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Analyzing bacterial persistence and dormancy: A bibliometric exploration of 21st century scientific literature

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ABSTRACT

In response to growing concerns about the efficacy of antibiotic treatment, there has been a significant increase in research on bacteria that are resistant to antibiotics over the past two centuries. Such investigations might bring a spotlight on the field's evolution and future prospects. The study was aimed at conducting a measurable bibliometric review of the scientific literature on bacterial persistence and dormancy in the 21st Century. A scientific literature published during 21st Century was analyzed to gain insights into and identify research trends and outputs in persistent bacteria. Bibliometrix (R language package) and the VOS viewer were used to conduct a bibliometric investigation to determine the globally indexed persistent bacteria research output. WoS Core Collection databases were searched for persistent bacteria selected as the subject. A total of 1,160 published documents from 495 sources from the preceding two decades were reviewed. Maximum publications of 112 were observed in 2021 with 860 citations; however, 82 publications appeared in 2015 and were able to get the highest number of citations (4,214), only 43 (3.7%) were single-authored, whereas 1,117 (96.3%) publications are the result of collaborative works. Out of the top 10 countries ranked for publications, the USA took the top spot for the most highly productive country with 435 articles. Dormancy' appeared 2,351 times, followed by '*Escherichia coli*" (1,744, and 'Growth' 1,184 times) in research publications on bacterial persistence research. The findings from this study will aid in the creation of strategies and guidelines for regulating and avoiding bacterial persistence status.

1. Introduction

Alarming increases in host immunosuppression, an emerging sophisticated evasion mechanisms developed by microbial pathogens, and/or the dramatic increase in antibiotic-resistant bacterial strains, lengths of hospitalization, and associated costs have resulted from the widespread failure of traditional antibiotic treatment (Pan et al., 2023). On the other hand, bacteria have evolved advanced and complicated ways of adapting to various environments over centuries, as well as diverse ways to outwit mankind's efforts to combat disease-causing pathogens since the dawn of the antibiotic era 60 years ago (Huemer et al., 2020). One of the more emerging approaches is persistence, which is caused by a modification to the genome that enables bacteria to replicate in the presence of previously inhibitory antibiotic concentrations. Bacteria are able to survive after being subjected to high levels of antibiotics by entering physiologically latent and slow-growing stages, at which point they are referred to as "persisters", There is growing evidence that persister development contributes to antimicrobial treatment failure (Khan et al., 2020; Xiao et al., 2023).

A bacterial subpopulation may avert antimicrobial therapy by attaining a state of reduced metabolic activity via a variety of processes, including biofilm, toxin-antitoxin modules, the rigorous response, and the SOS (Save Our Soul) system response (Pan et al., 2023; Wood, 2017). In contrast to antibiotic-resistant bacteria, which develop their resistance through the acquisition of mutations, persisters are phenotypically distinct variants that are drug-tolerant and can sustain development even after the antibiotics are no longer present (Brauner et al., 2016). Antibiotic resistance is more common in persistent pathogens, according to different studies (Mancuso et al., 2021). Persisters, which are a type of biofilm component, are significantly responsible for biofilms' resilience. There is evidence that persisters contribute to the formation of biofilms. Bacteria in a biofilm are kept alive by a highly hydrated extracellular matrix made of proteins, polysaccharides, lipids, and extracellular DNA (Zhao et al., 2020), such illnesses caused by biofilm-related infections are notoriously difficult to treat. Because their persistent nature is tied to the generation of biofilm-derived persisters. Hence, antibiotics and other novel substances are being developed to eradicate antibiotic-resistant bacteria known as "persisters" (Helaine et al., 2014).

Bibliometric analysis uses mathematical and statistical approaches to track shifts in variables including publication volume, article source, authorship, and subject. It is conceivable to compare the scholarly influence of two countries or two authors. Article quality, scholarly networking, and emerging research paradigms may also be assessed. The (Visualization of Similarities) VOSviewer also allows you to create bibliometric maps, which can shed light on both the qualitative and quantitative components of the study (Li et al., 2021; Yang et al., 2021). Some bibliometric studies have looked at the literature pertaining to biofilm and pathogenic bacteria (Ju et al., 2023, 2022).

As interest in bacterial persisters grows, it is crucial to provide a comprehensive analysis of the evolution of the area (Windels et al., 2019). This study sought to monitor the present state of research on bacterial persisters around the world and to detect developing trends in this field by conducting a bibliometric analysis of relevant papers published in the 21st century. Such assessments are important in the medical sector because they highlight current research developments and breakthroughs, motivate scientists to pinpoint outstanding nations and organizations, and spotlight areas for advancement. The results of the research can be used to create a foundation to guide subsequent evaluations and appraisals. It is intended to identify patterns and developments in this field of study as well as provide insight into prospective areas for further research and progress, so this study was aimed at conducting an illustrated and measurable bibliometric review of the scientific literature on bacterial persistence and dormancy in the 21st century.

2. Materials and methods

2.1. Design of study and database selection

A bibliometric analysis was carried out to significantly improve the quality of the literature review by providing an obvious, meticulous, and reliable review approach. It allows us to understand the landscape of scientific research, which assists us in recognizing patterns and trends in research publications about institutions, countries, authors, and research areas (Ellegaard and Wallin, 2015), additionally, these can aid in identifying the specific research emphasis within a particular field of research (Agarwal et al., 2016). Moreover, bibliometric methods are indispensable for anyone looking to stay abreast of the latest developments in the world of research.

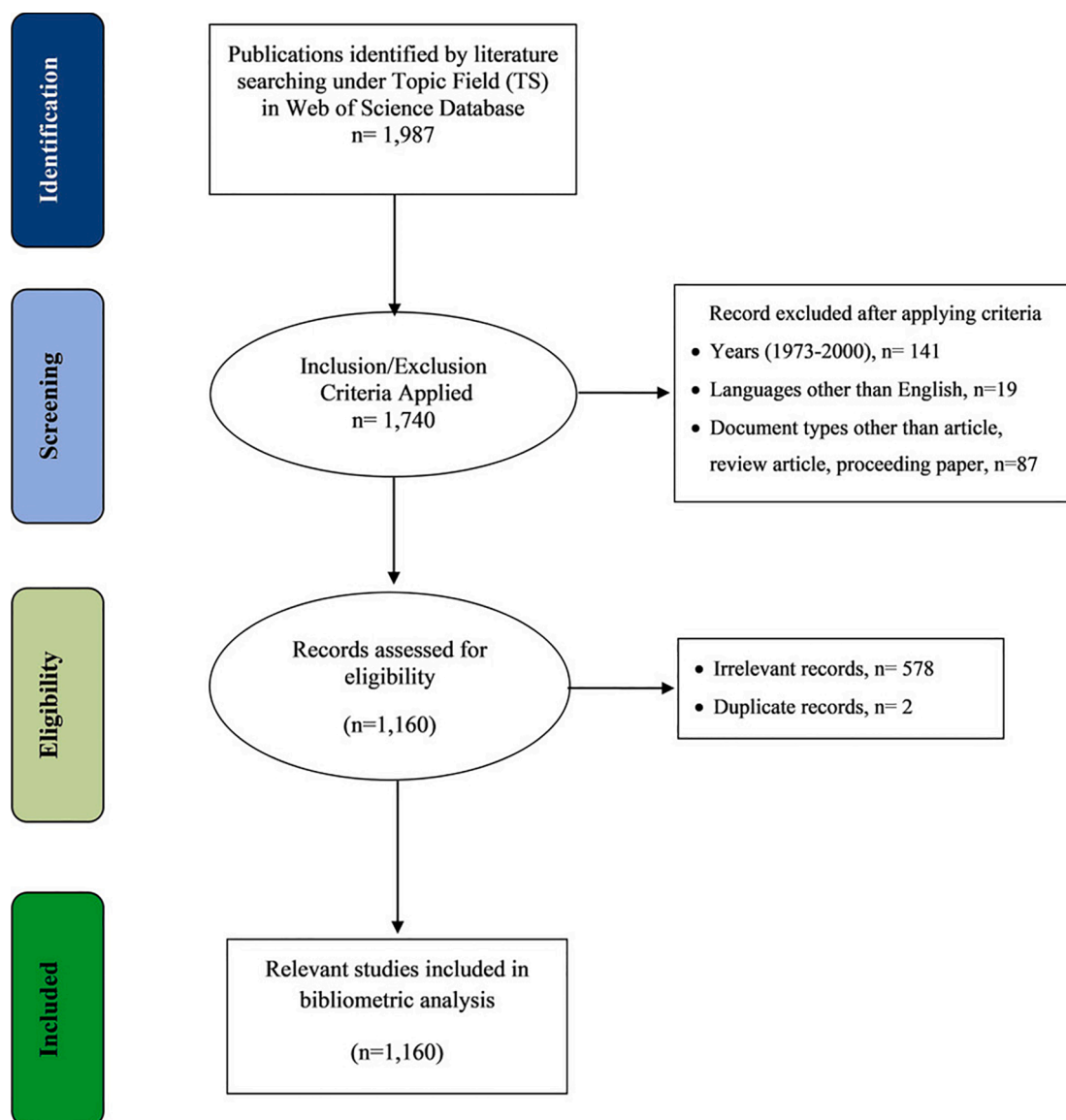The dataset for the current study was retrieved from the Web of

Fig. 1. Data extraction and filtering process for bacterial persistence and dormancy literature search from 2001 to 2023.

Science (WoS), a comprehensive, authoritative, and widely used scientific literature database. WoS is well-regarded because of its rigorous standards for document inclusion. The literature search took place on October 1, 2023. The Boolean search operators helped the authors retrieve the maximum number of relevant results. WoS Core Collection databases were searched for topic fields (TS: title, abstract, author keywords, and keywords plus).

2.2. Keywords selection

A thorough search strategy, mentioned in Fig. 1, was used to get and refine the retrieved data from the database. Appropriate keywords were prepared after conferring appropriate literature to run a search query in the WoS. The subsequent search query was run in the "Advanced" search option.

TS = ("Bacterial Persistence" OR "Persister cell*" OR " antibiotic tolerance" OR "Antibiotic tolerant cell" OR "bacterial infection" OR "biofilm formation" OR "Chronic infections" OR "coagulase negative staphylococci" OR "Dormant Mycobacteria" OR "Escherichia coli" OR "Genetic circuit" OR "guanosine pentaphosphate and tetraphosphate" OR "Mechanism of persistence" OR "Microbial" OR "PPGPP" OR "Pseudomonas aeruginosa" OR "Reactive oxygen species" OR "Reactive oxygen species (ROS)" OR "Staphylococcus aureus" OR "Mechanical Stress" OR "TA system" OR "Toxin overproduction" OR "toxin-antitoxin system" OR "bacteri*" OR "Physical Stress" OR "Bacterial matrix" OR "reduced metabolism" OR "energy production" OR "protein and nucleic acid synthesis" OR "DNA repair and protection" OR "protein degradation" OR "transporters/efflux systems" OR "transcriptional regulator") AND TS= (Dormancy).

2.3. Inclusion and exclusion criteria

To obtain accurate and comprehensive results, we strictly applied inclusion and exclusion criteria during our search for publications on bacterial persistence and dormancy. The search was carried out on the Web of Science Core Collection, and the query was limited to publications on dormancy, as indicated by the input of "dormancy" in the TS field tag (Topics). Only peer-reviewed documents were considered for the study. A list of irrelevant keywords which were excluded from the research can be found in the appendix. Fig. 1 contains a detailed list of the inclusion and exclusion criteria.

2.4. Data analysis

Various tools were employed for data analysis in this study. Microsoft Excel 2016 was used to clean the data and identify duplicate records, and it was also used to create Figs. 1–3. The manuscript was typed using Microsoft MS Word 2016. To construct and visualize bibliometric networks, VOSviewer version 1.6.19 was employed, resulting in Figs. 4 and 6a. Additionally, Biblioshiny, an application with a web interface for the bibliometrix R language package, was utilized to produce networking maps for Figs. 7a and 7b. ScientoPy a Python-based scientometrics analysis tool, was used to visualize Figs. 7a and 7b).

3. Data analysis and results

3.1. General overview and characteristics of publications on bacterial persistence and dormancy.

A total of 1,160 documents from 495 sources with an 8.1 percent annual growth rate were found on the topic of bacterial persistence and dormancy. 52,898 references were cited in these documents, and these 1,160 documents were cited 45,931 times with self-citations, and 43,317 times without self-citations by other documents. The average number of citations per document is 36.9, and the H-index is 103, as given in the WoS database.

3.2. Temporal analysis of publication productivity and citation growth

Based on the date criteria, the author retrieved a set of documents published in the 21st century. Fig. 2 illustrates the growth of publications and citations in bacterial persistence and dormancy research. The number of publications steadily increased, and the same is true of citations. Maximum publications of 112 were observed in 2021 with 860 citations; however, 82 publications appeared in 2015 and were able to get the highest number of citations (4,214). It is pertinent to mention that eleven publications in 2002 were the most impactful, getting 1,613 citations, with an average of 146.64 citations per publication.

3.3. Co-Authorship patterns and most prolific authors

We identified the authorship patterns of publications on bacterial persistence and dormancy research, which are shown in Fig. 3. It shows that out of the total 1,160 publications extracted from WoS, only 43 (3.7
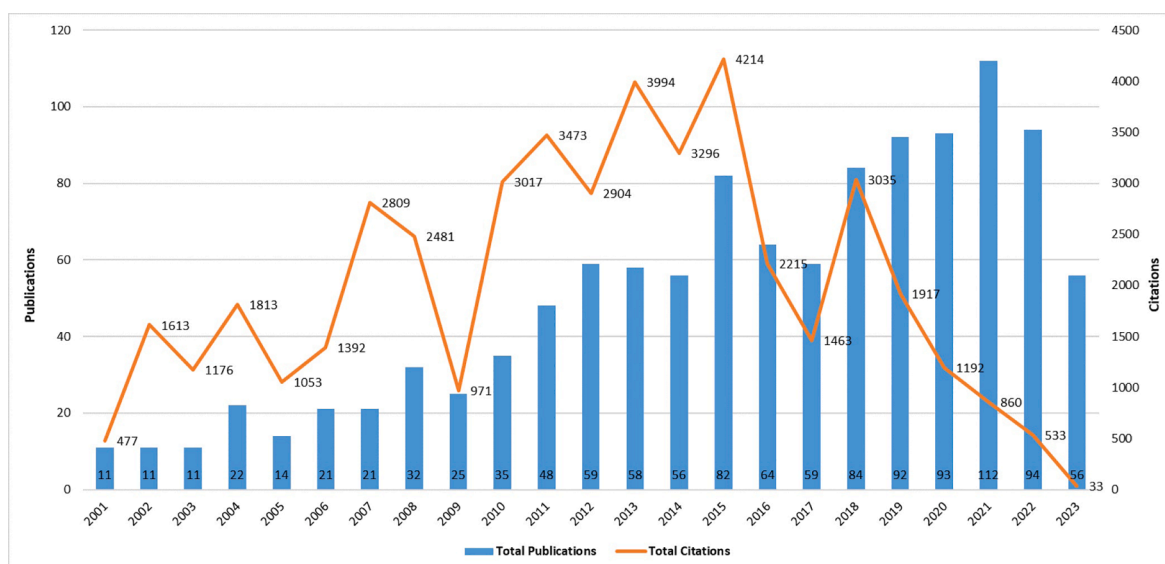

Fig. 2. Publications and citations distribution in bacterial persistence and dormancy research from 2001 to 2023.
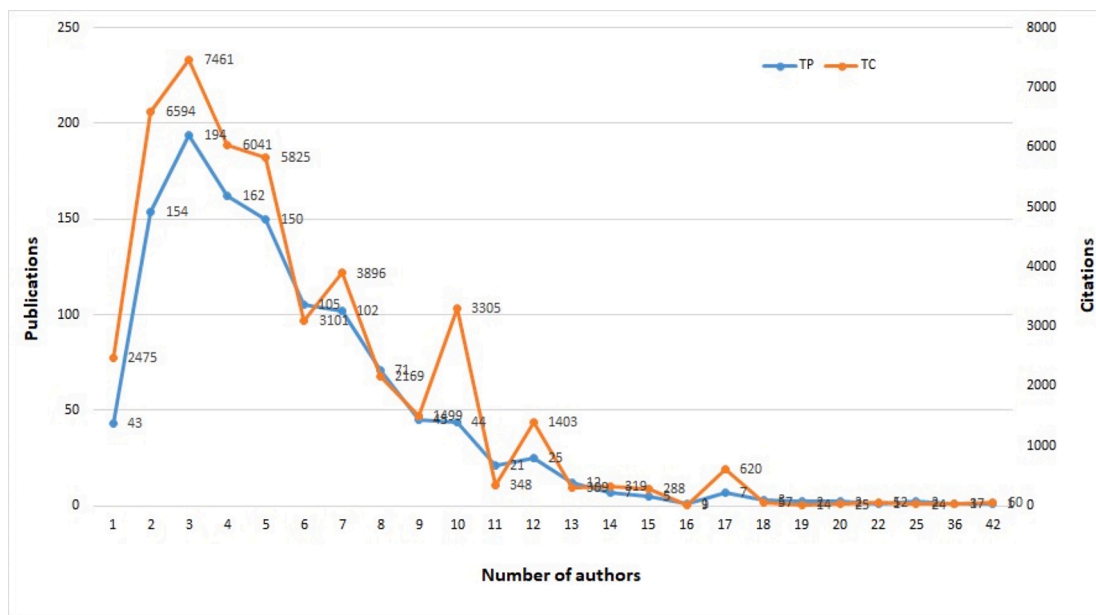
Fig. 3. Co-authorship patterns in publications and citations on bacterial persistence and dormancy research publications.
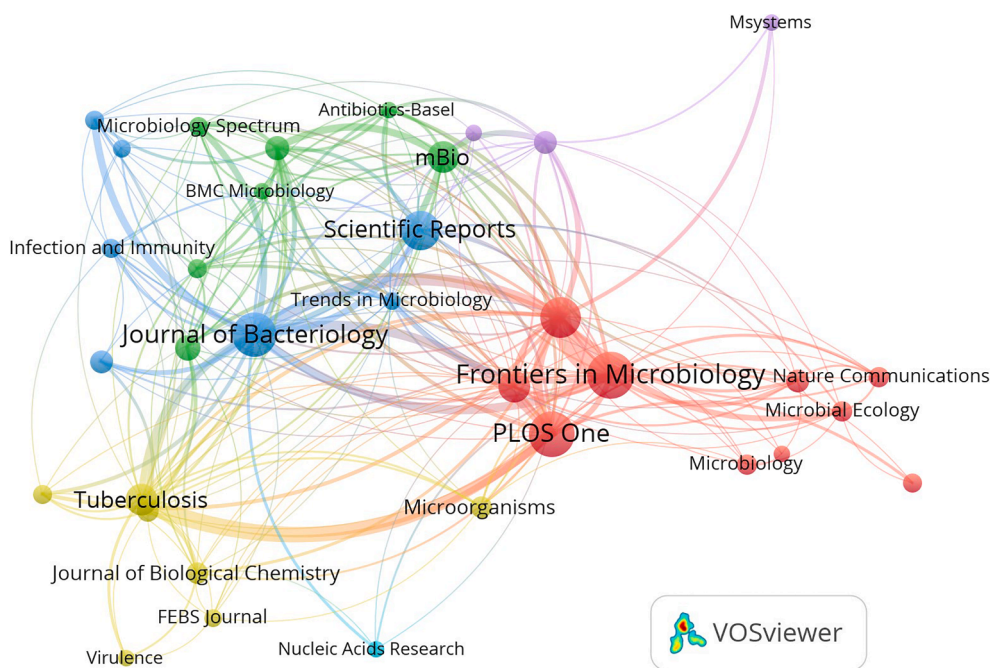

Fig. 4. Citation map of sources of publications with minimum 5 documents of a source. Out of 495 sources, 35 meet the thresholds.

%) were single-authored, whereas 1,117 (96.3 %) were the result of collaborative works. This analysis indicates that the highest number of authors is 42. The statistics show that the dominant authorship pattern is 3 authors (194 publications and 7,461 citations), followed by 4 authors (162 publications) and 2 authors (154 publications). The two-authored publications got the second-highest citations (6,594), followed by 6,041 citations for publications authored by 4 researchers.

Table 1 illustrates the most prolific authors publishing on bacterial persistence and dormancy in the 21st century. The top-10 authors in the table were ranked by their number of publications on bacterial persistence and dormancy, their total publications indexed in WoS and H-Index based on all their publications are given in the table. The leading author in bacterial persistence and dormancy research is Jay T. Lennon,

from Indiana University, Bloomington, USA, with 15 publications in our study and a total of 125 publications indexed in WoS, having a 43 H-index, followed by Arseny S. Kaprelyants, from the Russian Academy of Sciences, Moscow, Russia with 14 publications in this research area. Further analysis of the authors list shows that Thomas Wood from 'Fast Data Science Ltd., London, UK' has a 102 H-index for his 1,052 total publications, including 10 on bacterial persistence and dormancy.

3.4. Mapping source citations and preferred journals

A citation map of sources of publications, on the basis of the citations these sources got, is constructed as shown in Fig. 4. The size of each node represents the total number of links from the source, while the thickness
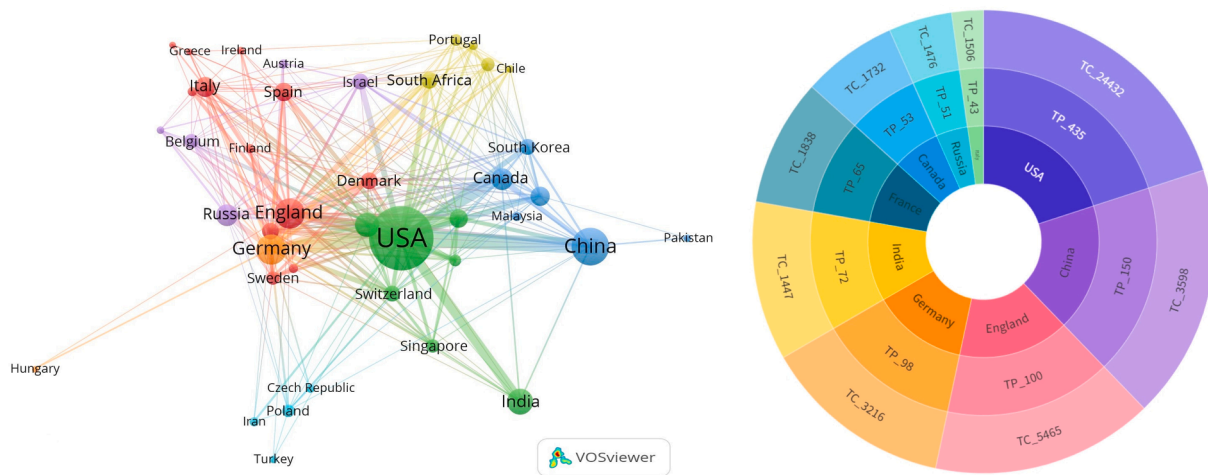
Fig. 5a. a) Co-authorship network map among countries with minimum 5 documents from a country. Out of 77, 41 meet the thresholds. b) Leading countries in bacterial persistence and dormancy research from 2001 to 2023.
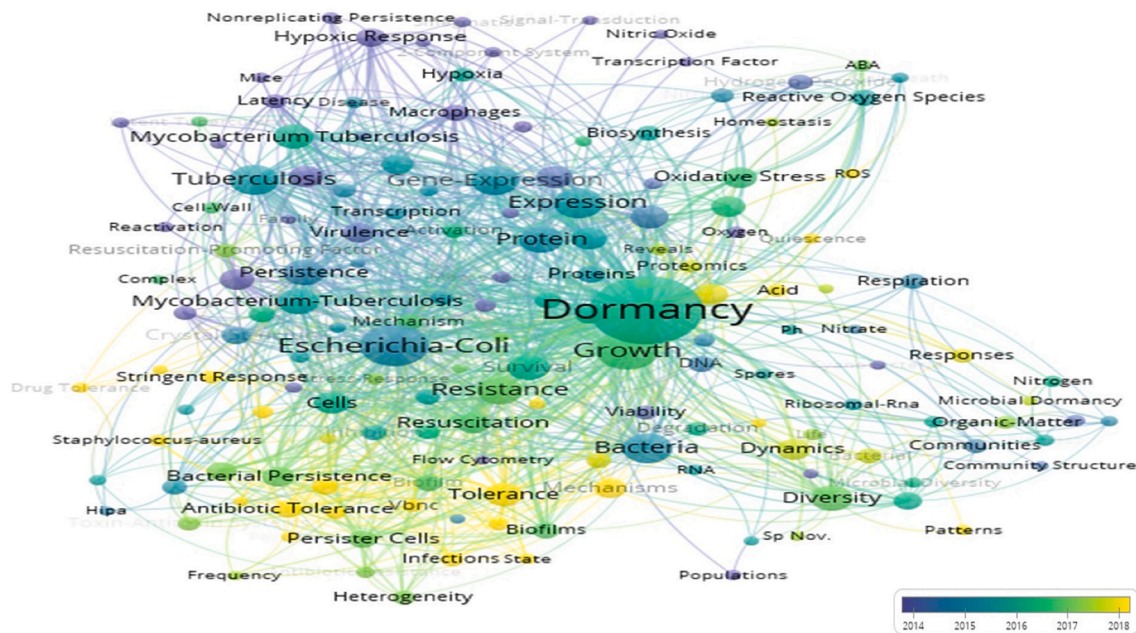
Fig. 6. Keyword co-occurrence network map of keywords used in bacterial persistence and dormancy research. Out of 3,946 keywords, 179 meet the thresholds.

Fig. 7. a) Keywords Evolution in Bacterial Persistence and Dormancy Research from 2001 to 2023. b) Keywords Trends in Bacterial Persistence and Dormancy Research from 2001 to 2020, and 2021 to 2023.

Table 1

Most Prolific Authors in Bacterial Persistence and Dormancy Research in 21st century.

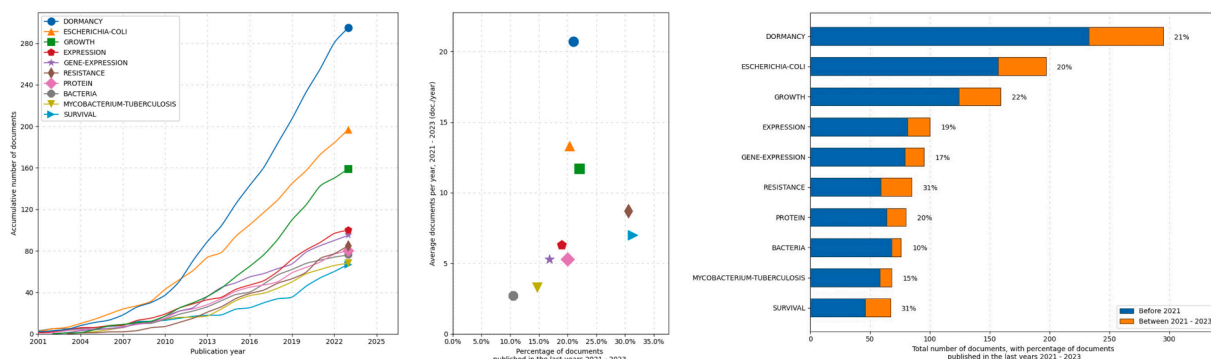| Rank	Researcher Profiles	Institute/Organization	TP (BP & D)	TP (WoS)	H-index
1	Lennon, Jay T.	Indiana University–Bloomington, USA	15	125	43
2	Kaprelyants, Arseny S.	Russian Academy of Sciences, Moscow, Russia	14	134	35
3	Tyagi, Jaya S.	All India Institute of Medical Sciences (AIIMS), New Delhi, India.	11	124	32
4	Wood, Thomas	Fast Data Science Ltd, London, UK	10	1052	102
5	Shleeva, Margarita	Russian Academy of Sciences, Moscow, Russia	10	44	14
6	Berisio, Rita	Consiglio Nazionale delle Ricerche (CNR), Naples, Italy	9	166	35
7	Blath, Jochen	Goethe University Frankfurt, Frankfurt, Germany	9	37	14
8	Franklin, Michael J. M.	University of Chicago, Chicago, USA	8	216	50
9	Ruggiero, Alessia	Istituto di Biostrutture e Bioimmagini (IBB-CNR), Napoli, Italy	8	95	22
10	Popham, David L	Virginia Polytechnic Institute & State University, USA	8	88	39

TP (BP & D), total publications on bacterial persistence & dormancy, TP (WoS), total publications in Web of Science.

of the links indicates the strength of the connection. For each of the 35 sources, the total strength of the citation links is 555 for 233 links. There are a total of six clusters. Top links are 28, 27, and 26 for 'Proceedings of The National Academy of Sciences of the United States of America', 'Journal of Bacteriology', and 'Frontiers in Microbiology," respectively, with average normalized citations of 2.97, 0.70, and 0.97.

The data shown in Table 2 represents the most preferred journals by the researcher in the area under study. The journals are ranked with respect to their total publications on bacterial persistence and dormancy research.

'Frontiers in Microbiology' is the leading journal with 40 publications (1,140 citations), followed by 'PLOS One' and 'Journal of Bacteriology' with 39 publications (1,663 citations) and 36 publications (1,347 citations), respectively. A total of 260 publications from these 10 journals were able to get 13,631 citations. The USA is at the top with 5 journals, 143 publications and 10,295 citations, followed by Switzerland

with 3 journals, 69 publications and 1,831 citations. Germany and Scotland have one journal each on this list. Further analysis shows that 3 journals fall in Q1, 5 in Q2, and 2 in Q3. There is no journal in the Q4 category of WoS.

3.5. Co-authorship network map among countries and identification of leading countries

Fig. 5a shows the network of the productive countries with publications greater than 5 and demonstrates the collaborative ties among countries, which is co-authorship. This figure demonstrates a network of co-authorship between countries publishing research on bacterial persistence and dormancy. The size of the node reflects the number of publications for each country, and the thickness of the line correlates to the strength of research collaboration. 41 items fulfilling the criteria made 7 clusters with 298 links a total link strength of 724.

The USA is in cluster 2 with Australia, France, India, New Zealand, Singapore, and Switzerland. The total number of publications in this cluster is 673, with 32,768 citations. The USA has a total of 35 links, and the total link strength is 223. England is in cluster 1, with 32 links and 125 total link strengths for its 99 publications. Saudi Arabia has 4 links and a total link strength of 5 for its 5 documents. The total link strength of this cluster is 408, for 305 publications and 15,153 citations. China is in Cluster 3 along with Canada, Japan, Malaysia, Pakistan, and South Korea. This cluster has 287 total publications and 7,107 citations, with Chinese share of 150 publications and 3,598 citations.

Out of the top 10 countries ranked for publications, as shown in Fig. 5b, the USA took the top spot for a highly productive country with 435 articles, while China came in second with 150 articles, followed by England with 100 publications. The USA also ranked first in terms of citations with 24,432 citations, followed by England with 5,465 citations and China with 3,598 citations. Japan has the lowest publications and citations at the bottom of the list. These top-10 countries have a total of 1,107 publications, which is 95.43 % of total publications.

Fig. 6 displays keyword co-occurrence among the publications on bacterial persistence and dormancy research. Each node represents the number of publications having these keywords and, and each line represents the network among these keywords.

There are 6 cluster with 10,324 links and 27,464 total link strength. 'Microbial 'Dormancy' is in cluster 1 with keywords 'Microorganisms', and 'Growth'. The sum of links in this cluster is 2,381, and sum of total link strength is 5,212. 'Persistence',

'Bacterial Persistence', 'Resistance', 'Persister', 'Antibiotic Tolerance', and 'Antibiotics' are placed in cluster 2. Sum of links for cluster 2 is 2,767 and 7,095 total link strength. The color of nodes shows their usage in accordance with the year. The yellowish keywords are the recently used keywords after the year 2018.

Table 2

Top 10 Preferred Journals by Researchers in Bacterial Persistence and Dormancy Research During 2001–2023.

Rank	Sources	Publisher	Country	TP	TC	IF 2022	JCI	Q 2022	Publishing model
1	Frontiers in Microbiology	Frontiers Media SA	Switzerland	40	1140	5.2	0.96	Q2	OA
2	PLOS One	Public Library Science	USA	39	1663	3.7	0.91	Q2	OA
3	Journal of Bacteriology	American Society for Microbiology	USA	36	1347	3.2	0.67	Q3	OA
4	Proceedings of the National Academy of Sciences of USA	National Academy of Sciences	USA	30	5062	11.1	2.51	Q1	OA
5	Scientific Reports	Nature Portfolio	Germany	29	530	4.6	1.06	Q2	OA
6	Tuberculosis	Churchill Livingstone	Scotland	19	975	3.2	0.49	Q3	NOA
7	mBio	American Society for Microbiology	USA	19	1152	6.4	1.40	Q1	OA
8	Applied and Environmental Microbiology	American Society for Microbiology	USA	19	1071	4.4	0.96	Q2	NOA
9	Frontiers in Plant Science	Frontiers Media SA	Switzerland	17	595	5.6	1.24	Q1	OA
10	Frontiers in Cellular and Infection Microbiology	Frontiers Media SA	Switzerland	12	96	5.7	0.83	Q2	OA

TC, total citations, TP, total publications, IF, impact factor, JCI, Journal Citation Indicator, Q, WoS quartile, OA, Open Access, NOA, Non-Open Access.

3.6. Keywords evolution and trends in bacterial persistence and dormancy

The most frequently used keywords were analyzed for their usage over the period from 2001 to 2023, and the results are given in Fig. 7a. The percentage of publications using these keywords in the last year, 2021–2023, is also shown. The keyword 'Dormancy' got the attention of the researcher working on this topic, and its usage has increased with time. The same trend can be seen in the last three years for 'Dormancy.' 'Bacteria' is the keyword, with a strong presence before 2021 but low visibility between 2021 and 2023. The accumulative growth of documents having these keywords can be seen in Fig. 7a. To compare the keywords used before 2021 and between 2021 and 2023, the author of this study analyzed the data with ScientoPy, and the results are shown in Fig. 7b. 'Dormancy' is the preferred keyword, as mentioned above; however, Fig. 7b shows that 21 percent of its documents were published in 2021–2023. 'Resistance' is used 31 % between 2021 and 2023 and 69 % before 2021. '*Escherichia coli*' is the second most used keyword, with 20 % usage between 2021 and 2023 and 80 % before 2021.

3.7. Characteristics of the most cited publications in bacterial persistence and dormancy research

Table 3 provides us with information about the most cited publications in bacterial persistence and dormancy research. These 10 (0.86 %) publications got 7,805 (17 %) citations, whereas the total citations for 1,160 publications were 45,931. 'Persister cells, dormancy and infectious disease," authored by Lewis and Kim and published in 'Nature Reviews Microbiology' is the highly cited article that got 1358 citations from 2007 until September 30, 2023. This article is followed by 'Evaluation of a nutrient starvation model of Mycobacterium tuberculosis persistence by gene and protein expression profiling' by Betts, JC et al. published in 'Molecular Microbiology' in 2002, which got 1,098 citations. Nature has three publications on this list, followed by 'Proceedings of the National Academy of Sciences of the United States of America' with two publications. These publications were able to get a maximum of 3330 citations during 2016–2020, followed by 1835 citations during 2021–2023, and 1790 during 2011–2015.

4. Discussion

Bibliometric analysis serves as a critical tool in understanding the evolving landscape of research, particularly in the context of persistent bacteria (Ellegaard and Wallin, 2015). This analysis enables a comprehensive examination of the existing body of literature, shedding light on trends, knowledge gaps, and areas warranting further investigation.

The current analysis represents an in-depth review of the retrieved publications regarding persistent bacteria, providing useful insights into the scope and magnitude of persistent bacteria research from 2001 to 2023. A total of 495 sources and, 1160 documents were identified during this period, with an annual growth rate of 8.1 %. The average document age is 7.31 years, and each document receives an average of 39.6 citations. The dataset comprises 52,898 references, and the

Table 3
Top Cited Articles in Bacterial Persistence and Dormancy Research from 2001 to 2023.

Title	Authors	ST	PY	TC	C/Y	2001–2005	2006–2010	2011–2015	2016–2020	2021–2023
Persister cells, dormancy and infectious disease	Lewis, Kim	Nature Reviews Microbiology	2007	1358	79.88	0	198	408	495	257
Evaluation of a nutrient starvation model of Mycobacterium tuberculosis persistence by gene and protein expression profiling	Betts, JC et. al.	Molecular Microbiology	2002	1098	49.91	122	250	293	301	132
Microbial seed banks: the ecological and evolutionary implications of dormancy	Lennon, Jay T.; Jones, Stuart E.	Nature Reviews Microbiology	2011	1050	80.77	0	0	218	492	340
Cross-biome metagenomic analyses of soil microbial communities and their functional attributes	Fierer, Noah et. al.	Proceedings of the National Academy of Sciences of the United States of America	2012	924	77	0	0	135	537	252
Inhibition of respiration by nitric oxide induces a Mycobacterium tuberculosis dormancy program	Voskuil, MI et. al.	Journal of Experimental Medicine	2003	742	35.33	67	205	218	183	69
Dormancy contributes to the maintenance of microbial diversity	Jones, Stuart E.; Lennon, Jay T.	Proceedings of the National Academy of Sciences of the United States of America	2010	596	42.57	0	3	185	258	150
The Soil Microbiome Influences Grapevine-Associated Microbiota	Zarraonaindia, Iratxe et. al.	mBio	2015	553	61.44	0	0	12	289	252
Ciprofloxacin Causes Persister Formation by Inducing the TisB toxin in Escherichia coli	Doerr, Tobias; Vulic, Marin; Lewis, Kim	PLOS Biology	2010	524	37.43	0	5	173	242	104
The Bacterial Cytoplasm Has Glass-like Properties and Is Fluidized by Metabolic Activity	Parry, Bradley R et. al.	Cell	2014	491	49.1	0	0	60	276	155
Activated ClpP kills persisters and eradicates a chronic biofilm infection	Conlon, B. P et. al.	Nature	2013	469	42.64	0	0	88	257	124

ST, Source Title, PY, Publication Year, TC, Total Citations, C/Y, Average Citations per Year.

document contents include 3946 Keywords Plus (ID) and 2898 Author's Keywords (DE). These findings serve as a foundational reference for the subsequent discussion.

The results of co-authorship patterns indicate that the majority of Bacterial Persistence and Dormancy publications are the outcomes of collaborative research, which unfolds the intricate web of collaborative ties among countries in the realm of bacterial persistence and dormancy research. With a threshold of more than five publications, it showcases a network of co-authorship, emphasizing the strength of collaborative efforts. Noteworthy clusters emerge, such as the USA in cluster 2, collaboratively contributing to 673 publications with a total link strength of 223. England, forming cluster 1, exhibits 99 publications with 32 links and a total link strength of 125. China, embedded in cluster 3, spearheads with 150 publications and 3,598 citations among the 287 total publications and 7,107 citations in the cluster.

The observed upward trend in publications on bacterial persistence and dormancy throughout the 21st century is indicative of a burgeoning interest in this field. Several factors contribute to this phenomenon. The growing concern surrounding antibiotic resistance and the related public health challenges have spurred an urgent need for a deeper understanding of bacterial behaviors (Majumder et al., 2020) This has driven both the scientific community and funding agencies to prioritize research in this domain.

Advancements in research methodologies and technologies have significantly contributed to the increase in publications (Mancuso et al., 2021) Researchers now have access to cutting-edge tools and techniques, enabling them to delve into the intricacies of bacterial persistence and dormancy. The evolving capabilities in data analysis, microscopy, and genetic studies have expanded the scope of research possibilities. This technological progress has allowed for more in-depth investigations and a higher level of precision in understanding these bacterial behaviors (Becker et al., 2021).

The COVID-19 pandemic may have also played a role in influencing research priorities. As the world grappled with a global health crisis, understanding bacterial behavior became even more vital (Scapaticci et al., 2022). This pandemic has underscored the importance of microbiological research, as well as the need to explore mechanisms that enable bacteria to persist and adapt, contributing to the increased research output in this field.

The prevalence of collaborative research in the study of Bacterial Persistence and Dormancy is a positive trend, underlining the multifaceted nature of the topic. Bacterial behavior, particularly persistence and dormancy, is a complex phenomenon that requires expertise from various scientific disciplines (Bakshi et al., 2021). Researchers in microbiology, genetics, bioinformatics, and medicine must combine their efforts to tackle the intricacies of this subject.

Collaborative research fosters an environment where ideas and knowledge flow freely across institutions and geographical borders. This cross-pollination of ideas often leads to innovative solutions and a more holistic understanding of bacterial persistence and dormancy. It encourages the sharing of resources, data, and expertise, ultimately benefiting the scientific community and public health initiatives. The high percentage of multi-authored publications suggests that teams of researchers are coming together to tackle the challenges associated with bacterial persistence and dormancy (Kaushik et al., 2022). Such collaborations promote the sharing of diverse perspectives and foster comprehensive investigations that can address the complex nature of bacterial behavior.

The prominence of the United States as a leader in bacterial persistence and dormancy research reflects the nation's substantial investment in scientific endeavors (Torres et al., 2021). The presence of multiple American institutions at the forefront of this field indicates the robust infrastructure and expertise available within the country. This leadership may be attributed to the long-standing commitment of the United States to advancing scientific knowledge and addressing public health concerns, including antibiotic resistance (Schlanger and Kirkcaldy, 2021).

Through delve into the institutional landscape of persistent bacteria research. The institution with the highest number of publications, the 'Russian Academy of Sciences,' stands out with 46 publications, contributing to 4 % of the total 1,160 publications. Notably, it demonstrates significant influence in bibliographic coupling, boasting 110 links and a total link strength of 1,163.21. This institution aligns with cluster 3, indicating a cohesive research focus. Interestingly, the 'Chinese Academy of Science' in cluster 5 exhibits comparable influence with 30 publications, 110 links, and a total link strength of 1,313.88. So the global dimension of this research is evident through the involvement of institutions such as the Russian Academy of Sciences and the Chinese Academy of Sciences. These institutions not only contribute significantly to the body of knowledge but also play an essential role in fostering international collaboration (Matveeva and Ferligoj, 2020). Their involvement in the study of bacterial persistence and dormancy demonstrates the cooperative nature of research in addressing global health challenges.

The frequent appearance of keywords such as 'Dormancy,' *'Escherichia-Coli,'* and 'Growth' highlights their central role in the research on bacterial persistence and dormancy. These keywords are not merely buzzwords but represent fundamental aspects of bacterial behavior that have garnered significant attention (Patacq et al., 2020). 'Dormancy' is particularly noteworthy, as it underscores the critical need to understand how bacteria enter and exit dormant states, affecting their susceptibility to antibiotics and their potential to cause recurrent infections. The identification of trending topics, including 'gene-expression,' 'mechanisms,' and 'infections,' offers a window into the evolving landscape of research in this field (Zhang et al., 2019; Nichols and Davenport, 2021; Ma et al., 2023). 'Gene-expression' points to the growing interest in understanding the genetic regulation underlying bacterial persistence and dormancy. 'Mechanisms' suggests a focus on uncovering the specific pathways and molecular processes that enable these behaviors, while 'infections' indicates the practical implications of this research for addressing real-world health challenges.

Highly cited publications have a lasting impact on the field of Bacterial Persistence and Dormancy. "Persister cells, dormancy and infectious disease" by Lewis, published in 'Nature Reviews Microbiology,' has been instrumental in shaping research directions. Its high citation count reflects its influence on subsequent investigations, making it a cornerstone reference for researchers in this area. Similarly, the article "Evaluation of a nutrient starvation model of Mycobacterium tuberculosis persistence by gene and protein expression profiling" by Betts, JC, et al., published in 'Molecular Microbiology,' has provided critical insights into the mechanisms of bacterial persistence and has guided further research efforts. The presence of these influential publications from journals like 'Nature' and 'Proceedings of the National Academy of Sciences of the United States of America' underscores the importance of reputable and high-impact outlets in disseminating key findings. Such publications are instrumental in shaping the discourse and driving the field forward.

The involvement of a diverse range of funding agencies in supporting research on bacterial persistence and dormancy underscores the global commitment to addressing antibiotic resistance and related health challenges. The 'United States Department of Health and Human Services,' 'National Institutes of Health (NIH)' (USA), and the 'National Natural Science Foundation of China (NSFC)' play pivotal roles in financing essential research in this field. These agencies allocate substantial resources to support scientific investigations aimed at understanding and combatting bacterial persistence and dormancy.

Collaboration between multiple agencies, both domestic and international, is a testament to the global nature of the challenge. The presence of four U.S. agencies funding a significant number of publications underscores the nation's commitment to tackling this issue from various angles.

5. Limitations and future research directions

The study has multiple limitations, including the fact that we only obtained data from Dimensions-indexed papers; also articles from other databases were not investigated which may have impacted the outcomes. Furthermore, only English-language publications were enrolled in the analysis, which may have led to language bias. Moreover, the quality of the most referenced articles was not reviewed, which could have biased the interpretation of the findings. finally, the true contribution of authors in the cooperative network was challenging to figure out since the program grouped authors with average weight. So a comprehensive research on the mechanisms of persister bacteria are compulsory, which will represent a future research trend, and it is anticipated that this will eventually contribute to the development of innovative anti-persister therapies which can benefit patients who have persistent infection.

6. Conclusion

In conclusion, the comprehensive analysis of current study results indicates that bacterial persistence and dormancy research is a dynamically growing and collaborative field driven by the urgency of antibiotic resistance and infectious diseases. This burgeoning interest is the result of a confluence of factors, including heightened concerns about antibiotic resistance, technological advancements, and the global health challenges posed by the COVID-19 pandemic. Collaboration among researchers from various disciplines and across borders is a hallmark of this field, ensuring a multifaceted and holistic approach to understanding bacterial behavior. The presence of influential publications and the influence of high-impact journals highlight the significance of the knowledge generated in this field. As various funding agencies around the world provide crucial financial support, research on bacterial persistence and dormancy is poised to make substantial contributions to scientific knowledge and public health, addressing the critical challenges posed by antibiotic resistance and infectious diseases.

Ethical approval

Because this study evaluated articles that had previously been published, an ethical clearance wasn't necessary. There are no authors of the included studies who were approached for further details regarding their honorable articles.

Declaration of competing interest

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

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Sample availability

Samples of the compounds are available from the author.

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