



RESEARCH ARTICLE

A REVIEW ON ANTIBIOTIC RESISTANCE PATTERNS OF STAPHYLOCOCCUS AUREUS AND ESCHERICHIA COLI ISOLATED FROM HOSPITAL WASTE WATER

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ABSTRACT

Hospital wastewater serves as a significant reservoir for pathogenic bacteria, including *Staphylococcus aureus* and *Escherichia coli*, showing alarming resistance patterns to various classes of antibiotics. In addition, *S. aureus* isolates from hospital wastewater have been found to be resistant to β -lactam antibiotics, especially methicillin, hence indicating the presence of MRSA strains. *E. coli* isolates exhibited multidrug resistance with notable resistance to cephalosporins, fluoroquinolones, and aminoglycosides, and the incidence of ESBL-producing *E. coli* is increasingly reported. The horizontal transference of antimicrobial resistance mediated by plasmids and integrons in the aquatic environment highlights the pressing requirement for integrated surveillance systems bringing together the microbiological, molecular, and environmental approaches needed to follow resistance trends and develop sustainable strategies to control antimicrobial resistance in the management systems of hospital wastewater.

INTRODUCTION

A complex mixture of contaminants coupled with the selective pressure in hospital wastewater acts as a potential breeding ground for the development of antimicrobial-resistant bacteria, such as *S. aureus* and *E. coli*. This encourages the development of resistant organisms and mobile genetic elements that can pose serious threats to public health. Antibiotics are secondary metabolites produced by microbes as well as chemically synthesized or semi-synthesized similar chemicals that can inhibit both the growth and survival of other microbes (Kumar M Jaiswal *et al.*, 2019). These compounds are used for the treatment of bacterial infections, to support surgical operations, to treat cancer, and as a preventative measure. They are also frequently used in aquaculture as growth promoters and in the veterinary care of domestic and livestock animals (La Page *et al.*, 2017). Antibiotic use is rapidly growing every year, and it is estimated that by 2030, use of antibiotics will have increased by 200% (Amangelsin *et al.* 2023). When these compounds are used for any given purpose, they do not become fully metabolized. The studies indicated that both humans and animals metabolized only small portions, while 20–90% was eliminated from the body via urine and feces as the parent compound or its metabolite. (Sabri, N van Holst. 2020). Antibiotics are emerging environmental pollutants of concern due to their possible adverse impacts on nontarget organisms and increasing resistance among bacteria (Wang *et al.* 2015). When antibiotics enter the environment, they can change the dominant flora, community composition, and structure, as well as microbial diversity and richness. However, some environmental conditions significantly moderate the severity of the impacts (Qiu, J. Chen *et al.* 2023). Antibiotic resistance is an adaptive genetic

characteristic that subpopulations of some bacteria exhibit and acquire, which enables them to survive and grow in the presence of therapeutic doses of an antibiotic agent. (Santos *et al.* 2016). This occurs because certain antibiotics, which are often released into the environment at low concentrations, exert significant selective pressure on bacterial communities, resulting in the development of their resistance (J.K. Chatterjee *et al.* 2022). The mechanism for bacterial resistance development is by genemutation or horizontal gene transfer. Resistance can therefore be developed towards a single antibiotic and then spread to a vast array of mobile genetic elements. Secondly, bacteria may acquire resistance towards multiple drugs, leading to difficulties in managing these cases in healthcare facilities. (Kunhikannan *et al.* 2021). It is difficult to assess and replace antibiotics to which resistance has arisen with newly developed ones in the quickest way possible. This reduces the number of therapy options, raises treatment expenses, lengthens hospital stays, results in unsuccessful treatments, and can cause deaths (Dires. S. Birhanu *et al.* 2018). One of the sources of antibiotics in the environment is hospital wastewater effluent. A variety of factors influence hospital wastewater production, including water supply, bed availability, general services such as air conditioning, kitchen, and laundry the types and number of units or wards, and management practices. All of these processes contribute to the total amount of wastewater produced (Khan, M.T Shah *et al.* 2021). For the purpose of removing contaminants from hospital wastewater, a variety of technologies, such as functionalized membrane filtration, persulfate activated degradation, heterogeneous photocatalysis, Fenton-like degradation, and adsorption, have been investigated (Vieira y pereira *et al.* 2021). Conventional wastewater treatment facilities are designed to remove

pollutants, such as total organic carbon, and nutrients, such as nitrates and phosphates. They are not intended to particularly remove micropollutants, such as antibiotics and antibiotic resistance genes (ARGs). The removal of antibiotics and ARGs in these systems varies by 1–2 log (Sabri *et al.* 2020). As a result, large amounts of antibiotics and ARGs are released into water bodies (Ben Y. Hu *et al.* 2021). Humans can receive resistant bacteria from contaminated food and water, infected animals—through direct contact, meat, or milk consumption contact with infected humans, and manure used as fertilizer (Chang, Q Wang *et al.* 2015). Even if antibiotic-resistant bacteria have been damaged or eradicated during wastewater treatment, ARGs may still be discharged into the environment and transformed into other bacteria. Previous research has found that ARGs are abundant in wastewater lagoons and municipal wastewater even after treatment (Zhang S Lu *et al.* 2020). This necessitates the development of effective antibiotic removal techniques that can also inhibit the spread of ARGs (Wang M Shen *et al.* 2017).

LITERATURE REVIEW

Petro Karungame, Anita Rugaika, Kelvin Mtei & Revocatus Machunda, (2023) studied on A study in Tanzania detected the following pathogens in treated hospital wastewater: *Klebsiella* spp. 39.3%, *E. coli* 27.9%, and *Pseudomonas* spp. 18.0%. *Klebsiella* spp. was highly resistant to tetracycline, gentamycin, ciprofloxacin, and sulfamethoxazole. Constructed wetland treatment was used.

Betsy Foxman, Elizabeth Salzman, Chelsie Gesierich, Sarah Gardner, Michelle Ammerman, Marisa Eisenberg, and Krista Wigginton, (2024) studied Antibiotic resistance is a major threat. Strategies include regulation, stewardship, education, and limiting agricultural use. Wastewater surveillance allows the detection of trends and emerging resistance, but this methodology must be improved for more precise tracking.

Mihret Tilahun, Agumas Shibabawand Metadel Adane, (2025) studied on Treatment systems in Ethiopia indicate that its wastewater and drinking water can be contaminated with bacteria, hence creating a public health risk: 82.57% and 42.18%, respectively. *Pseudomonas aeruginosa* most common, 41.25%. 65.26% of the wastewater samples contained multidrug-resistant strains. There is a dire need for better treatment and monitoring.

Prince Hotor, Fleischer C. N. Kotey and Eric S. Donkor, (2025) studied Poor monitoring and wastewater treatment in the region are quite urgent, while antibiotic-resistant bacteria such as *E. coli* (42.6%) and *K. pneumoniae* (32.1%) are predominant in West African hospital wastewater, with blaTEM and blaSHV being highly prevalent resistance genes (76% and 59.3%, respectively). Few studies have focused on toxin genes and antibiotic residues.

Gauri Kumara, Keshava Balakrishna, Chiranjay Mukhopadhyaya, and Vandana Kalwaje Eshwara, (2024) studied on It was observed that isolates from hospital wastewater were more resistant, at 86.7% MDR, when compared to municipal wastewater at 48.3% MDR. Resistance was higher in municipal wastewater post-monsoon. Integrons were detected in 17.7% isolates from hospitals and in 19.7% isolates from municipal samples, with the presence of trimethoprim and aminoglycoside resistance. WWTPs contribute to the dissemination of AMR.

Alisha Aky, Roya Chegenelorestani, Jila Shahvaisy-Zadeh, Arezoo Bozorgomid (2020) studied on A detected that 98% of *S. aureus* isolates from hospital wastewater in Iran were multidrug resistant. MRSA was detected in 11% of raw and 8% of treated samples. The common resistance genes are mecA, aacA-D, tetK (MRSA); tetM (MSSA). All MRSA isolates showed resistance to penicillin, oxacillin, and azithromycin. The finding thus indicates that careful wastewater treatment is required to avoid the spread of resistant *S. aureus*.

Brandon Bojar, Jennifer Sheridan, Rachele Beattie, Caitlin Cahak, Elizabeth Liedhegener, L Silvia, Krassimira Hristova, Troy Skwor (2021) studied on Antibiotic resistance patterns of *Escherichia coli* isolates from the clinic through the wastewater pathway, Results obtained indicated that the rate of AMR was highest in clinical UPEC at 46.8%, and in hospital wastewater, 37.8%; multi-drug resistance was most prevalent in hospital wastewater, 29.7%. Chlorine disinfection increased trimethoprim-sulfamethoxazole resistance, and hospital wastewater was a rich source of AMR and multi-drug resistant bacteria dominated by phylogroup A, while UPEC was dominated by phylogroup B2. La Thi Quynh Lien, Pham Thilan, Vishal Diwan, Ashok Tamhankar (2017) studied on In Vietnam, it was determined that 83% of *E. coli* isolated from hospital wastewater exhibited resistance to at least one antibiotic, including 32% displaying multi-resistance. The highest rates of resistance were recorded for co-trimoxazole at 70%, while the least frequent was imipenem at 1%. ESBL-positive *E. coli* were present at 43%, and genes such as blaTEM and blaCTX-M were identified; such bacteria in treated wastewater pose a threat to public health and demonstrate that better wastewater treatment is needed. G.Y. Liyanage, Pathmalal M. Manage (2017) studied on bacteria from the hospital effluent within Sri Lanka depicted high resistance against antibiotics. 68% resistant to 5+ antibiotics. Dominant bacteria: *Bacillus* sp., *Enterobacter* sp., *E. coli*. Resistance highest against AMX (28%) and AMP (21%). MIC: 60-660 µg/ml. Warns that antibiotic emission to the environment could reduce therapy effectiveness. Asim Shahzad, Abrar Hussain Mian, Tauseer, Tauseef Hamid (2021) studied on 7 bacterial pathogens were identified in the hospital wastewater; *S. aureus* and *E. coli* were identified to be the most common. Highly resistant to Gentamycin, Tetracycline, and Levofloxacin. Susceptible to Vancomycin, Cefixime, Tazobactam, and Doxycycline. Public health risk necessitates proper management protocols.

DISCUSSION

The results of our review have emphasized that hospital wastewater is an important reservoir for antibiotic-resistant bacteria, particularly *Staphylococcus aureus* and *Escherichia coli*. Both organisms in the present study have shown high resistance rates toward commonly used antibiotics. *S. aureus* isolates were highly resistant to β-lactam antibiotics, revealing the presence of MRSA strains, while *E. coli* were multidrug-resistant and included ESBL producers. These findings are consistent with previous studies that also detected similar resistance patterns among hospital effluents worldwide. The persistence of resistant strains even in treated wastewater points toward the inefficiency of conventional treatment systems in completely removing antibiotic residues and resistant bacteria. Continuous discharging of antibiotics and other chemical contaminants exerts selective pressure that supports the survival and transfer of resistance genes among bacterial populations. Such resistant organisms in hospital wastewater may become hazardous to the environment and public health, as they may enter community water sources and further spread resistance. Our findings emphasize that there is a need for immediate consideration of effective strategies in wastewater management, regular antimicrobial resistance monitoring, and proper use of antibiotics within the healthcare setup in order to reduce the spread of resistance through hospital wastewater.

CONCLUSION

The contribution of antibiotic-resistant bacteria, especially *Staphylococcus aureus* and *Escherichia coli*, to the hospital wastewater makes it a significant source. The presence of MRSA and ESBL-producing strains depicts serious public health concern. Inadequate treatment systems allow resistant bacteria and genes to enter the environment, enhancing the possibility of the spread of resistance. Wastewater treatment, stringent control of antibiotics, and monitoring become necessary in order to reduce resistance to antimicrobials and ensure the safety of public health.

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