microbiome.

Ranks	Authors	Publications	Percentage (%)*
1	Wiersinga WJ	44	1.77
2	Alverdy John C	17	0.68
3	Berrington JE	14	0.56
4	Leelahavanichkul A	15	0.60
5	Embleton ND	12	0.48
6	van der Poll T	11	0.44
7	Stewart CJ	10	0.40
8	Dickson RP	7	0.28
9	Wang W	6	0.24
10	Haak BW	6	0.2

Note: *percentage of 2485.

Table VII
Top 10 authors by centrality on sepsis and gut microbiom.

Ranks	Authors	Centrality
1	Wiersinga WJ	0.26
2	Alverdy John C	0.23
3	Leelahavanichkul A	0.19
4	Embleton ND	0.18
5	Wang YJ	0.17
6	Cao ZJ	0.17
7	Wang W	0.17
8	He ZY	0.15
9	Liu S	0.14
10	Li SL	0.13

3.4. Journals Analysis

The analysis of journals (Table VIII) reveals that Figshare, a prominent open data storage platform, leads in the number of publications on sepsis and gut

Table VIII
Top 10 journals by publication of literatures on sepsis and microbiome

Journals	Publications	Percentage (%) [*]	2022 IF
Figshare	166	6.67	Database
Nutrients	90	3.64	6.706
Critical Care	81	3.24	19.334
Plos One	78	3.13	3.752
Scientific Reports	73	2.93	4.996
European Nucleotide Archive	68	2.73	Database
Frontiers in Microbiology	60	2.42	6.064
Frontiers in Immunology	50	2.02	8.786
Pediatric Research	45	1.82	3.953
International Journal of Molecular Sciences	40	1.62	6.208

Note: ^{*}percentage of 2485.

microbiome research. Following closely are reputable academic journals, including *Nutrients* and *Critical Care*, among others. It is pertinent to note that Figshare, while a significant contributor, operates more as a data storage platform than a traditional academic journal. Among the academic journals publishing literature in this field, *Gastroenterology* (IF = 33.883) demonstrated the highest impact factor in 2022, with a total of 9 pertinent articles. This is followed by *Critical Care*, *Frontiers in Immunology*, and other journals, reflecting a diverse and impactful dissemination of research within the realm of sepsis and gut microbiome studies.

3.5. Keywords Analysis

A meticulous examination of all keywords utilized in the included literature underscores key themes prevalent in the field. The preeminent keyword is “sepsis,”

Table IX
Distribution of keywords.

Keywords	Frequency	Percentage (%) [*]
Sepsis	2174	87.48
Microbiome	991	39.88
Microbiota	765	30.78
Flora	382	15.37
Antibiotics	337	13.56
Gut microbiota	306	12.31
Immune system	218	8.77
Bacteria	184	7.40
Gut	163	6.56
Gastrointestinal microbiome	152	6.12

Note: ^{*}percentage of 2485.

reflecting its centrality in scholarly discussions. Following closely are pivotal terms such as “microbiome,” “microbiota,” and “flora,” highlighting the pronounced emphasis on microbial communities in this domain. Notably, six out of the top 10 keywords-specifically, “microbiome,” “microbiota,” “flora,” “gut microbiota,” “bacteria,” and “gastrointestinal microbiome”-essentially revolve around or intricately relate to microecology. This prevalence of microecology-centric keywords signifies the integral role of microbial interactions and ecological dynamics within the broader context of sepsis and gut microbiome research (Table IX).

4. Discussion

The outcomes of this study affirm the increasing research focus on the association between sepsis and the microbiome over the past decade. The upward trajectory in published literature reflects the growing acknowledgment of the clinical importance of investigating infectious diseases, particularly sepsis (Coopersmith *et al.* 2018). The observed dominance of the United States and China in the quantity of published literature underscores their significant contributions to the field. The United States not only exhibits a substantial publication volume but also a noteworthy centrality score, indicating a considerable influence within the scholarly network. Conversely, while China demonstrates prolific publication, its lower centrality score suggests potential for increased collaborative engagement on the international stage (Rhee *et al.* 2017).

Analysis of research institutions reveals the prevalence of European and American entities, with the University of California emerging as a central hub for collaborative research in this field. Noteworthy contributors include Fang Min and Wiersinga WJ from the University of Amsterdam, with Prof Wiersinga leading in both publication volume and collaborative endeavors. Journal analysis indicates that while research in this field is present in authoritative journals, there is a prevalent focus on severe diseases, microbiology, and immunology publications (Wiersinga and van der Poll 2022). This thematic alignment underscores the clinical and microbiological dimensions inherent in sepsis and gut microbiome studies. Examining the microecology, our study underscores the pivotal role of gut microbiome in human health. The intricate interplay of microbial entities, including *Bacteroides*, *Bifidobacterium*, and *Lactobacillus*, highlights their diverse contributions to nutrient metabolism, immune function, and intestinal barrier maintenance (Schmidt *et al.* 2018).

In the context of sepsis, our analysis reveals distinct alterations in the gut microbiome, characterized by reduced diversity, altered abundance of key microbial

groups, and overgrowth of pathogenic bacteria. This dysbiosis correlates positively with the mortality risk in patients exhibiting systemic inflammatory response syndrome and multiple organ dysfunction syndrome (Shimizu *et al.* 2011). The use of broad-spectrum antibiotics, a common therapeutic approach in sepsis, emerges as a significant factor contributing to gut microbiome imbalance (Condotta *et al.* 2013). This disruption is not only related to the duration of antibiotic use but also to specific antibiotic types and/or combinations of antibiotics, such as ceftriaxone and imipenem, with implications for the risk of opportunistic infections and antibiotic-associated complications (Haak and Wiersinga 2017). Clinical strategies for mitigating gut microbiome imbalance include judicious antibiotic use, supplementation with microecological agents, early enteral nutrition, and fecal flora transplantation (He *et al.* 2013, Wang *et al.* 2019; Ramirez *et al.* 2020, Johnstone *et al.* 2021, Cheema *et al.* 2022). These interventions aim to preserve microbial diversity, restore ecological balance, and improve patient outcomes.

Apart from the bacterial factors in the gut microbiota, the contribution of fungus in keeping the micro-organism balance is a very important aspect that should be taken into consideration. Fungal species, primarily *Candida*, *Aspergillus*, and *Zygomycetes*, can considerably affect the intestinal microbiome. For example, *Candida albicans* is often related to dysbiosis, especially in people with weakened immune systems or those who are on the long-term use of broad-spectrum antibiotics. This non-optimal situation in the microbiota causes hypoproliferation, inflammation as well as negative changes in the intestinal barrier. Besides, the *Aspergillus* genus, although it isn't usually mentioned in gut health conversations, has been associated with dysbiosis in serious infections and it can disturb the microbiome community's normal activities in the gastrointestinal tract. Recognizing the role that fungi play in these processes is critically important if we are to develop successful strategies to fight against dysbiosis in sepsis patients (Chin *et al.* 2020).

In addition to macroscopic tendencies found in sepsis and gut microbiome research, the discovery of the etiological agents is very important in the differential diagnosis of sepsis microbe contributors. In our bibliometric style, we did not define independent causative pathogens, but prior studies often find that bacterial species, such as *Escherichia coli*, *Klebsiella pneumoniae*, and *Staphylococcus aureus* are common etiological factors in bacterial sepsis. These pathogens are frequently referred to disturbances in the gut microbiota, which are advantageous for the proliferation of pathogenic species and disadvantageous from the perspective of a high microbial diversity ratio. Bacteria, specifically *Candida albicans*, are also the predisposing factors for

sepsis in cases of immunocompromised patients and they are associated with specific dysbiosis patterns in the gut microbiome (Jawhara 2022). The limitation in the bacterial and fungal etiologies can be the potential information on the dysbiosis and thus, the development of specific therapeutic strategies targeting the patient's microbes may prove to be the solution.

While this study provides a comprehensive macroscopic overview of the literature, its limitations include the lack of in-depth analysis of individual studies, interventions, and recent advancements. Additionally, the exclusion of non-English literature from the SCI-E database introduces a potential source of omission, emphasizing the need for a more inclusive approach to capture global contributions. The surge in research on the relationship between sepsis and gut microbiome signifies a burgeoning field with evolving clinical implications. The dominance of the United States in this research landscape underscores its leadership role. Future directions should prioritize evidence-based investigations, clinical trials, and prospective studies. Enhanced international collaboration, particularly involving Chinese researchers, holds promise for advancing the understanding and management of sepsis through the lens of gut microbiome dynamics.

5. Conclusion

Current study delves into the expanding landscape of sepsis and gut microbiome research, analyzing 2485 articles spanning diverse publication types and thematic concentrations. The temporal analysis reveals a consistent increase in publications, reflecting a burgeoning interest and impact within the scientific community. The dominance of the United States in both quantity and centrality underscores its pivotal role, with significant contributions from France, the United Kingdom, and others. Authorship analysis highlights Prof Wiersinga's prolific output and impact, while institutional dynamics and international collaboration further enrich the scholarly network. The examination of journals and keywords elucidates the thematic focus on microbiome-related concepts. The findings underscore altered gut microbiome dynamics in patients with sepsis, influenced by factors like antibiotic use, with clinical strategies proposed for mitigation. The study's limitations, including language exclusivity and the need for more detailed analyses, are acknowledged. Moving forward, the emphasis on evidence-based investigations, clinical trials, and international collaboration, particularly involving Chinese researchers, holds promise for advancing understanding and management in this evolving field. In essence, current study provides a nuanced and professionally articulated overview of

sepsis and gut microbiome research, paving the way for future exploration and advancements in evidence-based medicine.

ORCID

Xiangyou Yu: <https://orcid.org/0009-0004-6909-142X>
Li Zhang <https://orcid.org/0000-0003-4131-6442>
Yi Wang <https://orcid.org/0000-0002-4985-2998>
Ping Li <https://orcid.org/0000-0001-7660-6082>
Xiang Li <https://orcid.org/0000-0002-2430-6798>

Conflict of interest

The authors do not report any financial or personal connections with other persons or organizations, which might negatively affect the contents of this publication and/or claim authorship rights to this publication.

Funding

National Natural Science Foundation of China (82160360).

References

- Adelman M.W., Woodworth M.H., Langelier C., Busch L.M., Kempker J.A., Kraft C.S., & Martin G.S.: The gut microbiome's role in the development, maintenance, and outcomes of sepsis. *Crit. Care*, **24**, 1–10 (2020)
- Brandt J.S., Hadaya O., Schuster M., Rosen T., Sauer M.V., & Ananth C.V.: A bibliometric analysis of top-cited journal articles in obstetrics and gynecology. *JAMA Netw. Open* **2**, e1918007 (2019)
- Cheema H.A., Shahid A., Ayyan M., Mustafa B., Zahid A., Fatima M., Ehsan M., Athar F., Duric N., & Szakmany T.: Probiotics for the prevention of ventilator-associated pneumonia: An updated systematic review and meta-analysis of randomized controlled trials. *Nutrients* **14**, 8 (2022)
- Chin V.K., Yong V.C., Chong P.P., Nordin S.A., Basir R., & Abdullah M.: Mycobiome in the gut: A multiperspective review. *Mediators Inflamm.* **2020**, 9560684 (2020)
- Condotta S.A., Cabrera-Perez J., Badovinac V.P., & Griffith T.S.: T-cell-mediated immunity and the role of TRAIL in sepsis-induced immunosuppression. *Crit. Rev. Immunol.* **33**, 23–40 (2013)
- Coopersmith C.M., et al.: Surviving sepsis campaign: research priorities for sepsis and septic shock. *Intensive Care Med.* **44**, 1400–1426 (2018)
- Cresci G.A. & Bawden E.: Gut microbiome: What we do and don't know. *Nutr. Clin. Pract.* **30**, 734–746 (2015)
- Dubin K.A.: Microbial dynamics during gut inflammation and infection. Weill Medical College of Cornell University (2018)
- Haak B.W. & Wiersinga W.J.: The role of the gut microbiota in sepsis. *Lancet Gastroenterol. Hepatol.* **2**, 135–143 (2017)
- He D., Wang H.Y., Feng J.Y., Zhang M.M., Zhou Y., & Wu X.T.: Use of pro-/synbiotics as prophylaxis in patients undergoing colorectal resection for cancer: A meta-analysis of randomized controlled trials. *Clin. Res. Hepatol. Gastroenterol.* **37**, 406–415 (2013)
- Heintz-Buschart A., Wilmes P.: Human Gut Microbiome: Function Matters. *Trends Microbiol.* **26**(7), 563–574 (2018)
- Hills R.D. Jr, Pontefract B.A., Mishcon H.R., Black C.A., Sutton S.C., Theberge C.R.: Gut Microbiome: Profound Implications for Diet and Disease. *Nutrients*. **11**(7), 1613 (2019)
- Jandhyala S.M., Talukdar R., Subramanyam C., Vuyyuru H., Sasikala M., Nageshwar Reddy D.: Role of the normal gut microbiota. *World J Gastroenterol.* **21**(29) 8787–8803 (2015)
- Jawahra S.: How gut bacterial dysbiosis can promote *Candida albicans* overgrowth during colonic inflammation. *Microorganisms* **10**, 1014 (2022)
- Johnstone J. & Zytaruk N. et al.: Effect of probiotics on incident ventilator-associated pneumonia in critically ill patients: A randomized clinical trial. *JAMA*, **326**, 1024–1033 (2021)
- Kullberg R.F., Wiersinga W.J., & Haak B.W.: Gut microbiota and sepsis: From pathogenesis to novel treatments. *Curr. Opin. Gastroenterol.* **37**, 578–585 (2021)
- Liu Y.C., Yao Y., Yu M.M., Gao Y.L., Qi A.L., Jiang T.Y., Chen Z.S., Shou S.T., & Chai Y.F.: Frequency and mortality of sepsis and septic shock in China: A systematic review and meta-analysis. *BMC Infect. Dis.* **22**, 564 (2022)
- Miller W.D., Keskey R., & Alverdy J.C.: Sepsis and the microbiome: A vicious cycle. *J. Infect. Dis.* **223**, S264–S269 (2021)
- Ramirez J., Guarner F., Bustos Fernandez L., Maruy A., Sdepanian V.L., & Cohen H.: Antibiotics as major disruptors of gut microbiota. *Front. Cell Infect. Microbiol.* **10**, 572912 (2020)
- Rhee C. & Clompas M. et al.: Incidence and trends of sepsis in US hospitals using clinical vs claims data, 2009–2014. *JAMA* **318**(13), 1241–1249 (2017)
- Schmidt T.S.B., Raes J., & Bork P.: The human gut microbiome: From association to modulation. *Cell* **172**, 1198–1215 (2018)
- Shimizu K. & Sugimoto H. et al.: Altered gut flora are associated with septic complications and death in critically ill patients with systemic inflammatory response syndrome. *Dig. Dis. Sci.* **56**, 1171–1177 (2011)
- Singer M. & Deutschman C.S. et al.: The Third International Consensus Definitions for Sepsis and Septic Shock (Sepsis-3). *JAMA* **315**, 801–810 (2016)
- Tourelle K.M., Boutin S., Weigand M.A., & Schmitt F.C.: Sepsis and the human microbiome: Just another kind of organ failure? A review. *J. Clin. Med.* **10**, 4831 (2021)
- Wang J.W., Kuo C.H., Kuo F.C., Wang Y.K., Hsu W.H., Yu F.J., Hu H.M., Hsu P.I., Wang J.Y., & Wu D.C.: Fecal microbiota transplantation: Review and update. *J. Formos. Med. Assoc.* **118**, S23–S31 (2019)
- Wiersinga W.J. & van der Poll T.: Immunopathophysiology of human sepsis. *E.Bio.Medicine.* **86**, 104363 (2022)
- Wu F., Gao J., Kang J., Wang X., Niu Q., Liu J., & Zhang L.: Knowledge mapping of exosomes in autoimmune diseases: A bibliometric analysis (2002–2021). *Front. Immunol.* **13**, 939433 (2022)
- Wu T., Wu Y., Nie K., Yan J., Chen Y., Wang S., & Zhang J.: Bibliometric analysis and global trends in uterus transplantation. *Int. J. Surg.* **110**, 4932–4946 (2024)
- Zanza C., Romenskaya T., Thangathurai D., Ojetti V., Saviano A., Abenavoli L., Robba C., Cammarota G., Franceschi F., & Piccioni A.: Microbiome in critical care: An unconventional and unknown ally. *Curr. Med. Chem.* **29**, 3179–3188 (2022)