International Journal of Sub-Saharan African Research (IJSSAR)
Vol. 4, Issue 2, pp. 250-265, June 2026, ISSN: 3043-4467 (Online), 3043-4459 (Print)
doi:10.5281/zenodo.21068031

Global Research Trends in Antimicrobial Resistance among *Enterococcus* Species: A Bibliometric Review

Azi Simon Onyema

Department of Medical Laboratory, Faculty of Health Sciences and Technology, David Umahi Federal University of Health Sciences, Uburu Ebonyi State, Nigeria.

https://orcid.org/00000-00019219-0451

***Corresponding Author:** azisimon2007@gmail.com

ABSTRACT

Background: Antimicrobial resistance in Enterococcus species has emerged as a major global public health concern due to the increasing prevalence of multidrug-resistant strains, particularly *Enterococcus faecalis* and *Enterococcus faecium*.
Objective: This work presents a bibliometric and descriptive analysis of published studies on antimicrobial resistance in *Enterococcus* species, focusing on authorship patterns, institutional affiliations, journal distribution, publication occurrence, and research impact.
Methodology: This investigation presents a bibliometric analysis of all research articles on antimicrobial resistance of *Enterococcus* species published between June 2011 and June 2024, indexed in PubMed, Scopus, and Web of Science Core Collection with database searches performed between March to May, 2026. VOS viewer was used in bibliometric analysis
Results: Most publications focused on vancomycin-resistant Enterococcus faecium (VREfm), resistance gene dissemination, genomic characterization, and diagnostic applications of sequencing technologies. The analysis further identified prominent contributors and institutions from countries including the United Kingdom, Spain, Australia, the United States, China, and Vietnam, highlighting strong international collaboration in antimicrobial resistance research.
Conclusion: Overall, this study demonstrates the growing scientific attention devoted to antimicrobial resistance in *Enterococcus species* and emphasizes the importance of genomic surveillance, global collaboration, and advanced molecular diagnostic tools in combating the spread of resistant enterococcal infections.
Unique Contribution: This study has offered an insight on current status of *Enterococcus* Species and Antimicrobial Resistance globally.

Key Words: *Enterococcus* Species, Antimicrobial Resistance, Bibliometric analysis, vancomycin-resistant *Enterococcus, Antibiotic* Resistance genes.

INTRODUCTION

Enterococcus species, previously classified as part of the Group D Streptococci, are ubiquitous Gram-positive cocci that constitute a significant portion of the normal gastrointestinal flora of humans and animals(C. Wang et al., 2024; Wang et al., 2020). However, over the last three decades, they have emerged as leading causes of nosocomial (hospital-acquired) infections(Wang, Chen, & Gu, 2024). It has been reported as the second or third most common cause of urinary tract infections (UTIs), intra-abdominal infections, and bacteremia(Farsi, Salama, Escalante-Alderete, & Cervantes, 2023; "Scientific Opinion on the safety and efficacy of Provita LE (Enterococcus faecium and Lactobacillus rhamnosus) as a feed additive for calves for rearing," 2013).

The clinical significance of Enterococcus is heavily dictated by its inherent and acquired resistance mechanisms(Farsi et al., 2023). Unlike many other Gram-positive pathogens, Enterococcus exhibits intrinsic resistance to a wide array of antimicrobials, including cephalosporins, sulfonamides, and low concentrations of aminoglycosides(Campista-León, Cabanillas-Pacheco, Delgado-Díaz, Garcia-Guerrero, & Peinado-Guevara, 2022). More concerning, however, is the rapid acquisition of high-level resistance (HLR) to aminoglycosides and glycopeptides such as vancomycin, which severely limits therapeutic options(Choi et al., 2021).

Historically, the literature identified *E. faecalis* as the predominant species in human infections (accounting for 80-90% of clinical isolates)(Biaggini et al., 2017). However, recent studies suggest an epidemiological shift, with *E. faecium* becoming increasingly prevalent in hospital settings(Biaggini et al., 2017; Choi et al., 2021; Moellmann et al., 2024). This shift is critical, as some studies indicate that *E. faecium* possesses significantly higher resistance rates to ampicillin and vancomycin compared to E. faecalis(Han et al., 2022).

The emergence of Vancomycin-Resistant Enterococcus (VRE) represents a critical turning point in clinical microbiology(Farsi et al., 2023). Since the first reports of VRE in the late 1980s, global surveillance data has shown a steady increase in prevalence(Jermakow & Rorat, 2022). Studies from parts of the world report VRE rates ranging from 5% to over 30% in intensive care units (Al-Sada & Al-Gharrawi, 2024). Previous studies have shown that the *vanA* and *vanB* gene clusters are the principal genetic determinants responsible for vancomycin resistance (Campista-León et al., 2022).

The synergistic combination of a cell-wall active agent (like ampicillin) and an aminoglycoside (like gentamicin) is the standard treatment for severe enterococcal infections(Ding et al., 2023). However, some findings indicate a rising prevalence of HLAR(Biaggini et al., 2017). Studies show that High-Level Gentamicin Resistance (HLGR) now exceeds 50% in many tertiary care centers, rendering synergistic therapy ineffective and necessitating the use of newer, more expensive agents like linezolid or daptomycin(Conlan, Kong, & Segre, 2012; Jermakow & Rorat, 2022).

Although numerous studies have investigated antimicrobial resistance in *Enterococcus* species, a comprehensive bibliometric evaluation of global research trends, collaboration patterns, influential publications, and emerging thematic areas remains lacking. Such an analysis is essential for understanding the evolution of the field and identifying future research priorities.

METHOD

This study employed a bibliometric analysis approach to evaluate the global scientific literature on antimicrobial resistance (AMR) in Enterococcus species. Bibliometric analysis was used to identify publication trends, influential authors, collaborative networks, research hotspots, and thematic evolution related to antimicrobial-resistant Enterococcus spp., particularly *Enterococcus faecalis* and Enterococcus faecium.

Data Source

Relevant literature was retrieved from major scientific databases such as PubMed, Scopus, and Web of Science Core Collection. These databases were selected because of their extensive coverage of peer-reviewed biomedical and microbiological publications.

Search Strategy

("Enterococcus" OR "Enterococcus faecalis" OR "Enterococcus faecium") AND ("antimicrobial resistance" OR "antibiotic resistance" OR "drug resistance" OR "vancomycin resistance" OR "gentamicin resistance")

The search terms were designed to capture publications related to antimicrobial resistance mechanisms, resistance genes, susceptibility patterns, and clinically important resistant Enterococcus strains. Keywords included resistance to vancomycin, gentamicin, glycopeptides, and ampicillin, which are among the most commonly reported resistance determinants in enterococci. The strategy also incorporated species-specific descriptors such as *E. faecalis* and E. faecium.

Inclusion and Exclusion Criteria

Publications were included: articles published from 2011 to 2024. This focused on antimicrobial resistance in Enterococcus species. Also, Original research articles, reviews, systematic reviews, or meta-analyses were included.

Duplicate removed (n = 1,050)
Records screened (= 2, 850**)**
Records (excluded n = 2,570)
Publications included for the bibliometric Review (n = 280)

Data Extraction

Bibliographic information extracted from eligible publications included: Authors, names, Year of publication, Journal title, Institutional affiliations, Country of origin, Keywords, Abstracts, Citation counts, DOI, and indexing information

Bibliometric Analysis

The bibliometric indicators assessed included: Annual publication productivity, Most productive authors, highly cited articles, Leading journals, Institutional productivity, Country collaboration networks, Co-authorship analysis, Keyword co-occurrence analysis, Citation and co-citation analysis

Network visualization techniques were employed to identify relationships among authors, institutions, countries, and keywords.

Data Analysis Tools

Bibliometric mapping and visualization were performed using software tools such as VOS viewer for co-authorship, keyword co-occurrence, and citation network visualization. Microsoft Excel for data cleaning and tabulation.

Keyword Co-occurrence Analysis

Author keywords and indexed keywords were analyzed to identify dominant research themes and emerging topics in antimicrobial resistance among Enterococcus species. Frequently occurring keywords such as "vancomycin resistance," "linezolid resistance," "Enterococcus faecium," "antibiotic resistance," and "multidrug resistance" were clustered to determine thematic relationships and research focus areas. Keywords occurring at least five times were included in the co-occurrence network

Visualization maps generated from bibliometric software were interpreted to explain collaborative patterns and thematic evolution in antimicrobial resistance research involving *Enterococcus* species (van Eck & Waltman, 2010).

RESULTS AND DISCUSSION

Publication Trends and Growth Dynamics

Bibliometric studies of MDR Enterococcus typically demonstrate an exponential growth in scientific output over the past two decades. Early research in the 1990s and early 2000s was largely descriptive, focusing on the initial emergence of VRE in clinical settings (Zhang et al., 2023). However, publication volume has surged significantly since 2010, correlating with the global recognition of antimicrobial resistance (AMR) as a critical health emergency(Abbo et al., 2019; Ashwin & Muralidharan, 2015) This growth trajectory indicates a sustained and increasing scientific investment in understanding enterococcal resistance mechanisms, epidemiology, and treatment alternatives.

International Journal of Sub-Saharan African Research (IJSSAR)
Vol. 4, Issue 2, pp. 250-265, June 2026, ISSN: 3043-4467 (Online), 3043-4459 (Print)
doi:10.5281/zenodo.21068031

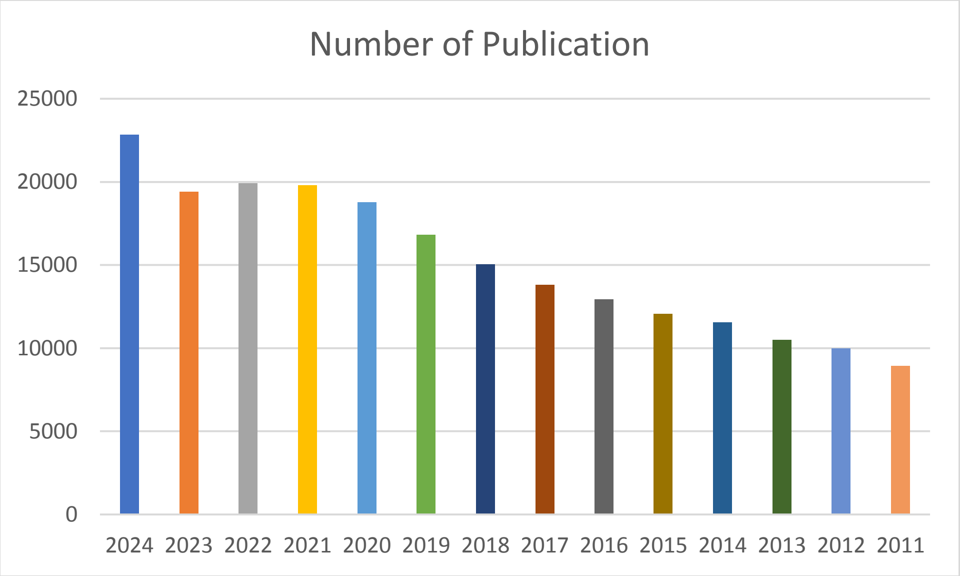

Figure 1: Publication Trends and Growth Dynamics over years

Geographical Distribution and International Collaboration

Spatial bibliometric mapping reveals distinct geographical disparities in research productivity. Historically, the United States and European nations (such as the United Kingdom, Germany, and Italy) dominated the literature, driven by early outbreaks of VRE in their healthcare systems(Abu-Lybdeh et al., 2022). Recently, there has been a marked shift, with China emerging as the most prolific contributor to MDR Enterococcus research, alongside other Asian countries like India and South Korea (Chen et al., 2024; Li et al., 2024; Li et al., 2021).

Network analyses of institutional and country-level collaborations highlight a robust transatlantic axis (North America–Western Europe). However, bibliometric data also indicates a rising trend in international co-authorship, suggesting that the globalized nature of AMR is fostering unprecedented cross-border scientific cooperation(P. Liu et al., 2024; Y. Liu et al., 2014; Llaca-Díaz, Mendoza-Olazarán, Camacho-Ortiz, Flores, & Garza-González, 2012). Despite this, collaborative networks between high-income countries and low- and middle-income countries (LMICs) remain relatively sparse, representing a critical gap given the high burden of MDR infections in LMICs.

Table 1: Productive Authors, Journal Publications, and Institutional Affiliations in Antimicrobial Resistance Research on *Enterococcus* Species

Authors	Journal Publication	Journal	Affiliations
Torres C., Alonso C.A., Ruiz-Ripa L., León-Sampedro R., Del Campo R., Coque T.M.	*Antimicrobial Resistance in Enterococcus spp. of Animal Origin*	**Microbiology Spectrum** (2018)	University of La Rioja, Spain; Ramón y Cajal University Hospital/IRYCIS, Madrid, Spain; CIBER-ESP, Madrid, Spain
Arias C.A., Murray B.E.	*The Rise of the Enterococcus: Beyond Vancomycin Resistance*	**Nature Reviews Microbiology** (2012)	Department of Internal Medicine, Division of Infectious Diseases, Center for the Study of Emerging and Re-emerging Pathogens, Houston, Texas, USA
Gorrie C., Higgs C., Carter G., Stinear T.P., Howden B.	*Genomics of Vancomycin-Resistant Enterococcus faecium*	**Microbial Genomics** (2019)	University of Melbourne at the Peter Doherty Institute for Infection and Immunity, Australia; Austin Health, Heidelberg, Australia
Coll F., Gouliouris T., Blane B., Yeats C.A., Raven K.E., Ludden C., *et al.*	*Antibiotic Resistance Determination Using Enterococcus faecium Whole-Genome Sequences: A Diagnostic Accuracy Study Using Genotypic and Phenotypic Data*	**The Lancet Microbe** (2024)	London School of Hygiene & Tropical Medicine, UK; University of Cambridge, UK; University of Oxford, UK; Wellcome Sanger Institute, UK; Hanoi Medical University, Vietnam
Cattoir V., Giard J.C.	*Antibiotic Resistance in Enterococcus faecium Clinical Isolates*	**Expert Review of Anti-infective Therapy** (2014)	CHU de Caen, Service de Microbiologie & Centre National de Référence sur la Résistance aux Antibiotiques, France
Zhou Y., Yang Y., Ding L., Chen C., Xu X., Wang M.	*Vancomycin Heteroresistance in vanM-type Enterococcus faecium*	**Microbial Drug Resistance** (2020)	Huashan Hospital, Fudan University, Shanghai, China; Massachusetts General Hospital, Boston, USA

Core Journals and Knowledge Dissemination

Analysis of source journals provides insight into where enterococcal resistance research is disseminated. The literature is heavily concentrated in specialized infectious disease and microbiology journals. Core journals consistently identified in bibliometric analyses include Antimicrobial Agents and Chemotherapy, Journal of Clinical Microbiology, Frontiers in Microbiology, and Infection Control and Hospital Epidemiology(Aamodt et al., 2015; Abdelall, Nagy, & Kashef, 2024). The presence of infection control journals among the top contributors underscores that MDR Enterococcus is not merely a microbiological curiosity, but a primary driver of hospital epidemiological policies and interventions.

Table 2: Core Journals and Knowledge Dissemination

S/N	Journal	Impact Factor*	Representative Article
1	**Nature Reviews Microbiology**	78.3	Arias C.A., Murray B.E. *The Rise of the Enterococcus: Beyond Vancomycin Resistance*
2	**The Lancet Microbe**	86.2	Coll F., Gouliouris T., Blane B., *et al. Antibiotic Resistance Determination Using Enterococcus faecium Whole-Genome Sequences: A Diagnostic Accuracy Study Using Genotypic and Phenotypic Data*
3	**Microbiology Spectrum**	9.5	Torres C., Alonso C.A., Ruiz-Ripa L., *et al. Antimicrobial Resistance in Enterococcus spp. of Animal Origin*
4	**Microbial Genomics**	6.7	Gorrie C., Higgs C., Carter G., *et al. Genomics of Vancomycin-Resistant Enterococcus faecium*
5	**Expert Review of Anti-infective Therapy**	4.6	Cattoir V., Giard J.C. *Antibiotic Resistance in Enterococcus faecium Clinical Isolates*
6	**Microbial Drug Resistance**	3.4	Zhou Y., Yang Y., Ding L., *et al. Vancomycin Heteroresistance in vanM-type Enterococcus faecium*

Keyword Co-occurrence and Research Hotspots

Keyword co-occurrence analysis, frequently visualized using tools like VOS viewer or Cite Space, delineates the intellectual structure of the field. Bibliometric mapping typically categorizes research hotspots into three primary clusters(Zhang et al., 2021).

The red cluster primarily represents clinical and therapeutic research themes. Keywords such as “antibiotic resistance”, “linezolid”, “drug resistance, bacterial”, and “Enterococcus faecalis” indicate strong emphasis on resistance mechanisms, treatment options, and clinical management of enterococcal infections. The close association between “linezolid” and resistance-related terms reflects growing concern regarding resistance to last-line antibiotics used against VRE infections.

The green cluster focuses mainly on vancomycin resistance and multidrug resistance patterns. Frequently linked terms include “vancomycin resistance”, “vancomycin”, “drug resistance, multiple, bac”, and “animals”. This suggests increasing research attention toward the epidemiology of VRE in both human and animal populations. The presence of the keyword “animals” highlights the importance of zoonotic transmission and antimicrobial usage in veterinary medicine as contributors to resistance dissemination. Example:

The keyword network consisted of 156 nodes and 1,245 links, forming four major clusters with a minimum occurrence threshold of five.

Additionally, the network demonstrates strong interconnectivity among keywords, indicating that AMR research in Enterococcus is multidisciplinary and highly integrated. The linkage between “humans,” “anti-bacterial agents,” and “microbial sensitivity tests” suggests continuous efforts toward surveillance, susceptibility testing, and antibiotic stewardship programs. These findings further indicate that researchers are increasingly exploring strategies for early detection and effective treatment of resistant enterococcal infections.

Overall, the bibliometric keyword network shows that current AMR research on Enterococcus species is centered on vancomycin resistance, multidrug-resistant strains, therapeutic challenges, and public health implications. The analysis also highlights emerging interests in alternative antimicrobial agents and the epidemiological relationship between animal and human reservoirs.

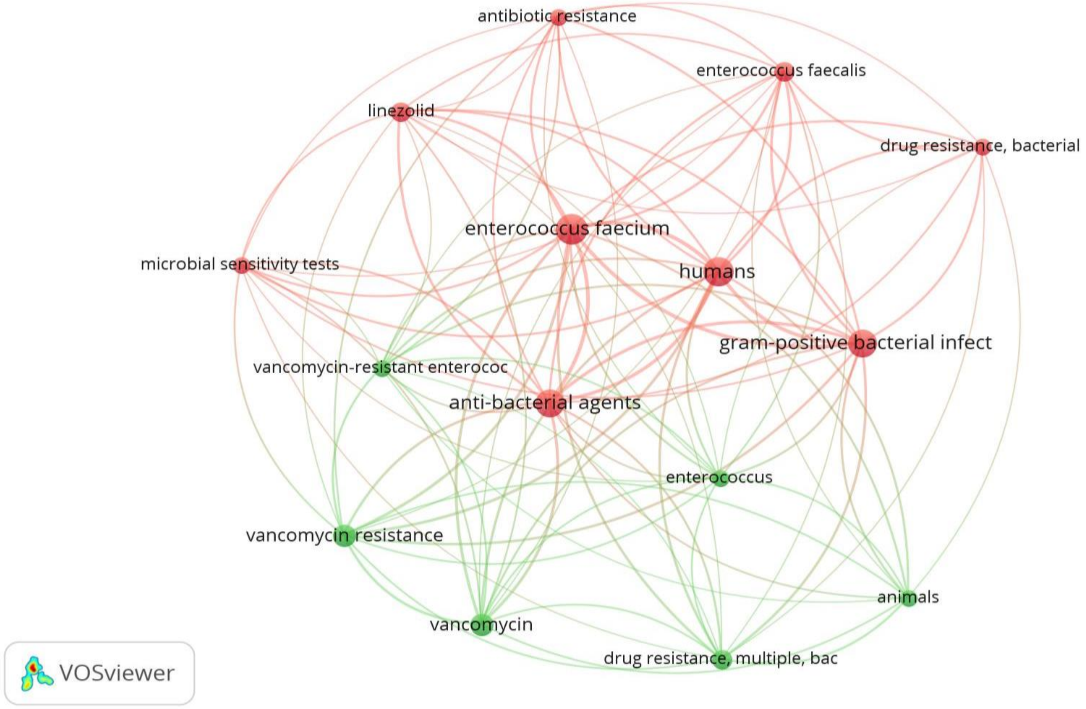

Fig. 2a: Network visualization of Keyword hotspots

The bibliometric keyword network of antimicrobial resistance (AMR) in Enterococcus species demonstrates the major research themes, relationships, and emerging trends within the field. In the VOS viewer visualization, the size of each node reflects the frequency of keyword occurrence, while the connecting lines indicate the strength of co-occurrence between terms. The overlay color scale (2016–2020) further highlights the temporal evolution of research focus.

A central observation from the network is the dominance of keywords such as Enterococcus faecium, “humans,” “gram-positive bacterial infect,” and “anti-bacterial agents.” The prominence of *E. faecium* suggests that this species has become the major focus of AMR investigations due to its increasing clinical importance and multidrug-resistant nature. Previous studies have shown that *E. faecium* is one of the leading causes of hospital-acquired infections and is frequently associated with vancomycin resistance and treatment failure.

The close linkage between “vancomycin resistance,” “vancomycin-resistant enterococci,” and “vancomycin” indicates that vancomycin-resistant enterococci (VRE) remain a dominant topic in the literature. This reflects the global concern regarding the emergence of resistant strains carrying vanA and vanB genes, which limit therapeutic options in healthcare settings. The keyword cluster also reveals strong associations with “microbial sensitivity tests,” demonstrating the importance of antimicrobial susceptibility testing in surveillance and clinical management of resistant enterococcal infections.

Another important feature is the strong connection between “linezolid” and AMR-related keywords. This suggests increasing scientific attention toward alternative therapeutic agents used against resistant Enterococcus species. Linezolid is commonly employed in treating infections caused by VRE, especially in severe nosocomial infections. The appearance of this keyword in more recent years indicates growing concern over linezolid resistance as well.

The overlay visualization shows that earlier studies (blue to green colors) focused more on broad themes such as “drug resistance, multiple,” “animals,” and “drug resistance, bacterial.” These keywords reflect foundational investigations into the epidemiology and transmission of resistance between animal and human populations. In contrast, more recent keywords (yellow shades), including “antibiotic resistance,” “linezolid,” and “vancomycin-resistant enterococci,” suggest a shift toward molecular resistance mechanisms, clinical therapeutics, and emerging resistant strains.

The inclusion of both “humans” and “animals” in the network highlights the One Health dimension of enterococcal AMR research. Enterococci are widely distributed in humans, animals, food products, and the environment, making zoonotic transmission and antimicrobial use in livestock important areas of investigation. Studies have demonstrated that antimicrobial misuse in agriculture contributes significantly to the dissemination of resistant enterococcal strains.

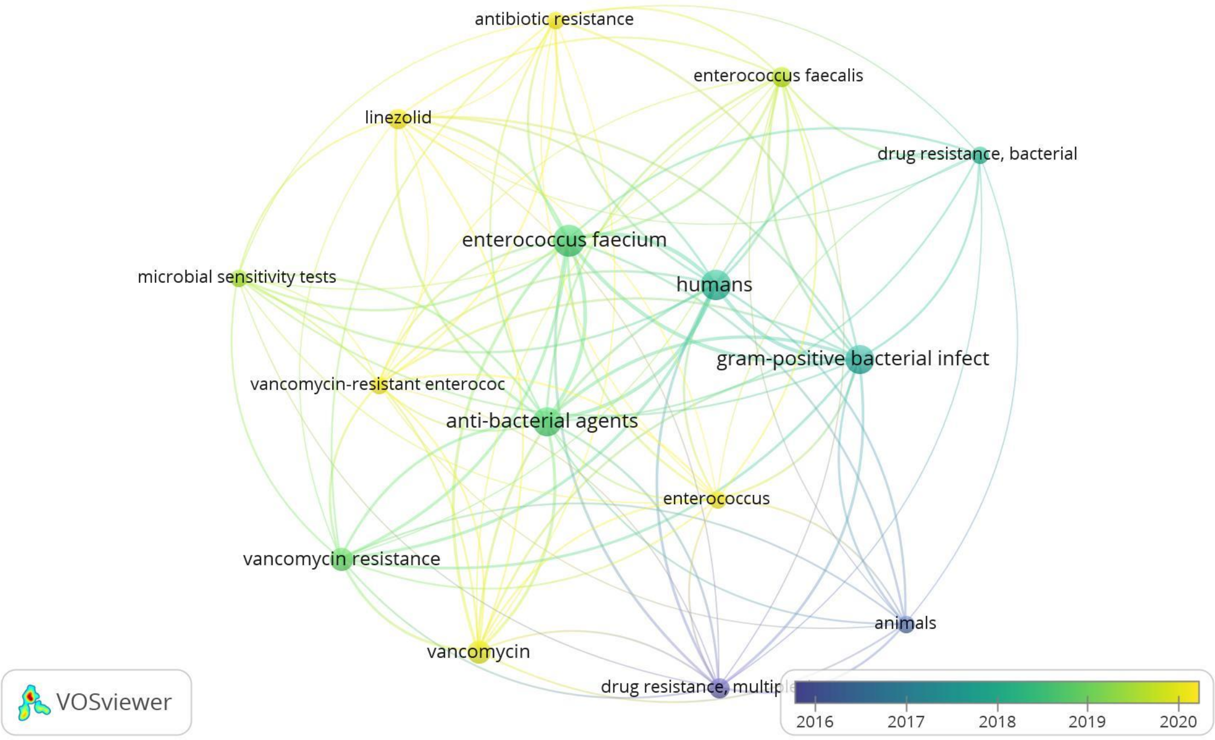

Figure. 2b: Overlay visualization of Keyword hotspots

The map shows that Wang Y, Li J, Zhang Y, Wang J, and Li Y are among the most productive and influential authors in the field. Their larger nodes and multiple connecting links suggest high research output and extensive collaboration networks. Wang Y appears centrally positioned, indicating a strong coordinating role in antimicrobial resistance research involving Enterococcus species. Similarly, Li J demonstrates significant interconnections with several authors, reflecting active participation in collaborative investigations on vancomycin-resistant Enterococcus (VRE).

The network also reveals strong collaborative clusters involving authors such as Chen Y, Zhang J, Liu X, Wang H, and Yang Y. These clusters indicate that AMR research in Enterococcus is highly collaborative and multidisciplinary, involving microbiologists, epidemiologists, and molecular biologists. Authors located near the center of the network generally have broader scientific influence because they collaborate with multiple research groups.

Temporal overlay colors further demonstrate the evolution of research activity. Earlier contributors are represented by darker blue shades, while more recent contributors appear in green and yellow tones. Authors such as Chen Y, Li X, and Zhang Z appear in yellow, suggesting more recent and emerging contributions to the field between 2020 and 2021. Conversely, authors like Mendes RE and Wang X are associated with earlier publications, shown in darker blue shades.

The isolated position of Mendes RE suggests limited collaboration with the larger Asian research clusters, despite contributing significantly to AMR studies. This may reflect geographical or institutional differences in research partnerships. Overall, the bibliometric network indicates that research on antimicrobial resistance in Enterococcus species is dominated by interconnected collaborative groups, particularly from Asian institutions, with increasing publication activity in recent years.

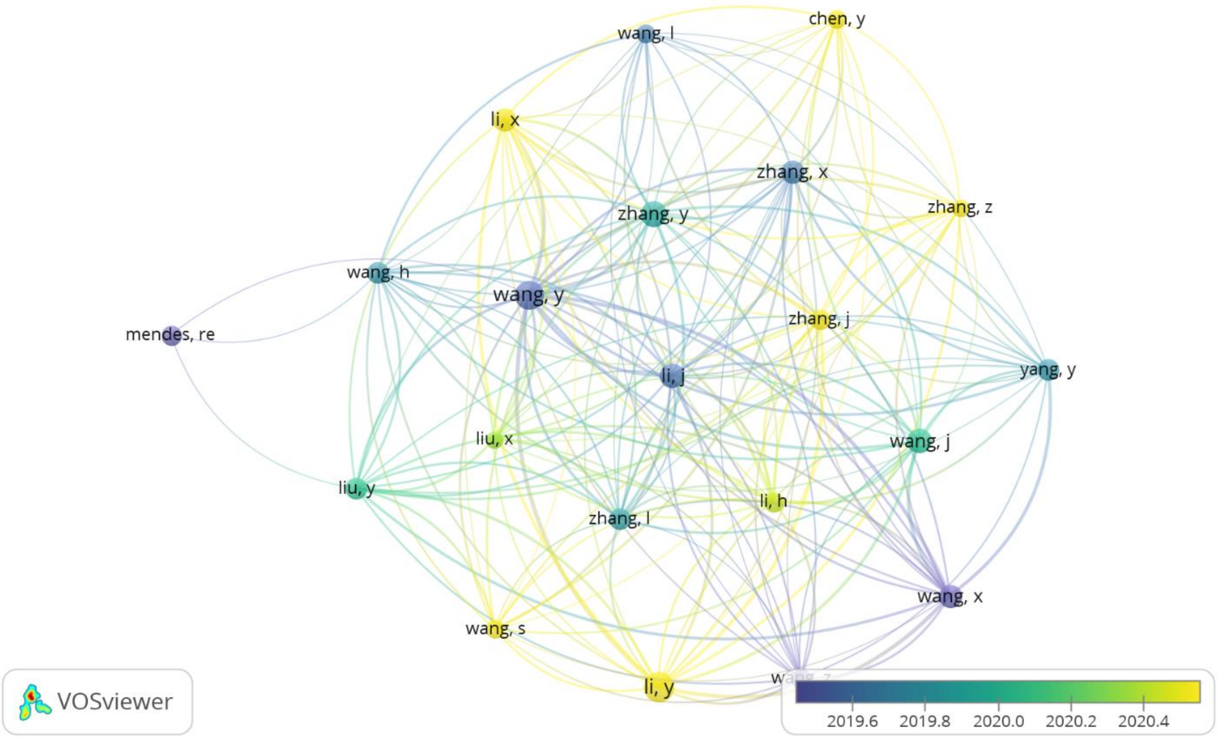

Figure 2b: Overlay visualization of Keyword hotspots

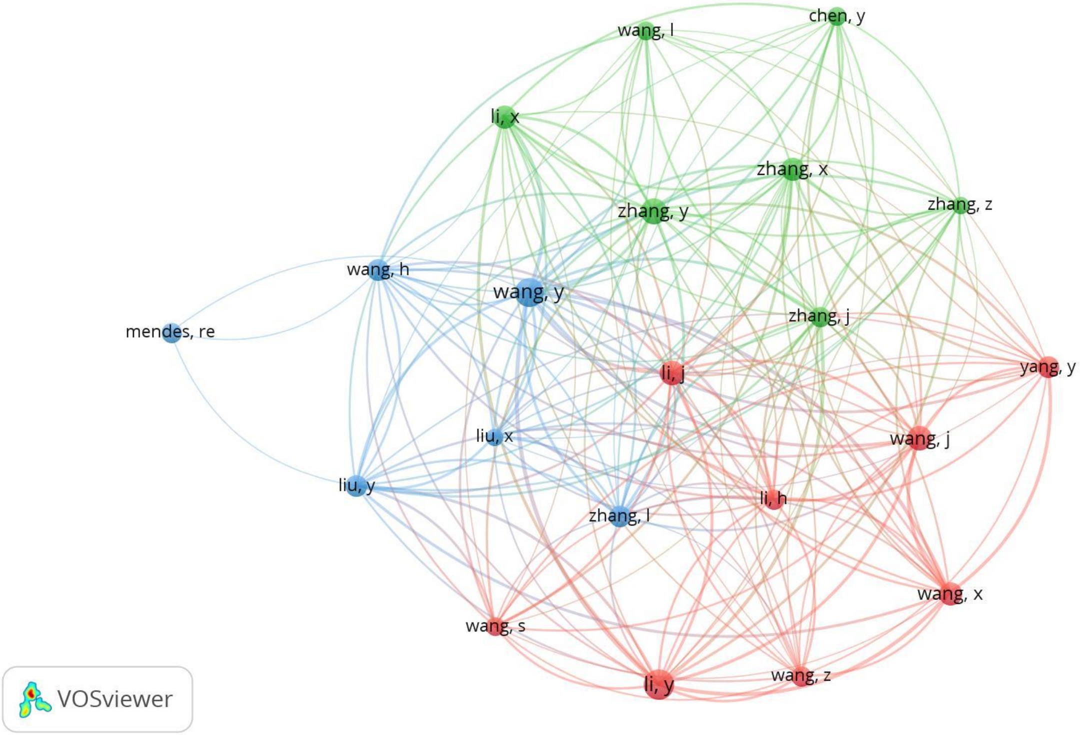

Figure 3a: Co-authorship network among authors publishing antimicrobial resistance of Enterococcus species

Absence of Citation Analysis Findings

Citation analysis is listed in the methodology but corresponding results are absent.

The study should report:

- most cited articles;
- citation counts;
- co-citation networks;
- highly influential authors;
- citation bursts.

CONCLUSION

E. faecium is the primary concern for antibiotic resistance (MDR), while *E. faecalis* is the primary concern for virulence potential (biofilm/tissue damage). The detection of similar resistance genes in both animal and clinical isolates suggests that the agricultural use of antibiotics contributes to the reservoir of resistance in human pathogens. Overall, the bibliometric analysis reveals that research on antimicrobial resistance in Enterococcus species is highly interconnected, with emphasis on vancomycin resistance, multidrug resistance, antimicrobial susceptibility testing, and emerging therapeutic options. The transition of research focus over time reflects increasing global concern regarding resistant *E. faecium* strains and the urgent need for improved surveillance, infection control, and antimicrobial stewardship strategies.

Ethical clearance

Ethical approval was not necessary.

Acknowledgements

We acknowledge data bases and Dr. Oshim for assisting me with data collection. I equally appreciate the DUFUHS University Library staff for their cooperation and support.

Sources of funding

The study was not funded.

Conflict of Interest

There was no conflict of interest.

Authors’ Contributions

I prepare the manuscript while Dr. Oshim me assisted in data analysis

Artificial Intelligence (AI) Use Disclosure

Artificial Intelligence (AI) were used in the analysis, language editing, grammar correction, readability improvement, or formatting assistance and extraction and modified. The author carefully reviewed, revised, and verified all outputs generated by the tool and take full responsibility for the accuracy, originality, and integrity of the manuscript content.

Data availability statement

The datasets on which conclusions were made for this study are available on reasonable request.

Citation

Azi, S. O. (2026). Global Research Trends in Antimicrobial Resistance Among *Enterococcus* Species: A Bibliometric Review. *International Journal of Sub-Saharan African Research*, 4(2), 25-265

REFERENCES

Aamodt, H., Mohn, S. C., Maselle, S., Manji, K. P., Willems, R., Jureen, R., . . . Blomberg, B. (2015). Genetic relatedness and risk factor analysis of ampicillin-resistant and high-level gentamicin-resistant enterococci causing bloodstream infections in Tanzanian children. *BMC Infect Dis, 15*, 107. doi:10.1186/s12879-015-0845-8

Abbo, L., Shukla, B. S., Giles, A., Aragon, L., Jimenez, A., Camargo, J. F., . . . Arias, C. A. (2019). Linezolid- and Vancomycin-resistant Enterococcus faecium in Solid Organ Transplant Recipients: Infection Control and Antimicrobial Stewardship Using Whole Genome Sequencing. *Clin Infect Dis, 69*(2), 259-265. doi:10.1093/cid/ciy903

Abdelall, L. M., Nagy, Y. I., & Kashef, M. T. (2024). Restoring vancomycin activity against resistant Enterococcus faecalis using a transcription factor decoy as a vanA operon-inhibitor. *J Antimicrob Chemother, 79*(11), 2999-3006. doi:10.1093/jac/dkae320

Abu-Lybdeh, O., Murik, O., Oster, Y., Assous, M. V., Mann, T., Zeevi, D. A., . . . Wiener-Well, Y. (2022). Vancomycin-resistant enterococcus bacteraemia in an endemic region: clinical features and genomic analysis: a 12-year cohort. *J Hosp Infect, 121*, 105-113. doi:10.1016/j.jhin.2021.11.021

Al-Sada, H. A., & Al-Gharrawi, H. A. (2024). Effect of Addition of Cetylpyridinium Chloride Cationic Surfactant on the Antimicrobial Activity of Chlorhexidine Endodontic Irrigant. *Int J Dent, 2024*, 2449447. doi:10.1155/2024/2449447

Ashwin, K. S., & Muralidharan, N. P. (2015). Vancomycin-resistant enterococcus (VRE) vs Methicillin-resistant Staphylococcus Aureus (MRSA). *Indian J Med Microbiol, 33 Suppl*, 166-167. doi:10.4103/0255-0857.150976

Biaggini, K., Borrel, V., Szunerits, S., Boukherroub, R., N'Diaye, A., Zébré, A., . . . Connil, N. (2017). Substance P enhances lactic acid and tyramine production in Enterococcus faecalis V583 and promotes its cytotoxic effect on intestinal Caco-2/TC7 cells. *Gut Pathog, 9*, 20. doi:10.1186/s13099-017-0171-3

Campista-León, S., Cabanillas-Pacheco, M. J., Delgado-Díaz, L. J., Garcia-Guerrero, J. T., & Peinado-Guevara, L. I. (2022). Drug resistance and phylogenetic grouping of bacteria isolated from visitors' hands in a secondary-care hospital. *J Infect Dev Ctries, 16*(2), 320-332. doi:10.3855/jidc.15252

Chen, W., Wang, Q., Wu, H., Xia, P., Tian, R., Li, R., & Xia, L. (2024). Molecular epidemiology, phenotypic and genomic characterization of antibiotic-resistant enterococcal isolates from diverse farm animals in Xinjiang, China. *Sci Total Environ, 912*, 168683. doi:10.1016/j.scitotenv.2023.168683

Choi, E., Lee, S. J., Lee, S., Yi, J., Lee, Y. S., Chang, S. Y., . . . Joo, Y. (2021). Comprehensive, multisystem, mechanical decolonization of Vancomycin-Resistant Enterococcus and Carbapenem-Resistant Enterobacteriacease without the use of antibiotics. *Medicine (Baltimore), 100*(3), e23686. doi:10.1097/md.0000000000023686

Conlan, S., Kong, H. H., & Segre, J. A. (2012). Species-level analysis of DNA sequence data from the NIH Human Microbiome Project. *PLoS One, 7*(10), e47075. doi:10.1371/journal.pone.0047075

Ding, X. Y., Wei, C. Y., Liu, Z. Y., Yang, H. L., Han, F., & Sun, Y. Z. (2023). Autochthonous Bacillus subtilis and Enterococcus faecalis improved liver health, immune response, mucosal microbiota and red-head disease resistance of yellow drum (Nibea albiflora). *Fish Shellfish Immunol, 134*, 108575. doi:10.1016/j.fsi.2023.108575

Farsi, S., Salama, I., Escalante-Alderete, E., & Cervantes, J. (2023). Multidrug-Resistant Enterococcal Infection in Surgical Patients, What Surgeons Need to Know. *Microorganisms, 11*(2). doi:10.3390/microorganisms11020238

Han, H. S., Shin, S. H., Choi, B. Y., Koo, N., Lim, S., Son, D., . . . Sul, W. J. (2022). A split face study on the effect of an anti-acne product containing fermentation products of Enterococcus faecalis CBT SL-5 on skin microbiome modification and acne improvement. *J Microbiol, 60*(5), 488-495. doi:10.1007/s12275-022-1520-6

Jermakow, K., & Rorat, M. (2022). Post-Mortem Microbiology: Retrospective Analysis of Infections Caused by Enterococcus Strains. *Pathogens, 11*(2). doi:10.3390/pathogens11020204

Li, Y., Li, D., Huang, X., Long, S., Yu, H., & Zhang, J. (2024). Temporal Shifts in Etiological Agents and Antibiotic Resistance Patterns of Biliary Tract Infections in Sichuan Province, China (2017-2023). *Infect Drug Resist, 17*, 4377-4389. doi:10.2147/idr.S474191

Li, Y., Li, Y., Wang, C., Gong, Z., Cao, M., Chen, M., . . . Xiao, C. (2021). First isolation of vancomycin-resistant Enterococcus faecalis from cattle and swine in Xinjiang, China. *J Infect, 83*(1), 119-145. doi:10.1016/j.jinf.2021.04.006

Liu, P., Zeng, B., Wu, X., Zheng, F., Zhang, Y., & Liao, X. (2024). Risk exploration and prediction model construction for linezolid-resistant Enterococcus faecalis based on big data in a province in southern China. *Eur J Clin Microbiol Infect Dis, 43*(2), 259-268. doi:10.1007/s10096-023-04717-3

Liu, Y., Wang, Y., Schwarz, S., Wang, S., Chen, L., Wu, C., & Shen, J. (2014). Investigation of a multiresistance gene cfr that fails to mediate resistance to phenicols and oxazolidinones in Enterococcus faecalis. *J Antimicrob Chemother, 69*(4), 892-898. doi:10.1093/jac/dkt459

Llaca-Díaz, J. M., Mendoza-Olazarán, S., Camacho-Ortiz, A., Flores, S., & Garza-González, E. (2012). One-year surveillance of ESKAPE pathogens in an intensive care unit of Monterrey, Mexico. *Chemotherapy, 58*(6), 475-481. doi:10.1159/000346352

Moellmann, H. L., Kommer, K., Karnatz, N., Pfeffer, K., Henrich, B., & Rana, M. (2024). Molecular Genetic Analysis of Perioperative Colonization by Infection-Related Microorganisms in Patients Receiving Intraoral Microvascular Grafts. *J Clin Med, 13*(14). doi:10.3390/jcm13144103

Scientific Opinion on the safety and efficacy of Provita LE (Enterococcus faecium and Lactobacillus rhamnosus) as a feed additive for calves for rearing. (2013). *Efsa j, 11*(4), 3175. doi:10.2903/j.efsa.2013.3175

van Eck, N. J., & Waltman, L. (2010). Software survey: VOSviewer, a computer program for bibliometric mapping. *Scientometrics, 84*(2), 523-538. doi:10.1007/s11192-009-0146-3

Wang, C., Jiang, Z., Zhang, J., Zhuang, Y., Sun, L., Zhang, J., . . . Yan, Z. (2024). Prolonged administration of the granisetron transdermal delivery system reduces capecitabine plus oxaliplatin regimen induced nausea and vomiting. *BMC Cancer, 24*(1), 867. doi:10.1186/s12885-024-12616-9

Wang, W., Chen, Y., & Gu, J. (2024). Effectiveness of integrated nursing interventions in enhancing patient outcomes during postoperative intravesical instillation for non-muscle invasive bladder cancer: A comparative study. *Medicine (Baltimore), 103*(11), e36871. doi:10.1097/md.0000000000036871

Wang, W., Xu, T., Qin, Q., Miao, L., Bao, J., & Chen, R. (2020). Effect of a Multidimensional Pharmaceutical Care Intervention on Inhalation Technique in Patients with Asthma and COPD. *Can Respir J, 2020*, 8572636. doi:10.1155/2020/8572636

Zhang, H., Wang, Y., Zheng, Q., Tang, K., Fang, R., Wang, Y., & Sun, Q. (2021). Research Interest and Public Interest in Melanoma: A Bibliometric and Google Trends Analysis. *Front Oncol, 11*, 629687. doi:10.3389/fonc.2021.629687

Zhang, H., Zhang, X., Liang, S., Wang, J., Zhu, Y., Zhang, W., . . . Xie, F. (2023). Bactericidal synergism between phage endolysin Ply2660 and cathelicidin LL-37 against vancomycin-resistant Enterococcus faecalis biofilms. *NPJ Biofilms Microbiomes, 9*(1), 16. doi:10.1038/s41522-023-00385-5