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The Association between the Global Threat of Ocean Pollution and Climate Change on the Distribution of Antibiotic Resistance: One Health Strategy

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ABSTRACT

Antibiotic resistance represents a fundamental issue affecting public health today. Antibiotic resistance occurs when bacteria alter their response to antibiotics. Pathogenic bacteria and their genes can diffuse throughout human and natural habitats. The complicated interactions between diverse bacterial communities that affect the health of people, aquatic animals, and the aquatic environment are an illustration of ecological issues. Pollution of the oceans by antibiotic-resistant bacteria (ARB) can disturb the natural equilibrium of the oceans and may spread to humans. Also, climate change (CC) significantly affects the health of marine environments. Rising temperatures, acidification, increased sea levels, an increasing number of invasive marine animals, changed biological systems, and a decrease in biodiversity are some of the major impacts on the oceans caused by CC. However, the elevated temperatures linked to CC facilitate the higher spread of bacterial infections in aquatic environments, aquatic animals, and humans with the emergence of antibiotic resistance. The present study aimed to provide a scientific understanding of the relationship between ocean pollution and CC, as well as their impacts on ocean health. Additionally, the present study presented the current status of ARB and its associated genes in the oceans, comparing to future projections based on previous studies. One Health (OH) concept strategies for reducing antibiotic pollution in the ocean were discussed. The present paper is a foundation for further studies to determine the prevalence of antibiotic resistance in the oceans, as well as to understand the current state and key highlights of ocean pollution.

Keywords: Climate change, Drug-resistant bacteria, Heavy metal resistance gene, Ocean pollution, One Health concept

INTRODUCTION

The oceans cover 71 percent of the Earth's total surface and play a crucial role in public health, providing essential resources such as food. Recently, oceans have been vital in addressing the growing demand for animal protein (Kraemer et al., 2019). The oceans are under threat from human activities, which makes them vulnerable to pollution. However, ocean pollution is a global threat (Landrigan et al., 2020). In addition, ocean pollution is considered one of the most important challenges globally (Komijani et al., 2021). These impacts have an effect on the dissolved oxygen (DO), pH, temperature, nitrates, and other chemical and physical characteristics of seawater in oceans (Alesci et al., 2022). The major anthropogenic pollutants found in the oceans are sewage, sludge, fertilizers, heavy metals, plastic particles, pesticides, and pharmaceutical residues such as antibiotics (Buelow et al., 2021). Through rivers, runoff, and direct discharge, pollutants eventually flow into the ocean. Discharges of partial or untreated wastewater from hospitals and nursing homes into oceans are leading to the introduction of human pathogens, multi-antimicrobial resistance bacteria, and many types of resistance to the food chain of oceans (Zacharias et al., 2021). In addition, agricultural and industrial discharges and rainfall may introduce metals, fertilizers, and chemicals into the marine environment (Bukha et al., 2022).

Ocean antibiotic pollution represents a global risk that harms marine ecosystems (Kulik et al., 2023). The improper use of antimicrobial agents in animal and human treatment is considered a major factor contributing to the development of antibiotic-resistant bacteria (ARB; Cáliz et al., 2022) and antibiotic-resistant genes (ARGs) among bacteria (Kulik et al., 2023). The existence of antibiotics in marine ecosystems poses a risk, as it promotes the growth of ARB and their carriers (Sosa-Hernández et al., 2021). The ARB and ARGs are often found in contaminated marine ecosystems, but their mechanisms are not fully understood (Gothwal and Thatikonda, 2017). Globally, many studies have reported the

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presence of antibiotic agents in marine environments as emerging contaminants (Agunbiade and Moodley, 2014; Lu et al., 2019; Maghsodian et al., 2022). Residues of antibiotic agents that remain in the marine environment are considered "persistent organic contaminants" (Ben et al., 2019). Antibiotic pollution in the marine environment can reach humans via contaminated seafood or swimming in affected areas (Sosa-Hernández et al., 2021). Nevertheless, the methods of transferring ARB to humans are not yet understood.

Today, Antibiotic resistance and climate change (CC) are major public health emergencies. Nevertheless, the complex relationship between ARB and CC is now established, and it has not yet been clarified (San Lio et al., 2023). Climate change leads to a rise in ocean temperature, and it is caused by humanity's use of resultant greenhouse gasses and fossil fuels (Ford et al., 2022). Climate change significantly contributes to the increased spread of different bacterial and vector-borne illnesses in humans, plants, and animals. In addition, it may be responsible for the prevalence of novel emerging pathogens. Therefore, using a coordinated strategy such as the One Health (OH) Concept is to address antibiotic pollution at the human, animal, and associated environmental levels on an international scale (Aslam et al., 2021).

Ocean pollution has become a global problem, as it originates from many sources, and so far, polluted oceans are widespread and difficult to control. Ocean pollution threatens the health of the marine environment and humans. The oceans contaminated by antimicrobial resistance have become a major global concern. Globally, ARB and ARGs spread silently among populations. Although several studies have been conducted on ocean pollution with antibiotics, information on the extent of prevalence and occurrence of antimicrobial resistance in the oceans is still limited (Wellington et al., 2013; Victoria et al., 2022).

Therefore, the objectives of this review include: (1) discussing the role of ocean pollution and CC in resistance evaluation among bacterial communities and the pathways of antibiotic resistance spread from hotspots to oceans; (2) highlighting the impacts of antibiotic resistance pollution on people and aquatic animal health, and the health of their associated marine environment; (3) show the current global policies and OH strategies concerned with addressing the impacts of antibiotic pollution and mitigating the spread of this pollution in the oceans.

REVIEW METHODOLOGY

This study was conducted through a bibliographic review, with emphasis on literature available on the internet relevant to scientific publications. A total of 174 academic articles were examined using different databases such as Scopus, Web of Science, Google Scholar, SciELO, PubMed, and many other sources of peer-reviewed journals. The inclusion criteria for articles in the review were the presence of specific keywords related to the review title: The Association between the Global Threat of Ocean Pollution and Climate Change on the Distribution of Antibiotic Resistance: One Health Strategy. On the other hand, the exclusion criteria were the irrelevance of the content to the topic of the study, the type of publication, and the date of publication. The review article was written comprehensively to ensure the consideration of all the relevant literature.

AN OVERVIEW OF ANTIBIOTIC RESISTANCE

Antibiotics are substances naturally manufactured by bacteria, actinomycetes, or fungi (Mohr, 2016). There are common antibiotics divided into 16 families based on Modes of action and chemical properties, including fluoroquinolones, aminoglycosides, tetracycline, β-lactams, sulfonamides, macrolides, trimethoprim, and glycopeptides (Dos Santos et al., 2017). Antibacterial agents have been commonly utilized to combat bacterial infections in animals and humans since the 1950s (Carvalho and Santos, 2016). They have a significant impact on reducing the morbidity and mortality rates for many infectious bacterial infections (Carvalho and Santos, 2016). Also, they are used to prevent bacterial infections in the fish farming industry (Giguère et al., 2013) and promote the growth of livestock (Liu et al., 2021). In contrast, a part of the antibiotics is absorbed in fish products, while the rest is released into the aquatic ecosystem via sewage effluents (Liu et al., 2021).

Recently, the use of antimicrobial drugs has increased around the world (Tiseo et al., 2020; Klein et al., 2024). Further, misuse of antimicrobials can lead to increased distribution of ARB in the environment with bacteria harboring ARGs (Kraemer et al., 2019). The ARGs are considered "emerging micropollutants" due to their increasing presence in marine environments (Kulik et al., 2023). Bacteria can gain resistance to antibiotic drugs and develop intrinsic resistance (Sun et al., 2022). Antibiotic resistance and ARGs have existed for billions of years and occur naturally in the environment (Zhuang et al., 2021). Antibiotic resistance can lead to treatment failure of bacterial diseases due to the inability of antibiotics to inhibit growth or destroy the bacteria due to the transfer of resistance genes from one bacterium to another, leading to a wider spread of resistance, or bacteria produce enzymes that breakdown the antibiotic (Authority et al., 2021). In addition, it reduces their effectiveness against many species of bacteria (Singh et al., 2022). Antibiotic pollution is a major global threat to humans and health in the 21st century. The World Health Organization (WHO) has ranked it as the most critical among six environmental challenges (Hazra et al., 2022). There is a list of 12 ARB families published by WHO (Amarasiri et al., 2020). The WHO has identified high (ARBs) such as *Escherichia coli*, *Staphylococcus aureus*, and *Klebsiella pneumoniae* (Huijbers et al., 2015).

A study was conducted in 76 countries in Europe over 5 years from 2000 to 2015, and the study concluded that antibiotic use has risen by 65% (Klein et al., 2018). Annually, antibiotic-resistant infections cause more than 30,000 deaths in countries in Europe, especially in Italy (Cassini et al., 2019). Aquatic environments are considered reservoirs and vectors for the spread of antibiotic resistance (ARB) (Amarasiri et al., 2020). The ARB and ARGs may accumulate in marine ecosystems through discharge from hospitals, farms, cities, and wastewater treatment plants (WWTPs). Increased spread of ARB and ARGs in the aquatic environment induced by human activities (Duan et al., 2020). Globally, numerous studies have documented seven families of antibiotics and their associated ARG subtypes (Zhuang et al., 2021).

The antibiotic resistance resistome is a group of all ARGs and their precursors in specific bacteria. In 2006, the antibiotic resistome term was named by Gerry Wright’s group (Kim and Cha, 2021). Antibiotic resistance is categorized into intrinsic and acquired resistance, while ARGs are categorized into intrinsic resistance. Intrinsic resistance originates from the producers themselves, while acquired resistance results from another bacteria through horizontal gene transfer HGT resistance (Hu et al., 2017; Eshrati et al., 2025). The antibiotic resistome is categorized into mobile and intrinsic resistome (Hu et al., 2017).

ANTIBIOTIC-RESISTANT BACTERIA AND ANTIBIOTIC-RESISTANT GENES IN AQUATIC ECOSYSTEMS

Several research investigations have been performed that confirmed the possibility of the presence of ARB and ARGs in marine ecosystems. These studies concluded that antibiotic-resistant consequences of excessive antibiotics in hospitals and farms lead to it reaching the aquatic environments through wastewater (Stoll et al., 2012). A study by Gambino et al. (2022) detected antibiotic-resistant Gram-negative bacteria and genes that confer resistance to sulfonamide and β-lactamase antibiotics in the collected seawater samples from Sicily Coasts, Italy. In contrast, in Sishili Bay of Yantai, China detected a high prevalence of 10 ARG subtypes that confer resistance to quinolones, tetracyclines, macrolides, and sulfonamides (Zhang et al., 2020). Whereas it was monitored the prevalence of twenty-four ARGs against (aminoglycoside, glycopeptides, β-lactamase, tetracycline, macrolides, chloramphenicol, trimethoprim, and sulfonamides) in collected water samples from Australia and Germany (Stoll et al., 2012). In addition, another study by Habibi et al. (2022) detected the presence of 402 ARGs on the shores of Kuwait, which showed resistance against β-lactamase. Several studies have reported that resistance genes of β-lactamase, sulfonamide, macrolide, and tetracycline are the most widespread types of ARGs in aquatic environments (Berglund, 2015; Huang et al., 2019; Grenni, 2022). Whereas, it was noted that the β-lactamase resistance genes are abundant in marine water, fish, and sea turtles (Stoll et al., 2012).

The collected water specimens from the Coast of Southeast Louisiana, USA, were tested to detect the presence of ARB (Belding and Boopathy, 2018). The result of this study revealed the presence of Enterobacter spp., *Escherichia coli*, and *Klebsiella*, which were resistant to tetracycline, carbapenem, penicillin, monobactams, cephalosporin, and sulfonamide antibiotics (Belding and Boopathy, 2018). Other studies by Leonard et al. (2025) documented the occurrence of antibiotic-resistant *E. coli* in coastal waters of the United Kingdom UK. In contrast, in the Veraval Coast of India, the prevalence of Enterobacteriaceae family resistant to multiple antibiotics, in both water and sediment samples, having 12 ARGs (Huang et al., 2019). Also, in coastal waters of Indonesia, Malaysia, China, and Vietnam, the presence of *E. coli*, *Enterobacter* spp., and *Klebsiella* spp. that were resistant to cephalosporin, sulfonamide, tetracycline, monobactam, penicillin, and carbapenem (Boopathy et al., 2015). Guzman-Otazo et al. (2019) who reported of multi-resistant *E. coli* in the river of Choqueyapu in Bolivia. In addition, multidrug-resistant bacteria have been isolated from the coastal waters of Tunisia (Ghozzi et al., 2023).

AN OVERVIEW OF OCEAN POLLUTION

The oceans provide more than 99% of the water resources on Earth. The global ocean splits into five ocean basins: the Atlantic, Indian, Arctic, Pacific, and Antarctic (Thushari and Senevirathna, 2020). On the other hand, the oceans are threatened by human activities, including domestic pollutants, industries, hospitals, and agriculture activities, which reach the marine environments through many different pathways, such as river and aquatic drainages, the atmosphere, and wastewater effluents (Dahms, 2014). Discharges of wastewater from hospitals and nursing homes into aquatic ecosystems are leading to the introduction of human pathogens, multi-antimicrobial resistance bacteria, and many types of resistance to the aquatic trophic chain (Zacharias et al., 2021). Furthermore, industrial discharges and rainfall may introduce metals, fertilizers, and chemicals into the marine environment. These compounds influence the health of aquatic ecosystems and accumulate in the biota (Hama Aziz et al., 2023). Marine pollution has negative impacts on aquatic life. However, these impacts affect the chemical and physical properties of seawater, such as pH, temperature, nitrates, and dissolved oxygen (DO) (Alesci et al., 2022). Pollutants can build up in the tissues of marine organisms and be transmitted through the marine food chain (Oudi et al., 2019) (Figure 1).

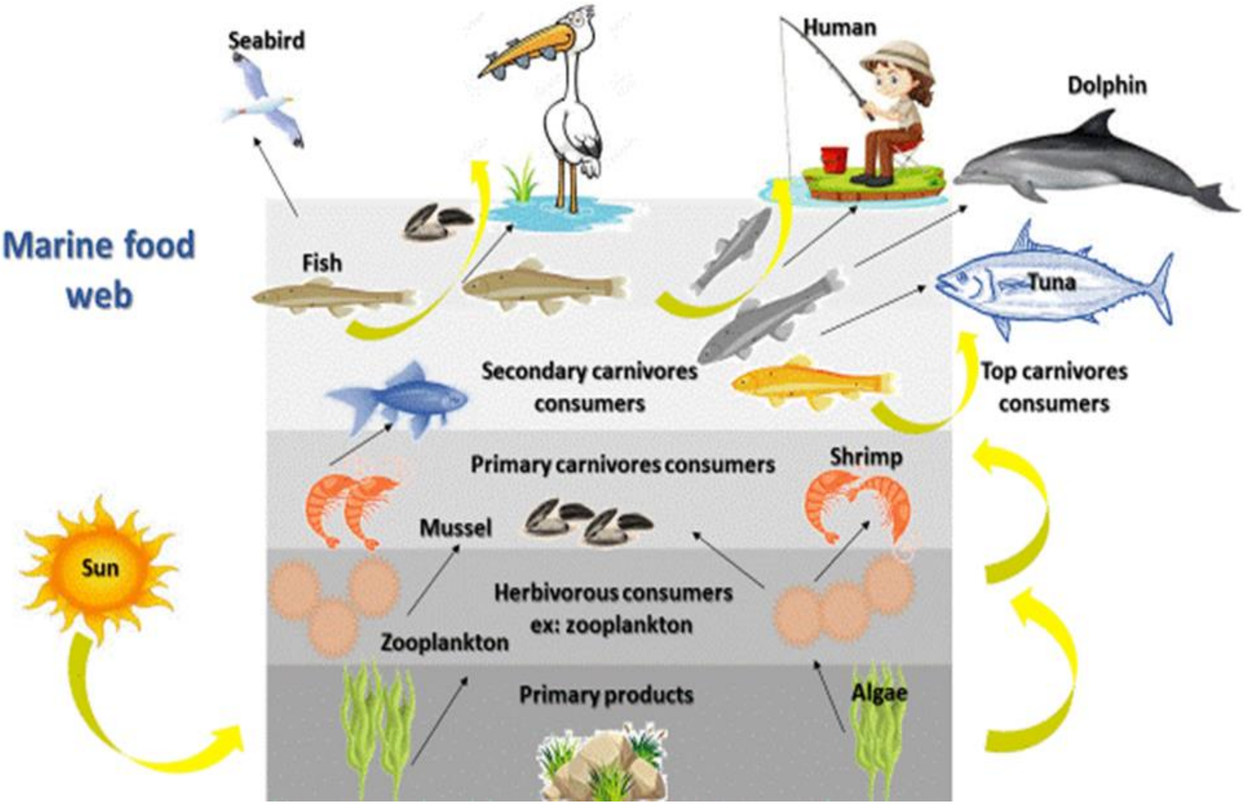

Figure 1. The marine food cycle shows the pollutants that can build up in the tissues of marine organisms and be transmitted through the marine food chain

Inadequate treatment of domestic, industrial, livestock industries, aquacultures, and hospital wastewater leads to antibiotic release into the oceans (Kraemer et al., 2019). Antibiotic pollution has become a serious threat to aquatic environments. The presence of antimicrobial agents in aquatic ecosystems may be affected by pH, temperature, bacterial populations, and dilution factors, which may lead to disturbances in their concentrations (Liu et al., 2021). However, antimicrobial agents are inadequately broken down and may find their way into aquatic environments through wastewater effluents (Chow et al., 2021). Antibiotic residues lead to increased rates of mutation and horizontal transfer among bacterial populations, even at sub-lethal or sub-inhibitory concentrations (Chow et al., 2021).

There is a difference in the pathways of ARB and ARG presence in marine environments compared with freshwater and sewage (Sucato et al., 2021). Antibiotic-resistant bacteria (ARB) and ARGs induce a negative impact on microbial populations by reducing their biodiversity. In addition, they induce changes in the ecological functions of marine and freshwater (Grenni et al., 2018). The influence of ARB and ARGs on the marine environment is related to their biodiversity, concentrations, and exposure time (Huijbers et al., 2015). In addition, they increase the risk to public health because antibiotics lose their effectiveness in treating bacterial diseases (WHO, 2023). The presence and persistence of ARB and ARGs in aquatic environments remain incomprehensible.

Currently, global oceans are threatened by plastic pollution. Plastic pollutants have become a dangerous concern for all parts of the global oceans. Moreover, the accumulated plastic debris in the oceans is divided into four forms based on their sizes, which include microplastic, megaplastic, macroplastic, and mesoplastic (Thushari and Senevirathna, 2020). Plastic debris is ubiquitous in anthropogenic aquatic ecosystems and serves as a reservoir for marine bacteria, ARB, and ARGs (Liang et al., 2023). Currently, ocean pollution is estimated to contribute to approximately 9 million deaths annually due to its impact on human health and marine environments (Landrigan et al., 2020).

EFFECTS OF CLIMATE CHANGE ON MARINE ECOSYSTEMS

Climate change (CC) correlates with shifts in rainfall and temperature patterns. Globally, over the past 50 years, an increase of 0.11°C in sea surface temperature has been recorded (Venegas et al., 2023). Similarly, in the last 130 years, sea surface temperature levels have climbed by 0.85°C (Scharsack et al., 2021). These observations highlight the ongoing trend of planetary heating and its impact on seawater temperatures.

Since the onset of the industrial revolution, there has been a sharp increase in greenhouse gas emissions, leading to a rise in atmospheric temperature at an average of 0.14^0 Fahrenheit per decade (Venegas et al., 2023). Between 1990 and 2010, there was a noticeable rise in levels of carbon dioxide CO_2 in the atmosphere, from 350 to 380 ppm, which correlated with changes in the climate (Doney et al., 2012; Coelho et al., 2013). If greenhouse gas emissions persist, we can anticipate a projected increase in the average temperature of 1.5°C by the middle of the 20th century, and by 2020, levels of atmospheric carbon dioxide CO_2 will have increased by 280 ppm to 413 ppm (Scharsack et al., 2021). In February 2023, it was observed that the atmospheric carbon dioxide CO_2 concentration reached 422.9 ppm (Venegas et al., 2023). The increase in atmospheric carbon dioxide CO_2 concentrations is absorbed by the surface of the oceans, leading to an increase in ocean acidity (Wei et al., 2023). However, the high levels of atmospheric carbon dioxide $CO_{2)}$ dissolve in the oceans and then react with seawater, leading to the formation of carbonic acid, which decomposes into hydrogen ions and bicarbonate. Therefore, a decrease in ocean pH is referred to as ocean acidification. Acidification is regarded as a significant environmental issue that affects marine environments (Doney et al., 2020). The ocean acidification changed from 8.13 to 8.08 PH (Coelho et al., 2013).

The rising release of greenhouse gases into the atmosphere results in increased accumulation of heat, with apportion being absorbed by the seawater surface, leading to an increase in internal temperature "ocean heat content" known as "ocean warming" through melting ice and thermal expansion (Bindoff et al., 2019). Global ocean warming has been occurring since the 1970s (Arias et al., 2021). Around the world, CC represents a significant risk to environments, animals, and humans that plays an important role in sea acidification, sea warming, and the rise of sea levels (Ford et al., 2022). Globally, from 1901 to 2010, the level of the sea rose by 0.11 meters (11 centimeters), while in the 1980s, the level of the sea increased at a rate of 3.2 millimeters per year (Muruganandam et al., 2023). The World Health Organization WHO considers CC the greatest risk to public health between 2030 and 2050; human mortality rates are expected to rise to 250000 annually (San Lio et al., 2023).

Historically, the Mediterranean Sea has been susceptible to significant CC, making it a notable hotspot for CC (Pepi and Focardi, 2021). At present, the Mediterranean Sea experiences an average temperature is seeing an average temperature rise of 1.4 compared to late 19th-century levels, with the increase being particularly noticeable during summer (Cramer et al., 2018). Lately, a substantial rise in CC levels has been detected in the ocean (Doney et al., 2012). Climate change (CC) has impacts on the physical and chemical properties of marine ecosystems, resulting in serious consequences to marine life, including dissolved oxygen concentration, pH, temperature, ice cover, and salinity of seawater (Cabral et al., 2019). Climate change affects the balance of marine ecosystems, leading to changes in the structure and biodiversity of marine organism populations (Assan et al., 2020). On the other hand, numerous research studies have reported that changes in ocean temperature may lead to alterations in the physiology of aquatic animals, resulting in changes in seasonal abundance, growth, fecundity, and feeding behavior (Doney et al., 2012) and invasive aquatic species (Neelmani et al., 2019).

CLIMATE CHANGE AND OCEAN POLLUTION

Pollution of the oceans and CC are some of the most pressing global challenges (Lu et al., 2018). Additionally, CC affects pollutants present in the oceans (Scharsack et al., 2021). These are two of the top health crises and should be prioritized by the public health system because they are interconnected (San Lio et al., 2023). Lately, many researchers have proposed that the combination of CC and ocean pollution is altering the biological structure and dynamics of marine environments (Jing et al., 2015). Limited data is available on the environmental hazards resulting from this mixture.

Heavy metals and petroleum accumulate in seawater and disrupt chlorophyll function in algae, reducing their photosynthetic capacity. This decline in photosynthesis decreases dissolved oxygen levels, negatively impacting marine animals. Furthermore, the accumulation of heavy metals in algae renders them toxic to marine animals that consume them, facilitating the transfer of these contaminants through the marine food chain (Lu et al., 2018). Ocean acidification resulting from increased CO_2 may increase the toxicity of some heavy metals and organic contaminants threatening the safety of coral reefs (Landrigan et al., 2020). In addition, heavy metals affect dissolved organic matter transport and the transformation of biotic and abiotic matter (Tang et al., 2022). Heavy metals have been used as bioindicators of CC in the environment (Tang et al., 2022).

Over time, these changes can devastate aquatic environments, and mitigating their adverse impacts can prove challenging (McCrink-Goode, 2014). The interaction between pollutants and CC may exacerbate ocean pollution. The presence of heavy metals, organic pollutants, excess nutrients, and plastics in the marine ecosystem raises challenges for reducing ocean pollution (Ford et al., 2022). Overall, the stressors of CC and the toxicity of contaminants can alter the biodiversity of aquatic organisms, such as fish, mollusks, and algae (Kibria et al., 2021) (Figure 2).

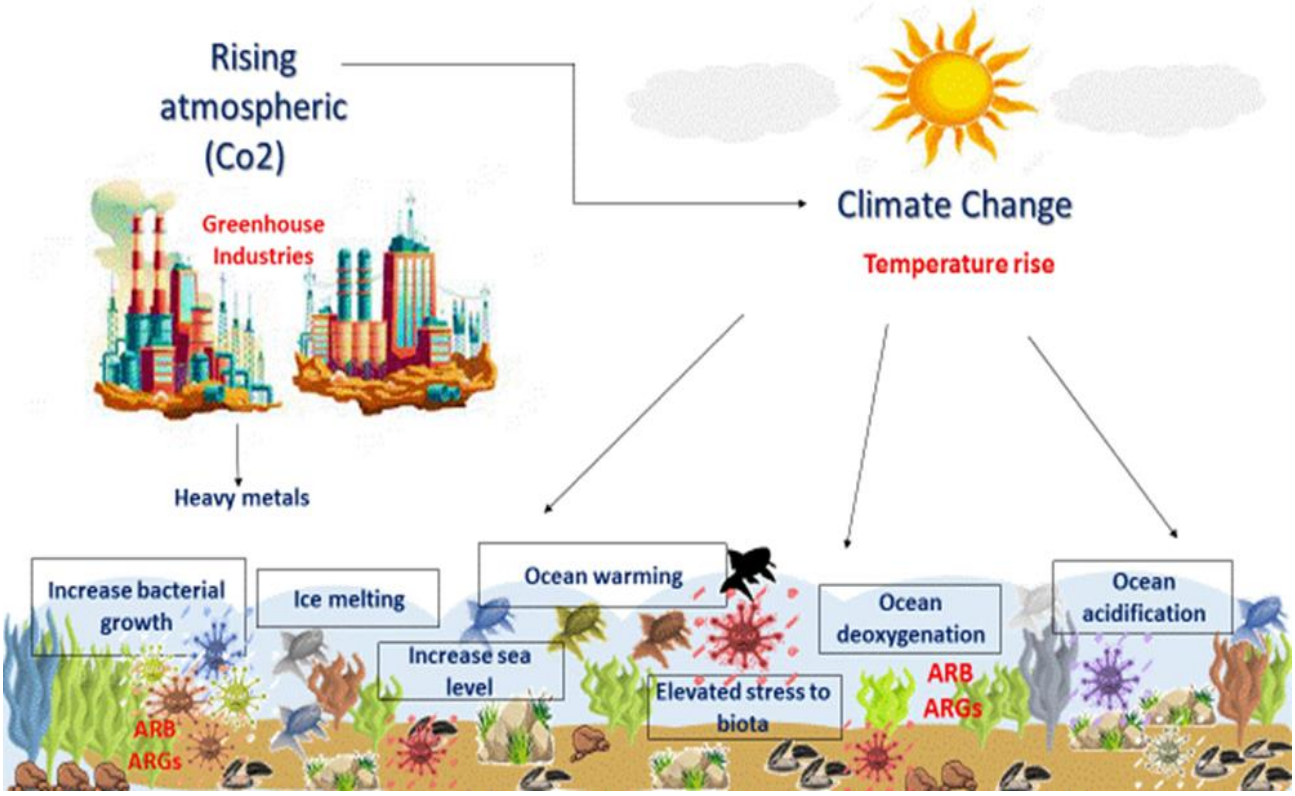

Figure 2. Negative impacts of climate change on coastal and ocean ecosystems.

CLIMATE CHANGE AND ITS ROLE IN AMPLIFYING OCEAN POLLUTION THROUGH ANTIBIOTIC-RESISTANT BACTERIA AND ANTIBIOTIC-RESISTANT GENES

Global CC is regarded as the primary driver of emerging infectious diseases (Li et al., 2022). Human activities have contributed to CC and ARB; hence, steps must be taken to mitigate their impacts. Temperature is closely related to bacterial growth, infections, the global distribution of bacteria, community composition, and survival in the presence of antibiotic agents (Philipsborn et al., 2016). Temperature rise speeds up HGT, which is a key factor in the development of antibiotic resistance. In addition, bacterial growth rates are often accelerated by temperature increases (Pietikäinen et al., 2005). Acquired ARGs are located on plasmids and can be transported to other aquatic bacteria through HGT, which is increased by increasing environmental temperatures (Zacharias et al., 2021). Many diseases are sensitive to climate, and temperature may increase the spread of bacterial infections in environments, animals, and humans (Harvell et al., 2002).

Mutations can occur in the presence of antibiotic resistance, which plays an important role in saving the life of the bacterial community (Li et al., 2022). Moreover, mutations that confer resistance to temperature stress can stimulate resistance to antibiotics and vice versa, a phenomenon known as cross-protection or collateral resistance (Okeke et al., 2022). Collateral resistance refers to the acquisition of resistance to a specific stress after prior contact with other stressor factors (Dragosits et al., 2013). The increased temperature may aid biofilm formation, as in the *Roseobacter* genus of *Rhodobacteraceae* growing at 33°C, resulting in the formation of a biofilm (Kent et al., 2018). Increased temperature induces a higher tolerance to antibiotics for marine bacteria (Kent et al., 2018). Within the United States, rising temperatures have been correlated with an increased prevalence of ARB among human bacteria (MacFadden et al., 2018; Li et al., 2022).

Numerous research studies have highlighted that the temperature increase forecasted by CC will drive an increase in antibiotic resistance in bacteria (MacFadden et al., 2018). A previous study was conducted in the USA from 1980 to 2010, collecting data on temperature and percentages of ARB from hospitals and laboratories across 41 states. The results of this study showed an association between temperature and antibiotic resistance (Pepi and Focardi, 2021).

Another study performed in 28 European countries from 2000 to 2006 reported the impact of temperature on antibiotic resistance (McGough et al., 2020). A recent review provided objective evidence that CC affects pathogenic bacteria (Cavicchioli et al., 2019). So far, there is limited research on CC and its impacts on infectious diseases. Likewise, numerous studies highlight CC impacts on the vectors of diseases more than on pathogenic bacteria. In addition, CC affects the spread of parasites, species of parasites, distribution changes, and abundance of hosts in marine environments (Assan et al., 2020). Currently, the impact of CC on the evolution of antibiotic resistance in ocean-based bacteria is not yet fully understood.

HOTSPOTS FOR THE TRANSMISSION OF ANTIBIOTIC-RESISTANT BACTERIA AND ANTIBIOTIC-RESISTANT GENES IN OCEANS

Domestic houses, healthcare settings, industrial plants, WWTPs, agriculture, aquaculture, and animal husbandry are considered "hotspots" for the spread of ARB and ARGs in the oceans (Kunhikannan et al., 2021; Gambino et al., 2022) (Figure 3). Therefore, pathogenic bacteria released from hotspots exposed to higher concentrations of antibiotics may increase their growth rates because of nutrient abundance in the ocean and may be selected before reaching marine environments (Azam and Malfatti, 2007).

Antimicrobial agents are lipophilic (Shokoohi et al., 2020) and incompletely metabolized in the human body, where they are released via the wastewater of hotspots with feces and urine (Sun et al., 2022). However, up to 70% of antibiotic agents cross the digestive tract of humans and are released via feces and urine (Shah et al., 2021). Several researchers have reported ARB and ARGs at high concentrations in hotspots. Marine environments have high levels of fecal matter, which arises from hotspots (Zieliński et al., 2021). Fecal pollution can introduce bacteriophages that harbor ARGs and pathogenic bacteria into marine environments. However, various substances in the marine environment, such as feces, soil, and plastics, act as potential reservoirs of antibiotic resistance (Amarasiri et al., 2020).

Figure 3. Impact of wastewater discharges on the marine food web.

HOSPITAL

Globally, hospitals are considered to be the most contaminated sector (Henriot et al., 2024). Antibiotics have been given extensively in hospitals for the treatment of bacterial infections in patients (Cai et al., 2021). Hospital wastewater contains the urine and feces of patients. In particular, some of these patients have taken antibiotic drugs for the treatment of their bacterial infections, which are included in the hospital wastewater as ARB and ARGs (Cai et al., 2021). The antibiotics given to the patients in the hospital are partially metabolized in their bodies, while the rest are added to the hospital wastewater through excretion (Sosa-Hernández et al., 2021). Hospital wastewater (HWW) treatment plants are considered host sites for the spread of ARB and ARGs in aquatic environments (Yuan and Pian, 2023). Effluents of hospital wastewater discharged from infections operating rooms and diagnostic laboratories contain antibiotics, hormones, organic pollutants, heavy metals, pathogenic bacteria, viruses, and parasites (Yuan and Pian, 2023). However, the term "antibiotic-resistant hospitals" is used when hospitals acquire pollutants associated with resistant bacteria (Donker et al., 2012) (Figure 4).

Some ARB can survive chlorine disinfection and can spread in the effluent after chlorination. On the other hand, ARB may be developed via propagation, and ARGs are propagated among the bacterial community through HGT by plasmids, integrons, and transposons (Kümmerer and Henninger, 2003; Jin et al., 2018). However, the spread of ARB and ARGs in aquatic environments has negative impacts and greater challenges for public health (Rowe et al., 2017). Indeed, hospital wastewater treatment plants (HWWs) are more likely than urban wastewater systems to spread ARB and ARGs (Zheng et al., 2018). Urban wastewater contains simple pollutants, whereas HWW contains pharmaceuticals, chemicals, and pathogens that require advanced treatment (Petrovich et al., 2020).

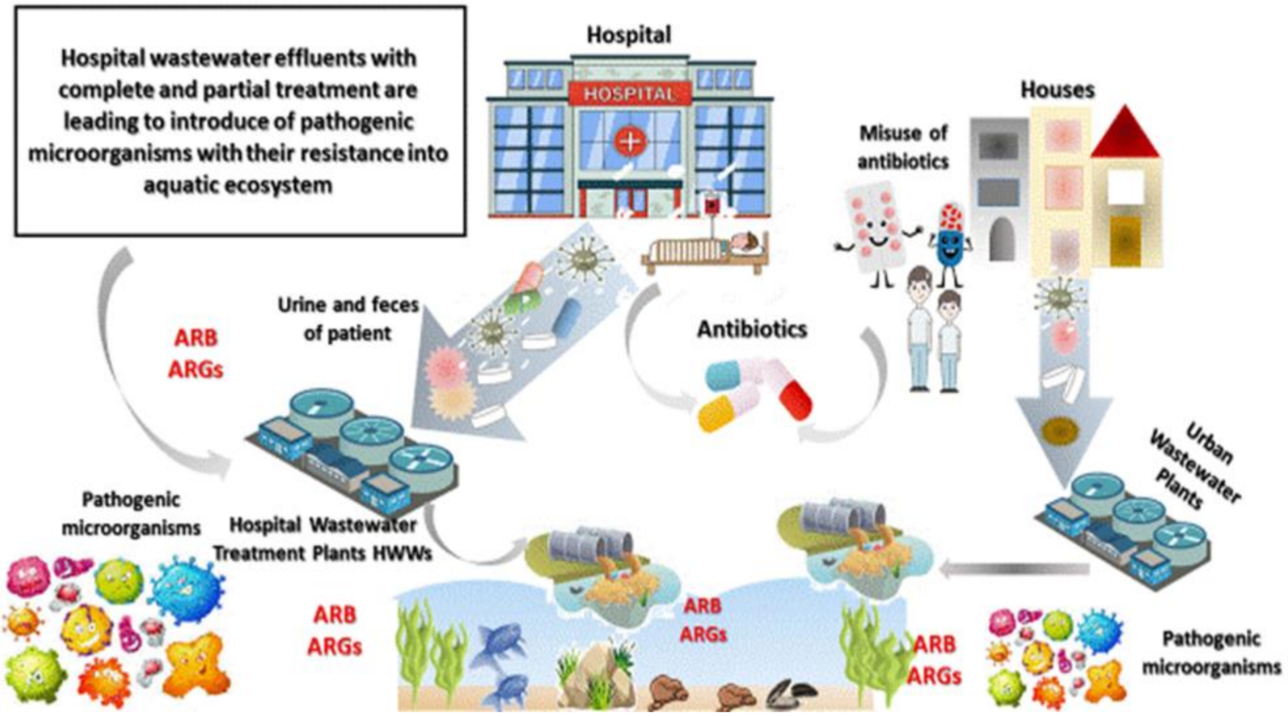

Figure 4. Hospital wastewater and urban wastewater as reservoirs for Antibiotic Resistance bacteria (ARB) and Antibiotic resistance genes (ARGs) in marine environments

In hospitals, antibiotics such as glycopeptides, vancomycin, carbapenems, piperacillin, and Cefotiam are used more frequently than in other sectors (Kümmerer and Henninger, 2003). The bacteria species commonly detected in HWWs include Vibrio spp., Salmonella, Shigella, Clostridium, Yersinia, Campylobacter, Leptospira, *Escherichia coli*, Klebsiella, Serratia, Enterobacter, *Staphylococcus aureus*, and *Acinetobacter baumannii* (Lien et al., 2017; Pulami et al., 2023). Another study has shown an increase in the presence of Gram-negative bacteria carrying *bla* genes such as *bla*$_{NDM}$, *bla*$_{KPC}$, *bla*$_{CTX\text{-}M}$, and *bla*$_{SHV}$ in HWWs, together with other drug-resistant ARGs (Le et al., 2016). Studies have also identified various bacterial species in HWWs, including *Salmonella* spp., *Aeromonas* spp., *Vibrio* spp., *Escherichia* spp., *Mycobacterium* spp., *Leptospira* spp., *Pseudomonas* spp., and *Legionella pneumoniae* (Yuan and Pian, 2023). Further, another study reported the persistent presence of a complex mixture of pathogenic bacteria, ARGs, antibiotics, and viruses in HWWs (Petrovich et al., 2020). The diversity and fate of the viral community in HWWs are not yet fully understood.

Globally, 10% of hospital infection outbreaks have been associated with antimicrobial resistance. The healthcare system in poor countries is more vulnerable to the effects of antibiotic resistance pollution in the environment compared to developed nations (Manaia et al., 2024). Currently, Extensively Drug-Resistant bacteria (XDR) are on the rise among strains. They pose a major concern in healthcare settings (Siri et al., 2024), as they can result in infections that are very challenging to manage and treat with antibiotics. Furthermore, XDR bacteria refer specifically to bacteria that are resistant to almost all available antimicrobial agents (Basak et al., 2016).

Currently, concerns about antibiotic pollution in hospitals have increased, therefore, many research studies have intensified in investigating the presence of ARB and ARGs in HWWs (Wang et al., 2018; Mehanni et al., 2023). Much research has been undertaken to detect antibiotics and residual bacteria in HWWs (Table 1).

Table 1. Isolated of Antibiotic Resistant Bacteria (ARB) and Antibiotic Resistant Genes (ARGs) from different hospitals around the world between 2023-2025

Location of study	**Type of isolates**	Year
Cambridge University Hospitals, Cambridge, United Kingdom	Tow $^{\beta}$- Lactam resistance genes (*bla*$_{\text{GES}}$ and *bla*$_{\text{OXA}}$)	2017
Beni- Suef University Hospital, Egypt	Three Multi-drug resistant bacterial isolates	2023
Three public hospitals in Xinxiang City, Central China	Escherichia and Acinetobacter were predominant in the Cultivable Multiple-antibiotic- bacteria (CMARB)	2018
Two hospitals in Singapore	The highest levels of ARGs are linked to resistance to $^{\beta}$- Lactam (*bla*$_{\text{KPC}}$), co-trimoxazole (*sull, sul2, dfrA*), amikacin, ciprofloxacin (*qnrA*), and intI1	2016
Hospital of Girona, Spain	Highest levels of ARGs linked to resistance to ($^{\beta}$- Lactam, macrolide, sulfonamide, and tetracycline)	2015
Ohashi Medical Center in Toho University, in Tokyo, Japan	Many ARB species, ARGs, and residual antibiotics	2021
Rural and urban hospitals in Vietnam	Antibiotic-resistant E coli isolated combined with ARGs	2017
Ayder Referral Hospital in North Ethiopia	Klebsiella spp, *Staphylococcus aureus,* and *Pseudomonas aeruginosa*, respectively, were frequently isolated from untreated wastewater, while Klebsiella spp, Pseudomonas aeruginosa, and Staphylococcus aureus, respectively, were frequently isolated from treated wastewater. These isolates were multi-drug resistant.	2017
Many hospitals in Benin	The highest levels of ARB are linked to resistance to Chloramphenicol and sulfamethoxazole.	2022
Regional High Specially Hospital of Ixtapaluca and the National Institute of Oncology in, Mexico	The presence of carbapenem resistance genes (CRGs) in Klebsiella spp	2022
Three hospitals in Cluj Country in, Romania	14 genes of ARGs confer resistance to $^{\beta}$- Lactam, aminoglycoside, chloramphenicol, macrolide-lincosamide-streptogramin B (MLSB) antibiotics, sulfonamide, and tetracycline	2017
Urban hospital in Japan	Proteobacteria, Bacteriodetes, Firmicute, Acinobacteria, and TM7, respectively were found in HWW before treatment.	2021

LIVESTOCK INDUSTRIES AND AGRICULTURE

Excessive antibiotic use by people and livestock may result in the discharge of partially metabolized antibiotics into the marine ecosystem through wastewater discharges. Because they are broken down or partially metabolized, most consumed antibiotics eventually enter sewer systems, either directly or indirectly (Faleye et al., 2018). The indirect release of consumed antibiotics into the marine environment through excretion is known as indirect antibiotic discharge. Unconsumed antibiotics are occasionally flushed directly into the sewer system (Aiken et al., 2014). Because of the high concentration of antibiotics, they are largely destroyed, but their active components still have an effect on the marine environment, which will eventually increase resistance in bacteria or may have ecotoxicological impacts (Aiken et al., 2014).

The rate of antimicrobial consumption in livestock reached 63.151 tons in 2010, with an expected increase of 67% by 2030 (Tiseo et al., 2020). Approximately 80% of antibiotics are distributed for veterinary use in the United States of America (Odoi et al., 2021). States in India, Canada, and Europe have strengthened their monitoring systems to spot emerging dangers or altering trends in the use of antibiotics in agriculture, particularly in settings where animals are produced (Nahrgang et al., 2018). Concerns over the rise of antimicrobial resistance have prompted many nations to implement stricter regulations on antibiotic use in veterinary practices, with the European Union notably banning the use of antibiotics as growth promoters in livestock since 2006 (European Union, 2006).

Nowadays, there is a lot of evidence suggesting that antibiotic use in livestock significantly contributes to the development of antibiotic resistance in some human infections (Collignon and McEwen, 2019). Antibiotic-resistant bacteria (ARB) and ARGs are widely distributed throughout most industrial wastes associated with animal husbandry-related sectors, and the antibiotic residue concentration in these enterprises is far higher than that in soil, hospitals, surface water, and groundwater. The continuous use of antimicrobials to enhance animal growth and prevent infections may lead to higher levels of antibiotic resistance in livestock farm wastes compared to human waste (Sim et al., 2011).

Fecal pollution creates physical contact, which increases the chances of gene transfer between environmental bacteria and bacteria that have been adopted into the intestinal tracts of people or domestic animals (Larsson and Flach, 2022). Numerous intestinal bacteria are also known to carry genetic elements, such as integrative conjugative elements, plasmids, insertion sequences, integrons, or transposons, that can help pathogens acquire genes and transmit them to other organisms (Larsson and Flach, 2022). The potential threat to human health from ARB and ARGs passing down the aquatic food chain has escalated in recent years due to the emergence of ARB and ARGs in livestock, aquatic products, and poultry meats (Rehaiem et al., 2016).

Soils have a natural abundance of ARB and ARGs. Reusing treated sewage effluents may put human health at risk if ARB and ARGs build up in agricultural soils. In addition, ARB and ARGs are mostly distributed in the soil by the use of manure in agriculture; these substances may travel to the ocean through wastewater effluents (Li et al., 2023). However, a major source of antibiotic resistance transmission to water-resistant genomes and soil is agricultural activities such as irrigation, soil fertilization, and animal rearing. Antibiotic-resistant bacteria (ARB), ARGs, and run-off chemicals are more likely to be present in intensive agricultural activities (Flores-Vargas et al., 2021). The discharge of ARB and ARGs from wastewater treatment plant effluents (WWTPs) into water sources contributes to the spread of ARB and ARGs in marine environments (Ondon et al., 2021). Antibiotic-resistant genes (ARGs) and heavy metal co-selection have been observed in agriculture-impacted resistome (Flores-Vargas et al., 2021).

INDUSTRIAL ACTIVITIES

Industrial activities such as aquaculture, medicine, and industry that cause ocean pollution may include chemical, pharmaceutical, food, and oil (Blanco-Picazo et al., 2020). The release of pollutants from industrial, wastewater treatment plants (WWTPs), and aquaculture operations (Jia et al., 2022) contribute to the prevalence of ARB and ARGs in marine environments (Baena-Nogueras et al., 2021). Nevertheless, industries that spread waste with heavy metals contaminate the soil and water sources, which causes bacteria to acquire heavy metal tolerance mechanisms. These bacteria may develop higher levels of heavy metal tolerance. The development of antibiotics and environmental studies are all significantly affected by the emergence of antibiotic and heavy metal resistance in aquatic bacteria (Tahmourespour, 2021).

There is rising global concern about antibiotic resistance and heavy metal pollution in oceans because heavy metal tolerance in pathogenic bacteria is responsible for the spread of antibiotic resistance. Studies have discovered a relationship between bacteria's resistance to heavy metals and antibiotics; comparable mechanisms exist in both situations to help bacterial growth in adverse conditions (Oves and Hussain, 2016). However, bacteria in marine environments can co-occur with ARGs and heavy metal resistance genes (HMRGs) (Håkonsholm et al., 2023). ARGs tend to be linked to gene cassettes that contain the class 1 integrons, a potentially mobile genetic element that is responsible for HMRGs and conjugative-mediated gene transfer (Lin et al., 2021). Therefore, the selection of multi-resistant bacteria and the spread of resistance into nature may be encouraged by the simultaneous existence of heavy metals and ARGs (Gambino et al., 2022). Bacteria often develop heavy metal resistance via a combination of passive and active mechanisms, such as sequestration, efflux, or alteration of metals within the microbial cell (Fardami et al., 2023).

Lead, cadmium, mercury, copper, chromium, and zinc are among the many examples of heavy metals that are frequently found in industrial operations and may constitute an important risk to both human health and the marine environment (Alghamdi et al., 2021). Copper and other heavy metals are used in fish farming as antifouling agents and feed additives. As a result, copper may contaminate the marine environment through feces, spilled feed, and nets from fish farms that have been metal-impregnated (Håkonsholm et al., 2023). Furthermore, heavy metals such as copper, arsenic, mercury, and silver have been used in different types of antimicrobials for many years and as antimicrobials in veterinary medicine and humans (Gufe et al., 2022). In addition, metals such as mercury, lead, chromium, and arsenic have carcinogenic and neurotoxic effects on both humans and animals (Morais et al., 2012). Overall, successfully mitigating the environmental effects of heavy metal pollution requires an in-depth understanding of the mechanisms via which heavy metal affects aquatic bacteria.

Over half of the seafood consumed worldwide is produced by fish farming. Fish farming uses antibiotic agents for growth and treats infections (Brunton et al., 2019). Aquatic environments can be exposed to antibiotic residues from various sources, including fish farming (Schar et al., 2021). There has been a rise in ARB and ARGs in aquaculture systems, according to several studies. The prevalence of ARB and ARGs in fish farming may have harmful effects on these industries (Kim and Cha, 2021). Many studies have shown that resistance can spread among human pathogens, aquatic bacteria, and fish pathogens (Shen et al., 2018; Pepi and Focardi, 2021). Antibiotic-resistant bacteria (ARB) and ARGs, including zoonotic pathogens, have been isolated from fish farming around the world as well as from water and products (Santos and Ramos, 2018).

WASTEWATER

Wastewater treatment plants (WWTPs) collect wastewater originating from healthcare settings, houses, companies, and other sources, making them inadvertent collection locations for ARB (Wengenroth et al., 2021). The transfer of resistance genes and storage of antibiotic resistance can occur within sewage and wastewater treatment plants (WWTPs). In addition, it has been suggested that they act as hotspots for HGT, which would allow the spread of ARGs within other bacterial species (Karkman et al., 2018). While the average bacterial density in sewage is between 10^5 and 10^8 cells per milliliter (Uluseker et al., 2021). The enhancement of biomass in contemporary biological WWTPs causes a threefold rise in bacterial density in the bioreactors, and selection by sedimentation produces dense bacterial aggregates. Microbial diversity and interactions are pervasive and frequent in WWTP bioreactors (Nielsen and McMahon, 2014).

Wastewater microbial populations are difficult to cultivate and mainly comprised of members from different phyla such as Bacteroidetes, Actinobacteria, Proteobacteria, and Firmicutes (Novo et al., 2013). Doxycycline, ofloxacin, ciprofloxacin, and norfloxacin concentrations in Swedish WWTP sludge were measured. Likewise, high levels of norfloxacin and ciprofloxacin were also found in samples of Swiss sewage sludge (Barancheshme and Munir, 2019). Moreover, β-lactamases can be easily broken down, whereas fluoroquinolones and tetracyclines are more persistent, allowing them to remain in the environment for longer and build up to higher concentrations (Hanna et al., 2023). A study by Mthiyane et al. (2024) reported that fifteen chosen antibiotics were monitored within the primary and secondary stages of WWTP.

However, the activated sludge process has been one of the most frequently used sewage treatment technologies for the removal of major contaminants from municipal sewage for more than a century (Uluseker et al., 2021). Through human and animal stool and urine, improper medicine disposal, and direct environmental contamination by wastewater from antibiotic production facilities, antibiotics are discharged into the environment (Singh et al., 2022). A study by Ng et al. (2023) reported azithromycin, erythromycin, clarithromycin, ofloxacin, and ciprofloxacin wastewater effluent samples from wastewater treatment facilities in 11 European countries, showing their presence throughout the continent's aquatic ecosystems. According to a study by Wang et al. (2019), macrolides and fluoroquinolones are the most prevalent antibiotics in the effluents of 18 designated WWTPs in Harbin City, China.

Because wastewater treatment processes are not intended to eliminate ARB and ARGs, WWTPs frequently include antimicrobial agents and other co-selective agents (Rodríguez-Molina et al., 2019). The potency of conventional treatment methods varies significantly among WWTPs, and it is still unclear how some treatment technologies work to eliminate antimicrobials, ARB, and ARGs (Pallares-Vega et al., 2019). The United Nations (UN) World Water Development Report 2020 reveals that 80% of wastewater globally is discharged into marine ecosystems without treatment (UNESCO World Water Assessment Program, 2020). In low-income countries, just 8% of wastewater undergoes treatment, while treatment rates reach 30% in lower-middle-income countries and 70% in higher-income countries (Buelow et al., 2021).

ROLE OF HORIZONTAL GENE TRANSFER IN THE DISSEMINATION OF ANTIBIOTIC-RESISTANT BACTERIA AND ANTIBIOTIC-RESISTANT GENES IN OCEANS

Bacteria can adapt to and live in settings contaminated with antibiotics according to their plastic genomes, which are supported through various genetic pathways such as conjugation, transformation, and transduction. Due to selection pressure, mutation, and gene transfer, ARB develops in bacteria (Kunhikannan et al., 2021). Horizontal gene transfer (HGT) in aquatic bacteria is the exchange of genetic material between various bacterial species in the marine environment (Eskova et al., 2022). Horizontal gene transfer (HGT) mechanisms include conjugation, transduction, and transformation. Horizontal gene transfer (HGT) is critical for assisting bacteria in sharing ARGs between species.

Horizontal gene transfer (HGT) is mediated by mobile genetic elements (MGEs) that include transposons, plasmids, bacteriophages, and integrons (Zhou et al., 2022). Although chromosomal mutations can result in antibiotic resistance in bacteria, HGT is a more prevalent method of ARGs in most cases of antimicrobial resistance (Michaelis and Grohmann, 2023). Bacteriophage transduction is a crucial method for the spread of ARGs throughout the populations of bacteria (Arnold et al., 2022). However, bacteriophages play an important role in spreading virulence genes and ARGs (Chiang et al., 2019).

Bacteria can develop resistance by degrading or modifying antibiotics, as well as by blocking their entry into cells or changing themselves. Bacteria can deactivate antibiotics by hydrolyzing them. The basic mechanism of antibiotic resistance involves antibiotic modification catalyzed by enzymes. Thousands of enzymes that can degrade and modify different antibiotics, including β-lactams, macrolides, aminoglycosides, and phenicol, have been discovered (Nordmann et al., 2011). Bacterial resistance is induced by the presence of ARGs. Pathogenic bacteria acquire ARGs via plasmid exchange at the gene level and develop antibiotic resistance. Horizontal gene transfer (HGT) of ARG-carrying plasmids, transposons, and integrons in bacteria can occur across strains of the same and distinct species (Jian et al., 2021). Different bacterial ARGs may develop resistance to various antibiotics.

About 70% of hospital-acquired infections are resistant to at least one antibiotic (Chow et al., 2021). Antimicrobials that dissolve in surface waters reach sub-inhibitory concentrations, influencing microbial ecology by raising mutation rates, generating HGT, and promoting ARB selection. Long-term exposure to sub-inhibitory antibiotic doses in the marine environment may be the primary cause of antibiotic resistance and ARG transmission (Atterby et al., 2021).

IMPACT OF ANTIBIOTIC-RESISTANT BACTERIA AND ANTIBIOTIC-RESISTANT GENES ON THE ONE HEALTH SCALE

Humans, animals, and the natural environment are interdependent, according to the OH concept (Robinson et al., 2016). A conceptual framework for creating interventions that maximize results for human, animal, and environmental health is provided by OH Concept (Gudipati et al., 2020). Despite the OH approach's propensity to emphasize zoonosis, it is crucial to consider the environmental impacts of capital-based development (Bukha et al., 2022). Because of the irresponsible and excessive use of antibiotics in many industries (human healthcare settings, livestock raising, and agriculture), antibiotic resistance is linked to each of these three factors (Velazquez-Meza et al., 2022). The improper use of antibiotics, contributing to the spread of resistance, is exacerbated by inadequate infection control, agricultural waste, environmental degradation, and the movement of humans and animals carrying resistant bacteria (Bürgmann et al., 2018). However, the OH concept underscores the interconnected health of humans, wild animals, domestic animals, and the environment. This concept emphasizes the necessity of interdisciplinary collaboration, particularly given the pressures of the rapid growth of the human population that is driven by CC, rising levels of contaminants, and the depletion of natural resources (McEwen and Collignon, 2018).

The marine ecosystems act as a significant reservoir of ARB and ARGs. The aquatic animals may consume ARB from the marine environment. On the other hand, their intestines provide an ideal environment for the horizontal transfer of ARGs via conjugation (Jia et al., 2022). Some studies have reported a high abundance of ARB and ARGs in the guts of zebrafish, this can be attributed to HGT that facilitates the ingest of ARB in water by aquatic animals (Fu et al., 2017). Resistant zoonotic bacteria can be detected in soil, where they can then infect plants, vegetables, and fruits. Antibiotic-resistant bacteria (ARB) are easily spread between and among many environments and humans (WHO, 2019). Antibiotic resistance can increase animal disease and mortality rates while also lowering productivity and causing economic losses (McEwen and Collignon, 2018).

According to current studies, the existence of ARGs and/or bacteria in wild animals is more a result of anthropogenic pollution than natural selection for resistance (Dolejska, 2020). Antibiotic-resistant bacteria (ARB) selection primarily occurs in environments with a human connection and areas with wildlife. Therefore, detecting the presence of clinically relevant ARB and ARGs in wild animals not undergoing antibiotics highlights the impact of environmental antibiotic resistance pollution (Ahasan et al., 2017). The rise of the ARB threatens both the aquatic ecosystems' health and human health, highlighting antibiotic pollution in the marine ecosystem as a critical issue (Zhuang et al., 2021) (Figure 5).

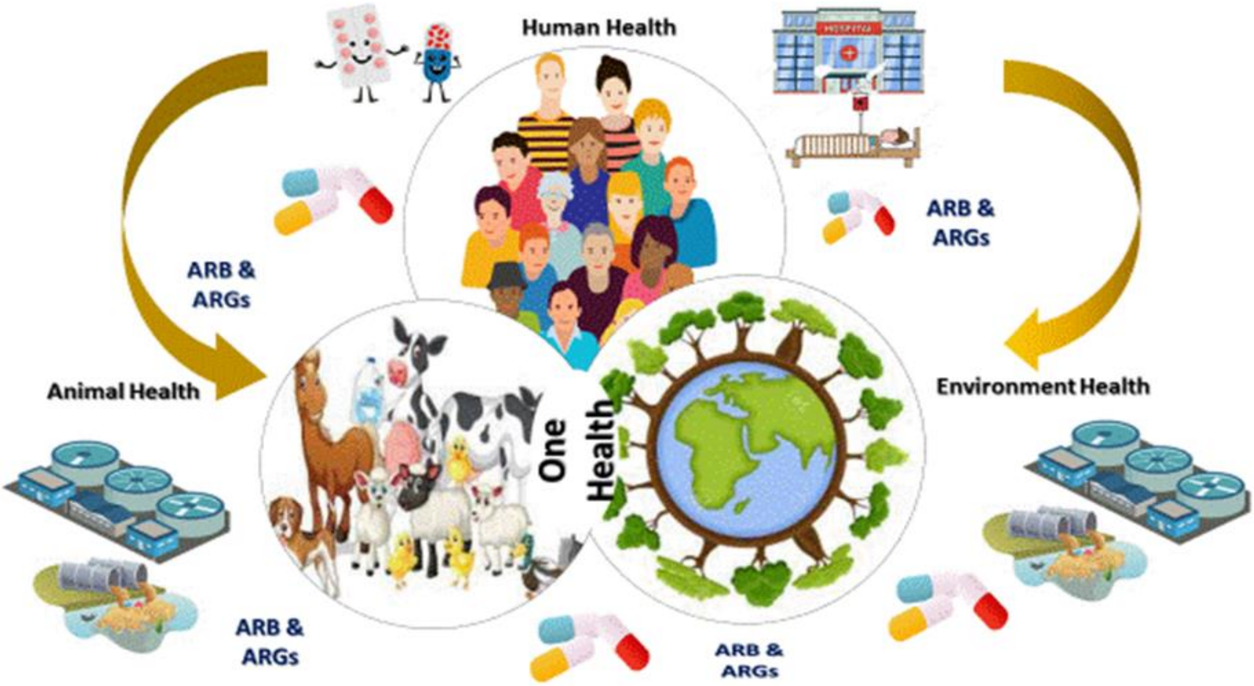

Figure 1. Spread of Antibiotic-Resistant Bacteria (ARB) and Antibiotic-Rsistant Genes (ARGs) at an On Health scale

RISKS OF ANTIBIOTIC RESISTANCE TO PUBLIC HEALTH

The rise in hospitalizations for infections caused by ARB is linked to clinically important antibiotic resistance. This situation can lead to unsuccessful treatments and increased mortality rates among patients (Ben et al., 2019). Particularly, bacteria that may colonize the human body (vectors) harbor ARGs simultaneously. To clone humans, vector bacteria must have the opportunity to come into contact with the human body, which necessitates that these bacteria occasionally or often share an environment with humans (Manaia, 2017). Antibiotic use impacts the intestinal flora, encourages resistance, and boosts the population of opportunistic bacteria, which leads to digestive issues and raises the risk of ARB (Li et al., 2021).

However, several ways may expose people to being infected with ARB, such as via ARB in medical settings, whereas it can be spread via human-to-human contact (Endale et al., 2023). Antibiotic-resistant bacteria can spread to human pathogenic bacteria when they infect the human body. Preventing and treating bacterial diseases becomes more challenging once harmful bacteria acquire resistance (Sanganyado and Gwenzi, 2019). Indirect transmission of waterborne enteric bacteria among residents in a community can also be made easier by poor sanitation (Collignon and Kennedy, 2015). Antibiotics can reach aquatic products mostly by ingestion, although they can also be ingested from sediments or surrounding water in relatively lower amounts (Maghsodian et al., 2022). Aquatic products gathered in Vietnam, China, Korea, and India contain antibiotic residues (He et al., 2016).

One of the most serious global health issues is antibiotic resistance, which causes over 33000 deaths and 67000 diseases annually in the European Union (ECDC, 2025). Globally, the threats associated with "super bacteria" or methicillin-resistant S. aureus (MRSA) are increasing due to its resistance to most antibiotics, making it one of the leading causes of death (Lin et al., 2021). The annual cost of treating infections caused by antibiotic resistance is projected to reach $35 billion in the USA, creating a considerable financial burden on the global economy (CDC, 2025). Surveillance research from 2000 to 2015 in 76 countries found a 65% growth rate in antibiotic usage, increasing it to 34.8 billion (Klein et al., 2018). According to estimates by the WHO, by the year 2050, ARB infections will cause the deaths of 10 million people annually (Chang et al., 2022; Sun et al., 2022).

GLOBAL ONE HEALTH STRATEGIES TO ADDRESS ANTIBIOTIC-RESISTANT BACTERIA AND ANTIBIOTIC-RESISTANT GENES IN THE OCEANS

To address the challenge of the antibiotic resistance crisis in the oceans, the WHO, FAO, and OIE have created a global action plan that incorporates the OH idea. The main objectives of OH are:

Awareness and knowledge of antibiotic resistance will be enhanced via education, productive communication, and training (McEwen and Collignon, 2018; Collignon and McEwen, 2019). Everyone should be aware of the basic principles of good hygiene, such as regular handwashing, disinfecting tools, and properly cleaning food. These practices help reduce the spread of diseases (WHO, 2015; Collignon and McEwen, 2019). Surveillance and research contribute to reinforcing the body of knowledge and evidence. Samples of the significant bacteria found in various animals, humans, and environmental settings, such as farms, veterinary offices, long-term care facilities, fish farming, hospitals, and community settings, should be taken as part of the OH surveillance of antibiotic resistance (WHO, 2015, 2017; Lozano-Munoz et al., 2021). Improve the administration of antibiotics to improve the health of humans and animals. While everybody can benefit from having a deeper understanding of the health aspects of antibiotic resistance, those in special need include farmers, people who keep pets, veterinarians, and those who work in the larger food industry (WHO, 2015).

Promote investment in new pharmaceuticals, vaccines, diagnostic tools, and other innovations by developing an economic case for sustainable investment that addresses the needs of all nations (Canada et al., 2015). Bacteriophages, immunomodulators, monoclonal antibodies, and enzymes encoded by phages are examples of novel treatment methods that have been developed as an outcome of increasing antibiotic resistance and a lack of new drug development. Novel therapeutic approaches may be important for treating serious infections and extending the useful life of antibiotics (Chang et al., 2022). The majority of action policies and laws fail to address the problem and do not expressly reduce the pollution of natural ecosystems by ARGs and antimicrobial agents. All national initiatives lack current regulations restricting the environmental release of antibiotics by pharmaceutical production facilities (Ifedinezi et al., 2024). When it comes to environmental preservation and conservation, global policies must be unified and unavoidable, requiring considerable investments in improving sanitary systems and wastewater management (Buelow et al., 2021).

One Health OH and global health are two interrelated approaches that must be used to fully understand the ARB problem and, more particularly, ARB transmission. The health of these systems is interconnected. Through this approach, it is possible to understand how ARB impacts not only humans but can also be transmitted from marine animals or the marine environment to humans (Hernando-Amado et al., 2020). A major approach to preventing antibiotic resistance is the prudent use of antibiotics in the aquaculture sector. This entails taking action to reduce needless antibiotic use and encouraging prudent consumption (WHO, 2015; Lozano-Munoz et al., 2021). It is crucial to implement national strategies following international norms. Restricted antibiotic use, monitoring of antibiotic resistance, and encouraging the adoption of alternative disease management techniques should be the main objectives of these programs, and to reduce ARB in marine ecosystems, the One Health approach is essential for developing integrated strategies and solutions. This approach emphasizes the importance of coordination and collaboration across various industries, such as aquaculture, public health, and environmental agencies (Lozano-Munoz et al., 2021). Sentinel species such as sea turtles can be used to track and maintain an eye on ARB in oceans. Effective measures require in-depth knowledge of the sources and factors that affect ARB in the oceans, such as WWTPs and human activities (Drane et al., 2021). Antibiotic resistance in aquatic bacteria can be monitored and noticed, which can be used to detect emerging resistance trends and guide intervention plans (Pereira et al., 2020). Despite CC, a health strategy that emphasizes simultaneously preserving the health of humans, animals, and the environment can help reduce the incidence of infections (Gudipati et al., 2020). Promoting awareness and educating the public on how antibiotic resistance is being impacted by CC in the oceans, with an emphasis on the importance of responsible antibiotic use and environmental conservation. Encouraging collaboration across disciplines among scientists working in various fields to better understand the complex connections between CC, antibiotic resistance, and ocean ecosystems (Gudipati et al., 2020).

CONCLUSION

Antibiotics are considered "pseudo-persistent” pollutants. They continually enter environments and their rate of entrance is higher than their rate of disposal. Despite this, the latest study suggests that the widespread administration of antibiotics over the past century has resulted in a selective pressure that has accelerated the acquisition and dissemination of ARGs among environmental bacteria. Moreover, this increases the possibility that these bacteria could be dangerous to human health, given their remarkable ability to swap genes**.** The unclear overlap of ARB and ARGs in the human microbiome and environment does not mean that there is no risk. Furthermore, the increase in infection rates and severity, coupled with the reduced effectiveness of antibiotics in healthcare settings, highlights the effects of this overlap on public health. Comprehending the transmission routes of ARB is crucial in tackling the issue of antibiotic resistance, which impacts not only public health but also the health of aquatic animals and marine environments to ensure the health of aquatic animals, humans, and marine environments. It is imperative to enhance cooperation among various health disciplines, engaging relevant institutions at local, national, and global levels. Applying an OH approach to understanding antibiotic pollution in oceans could lead to increased societal involvement and, ultimately, more effective policy.

DECLARATIONS

Authors' contributions

Khwla Khirallah Bukha collected the literature and wrote the first draft of the review article. Ibrahim Mohamed Eldaghayes contributed to the critical review, editing, and overall supervision of the manuscript. All authors have read, reviewed, edited, and approved the final version of the manuscript.

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The authors declare that there is no conflict of interest.

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Ethical considerations

Ethical issues (including plagiarism, consent to publish, misconduct, data fabrication and/or falsification, double publication and/or submission, and redundancy) have been checked by all the authors.

Availability of data and materials

All data generated during the research are relevant and included in this published article and will be available from the corresponding author upon reasonable request.

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