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Antibiotics and Resistant Bacteria in Hospital Wastewater: A Review of Their Presence and Implemented Removal Measures

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Abstract **-** Currently, antibiotics and resistant bacteria have been included among emerging microcontaminants that generate global concern. Due to prolonged exposure in the environment, they cause harmful effects on human health and aquatic ecosystems. Additionally, there is no standardized global regulation that governs their final disposal in hospital effluents and wastewater, leading to the indiscriminate discharge of antimicrobials into these effluents, which then reach wastewater treatment plants. This increases selective pressure on bacteria, resulting in the development of resistant bacteria and posing a risk to human health. This review explores antibiotics and resistant bacteria isolated from hospital effluents. It also provides information on methodologies used for isolating and identifying these bacteria, antibiotic resistance genes, and in situ methodologies for their removal. For this purpose, publications registered between 2021 and 2024 in the Scopus database were analyzed. As a result, it was found that no studies conduct a combined search for antibiotics and resistant bacteria in hospital effluents. Most studies focus on searching for bacteria and antibiotic resistance genes. Additionally, the methodologies presented for the removal of these microcontaminants show promising results and are proposed as a solution to be implemented within hospitals. In conclusion, there is an increase in the presence of bacteria resistant to antimicrobials due to the lack of regulatory standards, which increases the risk to human health and ecosystems. However, future prospects for their treatment are promising thanks to the use of biotechnology.

Keywords**:** Antibiotics, Resistant bacteria, Hospital wastewater, Antimicrobial resistance.

1. Introduction

Antibiotics are classified as chemical substances capable of combating bacterial infections in humans and animals by inhibiting growth or destroying bacteria [1,2]. These pharmaceutical compounds have been categorized based on their mechanism of action, chemical structure, and antimicrobial spectrum [2,3]. When describing the types of antibiotics, the most commonly mentioned are beta-lactams, macrolides, aminoglycosides, and tetracyclines, but we must also include sulfonamides, quinolones, and cephalosporins [2,4]. In the last decade, it has been reported that antibiotic consumption has increased by 65% globally, surpassing the 35% reported at the beginning of the 21st century [5,6]. This indiscriminate and excessive use has led to the emergence of resistant and multi-resistant bacteria, rendering antimicrobial treatments ineffective. Additionally, inadequate disposal of these medications causes them to reach water bodies, dispersing into the environment and promoting an increase in the occurrence of resistant bacteria [6-8]. This situation has led the World Health Organization (WHO) to consider the emergence of multi-resistant bacteria as one of the top 10 threats to health, considering it a major threat to ecosystems and human health [9-11].

In hospitals, antibiotics are routinely used to combat bacterial infections and prevent complications in patients diagnosed with respiratory infections (bacterial pneumonia), urinary tract infections, surgical wound infections, and sepsis [2,3]. Proper use of antibiotics in the hospital setting is vital to ensure patient recovery and minimize the risk of bacterial resistance, which can complicate the treatment of future infections. However, the uncontrolled increase in antibiotic use both publicly and commercially has led to the emergence and spread of bacteria resistant to most drugs worldwide. This has resulted in an increase in mortality rates due to infections contracted from so-called superbugs [12,13].

According to the WHO, during the COVID-19 pandemic, the excessive and unnecessary use of antibiotics in hospitals was a significant and widespread issue [14]. A report by the Pan American Health Organization (PAHO) (2021) indicated that antibiotic consumption in South America for 2019 (Argentina, Chile, Colombia, Costa Rica, Paraguay, and Peru) ranged between 18 to 36 defined daily doses per thousand inhabitants [15]. Additionally, very few studies have documented the presence of antibiotics in hospital wastewater, searching for the presence of amoxicillin (AMX), ampicillin (AMP), ciprofloxacin (CIP), metronidazole (MTZ), sulfamethoxazole (SMX), and neomycin (NEO) [16]. Hospital, agricultural, and industrial wastewater containing antibiotic residues has negative effects on the environment and significantly damages aquatic ecosystems, as antibiotics are considered toxic to aquatic organisms. They contribute to the development of resistant bacteria, and their prolonged exposure can have negative effects on human health [17].

It is estimated that by 2050, antibiotic-resistant bacteria could cause up to 39 million deaths, posing an increasing threat to global health and endangering millions of lives [18-20]. In Europe, infections caused by antibiotic-resistant bacteria are estimated to cause more than 30,000 deaths annually [8]. This figure is likely higher in regions such as Asia, Latin America, and the Caribbean, where morbidity and mortality rates will be the highest for all ages [20,21]. The presence of resistant bacteria in hospital wastewater has negative effects on the environment and human health because it facilitates the spread of resistance genes to other microorganisms, leading to the emergence of new resistant strains that are difficult to treat, disrupting aquatic ecosystems, and posing health risks to people due to exposure to hard-to-treat bacterial infections [16,22,23].

The 2030 Agenda for Sustainable Development, adopted by the 193 Member States of the United Nations, includes indicator 3.8, which mentions "access to safe, effective, quality, and affordable essential medicines and vaccines for all" within Sustainable Development Goal 3 (SDG 3), which promotes "Ensuring healthy lives and promoting well-being for all at all ages" [5,24,25]. However, while ensuring universal access to antimicrobials can save millions of lives, excessive and inappropriate use must be limited to prevent the development of antimicrobial resistance. Currently, different mechanisms of bacterial resistance have been described for almost all current antibiotics on the market, particularly in Latin America, where the situation is concerning due to the lack of data on surveillance and rational use of antibiotics. In this regard, the WHO has emphasized the importance of expanding microbiological analyses and generating quality data in all countries to address this threat, as the most common bacterial infections are becoming increasingly resistant to treatments [25,26].

2. Methods

2.1 Research Review Approach

An experienced team was formed, consisting of microbiologists with expertise in environmental contamination and public health (authors of this article). They were responsible for defining the research objective and problem, selecting the database to be used, designing the bibliographic search plan, establishing inclusion/exclusion criteria, and creating the data diagram, as detailed below.

The objective of this research was to determine, based on the most recent information, which antibiotics and resistant bacteria have been detected in water and what accessible methods exist for their removal. The Scopus database was chosen as the primary source for the study due to its prestigious online presence, extensive collection of international scientific publications, and expert peer reviews.

The inclusion criteria for this study were primary research articles published in English between 2021 and 2024, open-access, and containing relevant data on antibiotics and resistant bacteria in hospital wastewater, as well as methods or procedures implemented for their removal.

The exclusion criteria for this study were articles from reviews and non-primary research (e.g., reviews, letters to the editor, and comments) published in languages other than English and not open-access. Additionally, articles whose methodology was not adequately described (lacking detection and quantification limits of the equipment used) were excluded.

2.2 Search Strategy and Article Selection

This strategy included selecting appropriate databases, choosing specific keywords, formulating the search equation, and applying inclusion and exclusion criteria. The keywords included the following terms: antibiotics, antimicrobials, superbugs, resistant bacteria, hospital effluent, and contaminated water. Boolean operators “OR” and “AND” were used to formulate the search equation to obtain the maximum number of scientific publications related to the research topic. The search equation consisted of: ("antibiotics" OR "antimicrobials") AND ("superbugs" OR "resistant bacteria") AND ("hospital effluent" OR "contaminated water"). The information search was conducted in November 2024 using the Scopus electronic database, selecting the search field = article title, abstract, and keywords. Additionally, from January 2 to 4, 2025, a data verification was performed using an identical search string. The information was extracted into a data registration form where compliance with eligibility criteria (year, language, open access, sample type, and appropriate methodology) was evaluated. The registration was individually completed by each researcher and updated as the analysis of each article under evaluation progressed.

3. Results

3.1 Search Results and General Characteristics of the Study

The search process in the Scopus database up to 2024 revealed 164 publications, but for this study, 83 investigations published between 2021 and 2024 were considered. In 2021, 22 documents (26.5%) were published; in 2022, 16 documents (19.3%); in 2023, 24 documents (28.9%); and in 2024, 21 documents (25.3%). The results indicate that the number of publications has remained steady, with the highest increase occurring in 2023 with 24 documents published. This slight increase in the number of publications highlights the interest of research groups in the fields of health and the environment in investigating the issue of the presence of antibiotics and resistant bacteria as emerging contaminants in hospital wastewater and their potential effects on health and the environment (Figure 1).

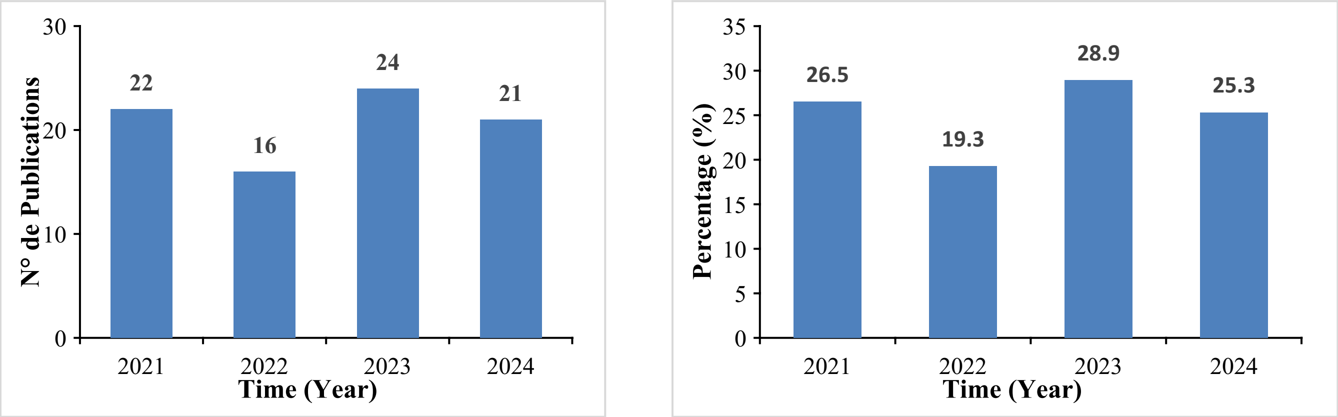

Fig 1. Trends in Scientific Publications on Antibiotics and Resistant Bacteria in Hospital Wastewater Reported in Scopus from 2021 to 2024**.** On the left side, the graph shows the number of publications per year. On the right side, the graph shows the percentage of publications per year.

Out of the 83 publications selected in this initial stage, 71% (n=59) correspond to articles, 21.7% (n=18) to reviews, and 7.3% (n=6) included book chapters, conferences, among others. Of the 59 articles, only 64.4% (n=38) are open-access publications in English, which were the eligible documents that proceeded to the next selection process. The result of the selection process and extraction of information from the articles, based on their relevance to the study's theme, yielded 18 articles for full retrieval and reading. A flowchart compatible with PRISMA 2020 was created (Figure 2) [27].

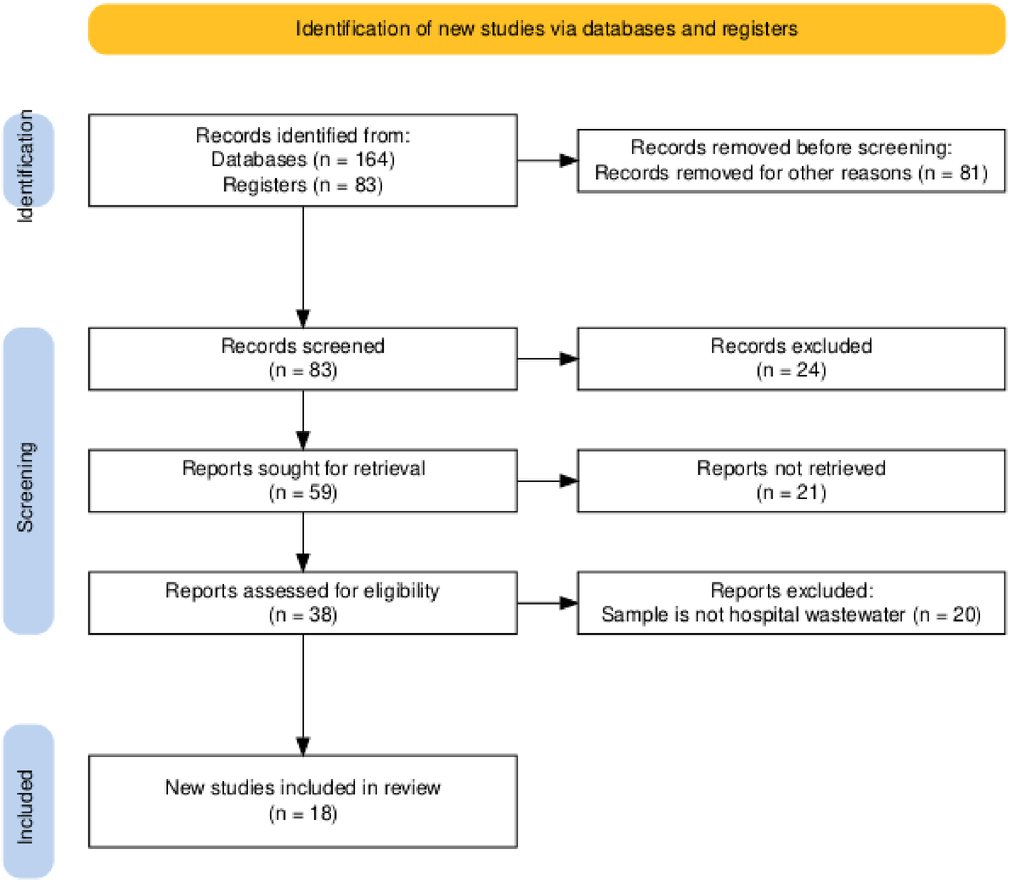

Fig 2. PRISMA Flow Diagram Used in the Information Search.

Table 1: Articles Included for the Integrative Review

Authors and Year	Country	Methodology	Relevant Results in Samples	Contribution to Treatment
Azuma et al. (2024)	Japan	Search for antibiotics: Not performed; Bacterial isolation: Chromogenic agars; Bacteria identification: DNA extraction and PCR on MiSeq (Illumina Inc.); Antibiogram: Not performed; Resistance genes: Quantitative PCR	Hospital wastewater contained: 78 CFU of CRE per mL; 131 CFU of ESBL-E per mL; 81 CFU of MDRA per mL; 215 CFU of MDRP per mL; 31 CFU of MRSA per mL; and 151 CFU of VRE per mL. 99% of CRE, ESBL-E, MDRA, MDRP, and VRE were rapidly inactivated after 0.5 minutes of UV [28]	Direct treatments with ultraviolet light and ultraviolet LED can inactivate antimicrobial-resistant bacteria (AMRB) and partially eliminate antimicrobial resistance genes (AMRGs).
Gonçalves et al. (2024)	Brazil	Search for antibiotics: Not performed; Bacterial isolation: Chromogenic agars; Bacteria identification: Vitek-2 system and PCR; Antibiogram: Vitek-2 system; Resistance genes: PCR	The presence of MDR bacteria was reported, such as *E. cloacae, K. pneumoniae, K. oxytoca*, and *Citrobacter farmeri* resistant to MER, IPM, ERT, AMC, AZT, CAZ, CPM, CRO, CIP, TZP, GEN, and C/T [23].	No contribution for eliminating MDR bacteria was presented.
Muhigwa et al. (2023)	Burkina Faso	Search for antibiotics: Not performed; Bacterial isolation: Antibiotic agars; Bacteria identification: API 20E system; Antibiogram: Kirby-Bauer method; Resistance genes: 2% agarose gel electrophoresis	*K. pneumoniae and K. oxytoca* are the predominant species resistant to multiple drugs. The presence of species such as *E. coli, K. pneumoniae, K. oxytoca, E. cloacae, C. diversus, C. freundii, P. vulgaris, P. mirabilis*, and *P. aeruginosa* resistant to AMX, CTX, and AMC was reported [29].	No contribution for eliminating MDR bacteria was presented.
Hamad & El-Sesy. (2023)	Egypt	Search for antibiotics: High-performance liquid chromatography (HPLC); Bacterial isolation: Not performed; Bacteria identification: DNA extraction and PCR; Antibiogram: Not performed; Resistance genes: Not performed	The presence of levofloxacin (4.7 mg/L) was reported. Treatments with copper oxide nanoparticles (CuONP) and zero-valent iron nanoparticles (nZVI) reduced levofloxacin concentrations by up to 85% and 95% respectively [30].	Treatments with copper oxide nanoparticles (CuONP) and zero-valent iron nanoparticles (nZVI) can be used as nanoadsorbents for the removal of the antibiotic levofloxacin.

Mannan et al. (2023)	Bangladesh	Search for antibiotics: Not performed; Bacterial isolation: Antibiotic agars; Bacteria identification: Vitek-2 system; Antibiogram: Vitek-2 system; Resistance genes: 2% agarose gel electrophoresis	*E. coli* resistant to AM, CRO, CXM, MER, and NIT; *A. baumanii* resistant to MER and AMP; *P. aeruginosa* resistant to MER, AMP, CRO, CXM, NAL, and CXM; and *E. cloacae* resistant to CRO, MER, CXM, AMP, MER, AMP, and NAL were reported [31].	No contribution for eliminating MDR bacteria was presented.
Mehanni et al. (2023)	Egypt	Search for antibiotics: Not performed; Bacterial isolation: Selective and differential agars; Bacteria identification: Biochemical tests; Antibiogram: Broth tests for antibiotics: TET, AMP, AMX, CLO, and ERI; Resistance genes: Not performed	*S. haemolyticus, E. faecalis*, and *E. coli* MDR resistant to TET, AMP, AMX, CLO, and ERI were reported [32].	No contribution for eliminating MDR bacteria was presented.
Girijan & Pillai (2023)	India	Search for antibiotics: Not performed; Bacterial isolation: Chromogenic agars; Bacteria identification: Biochemical tests and 16S rDNA sequencing; Antibiogram: Kirby-Bauer method; Resistance genes: PCR on ABI 3100 genetic analyzer	*E. coli* ESBL resistant to AMP, AMX, FOX, FEP, AMC, CAZ, CTX, CRO, CIP, NAL, ATM, TMS, AMI, GEN, and IMI; and *K. pneumoniae* ESBL resistant to AMP, AMX, AMC, CTX, FOX, CAZ, CRO, and FEP were reported [33].	No presento aporte para eliminar las bacterias MDR
Azuma et al. (2022)	Japan	Search for antibiotics: Not performed; Bacterial isolation: Chromogenic agars; Bacteria identification: Chromogenic agars; Antibiogram: Not performed; Resistance genes: Not performed	Methicillin-resistant *S. aureus* (MRSA) was reported [34].	No contribution for eliminating MDR bacteria was presented
Parashar et al. (2022)	India	Search for antibiotics: Not performed; Bacterial isolation: Selective and differential agars; Bacteria identification: Biochemical tests; Antibiogram: Kirby-Bauer method for antibiotics CIP and SMX; Resistance genes: Not perform	*E. coli* resistant to CIP and SMX was reported. Between 30% to 50% of resistant bacteria were eliminated when hospital wastewater was treated in wetlands [35].	The implementation of wetlands is an efficient alternative for effectively removing contaminants from wastewater.
Deguenon et al. (2022)	Benin	Search for antibiotics: MyBioSource® ELISA kit; Bacterial isolation: Antibiotic-supplemented agars; Bacteria identification: API 20E kit; Antibiogram: Not performed; Resistance genes: Not performed	*Acinetobacter* spp. and *Klebsiella* spp. were reported as the most frequently identified species. Residues of CIP (7.65 ± 2.272 ug/L), SMX (3.88 ± 3.088 ug/L), and AMP (1.90 ± 1.042 ug/L) were found [16].	No contribution for eliminating MDR bacteria was presented.
Roulová et al. (2022)	Czech Republic	Search for antibiotics: Not performed; Bacterial isolation: Cetrimide agar; Bacteria identification: Biochemical tests and NEFERMtest® 24; Antibiogram: Kirby-Bauer method for antibiotics PTZ, CAS, CIP, MER, GEN, AMI, and ATM; Resistance genes: Not performed	Bacterial isolation focused on the search for *P. aeruginosa*. It was found that 23% of *P. aeruginosa* strains were considered MDR due to resistance to PTZ, CAZ, MER, CIP, GEN, and AMI [36].	No contribution for eliminating MDR bacteria was presented.
Silva et al. (2022)	Portugal	Search for antibiotics: Not performed; Bacterial isolation: Antibiotic-supplemented agars; Bacteria identification: Multiplex PCR; Antimicrobial susceptibility: Kirby-Bauer method for antibiotics PEN, FOX, CIP, LNZ, GEN, KAN, TOB, ERI, CLI, TET, FUS, CLO, and TMS; Resistance genes: Not performed	Bacterial isolation focused on the search for methicillin-resistant *S. aureus* (MRSA). Strains of *S. aureus* resistant to PEN, FOX, CIP, GEN, KAN, TOB, ERI, CLI, TET, CLO, FUS, and TMS were found [37].	No contribution for eliminating MDR bacteria was presented.
Divyashree (2021)	India	Search for antibiotics: Not performed; Bacterial isolation: Selective and differential agars; Bacteria identification: Biochemical tests; Antibiogram: Kirby-Bauer method for antibiotics CTX, AMP, CAZ, COT, GEN, CIP, TET, CLO, NAL, NIT, MER, IMI; Resistance genes: 2% agarose gel electrophoresis	*Klebsiella* spp. resistant to NAL, TET, CTZ, CLO, CIP, AMP, GEN, NIT, IMI, MER, CTX, and PIT; *E. coli* resistant to NAL, TET, CTZ, CLO, CIP, AMP, GEN, NIT, IMI, MER, CTX, PIT; *Salmonella* spp. resistant to NAL, CTZ, CIP, AMP, GEN, IPM, MRP, CTX, PIT, ESBL; *Enterobacter* spp. resistant to NAL, CTZ, CIP, AMP, GEN, NIT, MER, and PIT; and *Proteus* spp. resistant to NAL, CTZ, CIP, CLO, AMP, GEN, MRP, CTX, and PIT were reported [38].	No contribution for eliminating MDR bacteria was presented.
Girijan & Pillai (2021)	India	Search for antibiotics: Not performed; Bacterial isolation: Selective and differential agars; Bacteria identification: Biochemical tests; Antibiogram: Kirby-Bauer method for antibiotics AZM, AMP, CLI, CLR, CLO, CIP, MFX, ERI, GEN, MET, OXA, STR, TMP, and VAN; Resistance genes: PCR on ABI 3100 genetic analyzer.	Bacterial isolation focused on the search for methicillin-resistant *S. aureus* (MRSA). Strains of *S. aureus* resistant to AMP, AZM, CLI, CLR, CLO, CIP, ERI, MET, OXA, STR, and VAN were found [39].	No contribution for eliminating MDR bacteria was presented.
Azuma &,Hayashi, T. (2021)	Japan	Search for antibiotics: Not performed, Bacterial isolation: Chromogenic agars, Bacteria identification: DNA extraction and PCR on MiSeq (Illumina Inc.), Antibiogram: Not performed, Resistance genes: Not performed.	Hospital wastewater contained: 1150 CFU of CRE per mL; 749 CFU of ESBL-E per mL; 81 CFU of MDRA per mL; 215 CFU of MDRP per mL; 31 CFU of MRSA per mL; and 151 CFU of VRE per mL. More than 90% of CRE, ESBL-E, MDRA, MDRP, and VRE were inactivated after 5 minutes of chlorination treatment, while 60% of MRSA were gradually inactivated after 30 minutes of treatment [40].	This study recommends implementing local chlorination treatment directly for hospital wastewater before discharging it to the wastewater treatment plant (WWTP).
Azuma &,Hayashi, T. (2021)	Japan	Search for antibiotics: Not performed; Bacterial isolation: Chromogenic agars; Bacteria identification: DNA extraction and PCR on MiSeq (Illumina Inc.); Antibiogram: Not performed; Resistance genes: Not performed	Hospital wastewater contained: 1,073 ± 1,162 CFU of CRE per mL; 568 ± 584 CFU of ESBL-E per mL; 274 ± 301 CFU of MDRA per mL; 123 ± 114 CFU of MDRP per mL; 77 ± 48 CFU of MRSA per mL; and 38 ± 51 CFU of VRE per mL. All AMRB were almost completely inactivated after 5 hours of irradiation. More than 90% of CRE, ESBL-E, MDRA, MDRP, and VRE were inactivated and eliminated after 2 hours, while the 100% inactivation of MRSA was slower, occurring gradually and after 5 hours of treatment [41].	This study recommends the use of natural solar irradiation for the treatment of resistant bacteria present in hospital wastewater.

Mijanur et al. (2021)	Bangladesh	Search for antibiotics: Not performed; Bacterial isolation: Selective and differential agars; Bacteria identification: Biochemical tests; Antibiogram: Kirby-Bauer method for antibiotics AZM, GEN, AMP, TOB, FEP, DOX, NIT, NET, CIP, CTX, CLO, AMI, OXA, STR, CFM, CAZ, and MET for only *S. aureus*; Resistance genes: Not performed.	*S. aureus* resistant to AMP, OXA, CHL, DOX, AZM, CIP, NET, TOB, FEP, CAZ, CFM, and CTX; *E. coli* resistant to AMP, OXA, CHL, AZM, CIP, STR, FEP, CAZ, CFM, and CTX; and Enterobacter spp. resistant to AMP, OXA, CHL, DOX, NIT, AZM, CIP, STR, FEP, CAZ, CFM, and CTX; and Pseudomonas spp. resistant to AMP, OXA, CHL, DOX, NIT, AZM, CIP, AMK, STR, FEP, CAZ, CFM, and CTX were reported [42].	No contribution for eliminating MDR bacteria was presented.
Azuma &,Hayashi, T. (2021)	Japan	Search for antibiotics: Not performed; Bacterial isolation: Chromogenic agars; Bacteria identification: DNA extraction and PCR on MiSeq (Illumina Inc.); Antibiogram: Not performed; Resistance genes: Not performed.	Hospital wastewater contained: 1,577 ± 918 CFU of CRE per mL; 1,471 ± 577 CFU of ESBL-E per mL; 378 ± 455 CFU of MDRA per mL; 64 ± 28 CFU of MDRP per mL; 50 ± 33 CFU of MRSA per mL; and 57 ± 20 CFU of VRE per mL. More than 90% of CRE, ESBL-E, MDRA, MDRP, and VRE were inactivated after 10 minutes of ozonation, while the 80% inactivation of MRSA was slower, occurring gradually and after 10 minutes of ozonation [43].	This study recommends the use of ozonation for the treatment of resistant bacteria at the discharge of hospital wastewater.

Antibiotics: Nalidixic Acid (NAL); Amikacin (AMI); Amoxicillin (AMX); Amoxicillin/Clavulanic Acid (AMC); Ampicillin (AMP); Azithromycin (AZM); Aztreonam (ATM); Cefepime (FEP); Cefixime (CFM); Cefotaxime (CTX); Cefoxitin (FOX); Ceftazidime (CAZ); Ceftriaxone (CRO); Ceftolozane/Tazobactam (C/T); Ciprofloxacin (CIP); Clindamycin (CLI); Chloramphenicol (CLO); Co-trimoxazole (COT); Doxycycline (DOX); Ertapenem (ETP); Streptomycin (STR); Gentamicin (GEN); Imipenem (IMI); Kanamycin (KAN); Meropenem (MER); Methicillin (MET); Metronidazole (MTZ); Netilmicin (NET); Neomycin (NEO); Nitrofurantoin (NIT); Oxacillin (OXA); Penicillin (PEN); Piperacillin/Tazobactam (PIT); Sulfamethoxazole (SMX); Tetracycline (TET); Trimethoprim-Sulfamethoxazole (TMS); Tobramycin (TOB).

Resistant Bacteria: Carbapenem-resistant Enterobacteriaceae (CRE); Extended-spectrum β-lactamase-producing *Enterobacterales* (ESBL-E); Multi-drug-resistant *Acinetobacter* (MDRA); Multi-drug-resistant *P. aeruginosa* (MDRP); Methicillin-resistant *S. aureus* (MRSA); Vancomycin-resistant *Enterococcus* (VRE).

4. Discussion

In recent years, the WHO, through national and regional surveillance systems in numerous countries worldwide, has collected information and reported that antibiotic use is steadily increasing, primarily in low- and middle-income countries. This has raised concerns about the harmful effects of these drugs on the environment [5,15,25], as studies have shown that many antimicrobials are not fully metabolized during therapeutic use and are excreted from the human body as active substances capable of contaminating the environment, leading to their increase in hospital and domestic wastewater [44]. Due to their widespread uncontrolled use, antimicrobials have been and continue to be discharged into the environment through human wastewater from various sources, including households (domestic), hospitals (clinical), veterinary and livestock activities, and pharmaceutical factories (industrial) [45].

The use and administration of antimicrobials occur most frequently in healthcare centers, making hospital effluents the most concentrated sources. The results of this study, shown in Table 1, indicate that 11% (n=2) of the investigations detected the presence of antibiotics (Levofloxacin, Ciprofloxacin; Sulfamethoxazole, and Ampicillin). The justification for the search for Levofloxacin is that it is a widely used fluoroquinolone for treating infectious diseases globally. It has also been observed in aquatic environments due to insufficient metabolism in the body [30]. The search for Ciprofloxacin, Metronidazole, Sulfamethoxazole, and Ampicillin was because they are the most commonly used antibiotics in West African countries due to their low cost in developing countries [16]. It is also worth noting that Sulfamethoxazole is excreted unchanged through urine, making it one of the most common substances found in the environment [30]. Both the United States and the European Union established surveillance of many antibiotics starting in 2018, focusing on clarithromycin, azithromycin, erythromycin, amoxicillin, and ciprofloxacin [46].

Information presented by Irfan (2022) indicates that approximately 3.57 million deaths in 2019 were associated with antimicrobial resistance [20,47]. Investigating antimicrobial resistance levels is crucial for public health, food safety, and the environment [32,34]. Monitoring antimicrobial resistance helps healthcare professionals select the most effective treatments and avoid unnecessary antibiotic use due to prolonged treatments that increase healthcare costs for patients. Environmentally, monitoring prevents contamination of aquatic ecosystems where resistant bacteria and their resistance genes can spread [23,28,31,39].

Antimicrobial-resistant bacteria in wastewater are a growing public health concern. They can enter wastewater from various sources, including human waste, hospital effluents, and agro-industrial residues that use antibiotics, increasing the risk of spreading these bacteria and their resistance genes to other bacteria in the environment. This exacerbates the problem of antimicrobial resistance, affecting both human health and ecosystems [32,35,37]. The results of this study, shown in Table 1, indicate that most investigations (90%) searched for resistant bacteria and/or antimicrobial resistance genes. These studies found that *E. coli, Acinetobacter* spp., *Klebsiella* spp., *Pseudomonas* spp., and *S. aureus* are the most commonly searched species due to their ability to accumulate or develop antimicrobial resistance genes. *E. coli* can acquire resistance to cephalosporins, carbapenemases, aminoglycoside methyltransferases, and quinolones [48,49]. *Acinetobacter* spp. can develop resistance to β-lactamases, aminoglycosides, and some strains are resistant to most commercially available antibiotics [50]. *Klebsiella* spp. can acquire resistance to extended-spectrum β-lactamases (ESBL) and carbapenemases [49]. *Pseudomonas* spp. has intrinsic resistance and can acquire resistance genes, leading to the frequent discovery of multi-drug-resistant strains [51]. *S. aureus* can acquire the mecA gene, reducing the efficacy of β-lactam antibiotics [52].

Table 1 also shows that the methodologies used for searching antibiotics, bacterial isolation and identification, antibiogram, and resistance genes include traditional reference methodologies based on bacteriological culture in selective, differential, and chromogenic agars, and biochemical tests. These are used for isolation, identification, and antibiogram to detect antimicrobial-resistant bacteria because these techniques are economical, relatively accurate, and convenient. With technological advancements, some traditional techniques have shown limitations, leading to the adoption of automated technologies like the VITEK2 system (BioMérieux) that help identify and determine antibiotic sensitivity in shorter times. Molecular techniques based on PCR are faster than culture-based approaches, allowing the discovery of various antimicrobial resistance genes in bacteria that were difficult to culture in laboratories. Currently, the most precise and accurate molecular tool for studying a specific organism and its resistance genes is whole genome sequencing (WGS) using platforms like Illumina (Illumina Inc.) or Nanopore MinIOn (Oxford Nanopore technology) [47].

Table 1 also shows that 33.3% (n=6) of the investigations contributed to the treatment of antibiotics and resistant bacteria in hospital wastewater, with Azuma, Takashi & Hayashi, Tetsuya being the researchers who made the most contributions (n=4) in this research area. This review shows that few hospital institutions have adopted and implemented in situ technologies to eliminate antimicrobial resistance and their resistance genes through chlorination, UV disinfection, ozonation, and solar photocatalysis processes [28,30,35,40,41,43]. In samples other than hospital wastewater, laboratory studies have been conducted on bioremediation processes with algae, extremophilic bacteria, phages, nanoparticles, and antimicrobial peptides to eliminate or remove antibiotics, antimicrobial-resistant bacteria, and antimicrobial resistance genes [45].

5. Conclusions

Antimicrobial resistance (AMR) has increased globally due to the rising and excessive use of antibiotics in healthcare centers, leading to increased discharge of these substances in hospital wastewater. As a result, there is a significant increase in carbapenem-resistant *Enterobacteriaceae* (CRE); extended-spectrum β-lactamase-producing *Enterobacterales* (ESBL-E); multi-drug-resistant *Acinetobacter* (MDRA); multi-drug-resistant *P. aeruginosa* (MDRP); methicillin-resistant *S. aureus* (MRSA); and vancomycin-resistant *Enterococcus* (VRE) in the studies utilized for this research.

The presence of antibiotics and antibiotic-resistant bacteria in hospital effluents is primarily due to inadequate treatment of these effluents, compounded by deficient supervision by environmental regulatory authorities. Together, this makes hospital effluents a real risk to health and the environment, necessitating the development and implementation of specific treatment plants within hospitals to address this problem.

To reduce the growing threat of antimicrobial resistance in aquatic environments, it is necessary to establish and universally apply strict limits on the release of antibiotics from point sources such as hospitals and ensure effective control through continuous monitoring to enforce regulations.

The proposed methodologies for the elimination of antibiotics and antibiotic-resistant bacteria show promising results, presenting a viable solution for implementation within hospitals. These techniques include chlorination, UV disinfection, ozonation, and solar photocatalysis. Implementing these processes will not only help reduce the presence of dangerous contaminants in hospital effluents but also contribute to protecting public health and the environment. For this to be effective, it is essential that hospitals receive the necessary support in terms of resources and training to adopt these solutions effectively.

Conflict of Interest

The authors declare no conflicts of interest.

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