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Multidrug-Resistant Bacteria and Antibiotics in Hospital Effluents: A Bibliometric Analysis of the Hidden Threat to Public Health

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This study presents a bibliometric analysis of the scientific literature on multidrug-resistant (MDR) bacteria and antibiotics in hospital effluents indexed in Scopus between 2010 and 2024, identifying key trends and applications. A total of 199 documents were processed using Boolean operators and tools such as VOSviewer and Biblioshiny-based RStudio. China, India, and Japan led publication output, followed by the United States and Brazil; in Europe, the United Kingdom and Germany stood out for their high levels of international collaboration. Original research articles accounted for 86% of the publications, while reviews made up 11%. Chen L., Diwan V., and Tamhankar AJ. emerged as the most prolific authors. The co-authorship map revealed five thematic clusters focused on genetic modeling, metagenomic characterization, chemical monitoring, bioremediation, and molecular mechanisms. Dominant methodologies included isolation on selective media, minimum inhibitory concentration assays, HPLC-DAD, LC-MS/MS, quantitative PCR, and shotgun metagenomics. Identified gaps include the lack of standardized protocols, limited coverage of Latin America and Africa, and insufficient integration of chemical and genomic data for predictive modeling. Future directions point to CRISPR-based biosensors, digital twins of treatment plants, artificial intelligence applications, and advanced purification technologies to mitigate the "hidden threat" posed by these effluents.

Keywords: multidrug-resistant bacteria, hospital wastewater, antibiotic resistance genes, wastewater-based epidemiology, advanced treatment technologies.

Introduction

Hospital wastewater (HWW) management faces an invisible challenge (Amin et al., 2025; Islam et al., 2021). Every drop of HWW released carries residues of antibiotics and other pharmaceuticals that the human body has not fully metabolized, along with millions of bacteria that have adapted to thrive in this drug-laden environment (Khan et al., 2021; Zhang et al., 2020a). Research indicates that, within treatment tanks, microorganisms freely exchange DNA fragments, plasmids, and integrons encoding efflux pumps, degradative enzymes, and protective mutations in a wide array of species. Consequently, hospitals inadvertently become breeding grounds for "superbugs" resistant to last-generation drugs, which can then enter and contaminate rivers and soils (Rolbiecki et al., 2024; Mutuku et al., 2022). Conventional wastewater treatment plants were never designed to retain bioactive compounds at nanomolar concentrations or to suppress the proliferation of multidrug-resistant (MDR) bacteria. Although isolated studies have quantified specific antibiotics or identified resistant strains in various settings, a holistic assessment is still missing (Brauer, 2022; Nadeem et al., 2020). Without standardized sampling protocols and longitudinal monitoring, regulators lack the data needed to develop effective policies, prioritize treatment technologies, and implement evidence-based antimicrobial-use strategies.

Since the first reports that hospital effluents represent a source of emerging contaminants, it has been clear that two intertwined risks exist: unmetabolized antibiotics persisting at detectable levels in wastewater, and bacterial communities in this milieu acquiring and sharing resistance genes via plasmids, integrons, and biofilms. Manage and Liyanage (2019) first described the environmental induction of antibacterial resistance by pharmaceutical residues, while Rizz et al. (2013) and Rodríguez-Mozaz et al. (2015) identified urban and hospital wastewater treatment plants as critical hotspots for the dissemination of MDR bacteria and antibiotic resistance genes (ARGs). Over the past decade, analytical methodologies have advanced from chemical-analytical techniques such as HPLC and LC-MS for antibiotic quantification to metagenomic approaches that unveil the full genetic arsenal of microbial communities in effluents. Ng et al. (2020) showed how sub-inhibitory antibiotic residues exert selective pressure favoring efflux pumps and deactivating enzymes, and Ory et al. (2016) documented the persistence of ciprofloxacin within hospital biofilms. More recent work by Evoung Chandja et al. (2024) and Mehanni et al. (2023) confirms that MDR dissemination extends beyond treatment plants, solidifying it as a global public-health threat.

At this crossroads, bibliometric analysis emerges as an invaluable tool for uncovering who, where, and how this threat to public and environmental health is being studied. By mapping collaboration networks, identifying thematic gaps, and pinpointing the methodologies employed, we can guide scientific efforts toward developing treatment systems capable of removing residual antibiotics, implementing epidemiological surveillance at hospital wastewater-treatment-plant effluent outlets, and proposing guidelines to moderate clinical antimicrobial use (Yu et al., 2023; Xiao et al., 2023). Only by doing so can we unmask and mitigate the hidden danger in these effluents and safeguard public health before superbugs become an insurmountable crisis.

Research on multidrug-resistant bacteria and antibiotics in hospital effluents is essential because it sheds light on a silent vector of contamination and resistance that, by escaping conventional regulatory and scientific scrutiny, undermines both drug efficacy and the health of exposed communities (Sun et al., 2022; Lu et al., 2020). Through this bibliometric analysis, we aim to fill knowledge gaps regarding the geographic distribution of studies, author networks, and prevailing methodologies, as well as underexplored thematic areas. By mapping who is researching what, where, and with what tools, we can prioritize empirical research, design standardized sampling protocols, and strengthen decision-making for the monitoring and treatment of hospital effluents, thus closing the gaps that currently hinder a coordinated response to this hidden threat (Sweileh and Moh'd Mansour, 2020; Wang et al., 2025).

Despite the growing volume of studies on multidrug-resistant bacteria in hospital effluents, a comprehensive synthesis that critically examines the field's evolution, key actors, and methodological directions remains lacking. This study addresses this gap by presenting the first exhaustive bibliometric analysis spanning the period 2010–2024, employing advanced scientific mapping tools such as VOSviewer and R-Studio to unravel collaboration networks, emerging thematic clusters, and technological trajectories. By systematically identifying geographical disparities, such as the underrepresentation of sub-Saharan Africa and Latin America, and highlighting the shift toward predictive approaches like artificial intelligence and CRISPR-based biosensors, this analysis not only maps the existing scientific landscape but also provides an empirical framework for prioritizing future research and evidence-based mitigation strategies.

The general objective of this research is to carry out a bibliometric analysis of scientific output on multidrug-resistant bacteria and antibiotics in hospital effluents, mapping trends, key actors, and knowledge gaps to inform the development of monitoring strategies, treatment technologies, and public health policies. The following specific objectives are proposed: i) To quantify the temporal and geographical evolution of publications in the field; ii) To identify the most influential collaboration networks among authors, institutions, and countries; iii) To characterize the predominant methodological approaches and analytical techniques; iv) To detect little-explored thematic and methodological areas; and v) To highlight research gaps and emerging trends to guide future investigations.

Methods

Scopus was chosen for its reputation as a comprehensive, peer-reviewed online database that indexes a vast number of publications from the international scientific community. Inclusion criteria restricted the analysis to English-language articles published between 2010 and 2024. This period was chosen because a preliminary search indicated that relevant scientific publications on this topic remained scarce prior to 2010. The bibliometric search was structured with Boolean operators ("OR" and "AND") to maximize retrieval of relevant studies (Donthu et al., 2021; Passas, 2024). *Table 1* shows the exact query used: (TITLE-ABS-KEY(("multidrug-resistant" OR "MDR" OR "antibiotic-resistant" OR "drug-resistant")) AND TITLE-ABS-KEY(("bacteria" OR "microorganism" OR "pathogen" OR "germ")) AND TITLE-ABS-KEY(("antibiotics" OR "antimicrobials" OR "medications" OR "drugs")) AND TITLE-ABS-KEY(("hospital wastewater" OR "hospital effluents"))) AND PUBYEAR > 2009 AND PUBYEAR < 2025 AND (LIMIT-TO(OA, "all")) AND (LIMIT-TO(LANGUAGE, "English"))

The search was conducted in June 2025 via Scopus, with fields limited to article title, abstract, and keywords. Retrieved records were exported to Microsoft Excel, VOSviewer, and analyses conducted through VOSviewer and Biblioshiny-based RStudio (VOSviewer, 2023; Aria and Cuccurullo, 2017). These tools enabled the creation of complex visualizations such as network graphs, overlay maps, and density maps, wich facilitate the interpretation of this information (Ahmad Bhat et al., 2023; Ab Rashid, 2023).

Results and Discussion

The results of this bibliometric study provide a comprehensive overview of the evolution, key contributors, and methodologies employed in research on multidrug-resistant bacteria and antibiotics in hospital effluents between 2010 and 2024. The analysis reveals sustained growth in scientific output, with Asia leading

Table 1. *Scientific literature search process*

Search criteria in scientific literature	
Terms, and search equation	(TITLE-ABS-KEY (("multidrug-resistant" OR "MDR" OR "antibiotic-resistant" OR "drug-resistant")) AND TITLE-ABS-KEY (("bacteria" OR "microorganism" OR "pathogen" OR "germ")) AND TITLE-ABS-KEY (("antibiotics" OR "antimicrobials" OR "medications" OR "drugs")) AND TITLE-ABS-KEY (("hospital wastewater" OR "hospital effluents"))) AND PUBYEAR > 2009 AND PUBYEAR < 2025 AND (LIMIT-TO (OA , "all")) AND (LIMIT-TO (LANGUAGE , "English"))
Database	Scopus
Period	2010–2024
Language	English
Total published documents	199

in publication volume, while European countries stand out for their high level of international collaboration. Influential authors were identified, along with collaboration networks organized into thematic clusters, and prevailing analytical techniques that have progressed from traditional methods to advanced molecular approaches.

Keyword mapping and thematic trend analysis highlight a clear shift from descriptive studies on contamination toward research integrating risk assessment, advanced treatment strategies, and epidemiological surveillance. However, significant gaps remain, including the lack of standardized methodologies, limited representation of regions such as Latin America and Africa, and weak coordination between scientific research and public health policy.

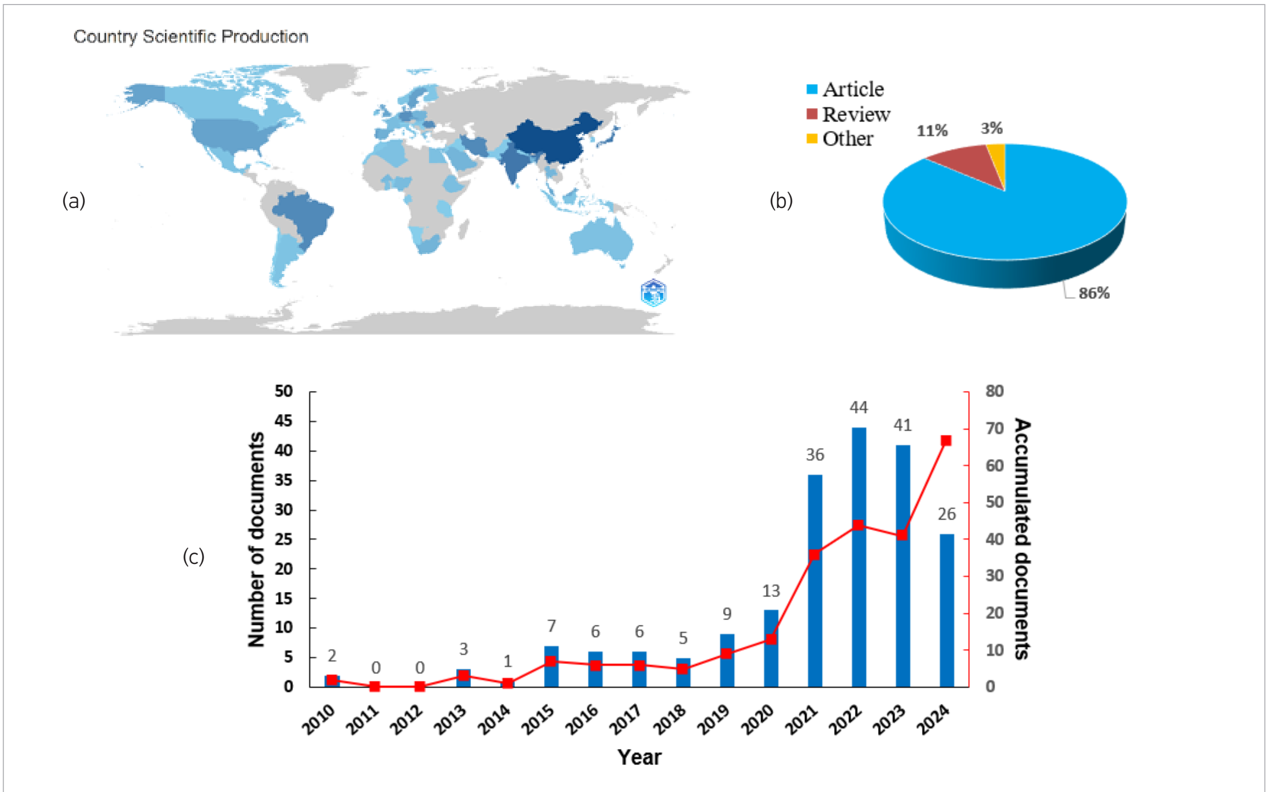
These findings lay the groundwork for strengthening future research agendas, guiding the development of more effective treatment technologies, and promoting integrated monitoring and control strategies to confront the hidden threat hospital effluents pose to public and environmental health.

Global scientific output, publication type, and temporal evolution of research in the field

Fig. 1 provides a comprehensive overview of the global scientific output on multidrug-resistant bacteria and antibiotics in hospital effluents, based on publications indexed in the Scopus database between 2010 and 2024. This figure illustrates the geographical distribution of scientific production (a), the types of documents published (b), and the temporal evolution of publications (c).

Fig. 1a shows that global academic output on multidrug-resistant bacteria and antibiotics in hospital effluents is dominated by China (122 articles), India (116), and Japan (64), followed by the United States (62) and Brazil (31). In Europe, the United Kingdom (24), Germany (22), Portugal (17), and Spain (17) make significant contributions, while Sweden, Italy, and France maintain moderate output coupled with a high degree of international collaboration. This geographic distribution reflects Asia's and the Americas' growing interest in antibiotic-resistance research. Established research

Fig. 1. *Global scientific output, publication types, and temporal evolution of publications indexed in the Scopus database between 2010 and 2024, focusing on academic literature related to multidrug-resistant bacteria and antibiotics in hospital effluents*



systems like Sweden's, where 86% of publications are collaborative, combine strong local output with multicenter networks, whereas India and China, despite leading in volume, show lower proportions of international co-publications. Latin America is represented by Brazil, which is emerging as a potential collaboration hub. These collaboration patterns underscore the importance of fostering interregional and interdisciplinary partnerships that integrate the fields of microbiology, environmental engineering, and data science to develop innovative solutions for monitoring, treating, and controlling hospital effluents and thus confront the global threat of antibiotic resistance.

Fig. 1c illustrates a rising trend in publication activity from 2010 to 2024. Annual output remained below five documents until 2014, then climbed steadily from 2019 onward, peaking at 44 publications in 2022. Although production dipped slightly to 41 in 2023 and more sharply to 26 in 2024, the cumulative total continued to grow, surpassing 70 publications by 2024. This surge parallels the global alarm over antimicrobial resistance and the pressing need for proper hospital-effluent management to protect public health and the environment.

Fig. 1b depicts document types: original research articles dominate at 86%, highlighting a strong emphasis on new empirical data; systematic and narrative reviews account for 11%, and other formats (book chapters, conference papers, brief communications) make up just 3%. While the prevalence of primary research accelerates evidence generation, the field would benefit from more critical reviews that synthesize findings and inform health-policy decisions.

Scientific output by author and co-authorship networks

Table 2 presents the leading authors who have contributed to the scientific output on multidrug-resistant bacteria and antibiotics in hospital effluents, based on publications indexed in Scopus. We can observe the contribution of researchers from different countries and continents, reflecting the international and collaborative nature of this field of study.

Table 2 highlights ten researchers whose careers reflect both productivity and impact. Leading the list is Chen L. (Shantou University, China), with four publications, an H-index of 4, and 263 citations; this author laid the groundwork for characterizing emerging contaminants in clinical wastewater over the past 30 years (Zhuang et al., 2021). Tied for second place in both publication count and H-index are Diwan V. (India) and Tamhankar A.J. (Sweden), each with four studies and 465 citations, underscoring their influence across diverse Asian and European communities. In fourth place, Azuma T. (Japan) also has four papers, an H-index of 3, and 74 citations for pioneering bioremediation approaches (Azuma and Hayashi, 2021; Azuma et al., 2022, 2024). Next is Bierbaum G. (Germany) with three works, an H-index of 3, and 176 citations, demonstrating a strong impact in clinical microbiology. Birošová L. (Slovakia) and Du H. (China) each appear with three publications and an H-index of 3, garnering 98 and 102 citations

Table 2. *Top authors by scientific output on multidrug-resistant bacteria and antibiotics in hospital effluent*

Rank	Author	NP	H-index	Country	Institution	TC
1	Chen L.	4	4	China	Shantou University	263
2	Diwan V.	4	4	India	Department of Public Health and Environment	465
3	Tamhankar Aj.	4	4	Sweden	Department of Public Health Sciences	465
4	Azuma T.	4	3	Japan	Osaka Medical and Pharmaceutical University	74
5	Bierbaum G.	3	3	Germany	University Hospital Bonn	176
6	Birošová L.	3	3	Slovakia	Slovak University of Technology	98
7	Du H.	3	3	China	Hospital of Soochow University	102
8	Flach C.-F.	3	3	Sweden	University of Gothenburg	92
9	Harnisz M.	3	3	Poland	University of Warmia and Mazury	71
10	Hayashi T.	3	3	Japan	Osaka Medical and Pharmaceutical University	62

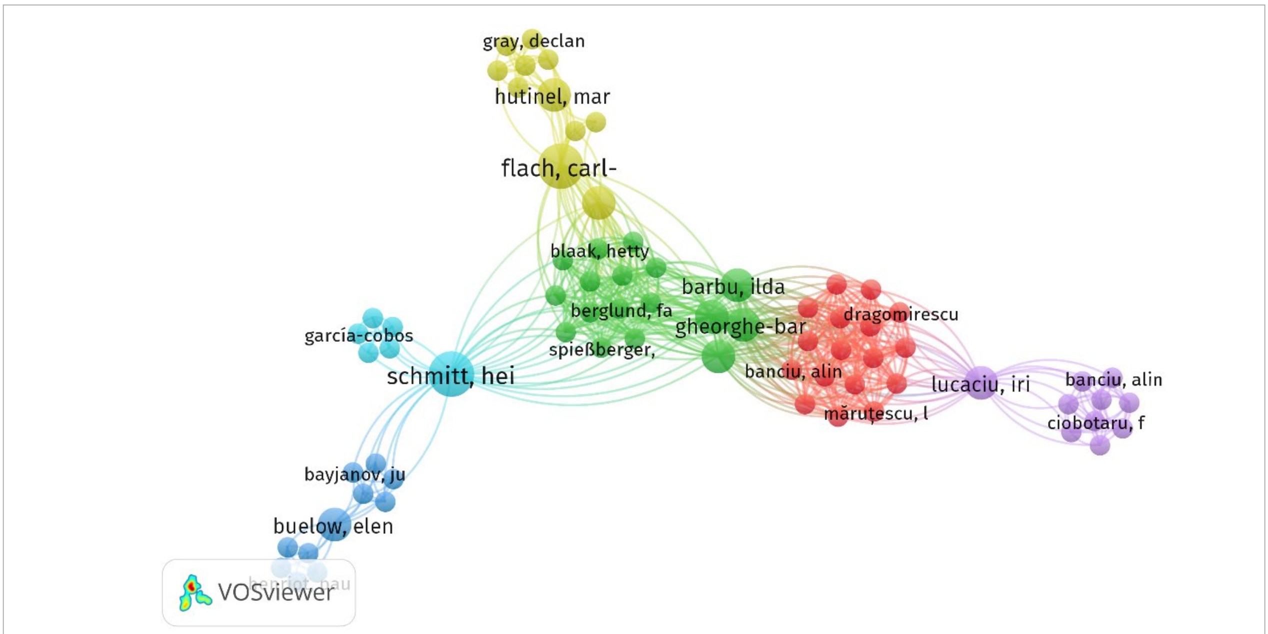
NP: Number of scientific publications

respectively, reflecting substantial contributions to effluent characterization and monitoring. In eighth position is Flach C.-F. (Sweden), with three papers, an H-index of 3, and 92 citations, focusing on antimicrobial resistance. Rounding out the top ten are Harnisz M. (Poland) and Hayashi T. (Japan), each with three publications, an H-index of 3, and 71 and 62 citations respectively. This ranking not only identifies the most prolific authors but also underscores the geographic diversity and interdisciplinary collaboration needed to confront the “hidden threat” posed by hospital effluents as reservoirs of bacterial resistance to public and environmental health.

Fig. 2 illustrates the collaboration network among authors who have investigated multidrug-resistant bacteria and antibiotics in hospital effluents during the period 2010–2024. This analysis, conducted using VOSviewer, highlights clusters of researchers grouped by affinity and frequency of co-authorship.

Fig. 2, generated with VOSviewer, illustrates the collaborative framework mapping interconnections among researchers studying multidrug-resistant bacteria and antibiotics in hospital effluents from 2010 to 2024. Each node represents an author, and its size proportional to their publication count, while links denote co-authorships and color intensity indicates distinct research communities. Five major color-coded clusters emerge: The blue group includes researchers such as Schmitt and Hei, focused on modeling the dissemination of resistance genes; the green group, formed by Spiessberger, Popa, and Marcel, stands out for their contributions in metagenomic characterization; the yellow group, with Genheden and Flach, emphasizes chemical monitoring strategies; The red group, composed of Surleac and Dragomirescu, focuses on emerging biotreatments; and the purple group, composed of Lucaciu and Banciu, delves into molecular mechanisms of resistance. Inter-cluster links, though fewer, bridge diverse methodological areas, facilitating the exchange of analytical approaches and sampling techniques. For example, Schmitt (blue) collaborates with authors in the yellow and light-blue clusters, highlighting synergies between computational modeling and advanced lab methods. This network reveals central “hubs” that disseminate knowledge and highlights emerging peripheral subnetworks. Conversely, the lack of direct ties between certain clusters, for example: between metagenomic characterization and electrochemical treatment, exposes fertile niches for integrated interdisciplinary studies. Overall, this visualization not only identifies key opinion leaders and emerging trends but also guides the planning of joint initiatives and resource allocation to confront the hidden threat hospital effluents pose to public health.

Fig. 2. *Author collaboration network on multidrug-resistant bacteria and antibiotics in hospital effluents (2010–2024)*



Predominant methodological approaches and analytical techniques.

Table 3 brings together the publications with the highest number of citations related to multidrug-resistant bacteria and antibiotics in hospital effluents, based on records indexed in Scopus. The publications presented reflect the influence and impact of key studies in consolidating the field, highlighting articles published in high-prestige journals.

Table 3 presents the most cited publications, reflecting high-impact, rigorously conducted studies. Topping the list is Samreen et al. (2021) with 363 citations and an annual citation rate (TC/year) of 72.6; their study is foundational for understanding resistance dynamics in clinical effluents. In second place, Majumder et al. (2021) has 246 citations (49.2 TC/year) and highlights innovative methods for removing residual pharmaceuticals. Zhuang et al. (2021) ranks third with 235 citations (47 TC/year), underscoring the severity of antibiotic pollution in aquatic ecosystems. The pioneering work of Diwan et al. (2010) follows closely with 220 citations, solidifying its status as a key reference for epidemiological and public-health research on hospital effluents. These metrics not only demonstrate the methodological quality achieved by combining microbiological, molecular, and chemical-analytical techniques, but also reflect the scientific community's keen interest in monitoring and mitigation strategies. Collectively, these landmark publications span advances from sampling and resistance-gene detection protocols to cutting-edge treatment technologies (photocatalysis, nanoparticles) and ecological risk-assessment models. Recognizing these contributions will help steer future research into emerging areas and bolster the interdisciplinary collaborations essential for countering the hidden threat hospital effluents pose to public and environmental health.

This bibliometric analysis reveals that, from 2010 to 2024, research methods have become progressively more sophisticated. Early investigations relied on spot-sampling of raw and treated wastewater at weekly or monthly intervals, with data quality ensured through ISO protocols (e.g., ISO 5667), refrigerated storage at 4°C, and the addition of degradation inhibitors. These measures guaranteed representativeness and reproducibility, enabling

Table 3. *Publications with the highest number of citations on multidrug-resistant bacteria and antibiotics in hospital effluents*

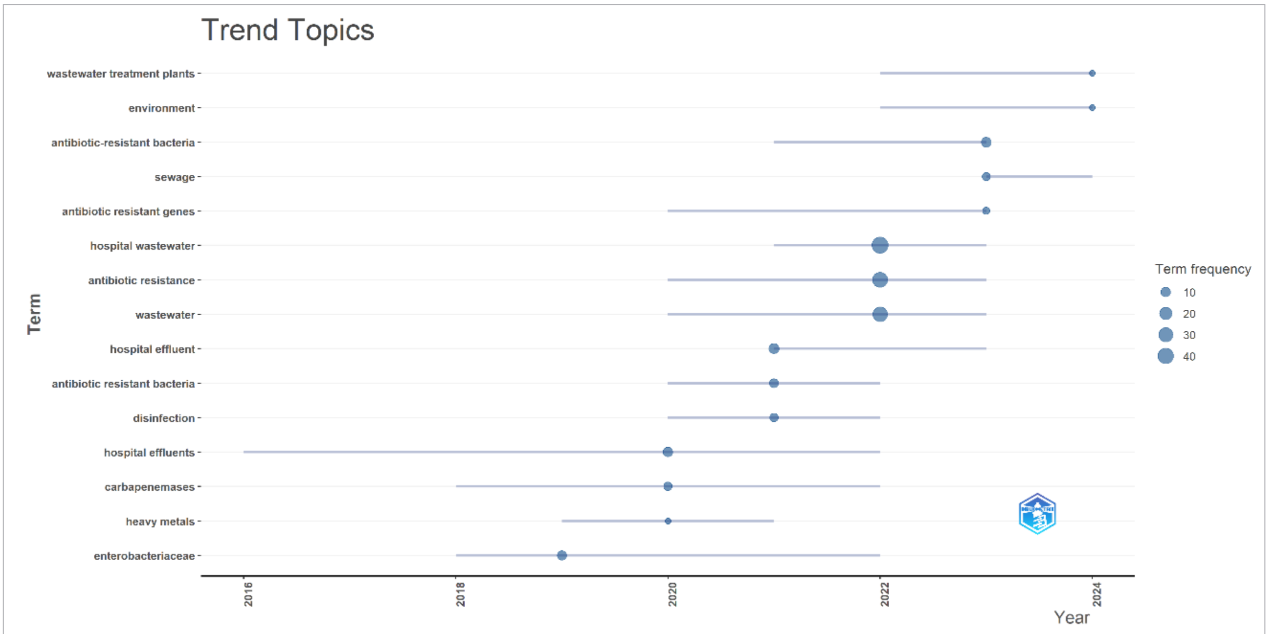
Author, year	Journal	DOI	TC	TC/ Year
Samreen et al., 2021	Journal of Global Antimicrobial Resistance	10.1016/j.jgar.2021.08.001	363	72.6
Majumder et al., 2021	Journal Environmental Chemical Engineering	10.1016/j.jece.2020.104812	246	49.2
Zhuang et al., 2021	Environmental Pollution	10.1016/j.envpol.2021.117402	235	47
Diwan et al., 2010	BMC Public Health	10.1186/1471-2458-10-414	220	13.75
Hassoun-Kheir et al., 2020	Science of The Total Environment	10.1016/j.scitotenv.2020.140804	177	29.5
Lien et al., 2016	International Journal Environmental Research Public Health	10.3390/ijerph13060588	157	15.7
Mutuku et al., 2022	World Journal of Microbiology and Biotechnology	10.1007/s11274-022-03334-0	139	34.75
Picão et al., 2013	Diagnostic Microbiology and Infectious Disease	10.1016/j.diagmicrobio.2013.02.001	139	10.69
Lamba et al., 2017	Environmental Science and Technology	10.1021/acs.est.7b03380	131	14.56
Varela et al., 2014	Water Research	10.1016/j.watres.2014.02.003	121	10.08
Amador et al., 2015	Journal of Environmental Science and Health	10.1080/10934529.2015.964602	121	11
Khan et al., 2019	Frontiers in Microbiology	10.3389/fmicb.2019.00688	105	15
Le et al., 2016	Antimicrobial Agents and Chemotherapy	10.1128/AAC.01556-16	94	9.4
Zhang et al., 2020b	Frontiers in Public Health	10.3389/fpubh.2020.574968	86	14.33
Ng et al., 2017	Frontiers in Microbiology	10.3389/fmicb.2017.02200	86	9.56

comparative assessments across treatment plants and regions (Radwan et al., 2024; Verlicchi, 2021). In microbiology, studies evolved from conventional isolation on selective media, such as MacConkey agar for Gram-negatives, to CHROMagar® for rapid species detection, and ultimately to automated identification via VITEK and MALDI-TOF systems. Antimicrobial susceptibility testing progressed from Kirby–Bauer disks to quantitative minimum inhibitory concentration (MIC) determinations by microdilution, following CLSI and EUCAST guidelines (Gonçalves et al., 2024; Silva et al., 2022; Rahman et al., 2021). This shift enabled standardized resistance measurements across *Escherichia coli*, *Pseudomonas aeruginosa*, and *Enterococcus* spp. Molecular-genetic methods marked a turning point: conventional PCR quickly gave way to quantitative (qPCR) and digital droplet PCR (ddPCR) for detecting specific resistance genes (blaCTX-M, blaKPC, mcr-1). Concurrently, shotgun metagenomics on platforms like Illumina MiSeq provided comprehensive "resistome" profiles, revealing integrons, transposons, and relative-abundance patterns, and tracing horizontal gene transfer routes (Azuma et al., 2024). In chemical analysis, liquid chromatography–tandem mass spectrometry (LC-MS/MS) became the gold standard. Early studies used solid-phase extraction (SPE) to concentrate samples, followed by high-resolution (LC-MS/MS) to quantify drugs (ceftriaxone, ciprofloxacin, vancomycin) at nanomolar levels. HPLC-DAD methods ran in parallel for validation, offering robust detection limits and recoveries, while the advent of UPLC systems and diverse internal standards further enhanced sensitivity and selectivity (Hamad et al., 2023; Deguenon et al., 2022). Finally, data analysis and ecological risk assessment integrated statistical and modeling tools. Predicted environmental concentration (PEC) versus no-effect concentration (PNEC) calculations and risk quotients (RQ = PEC/PNEC) enabled antibiotics to be ranked by ecotoxicological potential (Oldenkamp et al., 2024; Bouissou-Schurtz et al., 2014). Multivariate techniques (PCA, clustering) and bibliometric software (VOSviewer) rounded out the analysis, mapping thematic trends and collaboration networks. This blend of experimental rigor and strategic perspective provides a precise diagnosis of prevailing methodologies and lays out pathways for standardizing protocols in future research.

Thematic areas and scientific terms over time

Fig. 3 presents the main current topics addressed by researchers studying multidrug-resistant bacteria and antibiotics in hospital effluents during the period 2010–2024. The analysis shows how certain topics have gained relevance at different points in time. Likewise, it is possible to visualize the research lines that have been consolidated over the years.

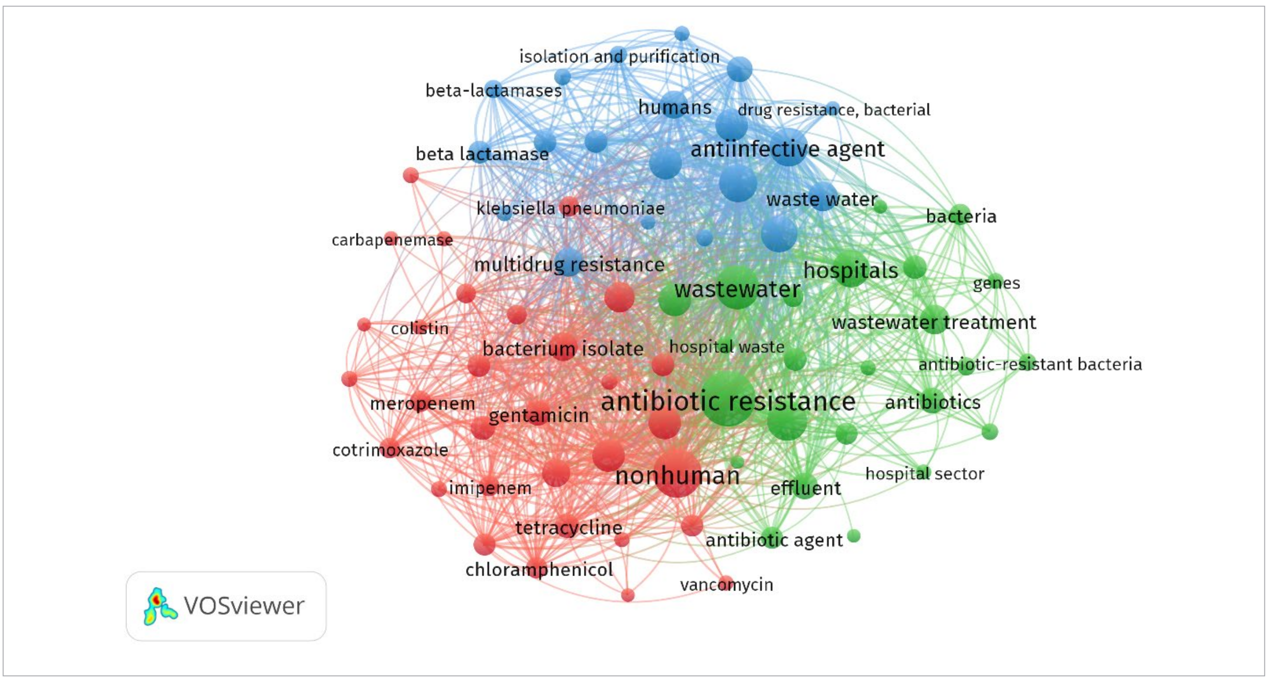
Fig. 3. *Trending topics among researchers studying multidrug-resistant bacteria and antibiotics in hospital effluents, 2010–2024*



Scientific interest in the environmental context of hospital discharges began around 2016, as evidenced by the emergence of terms like "wastewater treatment plants," "environment," and "sewage." In *Fig. 3*, the large circles along the 2020–2023 timeline show that most studies during this period evaluated emerging contaminants in rivers and urban sewer systems, as well as removal efficiency in conventional treatment plants, driven by both microbial populations and residual antibiotics in hospital effluents (Muhigwa et al., 2023; Hamad et al., 2023). From 2020 onward, concepts such as "antibiotic resistance," "antibiotic-resistant bacteria," and "antibiotic resistant genes" surged in prominence, underscoring concerns about the prevalence of resistant strains in clinical effluents. Numerous publications characterized microbial susceptibility profiles and identified antibiotics to which these populations had become resistant. These thematic trends not only track the occurrence of pharmaceuticals and their residues discharged from hospitals but also highlight the organisms' ability to tolerate them, directly linking medical practices to public-health risks. The appearance of "antibiotic resistant genes" and "hospital wastewater" between 2018 and 2022 intensified debates on resistance mechanisms and critical contamination points within medical facilities. The sustained co-occurrence of these terms, along with the consolidation of "hospital effluents," points to a methodological refinement: researchers began distinguishing antibiotic sources by specific hospital units (operating rooms, intensive-care wards, pediatric units, etc.) rather than sampling generic outflows. The term "disinfection," first observed in 2020, reflects growing interest in evaluating and optimizing microbial inactivation protocols before effluent discharge. Meanwhile, "carbapenemases" and "enterobacteriaceae" signal global concern over enzymes that deactivate last-line antibiotics, particularly among opportunistic pathogens that cause community and healthcare-associated infections. Overall, these evolving trends demonstrate a field maturing from merely documenting contaminant presence to probing their origins, resistance mechanisms, and containment strategies, highlighting fertile directions for future interdisciplinary collaboration.

Fig. 4 represents the key terms used by the scientific community investigating multidrug-resistant bacteria and antibiotics in hospital effluents during the period 2010–2024. The analysis, conducted with VOSviewer, organizes the concepts into colorcoded clusters, allowing the identification of the main thematic areas and their degree of interconnection.

Fig. 4. *Key terms used by the scientific community studying multidrug-resistant bacteria and antibiotics in hospital effluents (2010–2024)*



The co-occurrence analysis displayed in the VOSviewer map clusters high-frequency terms that appear together in studies from 2010 to 2024. Node size reflects how often each term is used in the academic discourse, while links indicate conceptual and methodological connections across research areas. Three major clusters emerge. *Fig. 4,* identifies three large clusters: Red cluster refers to the environmental characterization of antimicrobial resistance. Dominant terms include "multidrug resistance," "bacterium isolate," and specific antibiotic names such as "gentamicin," "tetracycline," and "chloramphenicol." Their frequent co-occurrence suggests that many studies focus on isolates from wastewater and assess their drug-specific susceptibility profiles (Gonçalves et al., 2024; Hamad et al., 2023; Mannan et al., 2023). Green cluster, groups terms oriented to the source and treatment of hospital effluents. Terms like "hospitals," "wastewater," "wastewater treatment," and "hospital sector" reveal that researchers view effluents as an integrated system, from contaminant generation to removal efficacy in conventional treatment plants. The rise of "treatment" and "hospital" in this cluster highlights technological advances over the past decade in ozonation, LED and UV disinfection, and nanoparticle filtration to reduce both antibiotic loads and resistant bacteria (Azuma et al., 2024; Hamad and El-Sesy, 2023; Azuma and Hayashi, 2021). Finally, the "Blue cluster" where terms such as "antiinfective agent", "humans", "drug resistance, bacterial" and "beta-lactamase" appear reflect a crossover between clinical microbiology and ecotoxicology. The frequent association of these nodes underscores the importance of contextualizing environmental findings with medical needs, with a focus on connecting environmental resistance with human infections, closing the "hospital-environment-hospital" loop.

Overall, this keyword map not only pinpoints where the scientific community has concentrated its efforts but also illustrates how sampling methods, analytical approaches, and clinical concerns intertwine. The holistic perspective it provides will help steer future research toward integrated environmental monitoring, optimized treatment strategies, and rigorous health-impact assessments, all of which are essential steps to mitigate the hidden threat posed by hospital effluents.

Research gaps and future research trends

Fig. 5 presents the thematic map generated in R-Studio based on publications on multidrug-resistant bacteria and antibiotics in hospital effluents during the period 2010–2024. The research topics can be visualized across four quadrants: Motor Themes, Basic Themes, Niche Themes, and Emerging or Declining Themes, according to their degree of relevance (centrality) and level of development (density). This figure provides a conceptual overview of the field and the evolution of its main lines of study, underscoring the interaction between clinical, microbiological, and environmental approaches. It also enables the analysis of research gaps and future trends in this area of study.

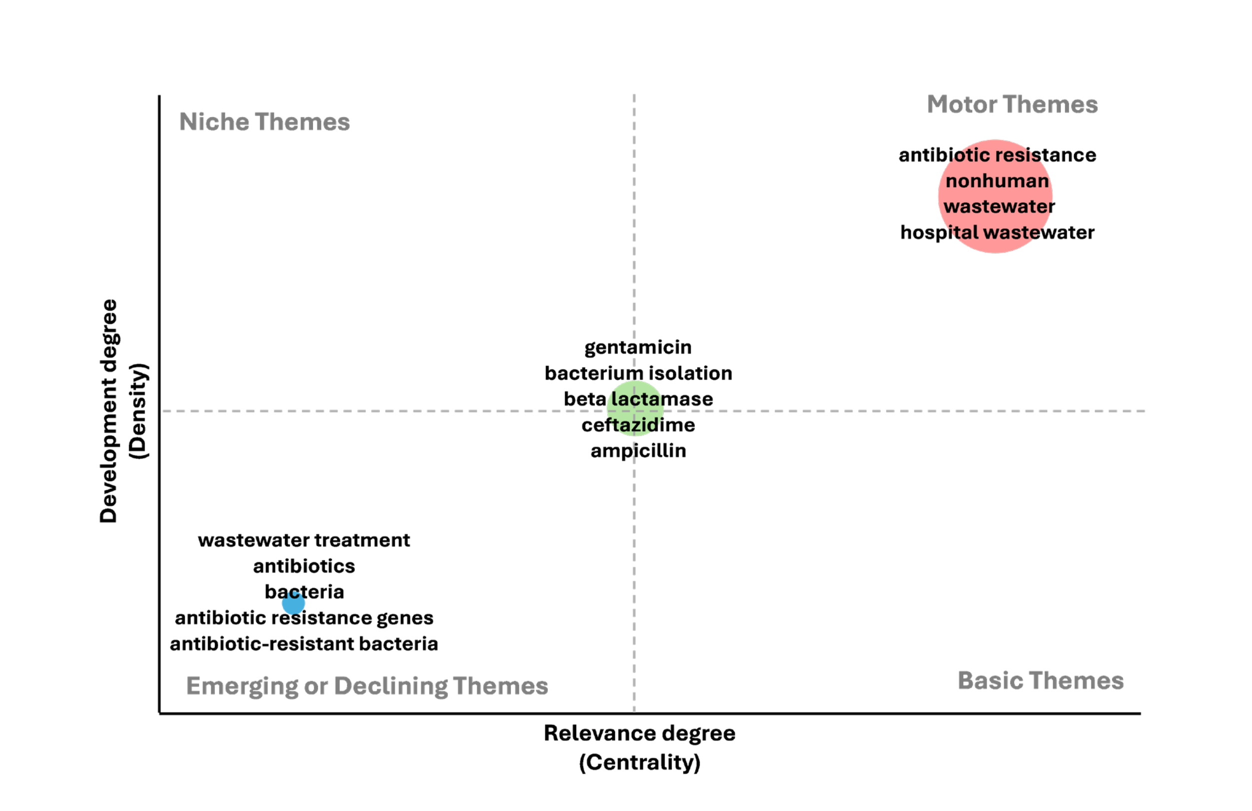
The thematic map generated in Biblioshiny-based RStudio (*Fig. 5*) organized the keywords into four quadrants according to two dimensions: centrality, which measures a theme's connection to the research core, and density, which reflects its internal development. This structure allows identification of the strategic role of each theme within the field.

In the upper right quadrant, "Motor Themes", the terms "antibiotic resistance," "non-human," "wastewater," and "hospital wastewater" appear, showing high centrality and high density. This indicates that current research focuses on understanding antibiotic resistance in non-clinical environments and hospital effluents. Their strategic position shows that these topics are frequent and connect to multiple research lines, acting as drivers of the field's progress.

The lower left quadrant, "Emerging or Declining Themes", groups terms such as "wastewater treatment," "antibiotics," "bacteria," "antibiotic resistance genes," and "antibiotic-resistant bacteria". These concepts display high centrality but low density and form the foundation of much research: optimization of wastewater treatment methods, quantification of residual antibiotics, and mapping the distribution of resistance genes in microorganisms and aquatic environments. Their sustained presence over the decade indicates that, despite new techniques, this base remains essential for validating approaches and comparing results across contexts.

The central area of the map gathers terms such as "gentamicin," "bacterial isolation," "beta-lactamase," "ceftazidime," and "ampicillin," representing classical research lines and potential targets for methodological renewal.

Fig. 5. *Thematic map generated in R-Studio for studies on multidrug-resistant bacteria and antibiotics in hospital effluents (2010–2024)*



These keywords recall the era when plate isolation and broad-spectrum antibiotic susceptibility profiles were pillars of resistance studies. Although many laboratories have shifted to high-throughput molecular techniques, this group remains relevant as a bridge to validate genomic approaches with well documented phenotypic data. Gentamicin, ampicillin and ceftazidime continue to be reference antibiotics in standard susceptibility tests; their co-occurrence with bacterial isolation indicates a tendency to return to conventional isolation methods to obtain strains of interest (especially Enterobacteriaceae and *Pseudomonas*) and to corroborate in situ results obtained by sequencing or qPCR. This is crucial when new resistance mechanisms are detected and it is necessary to compare enzymatic expression with actual drug susceptibility.

The "emergent" character of these terms stems from two factors: concern about reintroducing these antibiotics into first-line therapies, and the need to monitor the evolution of extended spectrum beta-lactamases and carbapenemases that mask emerging resistance. However, their proximity to the decline axis suggests the scientific community may be shifting attention toward next-generation molecules or pharmacological hybrids, relegating traditional phenotypic studies. This duality presents a methodological opportunity to integrate isolation protocols and minimum inhibitory concentration (MIC) determination for ceftazidime and ampicillin with metagenomic analyses of plasmidomes and functional beta-lactamase assays, promoting hybrid studies that link established phenotypic methods with genomics, proteomics and predictive artificial intelligence.

The "Basic Themes" (lower right) and "Niche Themes" (upper left) quadrants did not show well-defined term cores. This may be explained by the moderate publication volume (199 documents), the interdisciplinary nature of the field, which encompasses microbiology, analytical chemistry, environmental engineering and epidemiology, and the choice of a co-occurrence threshold that prioritized the most representative terms, concentrating clusters in the most relevant quadrants. During the analyzed period, fundamental concepts did not consolidate into dense, autonomous blocks but were strongly integrated into the motor themes, consistent with the field's evolution toward more predictive and integrative approaches.

Although research on multidrug-resistant bacteria and antibiotics in hospital effluents has expanded markedly in recent years, critical gaps remain. First, sampling and analytical protocols are heterogeneous, making reliable cross-study comparisons difficult. Second, geographic coverage is uneven: data abound for Europe, Asia, and the U.S., but studies from sub-Saharan Africa and Latin America are scarce. Third, most investigations focus on cephalosporins and quinolones, while emerging drug classes and their metabolites receive little attention. Finally, few studies integrate chemical and metagenomic datasets for predictive modeling of resistance-gene spread, compare long-term performance of conventional versus advanced treatment technologies, or link findings to health-policy recommendations via cost–benefit analyses and monitoring guidelines. Overcoming these limitations is essential to design effective containment strategies.

Looking forward, research in this field will evolve toward ever more predictive and integrated approaches powered by next-generation technologies. We anticipate the widespread deployment of real-time biosensors, built on CRISPR platforms and nanotechnology, to detect carbapenemase and other resistance variants directly within hospital sewer networks. At the same time, coupling next-generation sequencing (NGS) with clinical metadata will enable dynamic risk-mapping of horizontal gene transfer in aquatic systems and irrigated soils (Okesanya et al., 2025; Duan et al., 2023; Hajikhani et al., 2023). On the mitigation front, full-scale validation of advanced treatment systems, including electrochemical reactors, membrane-doped photocatalysis, and decentralized bioelectrochemical units, will assess their operational lifespan and cost–benefit profiles in diverse settings, especially in developing countries. Finally, integrating artificial intelligence and digital platforms in wastewater-treatment plants will allow simulation of extreme scenarios (e.g., flow surges, mixed contaminant loads) and standardization of protocols, closing the loop between research, policy, and environmental management to proactively counter the "hidden threat" of hospital effluents.

Conclusions

A sustained rise in scientific output was observed, driven primarily by China, India, and Japan, albeit with marked disparities in international collaboration. Europe, particularly Sweden and Germany, leads the multicenter networks.

The analysis successfully identified the most influential collaboration networks: coauthorship mapping revealed five distinct thematic groups focused on genetic modeling, metagenomic characterization, chemical monitoring, bioremediation, and the molecular mechanisms of resistance. Geographically, although China, India, and Japan led in publication volume, European countries especially Sweden, Germany, and the United Kingdom, demonstrated the highest levels of international and multicenter collaboration. This network structure underscores the importance of fostering interdisciplinary and interregional partnerships to effectively address this global challenge.

Research has clearly shifted from purely descriptive studies toward more integrated approaches combining microbiological, molecular, and chemical analyses. Techniques such as LC-MS/MS for antibiotic quantification and shotgun metagenomics for resistome profiling have become established, yet a pressing need remains to merge these methods into more robust predictive models.

Key gaps include a lack of standardized sampling and analytical protocols and the underrepresentation of regions such as sub-Saharan Africa and Latin America. Moreover, the weak linkage between scientific findings and public-policy formulation continues to impede a coordinated response to this threat.

Finally, the study points to future trends centered on emerging technologies such as CRISPR-based biosensors, artificial intelligence, and advanced treatment systems, underscoring the urgency of deploying preventive strategies to curb the spread of antimicrobial resistance from hospital settings into the broader environment.

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