Antibiotic-Resistant Bacteria Risks and Challenges for Human Health and Environment: An Overview

Suman Sarkar[1], Madhu Kamle[2], Ajay Bharti[1], Pradeep Kumar[3]*

[1]Department of Civil Engineering, North Eastern Regional Institute of Science and Technology, Nirjuli 791109, India.
[2]Applied Microbiology Laboratory, Department of Forestry, North Eastern Regional Institute of Science and Technology, Nirjuli 791109, India.
[3]Department of Botany, University of Lucknow, Uttar Pradesh-206007 India.

ABSTRACT

The purpose of this review was to examine the risks and challenges of antibiotic-resistant bacteria for human health and the environment. The evolution of Antibiotic Resistance Genes (ARGs) and Antibiotic-Resistant Bacteria (ARB) in Municipal Solid Wastes (MSW) landfills, hospital wastewater, and poultry farms are explored in-depth in this paper. MSW output has risen significantly in recent years. MSW landfills are the most popular method of MSW disposal. Landfills receive a variety of wastes, including unused and expired antibiotics, as well as bioactive wastes. As a result, MSW provides favorable conditions for the growth of antimicrobial resistance (AMR), as well as the transfer of ARGs from landfill bacteria to bacteria in the surrounding environment. Antibiotic usage that is unrestricted and excessive in healthcare facilities frequently results in an increase in antibiotic resistance and the dissemination of ARGs in the surrounding environment via hospital wastewater. The occurrence of ARB and the degree of resistance of bacterial strains from numerous landfills and hospital wastewater are discussed in this review. This is a critical concern for public health because once ARBs and ARGs enter the water environment, they can spread resistance genes to bacteria in the surrounding environment. The consequences of ARB and ARGs on the environment and public health are also described in this review. AMR is widely regarded as a major threat to public health systems worldwide, not only in developing countries. Antibiotics are commonly used in farm animals, and unmetabolized antibiotics, or ARGs and ARB, may be prominent in runoffs coming from animal wastes, posing a direct threat to surrounding water bodies.

Keywords: *Municipal solid waste, Landfill, Antibiotic resistance genes, Antibiotic-resistant bacteria*

INTRODUCTION

In 1910 salvarsan the first antibiotic was introduced. The introduction of antibiotics for clinical use in the 20th century was considered an exceptional medical breakthrough. In addition to treating bacterial infections, many modern medical procedures including organ transplants, open-heart surgery, and cancer treatment have been made possible by the use of various antibiotics. The rise of AMR has resulted from the misuse of antibiotics, resulting in some infections being effectively untreatable (Hutchings *et al.*, 2019). Medicine has been transformed by the use of antibiotics in many respects, and saved countless lives; the discovery of antibiotics was a turning point in medical history. The usage of these medications has accelerated the emergence of bacterial strains that are resistant to them. More than 20,000 potential resistance genes (r genes) of over 400 different categories have been reported in a recent database. When streptomycin was first used to treat tuberculosis in 1944, it caused the emergence of mutant strains of Mycobacterium tuberculosis that were resistant to

therapeutic doses of the antibiotic. A similar course of events was observed for other antibiotics. Many of these resistant strains have evolved to be multidrug-resistant (MDR). One example is *M. tuberculosis*, which is a major pathogen and is emerging in many nations around the world as the 20th-century version of the old pathogen (Davies & Davies, 2010; Taha *et al.,* 2022).

Modern times have witnessed a drastic rise in the generation of MSW. The main causes of this increase are population growth, fast urbanization, and rising living standards owing to economic growth (Sankhala *et al.*, 2021). MSW is a complicated collection of elements that are both biodegradable and not. The majority of the biodegradable garbage is made up of leather, food scraps, paper, leaves, and wood trimmings, while the non-biodegradable waste is made up of glass, metals, and plastics. Hazardous substances such as old batteries, paints, cosmetics, medicinal ingredients, and e-waste are also found in MSW. Studies by Gupta and Aurora (2016) have indicated that in India around 68.8 million tons of MSW is generated per year. Serious environmental and human health problems result from the poor management of MSW (Alanazi *et al.*, 2021; Sankhala *et al.*, 2021). Greenhouse gases (CH_4 and CO_2) are produced from the decomposition of food wastes and other organic wastes in MSW landfill sites. These gases have the most global warming

capacity. Despite rapid globalization, landfilling is one of the most commonly used methods for the disposal of MSW; these old-fashioned landfills are not designed to stop the percolation of leachate in the soil. Undesirable toxic materials such as organic pollutants, heavy metals, antibiotics, pharmaceutical, and personal care products, etc, that further pollute the sub-soil and the groundwater by percolating during rainfall are present in landfill leachate (Anand *et al.*, 2021). In addition to these chemical contaminants landfill leachate contains an abundance of ARB, ARGs, and pathogenic bacteria; which is a major concern because the ARGs may get transmitted to human pathogens via Horizontal Gene Transfer (HGT). Therefore, it is very important to remove medical wastes and PPCPs (Pharmaceutical and Personal Care Products) for the protection of aquatic life and to stop the transmission of ARGs from landfills to humans via human pathogens. Organic leachate produced from the decomposition of food scraps can significantly alter the bacterial community with time and temperature and proliferate the growth of pathogenic bacteria such as *Clostridium perfringens, Pseudomonas, Enterobacteria,* and *Salmonella* (Anand *et al.*, 2021). Ions of heavy metals can co-regulate the genes responsible for increased antibiotic resistance and reduce the susceptibility to antibiotics. The widespread emergence of MDR bacteria has been reported in recent years, which is an important constraint in the cure of infectious diseases (Alhussain *et al.*, 2021; Sankhala *et al.*, 2021).

Antibiotics are drugs used for preventing and treating bacterial infections. The ability of bacteria to resist the healing effects of an antibiotic to which they were previously sensitive is known as antibiotic resistance. Bacteria become antibiotic-resistant by either receiving ARGs or genetic mutations. ARB infections are reported to have morbidity and mortality rates and result in longer hospital stays. When bacteria change in response to these drugs then antibiotic resistance occurs. Not animals nor humans, but bacteria itself become antibiotic-resistant. Humans and animals may get infected by these pathogenic bacteria, and cause infections that are harder to treat than those caused by non-resistant bacteria. Ill effects of antibiotic resistance include higher medical costs, longer stays at hospitals, and increased mortality. There is an urgent need for the prescription and use of antibiotics in the medical world. Without behavioral change, the development of new medicines will not be enough to deal with antibiotic resistance. As more drugs are being developed with the advent of antibiotics, some of the serious infections are now treatable. Self-medication by patients and extensive use of antibiotics by medical personnel have increased the tolerance of microbes to these drugs. The use of antibiotics as additives in animal feed further complicates resistance. A major public health problem is created when untreated hospital wastes are improperly disposed of in rivers, roads, and drains, especially in developing nations is a major concern. Such improper disposal of hospital wastewater in an open environment facilitates the exchange of genetic materials with previously non-resistant bacteria (Adieze *et al.*, 2015). A selective pressure is exerted on consuming antibiotics (abiotic or biotic factors that change the behavior and fitness of an organism in a given surrounding) inside the gut, leading to antibiotic resistance in enteric bacteria. Around 21-66% of ARB was observed in chicken manure collected from farms that use GEN, kanamycin, AMX, and cephalexin. 8-20% of the ARB isolates were resistant to multiple drugs (Amarasiri *et al.*, 2020).

The purpose of this review was to examine the risks and challenges of antibiotic-resistant bacteria for human health and the environment.

RESULTS AND DISCUSSION

Antibiotic-resistant bacteria (ARB) in MSW landfills

Municipal Solid Waste (MSW) landfills are the most widely practiced for disposal of MSW. Landfills receive a variety of wastes including expired and unused antibiotics and bioactive wastes thus, MSW provides favorable conditions for the growth of AMR and transfer of ARGs from one landfill bacteria to the outer environmental bacteria (Chen *et al.*, 2017). Landfill leachate is a complex mixture of many hazardous and toxic organic pollutants, that can promote the modification of ARGs and ARB in the surrounding. It has many negative effects on the environment, wildlife, public health, soil, aquatic life, surface water, and groundwater. In conventional or poorly designed MSW landfills the leachate contains the ARGs and ARB will eventually percolate in the sub-soil and find its way into the underlying groundwater **(Figure 1)**. The appearance of ARB in humans can imbalance intestinal functions, and accelerate the growth of pathogenic bacteria causing intestinal imbalance, colon cancer, bowel cancer, and other untreatable diseases (Anand *et al.*, 2021). Infections caused by ARB have higher mortality rates, and higher morbidity resulting in longer hospitalization time. Antimicrobial resistance is a serious threat to achieving Universal Health Targets and it also hinders the sustainable goals for public health safety, clean water, food security, and sanitization (Adieze *et al.*, 2015). The presence of Multi-drug Resistance among microorganisms has become a major global concern. A mechanism has been developed by these microbes to resist the effects of various antibiotics currently being used. As the air currents move the pathogenic microorganisms from the soil into the atmosphere, possible air pollution is caused. It can also lead to the pollution of groundwater as the leachates from dumpsites get percolated in the subsoil and ultimately get mixed with groundwater. The atmospheric transport of pathogens has been identified as a key mode for the transmission of diseases and microbial dispersion (Odum *et al.*, 2020).

Mutations in microorganisms can be caused by the creation of selective pressure in the environment due to the presence of antibiotics, heavy metals used in households and industries, and products used in disinfection and sterilization. The growth of microorganisms is accelerated in landfills due to indiscriminate dumping of wastes, thus posing a danger to humans. Urban wastes contain a variety of components from various sources such as animal sheds, markets, and hospitals, and may contain AMR bacteria belonging to animal and human commensal flora, mainly *Enterobacteriaceae* (Waturu *et al.*, 2017). Many studies have identified landfills as a significant source of mobile genetic elements (MGEs), ARGs, and resistant bacteria **(Table 1)**. Resistant genes in bacteria may be innate or the result of selective pressure placed on the bacteria by a specific antibiotic. Antibiotics at high doses could thus play a key role in the development of resistance in resident microorganisms, as well as the spread of resistance to other microbes (Borquaye *et al.*, 2019). MSW landfills have been recognized as a hotspot for genetic elements (MGEs), ARGs, and resistant microbes. The presence of ARGs in microbes may be the result of selective

pressure imposed by a particular antibiotic on the microbial population or due to intrinsic changes in microbes. One of the main reasons for the development of ARB and the possible

dissemination of ARGs to other microbes is due to the presence of high levels of antibiotics (Borquaye *et al.*, 2019; Mai *et al.*, 2021).
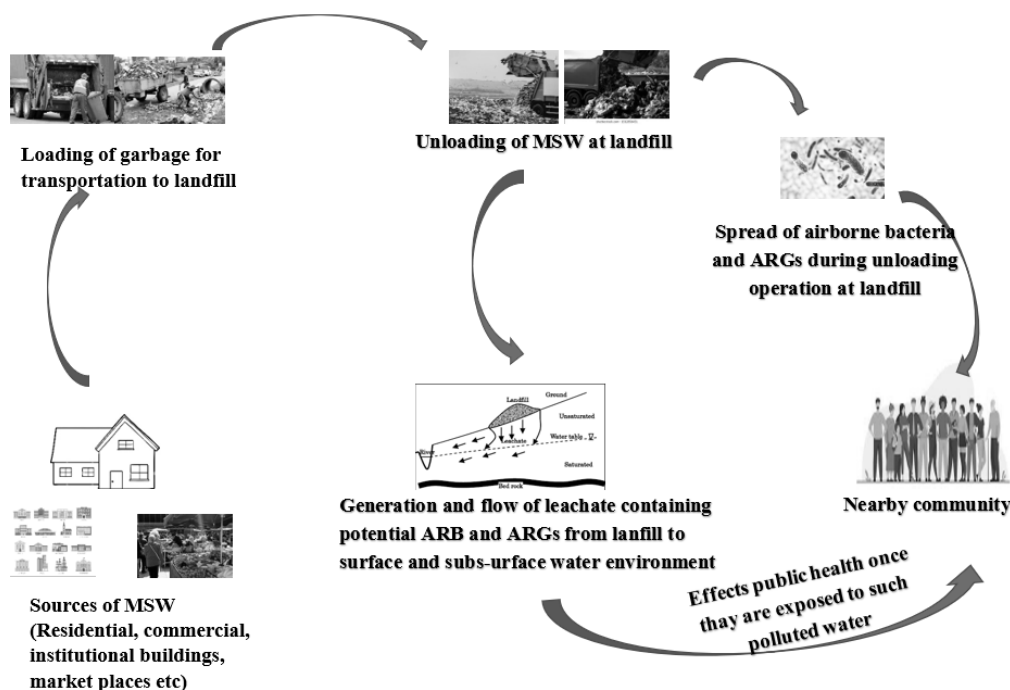
Figure 1. The diagram depicts the generation, and transportation of MSW to landfill, the proliferation of ARB and ARGs in landfill, and spread through leachate movement and during unloading operations, thus posing a health risk for nearby communities.

Table 1. Detection of Antibiotic Resistant Bacteria (ARB) MSW Landfill Samples

S/N	Location	Type and source of sample	Bacteria identification method	Bacteria Identified	Antibiotics used	Results and key findings	Reference
1	Cachar, Assam, India	soil samples from public grounds and uncultivable lands.	Morphological, biochemical, and Molecular	*Bacillus megaterium*, *Bacillus cereus*, *Pseudomonas aeruginosa*, and *Chromobacterium pseudoviolaceum*	GEN (50 µg), AK (30 µg), CN (30 µg), MET (30 µg), TE (30 µg), CTR (30 µg), AMP (25 µg), C (10 µg), AMX (10 µg), K (5 µg), OF (5 µg) and CFM (5 µg)	All of the isolates were resistant to penicillin and methicillin. The most resistant *P. aeruginosa* strain exhibited resistance to Cefdinir, Ampicillin, Kanamycin, Rifampicin, and Vancomycin.	Nath *et al.* (2019)
2	Ujjain City, Madhya Pradesh, India	soil samples from the waste dumping site	Biochemical and morphological	*Pseudomonas* sp., *Bacillus* sp., and *Enterobacter* sp.	AK (30 µg), AMC (30 µg), AMP (10 µg), AT (30 µg), CPM (30 µg), CTX (30 µg), CAZ (30 µg), C (30 µg), CIP (5 µg), DOR (10 µg), ETP (10 µg), GEN (10 µg), IPM (10 µg), LEV (5 µg), PIT (100/10 µg), PB B (300 units), TCC (30 µg) and TOB (30 µg).	Every antibiotic was effective against Enterobacter sp. About 52% of cultures were resistant to antibiotics, and 33% of cultures were multi-antibiotic resistant.	Sankhala *et al.* (2021)

#	Location	Sample source	Method of identification	Bacteria isolated	Antibiotics used	Findings	Reference
3	Kumasi, Ghana	soil samples and leachate from landfill sites	Biochemical and morphological	*Bacillus, Citrobacter, Pseudomonas, Klebsiella, Enterobacter, Proteus, Aeromonas, Listeria*, and *Shigella*	GEN, CIP, AK, AMP, AMX, CXM, E, TE, and P with specific concentrations (5–30 µg).	Two *Bacillus* spp. isolates exhibited resistance to AMP. Enterobacteriaceae (*Klebsiella, Enterobacter, Citrobacter, Proteus, and Shigella*) isolates were resistant to ampicillin, amoxicillin, and cefuroxime but susceptible to gentamicin, ciprofloxacin, and amikacin.	Borquaye *et al.* (2019)
4	Abraka, Delta State, Nigeria	Soil samples from the waste dumping site	Cultural, Morphological, and Biochemical	*Escherichia coli, Staphylococcus* spp., *Streptococcus* spp., *Proteus* spp., *Pseudomonas* spp., *Klebsiella* spp., *Neisseria* spp., *Micrococcus* spp., *Bacillus* spp., *Proteus* spp., *Klebsiella* spp., and *Bacillus* spp.	Antibiotic discs used against gram-positive organisms contained AX (30 µg), CXM (20 µg), AMX (30 µg), CTR (25 µg), CIP (10 µg), S (30 µg), COT (30 µg), E (10 µg), PF (10 µg) and CD (10 µg), while those used for gram-negative organisms contained COT (30 µg), C (30 µg), SPX (10 µg), AMX (30 µg), AMC (30 µg), GEN (10 µg), OF (10 µg), PF (10 µg), S (30 µg) and CIP (10 µg)	Pefloxacin was the least effective as 96% and 76.67% of gram-positive and gram-negative organisms respectively, were resistant to this antibiotic. All the isolates were observed to be MDR. A MAR index of 0.8 was recorded for 31.15% of the isolates tested while a MAR index of 1.0 was recorded for one isolate (*Bacillus* spp.). Only 3.28% of isolates tested showed low MAR indexes of 0.3 and 0.4.	Odum *et al.* (2020)
5	River Melayu, Southern Malaysia	River water sample	Molecular	*C. violaceum, E. coli, E. cloacae, K. pneumonia, S. maltophilia*, and *E. faecalis*	CX (FOX), CTX (CTX), CIP (CIP), E (E), GEN (GM), MRP (MEM), COT (SXT), TE (TE), and VA (VAN)	A total of 25% of *E. coli* and 44.4% of *P. monteilli* showed resistance to Meropenem. All *E. coli* and *K. pneumoniae*, 50% of *E. cloacae*, 33.3% of *P. Montville,* and 66.7% of *P. pseudoalcaligenes* displayed resistance to Tetracycline, while 14.2% of *E. faecalis* were only intermediate resistant.	Ho *et al.* (2021)
6	Bangladesh	Household Kitchen waste, dustbin, liquid wastes	morphological	*Staphylococcus* spp., *Salmonella* spp., *Pseudomonas* spp., *Vibro* spp., *Klebsiella* spp., *E.* coli, and *Bacillus* spp.	CAC (30/10 µg), MRP (10 µg), COT (25 µg), CIP (5 µg), AZM (30 µg), CFM (5 µg), CTR (30 µg), CXM (30 µg), AMX (30 µg), AK (10 µg).	All the Isolates were found to be MDR (resistant against two or more drugs). Isolates of *Klebsiella* spp. and *Bacillus* spp. showed resistance against CAC, CIP, and CFM. CAC and CFM resistance was exhibited by *Staphylococcus* spp. *Salmonella* spp. and *Vibrio* spp. were found to be resistant to COT.	Akter *et al.* (2020)
7	Nairobi, Kenya	Soil and water from Dumpsites and garbage Collection areas	Biochemical tests	*Escherichia coli*, and *Klebsiella*	AMP (10 µg), CPD (10 µg), CAZ (30 µg), CX (30 µg) CPM (30 µg), AMC (10/100µg ratio), CIP (10 µg), TE (30 µg), COT (30 µg), GEN (10 µg), C (30 µg), S (25 µg), NA (10 µg), and MRP (10 µg).	Most (61%) of the isolates were resistant to 1 - 3 antimicrobials. Another 23% of isolates were resistant to more than 3 antimicrobials and were thus MDR.	Waturu *et al.* (2017)

*Symbols used for Antibiotics

AK-Amikacin, AMX-Amoxicillin, AMC-Amoxicillin/Clavulanic acid or Amoxyclav, AMP-Ampicillin, AU-Augmentin, AZM-Azithromycin, AT-Aztreonam, CEC-Cefaclor, CN-Cefalexin, CDR-Cefdinir, CPM-Cefepime, CFM-Cefixime, CTX-Cefotaxime, CX-Cefoxitin, CPD-Cefpodoxime, CAZ-Ceftazidime, CAC-Ceftazidime/Clavulanic acid, CTR-Ceftriaxone, ZIN-Zinnacef, CXM-Cefuroxime, CN-Cephalexine, CEP-cephalothin, C-Chloramphenicol, CIP-Ciprofloxacin, CD-Clindamycin, COT-Co-trimoxazole, DOR-Doripenem, DOX-Doxycycline, ETP-Ertapenem, E-Erythromycin, FR-Furazolidone, GEN-Gentamicin, IPM-Imipenem, K-Kanamycin, LEV-Levofloxacin, LOM-Lomefloxacin, MRP-Meropenem MET-Methicillin, VA-Vancomycin, MO-Moxifloxacin, NA-Nalidixic acid, NET-netilmicin, NIT-Nitrofurantoin, OF-Ofloxacin, OX-Oxacillin, PF-Pefloxacin, P-Penicillin, PIT-Piperacillin/tazobactam, PB-Polymyxin, PB-Polymyxin, BPEF-Reflacine, RIF-Rifampicin, STX-Septrin, SPX-Sparfloxacin, S-Streptomycin, OFX-Tarivid, TE-Tetracycline, TCC-Ticarcillin/Clavulanic acid, TOB-Tobramycin, COT-Trimethoprime/sulphamethoxazole.

Antibiotic-resistant bacteria (ARB) in hospital wastewater

The excessive use of antibiotics in health establishments and hospitals for the treatment of diseases leading to resistance in microbes is a familiar problem, but the irrational use of such drugs and the resistance being developed as an environmental issue have been largely overlooked. Excessive and unrestricted use of antibiotics generally leads to an increase in ARB and causes the spread of ARGs in the surrounding through hospital wastewater. Hospital wastewater is considered a highly selective pollutant and is a contributor to high rates of ARB that

are being disseminated into the environment **(Table 2)**. Hospital wastewater aids in the selection of ARB by eliminating or inhibiting the growth of susceptible ones (Hauhnar *et al.*, 2018). Hospital wastewater is considered hazardous for ecological balance and public health due to its content of pathogenic microbes, chemical and pharmaceutical wastes, and radioactive wastes. Excessive and uncontrolled utilization of antibiotics by animals and humans leads to ARB and results in the spread of ARGs in the environment in the form of hospital wastewater. Studies have indicated that wastewater generated from hospitals is highly selective and contributes to high rates of resistant bacteria that are ultimately released into the natural environment. The selection pressure on bacteria is indicated by the number of antibiotics used in hospitals and effluents being released (Moges *et al.*, 2014; DO *et al.,* 2022).

During the span of the last two decades, a noticeable decline has been seen in the development and discovery of new antibiotics and a remarkable resistance has been observed to the antibiotics currently available. Selection pressure, mutation, and mechanism of genetic exchange have enabled many bacterial species to quickly adapt to an environment full of antibiotics. Unmetabolized antibiotics in a low concentration contained in untreated hospital waste disposals largely subsidize the development of ARB. Hence hospital wastewater is a hotspot for HGT of ARGs and thus proliferates resistant pathogenic bacteria. Global healthcare, travel, and medical tourism may contribute largely to the spread of ARB (Rabbani *et al.*, 2017, Dorobanțu *et al.*, 2022). Hospitals are thought to be the primary source of ARB; nevertheless, it has been seen that ARB is also disseminated to the community by colonized patients and through hospital wastewater disposal facilities. The incorrect and excessive use of antibiotics in human therapies, animal husbandry, aquaculture, etc. is the primary cause of ARB growth in the environment. Globally, 700,000 people die each year from diseases that are resistant to treatment; if appropriate steps are not taken, that number might rise to 10 million by the year 2050. A lack of consistent action to restrict AMR may result in the deaths of around 2.4 million individuals in high-income countries between 2015 and 2050, according to estimates (Rahman *et al.*, 2021; Rasueva *et al.*, 2023). The emergence of more infectious diseases, the revival of many infections that have been treated, and the recent increase in ARB in the environment a challenge for the medical community. The concept of ARB and ARGs is not new, but the sudden surge in ARB and the spread of ARGs is of great concern. Some of the major causes of the development and spread of ARB and ARGs are inappropriate use of antibiotics for medical purposes and negligence by patients in completing the prescribed medicines (Mustapha & Imir, 2019; Truong *et al.,* 2023).

Table 2. Detection of Antibiotic-Resistant Bacteria (ARB) from Hospital Wastewater Samples

S/N	Location	Type and source of sample	Bacteria identification method	Bacteria Identified	Antibiotics used	Results and key findings	Reference
1	Aizawl, Mizoram, India	Sewage dumping sites of hospitals	Morphological	*Morganella morganii*, and *Bacillus cereus*	AMP, K, CIP, C	It was found that the two strains were very resistant to the antibiotic Ciprofloxacin. The strain from Aizawl Civil Hospital (*Morganella morganii* designated as HC), showed a very high resistance to CIP and a very high concentration of 50 μg/ml could not eliminate the HC strains.	Hauhnar *et al.* (2018)
2	Owerri, Nigeria	Liquid wastes from hospitals	Morphological and Biochemical	*Klebsiella* spp., *Pseudomonas* spp., *E. coli*, *S. aureus*, *Coagulase negative*, *Staphylococcus* spp.*, Streptococcus* spp., *Salmonella* spp., *Proteus* spp., and *Enterobacter* spp.	PF, AMX, TE, NIT, ZIN, CIP, GEN E, C	*S. aureus* was observed to be the most resistant species isolated, being resistant to all the antibiotics tested. The coagulase-negative *Staphylococcus* was the most susceptible bacterial isolate and was susceptible to Pefloxacin, Nitrofurantoin, Zinnacef, Ciprofloxacin. Pseudomonas spp. and E. coli were susceptible to Zinnacef only.	Adieze *et al.* (2015)
3	Northwest Ethiopia	Untreated hospital wastewater	Biochemical	*Enterobacter* spp., *E*. coli, *Klebsiella* spp., *Pseudomonas aeruginosa*, *Enterococci* + CoNS, *S. aureus*, *Shigella* Spp., and *Citrobacter* spp.	AMP (10 μg), C (30 μg), CIP (5 μg), CD (2 μg), E (15 μg), GEN (10 μg), MET (5 μg), VA, (30 μg), S (10 μg), COT (5 μg), TE (30 μg), NA (30 μg), CEP (30 μg), CTX (30 μg), K (30 μg).	All the isolates of *S. aureus* were resistant to Ampicillin (100%). One isolate of *S. aureus* was resistant to 11 antimicrobials including Methicillin. However, no isolates of *S. aureus* were found to be VA-resistant. MDR was also common in gram-negative. All isolates of *E. coli*, *Citrobacter* spp. And *Enterobacter* spp. were 100% resistant to AMP. The overall resistance of gram-negative bacteria to Ampicillin was 97%.	Moges *et al.* (2014)

	Location	Sample	Identification	Antibiotics	Results	Reference
4	Dhaka City, Bangladesh	Wastewater samples from sewerage disposal points of hospitals	Biochemical and Fermentation tests	*E. coli*, and *K. pneumoniae*	CTX, CAZ, C, CIP, IPM, K, S, AMP, COT, GEN, CEC, CPM, CFM, CPD, CXM, CN, DOX, FR, LEV, LOM, MRP, MO, NA, OF, and TE.	Most of the *K. pneumoniae* isolates were MDR. When compared to *E. coli*, lower resistance was observed against all of the antibiotics in *K. pneumoniae* except Ampicillin (100%). Maximum resistance was observed in one *E. coli* isolate that was resistant to 21 out of 25 antibiotics.	Rabbani *et al.* (2017)
5	Maijdee, Noakhali, Bangladesh	Hospital wastewater samples	Morphological and Biochemical	*E. coli, Eterobactor* spp., *Klebisella* spp., *Shigella flexneri, Pseudomonas* spp., *Proteus* spp., *Vibrio* spp., *S aureus*, and *S epidermidis*	AZM (15 µg), GEN (10 µg) AMP (25 µg), TOB (10 µg), CPM (30 µg), DOX (30 µg), NIT (300 µg), NET (30 µg), CIP (5 µg), CTX (30 µg), C (30 µg), AK (30 µg), OX (1 µg), S (10 µg), CFM (5 µg), and CAZ (30 µg).	All the MAR bacteria (n = 30) were found to be resistant to antibiotics ampicillin oxacillin and cefixime. 29 isolates were resistant to cefotaxime. *E. coli Enterobacter* spp. and *Klebsiella* spp. showed 100% resistance to ampicillin oxacillin cefotaxime and cefixime whereas over 50% of them were found resistant to azithromycin and ciprofloxacin.	Rahman *et al.* (2021)
6	North-East Nigeria	Hospital sewage samples	Morphological and Biochemical	*Escherichia coli* (331 24.0%), *Salmonella enteric* (187 13.5%), *Pseudomonas aeruginosa* (113 8.20%), *Proteus mirabilis* (69 5.01%), *Klebsiella pneumoniae* (271 19.6%), *Vibrio cholera* (89 6.4%), *Morganella morganii* (77 5.59%), *Shigella* sp. (20114.5%), *Citrobacter fruendii* (51 3.70%), and *Moraxella catarrhalis* (48 3.48%)	OFX (10 µg); PEF (10 µg); CIP (10 µg); AU (30 µg); GEN (10 µg); S (30 µg); CEP (10 µg); NA (30 µg); STX (30 µg) and AMP (30 µg)	All the isolates were found to be MDR, except *M. morganii*. All the isolates were resistant to Nalidixic acid and among the isolates, *E. coli* showed complete resistance (100%) to all the antibiotics, followed by *P. aeruginosa* and *P. mirabilis* (70% each), *K. pneumoniae* (60%), *C. fruendii* and *S. enteric* (50% each), *M. catarrhalis, V. cholera,* and *Shigella spp.* (40% each) while *Morganella morganii* (20%) was the least resistant.	Mustapha and Imir (2019)
7	Noakhali, Bangladesh	Hospital wastewater	Morphological and Biochemical	*Escherichia coli*	AMP (10 µg) CIP (5 µg) TE (30 µg) C (30 µg) CAZ (30 µg) GEN (10 µg) AZM (15 µg) CTX (30 µg)	Among the isolated *E. coli*; the 100%, 80%, 80%, 70%, 30%, 20%, 20%, and 10% isolates were resistant to AMP, CAZ, CTX, TE, C, GEN, CIP, and AZM antibiotics respectively. Isolate numbered 4 was resistant to all antibiotics.	Akther *et al.* (2018)

Antibiotic-resistant bacteria (ARB) in poultry farm

Poultry production is considered a means of economic development and poverty alleviation. The demand for quality sources of animal products is increasing by the day as low-income nations transition into higher incomes along with the fast-growing urban population. To meet this growing demand poultry production continues to change from traditional practices to intensive production using antibiotics. Rigorous poultry production may lead to an increase in AMR in facilities lacking biosecurity measures. AMR remains an emerging threat for animal and human health decreasing the ability to treat pathogenic bacterial infections and increasing the risk associated with mortality and morbidity due to resistant bacteria. It remains a pressing issue for both human and veterinary medicine to ensure the effectiveness of antibiotics in treating bacterial infections (Hedman *et al.*, 2020; Rasueva *et al.*,

2023). Apart from the antibiotics used in human therapy its use in agriculture and livestock farming is also considered a major source of ARB and ARG generation (Tripathi & Tripathi, 2017; Jain *et al.*, 2023). One of the important reasons for the generation of new ARGs and ARB to these antibiotics and genetic mutation in pathogenic bacteria is the irrational use of these antibiotics in treatment as well as growth promoters. This may also affect the commensal bacteria normally present in the gastrointestinal tract and may produce ARGs that may get transferred to the pathogenic bacteria by HGT and may give rise to a new ARB strain. ARB in poultry farms causes noticeable losses by spending a huge amount on the disinfection and treatment of poultry farms after infection (Hamed *et al.*, 2021). Antibiotics may be regulated to whole flocks rather than individuals in densely reared animals. Food animals such as turkeys and broilers may be fed with antimicrobials like

antimicrobial growth promoters (AMGP). However, the spread of ARB and ARGs from farm animals to humans is controversial (Van den Bogaard *et al.*, 2001).

Effects of ARB on human health

Consumption of antibiotics can influence the emergence of ARB by altering gastrointestinal functioning which could stay in the human gut for a very long duration. The proliferation of pathogenic bacteria may be caused by human gut microbiota imbalance may cause serious diseases like intestinal imbalance and colorectal cancer (Anand *et al.*, 2021). Even though antimicrobial resistance has attracted the interest of both the general public and the medical community the extent of the influence of ARB on health and economic outcomes is largely unknown. Antimicrobial-resistant infections have a variety of effects on patient outcomes. ARGs can change a bacterial pathogen's fitness making it more or less dangerous; resistance in a bacterial pathogen can cause a delay in the effect of a suitable antibiotic treatment process; and the antimicrobial therapies required to treat infections caused by ARB might be harmful or insufficient (Eliopoulos *et al.*, 2003). AMR is seen as a danger to public health systems across the world not just in developing countries. Antibiotics are no longer effective in treating infectious diseases implying that health care has an uncertain future. AMR infection causes significant diseases lengthier hospital stays greater healthcare expenses higher second-line medicine prices and treatment failures. Every year more than two million individuals in the United States fall ill with antibiotic-resistant illnesses resulting in at least 23000 fatalities according to the CDC (Centers for Disease Control and Prevention). Antibiotic resistance impairs the human immune system's ability to fight infectious infections, as well as causes complications in individuals undergoing dialysis, chemotherapy, or joint replacement. People with chronic conditions like diabetes, rheumatoid arthritis, and asthma will be particularly affected by antibiotic resistance. AMR results in significant morbidity and mortality consequences for patients. When compared to non-resistant bacteria, resistant bacteria have a twofold increase in the risk of having a serious health problem and a triple increase in the risk of death (Dadgostar, 2019).

Effects of ARB on the water environment

Antibiotics enter the environment through human excretions (urine and feces) incorrect disposal and/or handling of unused medications direct environmental contamination in aquaculture or plant cultivation and waste streams from antibiotic manufacture (Larsson & Flach, 2022). Human exposure to ARB and ARGs in aquatic habitats has been regarded as an effective setting for the acquisition and spread of antibiotic resistance. Human exposure to ARB and ARGs in aquatic environments may constitute an extra health risk (Amarasiri *et al.*, 2020). Disinfection and sterilizing products as well as heavy metals used in industries and households as well as antibiotics create selection pressure in the environment resulting in microorganism mutations (Waturu *et al.*, 2017). There is a risk that ARGs from ambient bacteria will be transmitted to infectious bacteria that can cause diseases in humans posing a public health risk (Hauhnar *et al.*, 2018). Antimicrobials are widely used in food animals and discharge from animal waste may contain unmetabolized antibiotics ARBs

and ARGs which have a direct influence on nearby water bodies (Landers *et al.*, 2012). The release of antimicrobials ARB and ARGs into the environment through human and animal waste is a global issue with major public health implications. In 2015 the World Health Organization (WHO) released a worldwide action plan on AMR with five strategic objectives one of which was to improve awareness of the spreading of AMR by monitoring and research. Whether effluents are intended for disposal into the environment or reuse for irrigation knowledge of the removal efficiencies of technologies used at Waste Water Treatment Plants is crucial for AMR surveillance (Ng & Gin, 2019; Krestonoshina *et al.*, 2022).

CONCLUSION

The rapid development of the world's population has resulted in the expansion of cities industries and hospitals which has increased the amount of trash produced. MSW management is a major issue that all developing cities must deal with. MSW generation is rapidly increasing posing a significant danger to world health and is also a significant environmental burden. Toxic contaminants such as ARGs, ARB, ECs, MGEs, and other inorganic contaminants are found in leachate from MSW landfill sites. These contaminants sink with the leachate but might be transferred with the plume where they mix with groundwater and are distributed further in the natural environment. It is critical to establish strategies for segregating wastes with the potential to generate ARBs and ARGs in MSW landfills. Because of poor pharmaceutical waste disposal, MSW landfills may cause antibiotic resistance in bacterial bioaerosol. The bacteria's resistance may have developed as a result of the species' lengthy exposure to antibiotics in the landfill site which must have allowed the bacteria to develop methods to evade the drug's actions. The capacity of resistant bacteria to pass on their ARGs to other infectious bacteria that can cause mortality is a critical issue that must be addressed. Antibiotics and other toxic contaminants contaminate water causing resistance to develop as a result of selection pressure. As a result, a suitable wastewater treatment facility should be created and hospitals should employ increased hygienic measures. Hospital wastewater must be properly treated before discharging into the environment and all other wastewater must be drained in an isolated place and not directly into irrigation fields ponds channels or rivers.

REFERENCES

Adieze, I. E., Nnadi, C., Braide, W., Azubuike, C., & Nduka, I. (2015). Antibiotic resistance pattern of bacterial isolates of liquid wastes and waste dump soils of hospitals in

Owerri, Nigeria. *Nigerian Journal of Microbiology*, *29*, 3002-3011.

Akter, A., Ahmed, S., Islam, T., & Munshi, S. K. (2019). Occurrence of drug resistant bacteria in household waste samples. *Stamford Journal of Microbiology*, *9*(1), 15-18.

Akther, S., Debnath, T., & Chowdhury, M. M. H. (2018). Multidrug resistant E. coli in hospital waste water: A potential concern for public health. *Advances in Biotechnology & Microbiology*, *8*(1), 555729.

Alanazi, A. M., Alawfi, A. H., Alrashidi, E. F. A., Alazmi, S. E. M., Alharbi, B. B. G., Alhowaish, K. F., Almasoudi, F. M., Al Sulail, A. J., Alanazi, L. M., & Alrashidi, B. S. (2021). An overview on antibiotics use in endodontic management. *Pharmacophore*, *12*(6), 10-14. doi:10.51847/5gRcbQKxpG

Alhussain, B. S., Alfayez, A. A., Alduhaymi, A. A., Almulhim, E. A., Assiri, M. Y., & Ansari, S. H. (2021). Effect of various antibacterial materials in dental composites: A systematic review. *Annals of Dental Specialty, 9*(3), 39-44. doi:10.51847/FlBp7cmL4q

Amarasiri, M., Sano, D., & Suzuki, S. (2020). Understanding human health risks caused by antibiotic resistant bacteria (ARB) and antibiotic resistance genes (ARG) in water environments: Current knowledge and questions to be answered. *Critical Reviews in Environmental Science and Technology*, *50*(19), 2016-2059.

Anand, U., Reddy, B., Singh, V. K., Singh, A. K., Kesari, K. K., Tripathi, P., Kumar, P., Tripathi, V., & Simal-Gandara, J. (2021). Potential environmental and human health risks caused by antibiotic-resistant bacteria (ARB), antibiotic resistance genes (ARGs) and emerging contaminants (ECs) from municipal solid waste (MSW) landfill. *Antibiotics*, *10*(4), 374.

Borquaye, L. S., Ekuadzi, E., Darko, G., Ahor, H. S., Nsiah, S. T., Lartey, J. A., Mutala, A. H., Boamah, V. E., & Woode, E. (2019). Occurrence of antibiotics and antibiotic-resistant bacteria in landfill sites in Kumasi, Ghana. *Journal of Chemistry*, *2019*.

Centers for Disease Control and Prevention. (2019). *Antibiotic resistance threats in the United States, 2019*. US Department of Health and Human Services, Centres for Disease Control and Prevention.

Chen, Q. L., Li, H., Zhou, X. Y., Zhao, Y., Su, J. Q., Zhang, X., & Huang, F. Y. (2017). An underappreciated hotspot of antibiotic resistance: The groundwater near the municipal solid waste landfill. *Science of the Total Environment*, *609*, 966-973.

Dadgostar, P. (2019). Antimicrobial resistance: Implications and costs. *Infection and Drug Resistance, 12*, 3903-3910.

Davies, J., & Davies, D. (2010). Origins and evolution of antibiotic resistance. *Microbiology and Molecular Biology Reviews*, *74*(3), 417-433.

Do, D. T., Nguyen, H., Tran, M. D., Nguyen, N. L., & Nguyen, T. B. T. (2022). A study on determinants influencing performance of accountants of SMEs in Vietnam. *Journal of Organizational Behavior Research, 7*(1), 58-71.

Dorobanțu, F. R., Hodoșan, V., Tîrb, A. M., & Carmen, D. (2022). Pattern of newborn antibiotic use in a tertiary level maternity for five years. *Pharmacophore*, *13*(3), 57-63. doi:10.51847/pq4Px0rkxG

Eliopoulos, G. M., Cosgrove, S. E., & Carmeli, Y. (2003). The impact of antimicrobial resistance on health and economic outcomes. *Clinical Infectious Diseases*, *36*(11), 1433-1437.

Hamed, E. A., Abdelaty, M. F., Sorour, H. K., Roshdy, H., AbdelRahman, M. A. A., Magdy, O., Ibrahim, W. A., Sayed, A., Mohamed, H., Youssef, M. I., et al. (2021). Monitoring of antimicrobial susceptibility of bacteria isolated from poultry farms from 2014 to 2018. *Veterinary Medicine International*, *2021*.

Hauhnar, L., Pachuau, L., & Lalhruaitluanga, H. (2018). Isolation and characterization of multi-drug resistant bacteria from hospital wastewater sites around the city of Aizawl, Mizoram. *Advances in Bioscience and Biotechnology*, *9*(07), 311-321.

Hedman, H. D., Vasco, K. A., & Zhang, L. (2020). A review of antimicrobial resistance in poultry farming within low-resource settings. *Animals*, *10*(8), 1264.

Ho, J. Y., Jong, M. C., Acharya, K., Liew, S. S. X., Smith, D. R., Noor, Z. Z., Goodson, M. L., Werner, D., Graham, D. W., & Eswaran, J. (2021). Multidrug-resistant bacteria and microbial communities in a river estuary with fragmented suburban waste management. *Journal of Hazardous Materials*, *405*, 124687.

Hutchings, M. I., Truman, A. W., & Wilkinson, B. (2019). Antibiotics: Past, present and future. *Current Opinion in Microbiology*, *51*, 72-80.

Jain, C. (2023). Evaluation of Chromogenic agar media for isolation, identification and direct antibiotic susceptibility testing of uropathogens. *International Journal of Pharmaceutical Research & Allied Sciences*, *12*(2), 7-12. doi:10.51847/Kd4vp42v9B

Krestonoshina, K., Maslakova, K., Yangirova, L., Kinareikina, A., & Silivanova, E. (2022). Insect resistance to insecticides and approaches to its identification. *Entomology and Applied Science Letters, 9*(4), 41-47. doi:10.51847/pALDPlwPDj

Landers, T. F., Cohen, B., Wittum, T. E., & Larson, E. L. (2012). A review of antibiotic use in food animals: Perspective, policy, and potential. *Public Health Reports*, *127*(1), 4-22.

Larsson, D. J., & Flach, C. F. (2022). Antibiotic resistance in the environment. *Nature Reviews Microbiology*, *20*(5), 257-269.

Mai, C. N., Mai, A. N., Nguyen, H. N. T., & Nguyen, H. T. (2021). Factors affecting endogenous income of informal laborers suffering economically social exclusion in Vietnam's northern mountainous area. *Journal of Organizational Behavior Research, 6*(1), 59-70.

Moges, F., Endris, M., Belyhun, Y., & Worku, W. (2014). Isolation and characterization of multiple drug resistance bacterial pathogens from waste water in hospital and non-hospital environments, Northwest Ethiopia. *BMC Research Notes*, *7*, 1-6.

Mustapha, A., & Imir, T. (2019). Detection of multidrug-resistance gram-negative bacteria from hospital sewage in North East, Nigeria. *Frontiers in Environmental Microbiology*, *5*(1), 1-7.

Nath, S., Paul, P., Roy, R., Bhattacharjee, S., & Deb, B. (2019). Isolation and identification of metal-tolerant and antibiotic-resistant bacteria from soil samples of Cachar district of Assam, India. *SN Applied Sciences*, *1*, 1-9.

Ng, C., & Gin, K. Y. H. (2019). Monitoring antimicrobial resistance dissemination in aquatic systems. *Water*, *11*(1), 71.

Odum, E. I., Idise, O. E., & Ogogo, D. I. (2020). Multidrug resistant bacteria in dumpsite soils within Abraka, Delta State, Nigeria. *FUDMA Journal of Sciences*, *4*(2), 639-644.

Rabbani, M. A. G., Howlader, M. Z. H., & Kabir, Y. (2017). Detection of multidrug resistant (MDR) bacteria in untreated waste water disposals of hospitals in Dhaka City, Bangladesh. *Journal of Global Antimicrobial Resistance*, *10*, 120-125.

Rahman, M. M., Devnath, P., Jahan, R., & Talukder, A. (2021). Detection of multiple antibiotic-resistant bacteria from the hospital and non-hospital wastewater sources of a small town in Noakhali, Bangladesh. *Journal of Applied Biology and Biotechnology*, *9*(3), 59-65.

Rasueva, M. K., Medalieva, A. Z., Shengelaya, P. D., Allahverdiyeva, D. C. K., Pule, A. K., & Gasanov, Z. A. (2023). The effectiveness of the use of macrolide antibiotics in infectious diseases. *Pharmacophore*, *14*(1), 87-92. doi:10.51847/divREXrE3e

Sankhala, T., Vyas, A., & Vyas, H. (2021). Characterization and antibiotic susceptibility pattern of bacteria isolated from waste dumping site in Ujjain city India. *Current World Environment, 16*, 277-281.

Taha, O. M. A., Ali, A. H. I., Alsalamah, S. A. A., Alghonaim, M. I. A., Almuhaini, A. M. Z., Ibrahim, N. A., & Alsaif, K. S. S. (2022). Molecular detection of some high resistance genes Metallo β-lactams of *Klebsiella Pneumoniae* using multiplex PCR. *Entomology and Applied Science Letters, 9*(3), 18-24. doi:10.51847/Ef36v0dx8n

Tripathi, V., & Tripathi, P. (2017). Antibiotic resistance genes: An emerging environmental pollutant. *Perspectives in Environmental Toxicology*, 183-201.

Truong, T. H. L., Le, T. N. Q., Le, T. T., & Phan, H. M. (2023). Fintech driven financial inclusion: The case of Vietnamese households. *Journal of Organizational Behavior Research, 8*(1), 52-73.

Van den Bogaard, A. E., London, N., Driessen, C. A. G. G., & Stobberingh, E. E. (2001). Antibiotic resistance of faecal Escherichia coli in poultry, poultry farmers and poultry slaughterers. *Journal of Antimicrobial Chemotherapy*, *47*(6), 763-771.

Waturu, G., Mutai, W., Kiiru, J., Musyoki, M., & Ochieng, L. (2017). Antimicrobial resistance encountered in garbage collection areas and dumpsites in Nairobi, Kenya using Escherichia coli and Klebsiella as indicator species. *Advances in Microbiology*, *7*(9), 653-665.