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Integrating Naqli and Aqli perspectives into bibliometric research on antimicrobial resistance in Enterococcus faecalis and Enterococcus faecium

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Abstract

Introduction: Antimicrobial resistance (AMR) in *Enterococcus faecalis* and *Enterococcus faecium* is a major global health challenge because of multidrug resistance and persistent healthcare-associated infections. From the Naqli–Aqli perspective, addressing AMR reflects the Islamic principles of preserving human life (Hifz al-Nafs), seeking beneficial knowledge, and exploring Allah SWT's creation through scientific inquiry. Aim: To analyse global research trends in AMR involving *E. faecalis* and *E. faecium* using bibliometric methods. Methods: Scopus records published from 2020 to 2024 were retrieved and analysed using BiblioMagika version 2.10.1 (Ahmi 2025), VOSviewer version 1.6.20 (Van Eck and Waltman 2025), and OpenRefine. Results: A total of 918 publications from 97 countries were identified, demonstrating an increase in research output. The United States, China, and India were the leading contributors. Author productivity followed Lotka's Law, while co-authorship analysis revealed limited international collaboration. Keyword analysis identified antimicrobial resistance, antibiotic resistance, *E. faecalis*, and *E. faecium* as dominant terms; the occurrence of nonhuman-related keywords also points to the relevance of a One Health perspective. Conclusion: Strengthening international collaboration and cross-sectoral research is important for addressing AMR. Integrating Naqli and Aqli perspectives offers an ethical framework for collaborative research that supports the preservation of human life.

Keywords:
Enterococcus faecalis, *Enterococcus faecium*, Bibliometric Analysis, antimicrobial resistance.

INTRODUCTION

Islam places great emphasis on the pursuit of knowledge and encourages humanity to observe, reflect upon, and investigate the natural world as manifestations of Allah SWT's signs (*āyāt*). The emergence of antimicrobial resistance (AMR) represents not only a scientific challenge but also an ethical responsibility, as preserving human health aligns with one of the primary objectives of *Maqasid al-Shariah*, namely *Hifz al-Nafs* (preservation of life). Therefore, scientific investigations that improve understanding of antimicrobial resistance contribute to fulfilling this objective by supporting evidence-based strategies to reduce morbidity and mortality associated with resistant pathogens.

Allah SWT says:

"Indeed, in the creation of the heavens and the earth and the alternation of the night and the day are

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signs for those of understanding." *(Surah Ali 'Imran 3:190)*
This verse encourages rational reflection (*Aqli*) upon creation, providing a foundation for scientific exploration. Likewise, Allah SWT commands:
"Read in the name of your Lord who created." *(Surah Al-'Alaq 96:1)*

This first revealed command establishes knowledge acquisition as a fundamental principle in Islam. Consequently, bibliometric analysis serves as an intellectual tool that enables researchers to identify scientific trends, research gaps, and collaborative opportunities, thereby supporting the development of effective interventions against antimicrobial resistance. Integrating Naqli and Aqli perspectives reinforces that scientific excellence, and spiritual values are complementary rather than contradictory, encouraging responsible stewardship of knowledge for the benefit of humanity.

Antimicrobial resistance (AMR) is one of the most important problems of the 21st century, risking global health security by reducing antibiotic efficacy. *E. faecalis* and *E. faecium* occupy a distinctive and significant role among numerous bacterial pathogens associated with AMR (Abdullah et al. 2025). Once considered harmless gut commensals, they have transitioned into dangerous opportunistic pathogens linked to healthcare-associated infections (HAIs). These infections encompass urinary tract infections, intra-abdominal abscesses, bacteremia, surgical site infections, and infective endocarditis, many of which are challenging to treat due to the pathogens' inherent and acquired resistance mechanisms (Sheerah et al. 2025). These bacteria possess natural resistance to some drugs and have rapidly developed resistance to vancomycin, leading to the global spread of vancomycin-resistant enterococci (VRE) since the late 1980s. Carrying the vanA and vanB genes, these resistant strains cause serious treatment challenges, increasing illness and death rates (Ahmed et al. 2018). The World Health Organization (WHO) lists VRE as high-priority pathogens (WHO 2017), and the U.S. Centers for Disease Control and Prevention (CDC) categorises them as a serious threat (Centres for Disease Control and Prevention 2019).

While a large body of research addresses their epidemiology and molecular mechanisms, the landscape remains fragmented across microbiology, clinical medicine, and environmental sciences (Tang et al. 2023). Traditional reviews often fail to capture macro-level collaboration patterns or emerging fronts like CRISPR-Cas systems, whole-genome sequencing (WGS) surveillance, and One Health integrations (Salinas 2022). Unlike broader studies grouping enterococci within the general "ESKAPE" category (Boccella et al. 2021), this study addresses the literature gap by providing a dedicated, systematic bibliometric analysis focused exclusively on *E. faecalis* and *E. faecium* from 2020 to 2024.

METHODOLOGY

Study design

This study employed a bibliometric analysis to evaluate global research output on antimicrobial resistance (AMR) in *E. faecalis and E. faecium*. Bibliometric analysis is a quantitative approach to examining scholarly literature, enabling assessment of publication patterns, citation impact, collaboration networks, and subject analysis within a defined research domain.

Data sources

A multidisciplinary citation database was selected for this analysis: Scopus. This database was chosen because it provides comprehensive coverage of peer-reviewed journals, including robust metadata and allows export of records in formats compatible with bibliometric software.

Search strategy

The search string reported in the submitted manuscript combined *E. faecalis* terms AND *E. faecium* terms AND resistance terms. This structure may preferentially retrieve records mentioning both species and may exclude relevant publications focused on only one species. The search must therefore be re-run before the results can be finalised. A proposed inclusive Scopus Advanced Search query is:

TITLE-ABS-KEY(("Enterococcus faecalis" OR "E. faecalis" OR "Enterococcus faecium" OR "E. faecium") AND ("antimicrobial resistance" OR "antibiotic resistance" OR "drug resistance" OR "multidrug

resistance" OR "vancomycin resistant" OR "linezolid resistance" OR "ampicillin resistance")) AND PUBYEAR > 2020 AND PUBYEAR < 2025

This query is a proposed revision and must be tested in Scopus, with the exact executed query, search date, number of retrieved records, and filters saved for reporting. Because the query uses OR between the two species, it captures studies directly addressing either organism; title/abstract screening then determines whether AMR is a substantive focus. If the intended research question requires studies reporting both species in the same record, that narrower objective should instead be stated explicitly and analysed separately.

Data retrieval and cleaning

Searches were performed in July 2025. Metadata, including titles, abstracts, author keywords, index keywords, author names, affiliations, journal titles, publication years, references and citation counts were exported. Records from Scopus were downloaded in CSV format. Articles that only mentioned *E. faecalis* and *E. faecium* tangentially (e.g., within mixed microbial communities without a resistance focus) were excluded after screening titles and abstracts. The final dataset included 918 records.

Inclusion and exclusion criteria

Inclusion criteria:

i. Publications explicitly addressing AMR in *E. faecalis* and *E. faecium*.
ii. Research presenting experimental, clinical, epidemiological, or review-based findings.
iii. Indexed in Scopus during the study period.

Exclusion criteria:

i. Articles focusing exclusively on other species unless *E. faecalis* and *E. faecium* resistance data were explicitly reported.
ii. Articles lacking sufficient bibliographic metadata.

RESULTS AND DISCUSSION

Annual publication trends

The dataset revealed 918 publications between 2020 and 2024 (Figure 1). The annual publication volume demonstrated a steady upward trajectory, indicating sustained scholarly engagement and growing interest in the field. Conversely, annual citations followed a different pattern. Total citations peaked at 3,581 during the midpoint of the observed period, reflecting the impact of foundational studies. This was followed by a gradual decline to 1,611 in the most recent year, a predictable trend given that newer publications have had less time to accumulate citations.

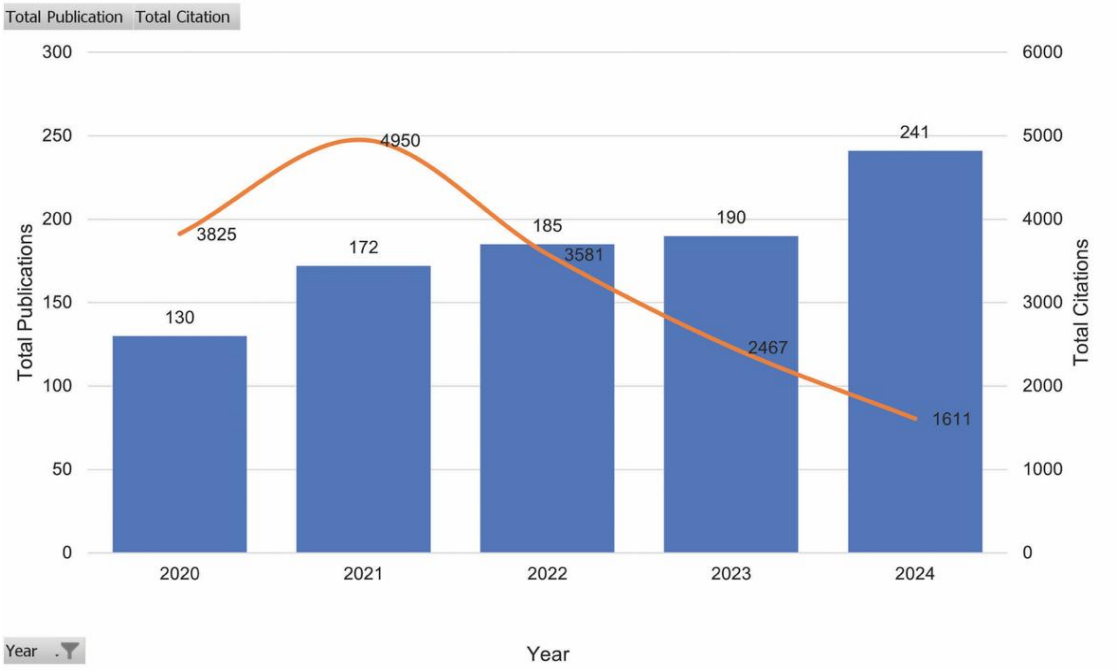


Figure 1. Annual publications on antimicrobial resistance in *E. faecalis* and *E. faecium* from 2020 to 2024.

Authorship analysis

The analysis of author productivity identified the 10 most prolific contributors to research on antimicrobial resistance (AMR) in *E. faecalis* and *E. faecium* (Table 1). Coombs, G.W. ranked first with 10 publications (1.09%), followed by Mowlaboccus, S. with eight publications (0.87%) and Daley, D.A. with seven (0.76%). Seven additional authors- Zhuo, C., Zhu, D., Yu, H., Su, D., Jin, Y., Huang, X. and Hu, F.- each contributed six publications (0.65%). These counts describe publication productivity within the retrieved dataset and should not, by themselves, be interpreted as measures of research quality or influence.

Table 1. The 10 most prolific authors contributing to this research area, generated using BiblioMagika version 2.10.1 (Ahmi 2025).

Author Name	TP	%
Coombs, G.W.	10	1.09%
Mowlaboccus, S.	8	0.87%
Daley, D.A.	7	0.76%
Zhuo, C.	6	0.65%
Zhu, D.	6	0.65%
Yu, H.	6	0.65%
Su, D.	6	0.65%
Jin, Y.	6	0.65%
Huang, X.	6	0.65%
Hu, F.	6	0.65%

Most Influential Institutions by Total Citations

Table 2 presents the most influential institutions contributing to research in this domain, ranked by total citation count (TC). The findings reveal that several universities and medical centres from diverse geographical regions, particularly Asia, Europe, and North America have made substantial contributions to the field.

Ajman University (United Arab Emirates) emerged as the most influential institution, achieving 1,012 total citations from only two publications, with an exceptionally high citation average of 506 citations per paper (C/P). Similarly, King Faisal University (Saudi Arabia), despite producing just one publication, also achieved 506 citations, highlighting its remarkable research impact.

Henry Ford Hospital (USA) followed closely, producing six papers that collectively received 602 citations, resulting in a strong average of 100.33 citations per paper, supported by an h-index of 5 and g-index of 6, indicating both productivity and consistent citation influence. Other high-impact contributors include Zoetis Reference Laboratory (USA) and the United States Department of Agriculture (USA), which recorded 467 and 456 total citations, respectively. Their citation averages (116.75 and 152.00) further demonstrate the global relevance of their research outputs, particularly in antibacterial and molecular studies.

A few European and Asian institutions displayed consistent research productivity. For instance, Normandie University (France), Hospital Universitário de Brasília (Brazil), and Hospital de Clínicas de Porto Alegre (Brazil) each produced between five and six publications with moderate citation averages (57–69 citations per paper), and high h- and g-indices (5–6), suggesting balanced productivity and influence.

Notably, medical and health-related institutions dominate the list, such as Agios Nikolaos General Hospital, Hospital São Lucas, and Children's Hospital of Jiangxi Province, reflecting the strong clinical and translational orientation of the research field. In addition, North American institutions like the University of Pennsylvania Perelman School of Medicine and Rush University Medical Centre demonstrated high citation averages (66.2 and 138.0 citations per paper, respectively), reinforcing their continued global leadership in biomedical research.

Table 2. Top 10 Influential Institutions by Total Citations.

Institution Name	Country	TP	NCA	NCP	TC	C/P	C/CP	h	g	m
Ajman University	United Arab Emirates	2	NR	2	1012	506.00	506.00	2	2	0.667
Henry Ford Hospital	United States	6	NR	6	602	100.33	100.33	5	6	0.833
King Faisal University	Saudi Arabia	1	NR	1	506	506.00	506.00	1	1	0.333
Zoetis Reference Laboratory	United States	4	NR	4	467	116.75	116.75	4	4	0.800
United States Department of Agriculture	United States	3	NR	3	456	152.00	152.00	3	3	0.500
Normandie Univ	France	6	NR	6	348	58.00	58.00	6	6	1.000
NHO Sagamihara National Hospital	Japan	3	NR	3	348	116.00	116.00	3	3	0.600
South China Agricultural University	China	4	NR	4	347	86.75	86.75	3	4	0.500
Hospital Universitário de Brasília	Brazil	6	NR	6	344	57.33	57.33	6	6	1.000
Hospital de Clínicas de Porto Alegre	Brazil	5	NR	5	343	68.60	68.60	5	5	1.000

These data were generated using BiblioMagika version 2.10.1 (Ahmi 2025).
Note: TP = total number of publications; NCA = number of contributing authors; NCP = number of cited publications; TC = total citations; C/P = average citations per publication; C/CP = average citations per cited

publication; h = h-index; g = g-index; m = m-index; NR = not reported.

Author Productivity Based on Lotka's Law

A total of 97 countries contributed to the literature. The United States led global production with 156 publications (16.99%), followed by China with 113 publications (12.31%), and India with 76 publications (8.28%). When normalised by GDP, smaller nations such as Portugal, Greece, and Denmark demonstrated disproportionately high research densities due to concentrated centres of microbiology excellence.
Publications were distributed across 339 peer-reviewed journals, with a heavy concentration in specialised outlets. The journal *Antibiotics* ranked first, accounting for 131 publications (38%), followed closely by *Frontiers in Microbiology* and *Animals*. Open-access portals like *Infection and Drug Resistance* and *International Journal of Molecular Sciences* also emerged as vital publication venues.

Geographic distribution of publications

A total of 97 countries contributed to publications in this field. Table 4 summarises the top 10 most productive countries.

i. The United States led with 156 publications (16.99%), reflecting strong investment in AMR surveillance, molecular microbiology, and clinical studies.
ii. China ranked second with 113 publications (12.31%), showing remarkable growth, particularly after 2010, largely driven by hospital-based studies and genomic analyses.
iii. India (76; 8.28%) and United Kingdom (70; 7.63%) followed, reflecting increasing contributions from emerging economies.
iv. Among European nations, Spain (5.23%), Italy (7.52%), and Germany (5.88%) were leading contributors.

When normalised by gross domestic product (GDP), smaller nations such as Portugal, Greece, and Denmark demonstrated disproportionately high research productivity relative to their size, likely due to concentrated centres of excellence in microbiology and clinical infectious diseases.

Leading Journals

Publications were distributed across 339 peer-reviewed journals. The top 5 journals accounted for nearly 87% of all publications, reflecting concentration in specialised outlets.

i. The Antibiotics ranked first with 131 publications (38%), reflecting their focus on AMR.
ii. Frontiers in Microbiology and Animals followed closely.
iii. Specialty microbiology journals (Pharmaceuticals, Pathogens and Probiotics and Antimicrobial Proteins) were major outlets.
iv. Open-access journals, particularly Infection and Drug Resistance and International Journal of Molecular Sciences, emerged as important publication platforms.

Table 3. Productivity Patterns of Authors and Research Contributions

Document Written	N. of Authors	Proportion of Authors	Lotka's Law
1	5070	93.70%	60.00%
2	271	5.01%	15.00%
3	51	0.94%	6.67%
4	11	0.20%	3.75%
5	3	0.06%	2.40%
6	2	0.04%	1.67%
7	1	0.02%	1.22%
8	1	0.02%	0.94%
10	1	0.02%	0.60%
Grand Total	5411	100.00%	92.25%

Source: Generated by the author using BiblioMagika version 2.10.1 (Ahmi 2025).

Table 4. Top 10 most productive countries in AMR research on *E. faecalis* and *E. faecium.*

Rank	Country	Publications (n)	Percentage of total	Average citations per paper	h-index
1	United States	156	16.99%	22	29
2	China	113	12.31%	24.53	26
3	India	76	8.28%	21.55	17
4	United Kingdom	70	7.63%	21.32	17
5	Italy	69	7.52%	21.82	21
6	Germany	54	5.88%	14.04	14
7	Spain	48	5.23%	20.86	15
8	Australia	48	5.23%	20.40	15
9	Brazil	45	4.90%	18.70	13
10	South Africa	29	3.16%	31.12	10

These results highlight the countries with the highest publication counts in the retrieved dataset. Source: Generated by the author using BiblioMagika version 2.10.1 (Ahmi 2025).

Citation analysis and landmark papers

The citation analysis showed that the most cited study is a narrative review by Ghazala Muteeb et al. (2023) (Muteeb 2023) published in *Pharmaceuticals* (506 citations), which provides a comprehensive discussion on the origin of antibiotics, the emergence of resistance, and their implications for future drug development. This broad thematic coverage accounts for its high citation impact. The second most cited work by Rojita Mishra et al. (2020) in *Frontiers in Microbiology* (330 citations) focuses on natural anti-biofilm agents as promising strategies to control biofilm-associated pathogens, a particularly relevant area in *E. faecalis* and *E. faecium* infections given the species' strong biofilm-forming capacity (Mishra 2020). The third most cited article by Jessica C. Ezeji et al. (2021) in *Gut Microbes* (220 citations) examines the dual roles of *Parabacteroides distasonis* as both a gut commensal and emerging resistant pathogen, highlighting the broader interplay between gut microbiota, resistance mechanisms, and human health (Ezeji 2021). Similarly, the review by Argyrios Periferakis et al. (2022) in *International Journal of Molecular Sciences* (213 citations) emphasises the antimicrobial potential of kaempferol, a natural flavonoid, underscoring the growing interest in phytochemicals as alternative therapies against resistant pathogens, including *E. faecalis* and *E. faecium* (Periferakis, 2022). Finally, Marta Reyman et al. (2022) in *Nature Communications* (189 citations) report findings from a randomised trial on the impact of early-life antibiotic exposure on the infant gut microbiome, demonstrating how antibiotic use in early development can shape resistance reservoirs (Reyman et al., 2022). Collectively, these highly cited works highlight the central themes driving AMR research in *E. faecalis* and *E. faecium*: the global threat of resistance, the role of biofilm formation, the contribution of the gut microbiome as a resistance reservoir, and the potential of natural compounds as alternative antimicrobial agents.

The institutional citation results should be interpreted cautiously because citation indicators may be disproportionately influenced by a small number of highly cited publications. Although Ajman University recorded 1,012 citations from two publications (506 citations per publication), this figure alone does not establish sustained institutional leadership in research specifically addressing antimicrobial resistance in *Enterococcus faecalis* and *Enterococcus faecium*. The contribution of highly cited review articles, including the paper by Muteeb et al. (2023), should be considered alongside the number and nature of the publications attributed to each institution. Accordingly, institutional citation counts in this study represent citation visibility within the analysed dataset rather than a direct measure of research quality, sustained empirical productivity, or institutional specialisation in enterococcal antimicrobial resistance. A more balanced interpretation requires consideration of publication type, species-specific relevance, the distribution of citations across individual publications, and the volume of original research. This distinction is particularly important when institutional rankings are based on a small number of publications.

Author collaboration

The co-authorship analysis was conducted using VOSviewer version 1.6.20 (Van Eck and Waltman 2025) to identify collaboration patterns among the most productive authors in the field. With a threshold of at least three documents and 54 citations per author, the top 25 authors were selected for mapping. The visualisation revealed that while these authors are highly productive in terms of publication output, their collaborative links are relatively weak**.** The network map appeared scattered (Figure 2)**,** with many authors forming isolated nodes rather than being part of a larger interconnected network. This suggests that most authors collaborate within their own limited research groups rather than across wider international networks.

Out of the 25 most productive authors, only four were found to be directly connected in the first analysis. (Figure 3) When the parameters were adjusted, the number of connected authors increased slightly, with five authors showing collaborative links (Figure 4)**,** yet the overall structure remained fragmented. This pattern highlights the low level of co-authorship connectivity, indicating that research on *E. faecalis* and *E. faecium* antimicrobial resistance is driven by multiple independent groups with limited cross-group collaboration.
The findings emphasize a contrast between high research productivity and low network integration**.** Although the top authors contribute significantly to the literature, their research efforts appear to be conducted largely in parallel, with few strong linkages bridging different research clusters. This underscores the need for greater international collaboration and networking to strengthen the research community and enhance knowledge sharing in this domain.



Figure 2. Co-authorship network of the most productive authors in antimicrobial resistance research on *E. faecalis* and *E. faecium*. Each node represents an author, with node size proportional to the number of publications. The colours indicate different clusters of collaboration, while the lines represent co-authorship links between authors (Van Eck and Waltman 2025).

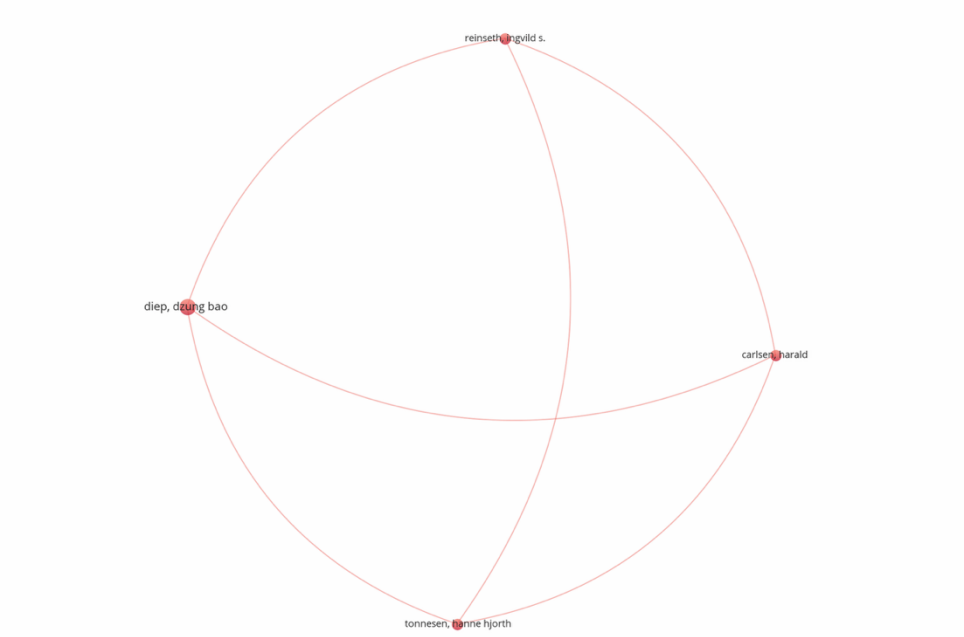


Figure 3. Author collaboration network based on the applied threshold (minimum of 3 documents and 54 citations per author) (Van Eck and Waltman 2025).

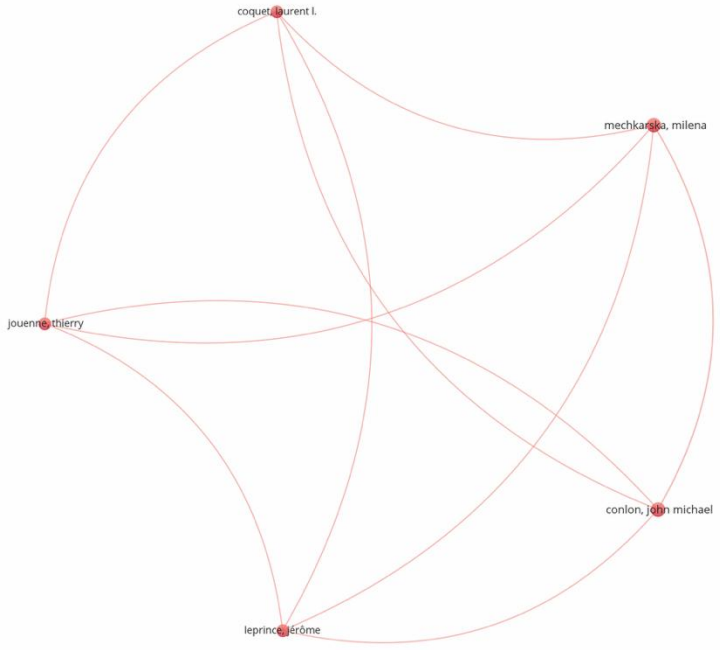


Figure 4. Author collaboration network based on the applied threshold (minimum of 3 documents and 10 citations per author) (Van Eck and Waltman 2025).

Keywords Analysis

Keyword analysis provides a thorough and quantitative overview of the thematic structure within the research domain. By using bibliometric indicators such as total link strength, citation counts, and normalised citation scores, this analysis will be able to systematically identify the most influential keywords, determine the interrelationships between them, and evaluate their relative significance in the collection of scholarly publications. This approach will not only reveal the conceptual focus of the field but also highlight the degree

of intellectual connectivity among recurring research themes.
Based on the results, it indicates that the research field is mainly characterised by recurring themes associated with antimicrobial resistance, *E. faecalis* and *E. faecium*. This emphasises a focused academic interest in microbial resistance mechanisms, clinical epidemiology, and the broader public health consequences from the emergence and dissemination of resistant bacterial strains. Based on the column Total Link Strength, it shows the amount of co-occurrence among keywords, which demonstrates how closely these study concepts are related to each other. Strong thematic consistency across studies can be seen through the high link strength values (>30,000) for these bacteria and antimicrobial resistance. It clearly suggests that these terms are central nodes within the research network.

Data from 2022 strongly indicate that this research area remains relevant and is actively developing, as many studies have been published in recent years. The average number of citations per document, which ranges from 12 to 19, together with normalised citation scores close to 1.0, suggests that the research in this field has been consistent and has been recognised for its impact globally. Furthermore, the results strongly show that there is no preference toward any single topic, meaning that attention is evenly distributed among the main themes.

Interestingly, the keywords "antibiotic resistance" and "nonhuman" have slightly higher citation averages, approximately 19 citations per article. This suggests that these subjects are more widely relevant across diverse scientific areas, including veterinary medicine, environmental microbiology, and public health. This trend also supports the One Health approach, which emphasises the close relationship between human, animal, and environmental health in addressing antimicrobial resistance.
Conceptually, the keyword clustering indicates that current research is primarily focused on resistance epidemiology, clinical microbiology, and infection control. Since the frequent appearance of the term nonhuman as a co-occurring keyword in the results is high, it highlights the importance of the One Health perspective, which identifies the close connections between human, animal, and environmental health in combating antimicrobial resistance.

To add, the existence of general terms such as “article” suggests that the dataset includes a variety of publication types, including original research papers, review articles, and meta-analyses. From these varieties of publication types, it can be concluded that the topic of antimicrobial resistance has been explored through multiple research approaches and methodologies.

This bibliometric analysis of 918 publications (2020–2024) provides the most comprehensive overview to date of research activity on antimicrobial resistance (AMR) in these bacteria. The results demonstrate a steady increase in publications every year, reflecting the enduring clinical and scientific relevance of this organism. The United States and China emerged as leading contributors, with Europe and India also making substantial contributions. Analysis of co-authorship networks highlighted fragmented collaboration networks with limited international integration, particularly after 2020. Thematic mapping identified four primary research clusters: Medicine, Immunology and Microbiology, Biochemistry, Genetics and Molecular Biology.

Our findings align with broader bibliometric studies of AMR, which also report significant growth since the 2020s, driven by global recognition of antibiotic resistance as a public health crisis. For instance, global bibliometric analyses on multidrug-resistant Gram-negative pathogens have shown similar growth trajectories, though *E. faecalis and E. faecium* occupy a unique niche. Unlike *Klebsiella pneumoniae* or *Acinetobacter baumannii*, which are associated primarily with hospital outbreaks, *E. faecalis and E. faecium* are part of the human microbiota and opportunistically cause infections, complicating strategies for surveillance and control (Krawczyk et al. 2021). The dominance of the United States is consistent with its leadership in AMR research overall, supported by agencies such as the Centres for Disease Control and Prevention (CDC) and National Institutes of Health (NIH) (Sullivan et al. 2025). China’s rapid ascent, however, is noteworthy: while its average citation impact is currently lower than that of the USA or Europe, its expanding volume of research suggests growing influence. This mirrors patterns seen in other biomedical domains where China has transitioned from high-output but lower-impact publications toward increasingly influential work. The strong representation of India highlights the contribution of emerging economies, likely driven by the high clinical burden of resistant *E. faecalis and E. faecium* in these regions. Nevertheless, collaboration patterns indicate that while North America and Europe are highly interconnected, Asian and Latin American institutions remain comparatively less integrated into global research networks. Strengthening South–South and North–South collaborations may accelerate both the quality and translational impact of research from these regions (Guan et al. 2024). The keyword analysis revealed that these bacteria and antimicrobial resistance are the two most dominant and

interconnected themes in the dataset, both exhibiting exceptionally high total link strengths exceeding 40,000. This indicates a strong conceptual and methodological alignment across studies in the field. The prominence of these bacteria corresponds to their growing recognition as one of the ESKAPE pathogens, a group of bacteria notorious for evading conventional antibiotics and posing critical threats to global healthcare systems. The consistent co-occurrence between these bacteria and antimicrobial resistance demonstrates the extensive research efforts focused on understanding resistance mechanisms, molecular epidemiology, and the clinical outcomes associated with multidrug-resistant *Enterococcus* infections (Wei et al. 2024).

The presence of *antibiotic resistance* and *nonhuman* as frequently cited keywords further highlights the multidisciplinary nature of this research domain. Studies have increasingly emphasised the *One Health* framework, which recognises the interconnectedness of human, animal, and environmental health in the propagation of antimicrobial resistance (AMR) (Singh et al. 2021). The high citation rate of keywords such as *nonhuman* (average ≈ 19 citations per document) indicates that AMR research extends beyond clinical settings to include environmental reservoirs, livestock management, and food safety (Aljeldah 2022). This pattern reinforces the notion that tackling AMR requires coordinated surveillance and stewardship across sectors rather than an isolated, hospital-based approach. The average publication year of 2022 across all top-ranked keywords demonstrates that AMR and these bacteria remain highly active and evolving areas of investigation. Recent years have seen the integration of molecular tools such as whole-genome sequencing (WGS), metagenomics, and transcriptomics to elucidate resistance genes and transmission dynamics (Turner et al. 2021). The consistent normalised citation scores (~1.0) across multiple keywords also suggest that research productivity and impact in this field are balanced, with no single topic dominating scientific attention. This indicates a mature yet dynamic research landscape where clinical, molecular, and ecological dimensions of AMR are being explored simultaneously.

Interestingly, the inclusion of the general keyword *article* implies the presence of diverse publication formats ranging from original research to reviews and meta-analyses, reflecting the methodological heterogeneity of the field. Review papers often play a pivotal role in consolidating fragmented data on AMR, while experimental studies continue to provide insights into novel antimicrobial agents, resistance determinants, and infection control strategies. This diversity of publication types contributes to the high citation volume observed for the top keywords, signalling broad engagement and interdisciplinary collaboration among researchers.

Species-Specific Resistance Mechanisms and Emerging Molecular Determinants

Although *E. faecalis* and *E. faecium* share several resistance mechanisms, their antimicrobial susceptibility profiles and epidemiological characteristics differ. Ampicillin resistance is more frequently encountered among clinical *E. faecium* isolates, in part because of alterations in PBP5, whereas *E. faecalis* isolates are generally more likely to remain susceptible to ampicillin. In healthcare settings, vancomycin-resistant *E. faecium* and the dissemination of hospital-adapted lineages, including CC17-associated lineages, have attracted considerable research attention. Nevertheless, acquired glycopeptide resistance mediated by vanA or vanB can occur in both species.

Resistance research also extends beyond glycopeptides and β-lactams. The transferable determinants optrA, poxtA and cfr are relevant to linezolid resistance, while changes affecting PBP5 and other cell-wall-associated pathways may contribute to reduced β-lactam susceptibility. These mechanisms illustrate the diversity of molecular pathways investigated in enterococci and the importance of considering antimicrobial class, bacterial species and genetic context when interpreting resistance research.

For bibliometric interpretation, however, the presence of these mechanisms in the broader literature should not be equated with their prominence in the present dataset. Their representation must be established through analysis of the eligible publications and their keyword and thematic profiles. Accordingly, species-specific and determinant-specific findings should be reported only where supported by the analysed records.

Integrating Naqli and Aqli Perspectives: An Ethical One Health Framework for Enterococcal Antimicrobial Resistance

The findings of this bibliometric study can be interpreted through complementary Naqli and Aqli perspectives, providing a framework that connects scientific evidence with ethical responsibility. The Aqli perspective is reflected in the systematic analysis of publication trends, citation patterns, research themes and collaboration networks related to antimicrobial resistance (AMR) in *Enterococcus faecalis* and *Enterococcus faecium*. These bibliometric indicators help identify areas of scientific attention, the development of research priorities and patterns of knowledge exchange. However, citation counts and publication networks represent

scholarly activity rather than direct measures of AMR prevalence, clinical outcomes or the effectiveness of antimicrobial stewardship interventions. Their interpretation must therefore remain grounded in the scope and limitations of the available data.

From the Naqli perspective, the principle of *Hifz al-Nafs*, or preservation of life, provides an ethical basis for emphasising the prevention and appropriate management of resistant infections. The clinical significance of enterococcal AMR highlights the importance of responsible antimicrobial prescribing, infection prevention and control, and continued research into resistance mechanisms and effective interventions. In this context, *Hifz al-Nafs* can inform the ethical purpose of AMR research by emphasising the protection of patients and communities. Nevertheless, the identification of a research trend through bibliometric analysis does not, by itself, demonstrate whether these ethical objectives have been achieved in clinical practice.

The principle of *Khilafah*, understood here as stewardship and responsibility, further extends the discussion beyond individual patient care. Antimicrobial effectiveness is a shared resource that requires responsible use, coordinated surveillance and attention to the movement of resistant organisms and resistance determinants across interconnected human, animal and environmental settings. The One Health framework offers a practical approach to this shared responsibility by encouraging collaboration among healthcare professionals, veterinarians, environmental scientists, microbiologists and public health authorities. Applied to enterococcal AMR, this perspective supports integrated research and surveillance that can help identify resistance patterns and inform context-appropriate interventions.

The Naqli–Aqli integration also has implications for international research collaboration and equity. Bibliometric collaboration networks can reveal patterns of cooperation among countries and institutions, but they should not be interpreted as direct measures of fairness or research capacity. Where the findings indicate uneven participation or concentration of research output, these patterns may prompt further consideration of equitable partnerships, shared access to research capacity, transparent data sharing and the recognition of contributions from underrepresented settings. Such measures are relevant to responsible AMR research because resistance is not confined by national borders, while the resources available for surveillance, laboratory investigation and intervention may differ substantially between settings.

Taken together, the Naqli–Aqli perspective positions empirical analysis and ethical reflection as complementary rather than interchangeable approaches. Aqli reasoning supports the systematic examination of evidence and the critical interpretation of research patterns, while Naqli principles provide a normative basis for considering how scientific knowledge should inform responsibility, justice and the protection of life. Through One Health, these perspectives can be connected to a shared agenda for evidence-informed antimicrobial stewardship, interdisciplinary collaboration and equitable responses to enterococcal AMR. This framework offers an ethical interpretation of bibliometric evidence without suggesting that citation or publication metrics alone establish the success of AMR policies or interventions.

CONCLUSION

This bibliometric analysis demonstrates that research on antimicrobial resistance in *Enterococcus faecalis* and *Enterococcus faecium* continues to expand globally, although international collaboration remains fragmented. The increasing adoption of the One Health paradigm reflects the growing recognition that antimicrobial resistance must be addressed through coordinated efforts spanning human, animal, and environmental health. From the Naqli–Aqli perspective, these findings reinforce the Islamic principle that scientific knowledge should be pursued responsibly to preserve life (*Hifz al-Nafs*), protect public health, and promote societal well-being. The integration of revealed knowledge (Naqli) and rational scientific inquiry (Aqli) provides a comprehensive framework for guiding future antimicrobial resistance research, encouraging ethical innovation, stronger global collaboration, and sustainable healthcare solutions that benefit humanity while fulfilling mankind's responsibility as stewards (*khalifah*) of Allah SWT's creation.

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CONFLICT OF INTEREST

The author declares no conflicts of interest related to this study.

ETHICS STATEMENT

This study was conducted in accordance with accepted ethical standards. Informed consent was obtained from all participants, and their confidentiality and anonymity were strictly maintained. Artificial Intelligence tools were used only to assist in data organization and writing support.

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