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REVIEW /REVISIÓN

DRUG-RESISTANT BACTERIAL MICROBIOTA, AN ADDITIONAL HEALTH RISK FACTOR DUE TO CHEMICAL CONTAMINATION IN WATER BODIES

Microbiota bacteriana resistente a tóxicos, un riesgo adicional a la salud debido a la contaminación química en cuerpos de agua

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ABSTRACT

Environmental pollution caused by anthropogenic chemical compounds is a serious problem that requires new economic policies and greater social awareness to mitigate and prevent biodiversity loss and adverse effects on human health. This review aims to determine whether pollutants in freshwater bodies can lead to the development of resistant bacteria to these contaminants and affect the effectiveness of antibiotics used to treat infections in both humans and livestock. Evidence suggests that areas surrounding rivers and lakes contaminated with toxic substances face a higher risk of infections caused by this type of resistant bacteria, which also show resistance to metals, dyes, pesticides, hydrocarbons, and even to various treatments for potable water. Co-resistant organisms are emerging in surface water bodies, airborne particles, and garbage dumps. When they come into contact with potential hosts, they alter the hosts' microbiota to favor their own survival. The case of the Atoyac River Basin in Central Mexico is described, where co-resistant bacteria have been found in tributaries, leading to an increase in the frequency of antibiotic-resistant infections among riverside communities. This review underscores the urgency of raising public awareness about these issues and implementing measures for the proper management of industrial materials and consumer products. By replacing polluting energy sources, minimizing the use of toxic substances in industry, and improving waste management, we can help reduce pollutant generation and safeguard health, biodiversity, and the environment.

Palabras clave: ríos contaminados, contaminación tóxica, resistencia a antibióticos.

RESUMEN

La contaminación del medio ambiente con compuestos químicos de origen antrópico es un problema grave que exige nuevas políticas económicas y una mayor conciencia social para mitigar y prevenir la pérdida de biodiversidad y de la salud humana. Esta revisión tiene como objetivo determinar si los contaminantes en ríos y lagos pueden inducir el desarrollo de bacterias resistentes a estos contaminantes y, simultáneamente, a los antibióticos utilizados para tratar infecciones tanto en humanos como en ganado. La evidencia sugiere que, en las cercanías de ríos y lagos contaminados con sustancias tóxicas, existe un mayor riesgo de infecciones causadas por este tipo de bacterias resistentes, que a la vez muestran resistencia a metales, colorantes, pesticidas, hidrocarburos e incluso a varios tratamientos utilizados para potabilizar el agua. Tanto en cuerpos de agua superficial como en partículas en el aire y vertederos están surgiendo organismos corresistentes que, cuando entran en contacto con posibles hospederos, alteran su microbiota para favorecer su propia supervivencia. Se describe el caso de la cuenca del río Atoyac en el centro de México, donde se han encontrado bacterias corresistentes en los afluentes, al tiempo que la frecuencia de infecciones resistentes a los antibióticos ha aumentado entre los habitantes de las comunidades ribereñas. Esta revisión subraya la urgencia de aumentar la conciencia pública sobre estos problemas e implementar medidas para la gestión adecuada de materiales industriales y productos de consumo, de modo que, al sustituir fuentes de energía contaminantes, reducir el uso de tóxicos en la industria y gestionar adecuadamente los residuos, podamos contribuir a reducir la generación de contaminantes y proteger la salud, la biodiversidad y el medio ambiente.

INTRODUCTION

So far this century, environmental pollution has emerged as a global crisis and has been identified by the World Health Organization (WHO) as the main cause of premature death, claiming between nine and 12 million lives a year worldwide due primarily to air pollution and secondly to water contamination (Landrigan et al. 2020). The rapid industrialization of developing countries, combined with lax environmental regulations and decision-makers lacking technical expertise, has exacerbated pollution issues. This has resulted in the overexploitation of natural resources and accelerated the deterioration of soil, airsheds, and waterways, as industries discharge waste into the air, rivers, and soil—often on land that was once farmland (Vineis and Xun 2009). Consequently, numerous countries undergoing this economic transformation—particularly in Latin America and Asia—have experienced a sharp rise in non-transmissible chronic illnesses. Their biodiversity has suffered significant damage, yet these changes have not led to substantial improvements in the population’s living standards (Landrigan et al. 2018).

The pollution of freshwater bodies has evolved from contamination by organic material and microorganisms from household sanitation systems to include all types of industrial waste. Studies have examined the interactions between these organic and inorganic chemical compounds and microorganisms in the environment. Some findings reveal beneficial effects, such as certain bacteria—like those of the *Proteus* genus—capable of degrading petroleum hydrocarbons (Drzeiwiecka et al. 2016). However, in other cases, bacterial activity increases the bioavailability of inorganic compounds for higher organisms, leading to devastating consequences for both biota and human health, such as the transformation of mercuric chloride into methylmercury in the Minamata River, a process driven by river microbiota that led to Minamata disease (Yorifuji et al. 2009, Bravo and Cosío 2020). These two examples illustrate how microorganisms interact with chemical compounds in open environments, often with unpredictable results. While previous studies have focused on free-living bacteria, evidence also points to highly dangerous and undesirable interactions between toxic compounds and pathogenic bacteria, eukaryotes, and viruses present in sewage, which now mix with industrial waste, as well as discharges from industrial farms or from hospitals, amplifying their risks (Xu et al. 2017).

Given these circumstances, this review aims to assess the extent of existing research on these interactions in bacteria and their potential health risks. The goal is to alert health authorities in developing countries that fail to adequately monitor environmental quality and to advocate for the protection, restoration, and recovery of surface water bodies for the benefit of human populations and biota. To this end, the study examines the case of the Atoyac River Basin in Central Mexico, one of the country's most polluted water systems.

MATERIAL AND METHODS

A search was conducted using Web of Science, Scopus, and PubMed to identify reviews and analyses on surface water contamination by toxic compounds. The rationale followed in the present review is shown in **figure 1**. The search covered the period from 2000 to 2025 and included the following keywords: surface water, aquifers, microbiota, microbiome, antibiotic-resistant bacteria, antibiotic-resistant genes, chemical contamination, environmental and health effects. A total of 171 articles were retrieved. Of these, 60 studies focused on infectious diseases caused by fecal contamination from urban or agricultural areas without addressing chemical pollution, and one study examined plastics in coral reefs; therefore, they were excluded from the review. Of the remaining 110 articles, 27 papers described the presence of human excreta in drain discharges from cities, rural communities, and medical facilities, alongside chemical compounds and medicinal drugs, including antibiotics; 40 studies examined industrial and agro-industrial activities polluting rivers with various toxic chemicals, as well as antibiotic metabolites in animal excreta; 13 studies provided data on water management practices and industrial and municipal water treatment plants, highlighting their role in facilitating the horizontal transfer of antibiotic-and-toxic-chemical-resistance genes among microorganisms; six papers explored microplastics as a support structure for biofilm formation and horizontal transfer; 47 articles analyzed the composition of river or human microbiota, resistance development, mutations, and horizontal transfer;

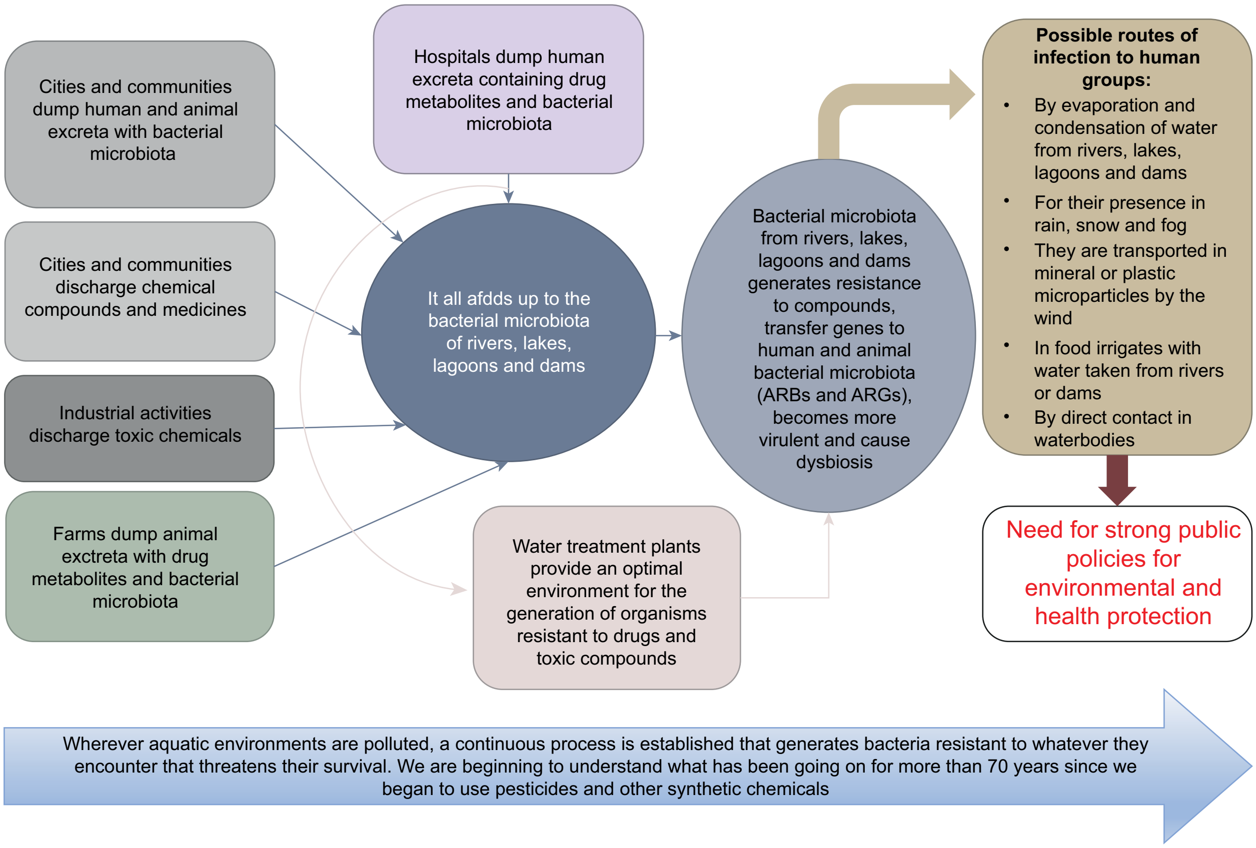


Fig. 1. Conceptual model followed for this review.

14 studies discussed possible routes of human exposure to pollution from rivers; and 57 papers contained information about health risks associated with resistant bacteria and the need for effective public policies to prevent human and animal exposure. Since more than one subject was addressed within several papers, the total count does not sum precisely to 110. The third section of this work centers on a representative case study in Mexico: the Atoyac River Basin. Of the total 110 articles, 23 focused on this region, examining the presence of pollutants and microorganisms, particularly in relation to antibiotic resistance.

WATER POLLUTION OVERVIEW

When discussing polluted water, health authorities in tropical countries often focus on organic matter, feces, and pathogenic microorganisms responsible for intestinal infections and other severe and dangerous illnesses such as cholera, dysentery, malaria, and poliomyelitis. Diarrheal diseases alone result in approximately 800 000 deaths annually due to fecal-contaminated water, with children accounting for one-third of these fatalities. The WHO estimates that two billion people lack access to adequate drinking water facilities, forcing them to rely on microorganism-contaminated water, thereby putting their health at serious risk (WHO 2023).

Health authorities have overlooked the fact that, beyond the risks of infections, chemical contamination of water led to 1.3 million deaths in 2015 due to inadequate sanitation and unsafe water sources, according to a study by Landrigan et al. (2018). Chemical contamination of water has become increasingly complex, originating nearly a century ago with the use of agrochemicals, including crop pesticides, and nitrate- and phosphate-based fertilizers intended to boost soil productivity. In this millennium, these pollutants have been joined by additional, previously unrecognized risks, including vast quantities of carcinogens, mutagens, and endocrine disruptors released by various industries (WHO 2023).

Currently, the recognized sources of river pollution include industrial effluents, agricultural runoffs, and human waste—often containing antibiotics and antiseptics that create selective pressure on bacterial populations promoting resistance (Barnett-Itzhaki et al. 2016, Maruzani et al. 2020, Purohit et al. 2020).

Despite the risks to human health, efforts to prevent chemical contamination remain under the jurisdiction of environmental ministries, which hold less power, have less influence, and have limited funding (Landrigan et al. 2020). Meanwhile, mounting evidence suggests substantial alterations in riverine microbiota that favor the survival of chemical-resistant bacteria.

HOW DOES CHEMICAL POLLUTION AFFECT THE MICROBIOTA OF RIVERS?

The pollution caused by human activities has undeniably impacted ecosystems worldwide. Countless rivers now have dead sections along their courses, where life chains have collapsed, leaving only a few surviving organisms. Often, these polluted stretches are sources of disease for human populations, with notable examples including the Minamata River (Yorifuji et al. 2009), the Mississippi River (Joyce 2000), the Nile River (Soliman et al. 2006), the Ganges River (Richards et al. 2023), and the Yang-Tse River (Zhang et al. 2013). Mexican rivers are no exception, with many deteriorating over the years without restoration efforts—treated as though this degradation were a natural and acceptable process (Guevara et al. 2014, Arellano et al. 2015, Montero-Montoya 2020).

Despite the presence of pollutants and dead zones, these water bodies still harbor microorganisms that constitute the river's microbiota. Much like the intestinal microbiota, this microbial community consists of numerous species of bacteria, viruses, and phages. The normal bacterial microbiota of freshwater bodies is detailed in **table I** (Zwart et al. 2002).

Chemical contamination first impacts the physical and chemical conditions of a water body, including pH, temperature, salinity, and trophic state. These conditions, along with light availability and climate, shape the diversity of microorganisms present. Metals, phosphorus, and nitrogen concentrations are assessed in environmental monitoring (Wu et al. 2019), which are affected by agricultural spills from fertilizers and pesticides. As a result, microbiota composition undergoes notable alterations, as seen in **table I**, which shows reduced biodiversity by the persistence of more resistant organisms. It is also observed that, even in polluted rivers, the relative abundance of highly pathogenic phyla for humans—such as Pseudomonadota, which includes the genus *Enterobacter*, known to cause diarrhea, pneumonia, and other diseases—remains low. In contrast, the more abundant phyla are also found in the intestinal microbiota, such as Bacteroidota and certain Pseudomonadota classes, including alpha, beta, and gamma Proteobacteria (**Table I**).

TABLE I. COMPARISON OF THE DIVERSITY OF BACTERIAL MICROBIOTA BETWEEN PRISTINE FRESHWATER SITES AND SITES CONTAMINATED BY HUMAN ACTIVITIES.

Phyla/class/order	Pristine freshwater sites (%)	Urban/ agriculture (%)	Industrial (%)
Actinobacteriota/—/—	10	12	18
Pseudomonadota/alpha-proteobacteria/—	12	12	18
Pseudomonadota/beta-proteobacteria/—	10	12	18
Bacteroidota/Cytophagia/Cytophagales	8	12	—
Bacteriodota/Bacteroidia/Flavobacteriaceae	8	12	—
Bacteroidota/Bacteroidia/Bacteroides	8	12	9
Verrucomicrobiota/—/—	7	6	9
Pseudomonadota/gamma-proteobacteria/—	6	6	18
Pseudomonadota/delta-proteobacteria	6	3	—
Planctomycetota/—/—	5	3	—
Acidobacteriota/Holophagae/Holophagaceae	4	—	—
Chloroflexota/—/—	5	—	—
Fusobacteriota/—/—	2	—	—
OP10**/—/—	2	3	—
Bacteroidodota/—/—	2	—	9
Cyanobacteriota/—/—	2	6*	—

/—/ Class or order was not reported.

*Among the genera reported is Microcystis, related to toxic algal blooms (Zwart et al. 2002, Cottrell et al. 2005, Newton et al. 2011, Mittal et al. 2019).

**OP10 Phylum was reported by Hugenholtz et al. 1998.

Phyla, class and order nomenclature is approved by the National Center for Biotechnology Information, Taxonomy Checklist Dataset (NCBI 2011).

TABLE II. XENOBIOTIC METABOLISM OF TRANSPORT PATHWAYS, ANTIBIOTIC RESISTANCE, METAL TOLERANCE, AND VIRULENCE FACTORS IDENTIFIED IN BACTERIA OF RIVERS CONTAMINATED BY INDUSTRIAL DISCHARGES AND OTHER SOURCES OF POLLUTION.

Xenobiotic metabolism or transport pathways	Antibiotic resistance	Metal tolerance	Virulence factors
Degradation of: - Atrazine - Benzoate - Bisphenol - Chlorobenzene -Chlorocyclohexane - Toluene - Xylenes - Benzene - Phenol - Ethylbenzene - PAHs - Naphthalene - Nitrotoluene	Efflux pumps. Peptidoglycans biosynthesis inhibition. Hydrolytic degradation. Transferases.	Efflux pumps. Metabolism: - oxidation - reduction - methylation - demethylation	Offensive: - production of bacterial toxins, - secretion and adherence systems. Virulence factors: - flagella, - type IV pili, - encapsulation with lipo-oligosaccharides and lipopolysaccharides.

Elaboration from Tang et al. (2021), Xu et al. (2017), Lekunberri et al. (2018), Mittal et al. (2019).

Physiologically, the metabolic activity of a river's microbiota is highly dynamic, encompassing toxic substance activation and detoxification, metal and antibiotic resistance pathways, and the activation of virulence mechanisms (Stanley et al. 2014, Brown et al. 2015, Mittal et al. 2019). This demonstrates an intense response to toxic environmental conditions (**Table II**).

In polluted rivers with a high abundance of xenobiotic compounds, microbes tend to acquire genes and pathways that enable the transformation or transport of these chemicals as part of their survival mechanism (Mittal et al. 2019; **Table III**). These bacteria not only persist in these environments but also develop properties that make them resistant to medical treatments or enhance their pathogenicity when infecting living organisms. In addition to the induced physiological activity, a large number of mutations occur due to the presence of mutagenic agents. These mutations are inherited by offspring or transmitted horizontally to other organisms, e.g., from a non-pathogenic species to a pathogenic species. This is due to the ubiquitous presence of mobile genetic elements, including transposases (Tn3, Tn21, Tn1721, Tn2501, and Tn3926) or integrases (intl1, intl2, and intl3), which promote the incorporation of new genes (Lekunberri et al. 2018, Mittal et al. 2019, Salma et al. 2025).

Strikingly, co-resistance to antibiotics and metals has been identified in highly polluted sites (**Table III,** bottom), where resistance genes appear to be present in the same plasmid as observed by Xu et al. (2017, 2025) in several multi-resistant bacterial species (**Table IV**). Additionally, Gupta et al. (2022) found that metal concentrations were positively correlated with the relative abundance of antibiotic resistance genes (ARGs) and metal resistance genes (MRGs), suggesting that metals promote horizontal transfer and co-selection of resistance mechanisms in the environment.

Beyond metals, Qiu et al. (2022) established that stress caused by pesticides—such as glyphosate,

TABLE III. SOME GENES ASSOCIATED WITH ANTIBIOTIC RESISTANCE, METAL TOLERANCE, OR ANTIBIOTIC AND METAL CO-RESISTANCE DETECTED IN RIVERS CONTAMINATED BY INDUSTRIAL DISCHARGES AND OTHER SOURCES OF POLLUTION.

Antibiotic resistance genes		Heavy metal resistance genes
To sulfamide:		To copper:
- *sul* (*sul*1, *sul*2, *sul*3)		- *cop*B, *cop*D
To tetracycline:		To zinc and cadmium:
- *tet (tetA, tetB, tetW, tetM, tetQ, tetO)*		- *czc*A, *czc*D, *zra*P
To quinolones (through plasmids):		To lead:
- PMQR (*qnrA, qnrB, qnrD, qnrS, qepA*)		- *phr*R, *phr*T
To fluoroquinolones:		To mercury:
- *gyrA*		- *operon mer* (*mer*A, *mer*R)
To macrolides:		To arsenic:
- *erm* (*erm*B y *erm*C)		- *ars (arsR, arsA, arsB, arsC, arsD, arsH, arsM*)
To β-lactam:		
- Class A (*CARBs, Tla*)		
- Class B (*cephA3, cphA6*)		
- Class C (*CMY, MIR, PDC, DHA, OCH*)		
- Class D (*OXA b-lactamasa*)		
- Carbapenems (*IMP, VIM, OXA*)		
- Metallo-b-lactamases (*bla*$_{\text{NDM-1}}$, *bla*$_{\text{NDM-8}}$, *bla*$_{\text{AIM-1}}$, *SMB-1*, *bla*$_{\text{IMP-1}}$, *bla*$_{\text{IMP-25}}$, *imiH*, *bla*$_{\text{VIM-2}}$)		
To rifampicine:		
- *rpoB*		
To daptomycine:		
- *rpoC*		
Multidrug:		
- *mexW, mexB, mexF, oprN*		
Genes of co-resistance to antibiotics and metal in the same plasmid		
Antibiotic resistance genes*:*		Metal tolerance genes*:*
qepA, qnrA, qnrB, qnrD	------	*czcA, czcD, zraP*
ermB	------	*copB, copD*
tetA or *tetW*	------	*copB* and *merR*
sul3	------	*copB, copD, czcA, czcD, zraP, merA, merR*
tetA, tetR, blaCMY-2, strA, strB	------	*operon mer*

Elaborated from Tang et al. (2021), Xu et al. (2017), Mittal et al. (2019).

TABLE IV. CO-RESISTANCE TO CHEMICALS, ANTIBIOTICS, AND ANTISEPTICS FOUND IN BACTERIAL SPECIES.

Organism	Co-resistance	Authors
Bacillus cereus *Bacillus megaterium* *Bacillus thuringiensis* *Shewanella oneidensis* *Acinetobacter baumanii*	Cu, Zn, Cd, tetracycline, sulfamethoxazole, ciprofloxacin	Xu et al. (2017)
Acinetobacter spp.	Methylene violet, acridine orange, SDS, benzalkonium, chlorine, rhodamine, sodium deoxycholate	Aishwarya et al. (2021)
Proteus spp.	Antibiotics, metals, and other toxics	Drzeiwiecka (2016)
Bacillus spp. *Pseudomonas* spp. *Klebsiella* spp.	Sodium hypochlorite, EDTA, phenol, trimethoprim, chloramphenicol	Debarati et al. (2019)
Escherichia coli *Salmonella* spp. *Campylobacter jejunii*	Cyclohexane, triclosan, ampicillin, tetracycline, fluoroquinolone	Debarati et al. (2019)

2,4-D, and pesticide mixtures—increases bacterial antibiotic resistance through multiple mechanisms, including activation of efflux pumps, inhibition of outer membrane pores, and induction of gene mutations. Acquired ARGs can be transmitted horizontally via conjugation or mobile genetic elements (MGE) (Wang et al. 2024), a process facilitated by pesticides that increase membrane permeability. Bacteria that emerge through this process are termed antibiotic-resistant bacteria (ARB).

Furthermore, microorganisms in rivers highly contaminated with metals, plastics, pesticides, fertilizers, medicinal products, fats, oils, petroleum, and other organic compounds, not only exhibit metabolism of sulfur, methane, nitrogen, as well as hydrocarbon degradation, but also display several mechanisms contributing to antibiotic resistance through beta-lactamases and biofilm formation (Aishwarya et al. 2021). Biofilms protect bacterial communities, enabling them to survive and propagate ARGs (Xiao et al. 2024). In addition, some bacteria release toxic peptides, further polluting the water. **Figure 2** illustrates these complex transformations. These bacterial activities—methane and CO_2 production during acetate decarboxylation—contribute to greenhouse gas formation (Aishwarya et al. 2021).

Another negative aspect of microbiota alteration in polluted water bodies is the ability of these microorganisms to overcome the physiological cost of acquiring antibiotic resistance due to constant pressure. Horizontal transfer further includes the acquisition of plasmids, mobile genetic elements, or phage DNA that may encode virulence factors, as well as the sequences needed for genetic mobility, thereby enabling bacteria to survive within host tissues (Shames et al. 2009). Virulence factors, as shown in **table II**, were found in abundance in the study of Tang et al. (2021). ARGs and virulence factors were correlated in species such as *Escherichia coli*, *Staphylococcus aureus*, *Streptococcus pneumoniae*, *Burkholderia glumae*, and *Klebsiella pneumoniae*, which rank among the pathogens responsible for the highest number of infections worldwide (ARC 2022). However, these events extend beyond human pathogens. ARGs and virulence factors have also been found in fungal species affecting rice and grass, such as *Fusarium graminearum* and *Magnaporthe oryzae* (Tang et al. 2021). In other words, food production is also at risk.

EVIDENCE FOUND IN OPEN ENVIRONMENTS

The presence of toxic industrial chemicals, drugs, and antibiotics exerts significant pressure on the natural selection of both free-living microbial organisms and those that colonize humans, leading to the widespread presence of ARB and ARGs. There is also a risk that ARGs may recombine within clinically important pathogens, fostering the emergence of superbugs resistant to traditional medical treatments.

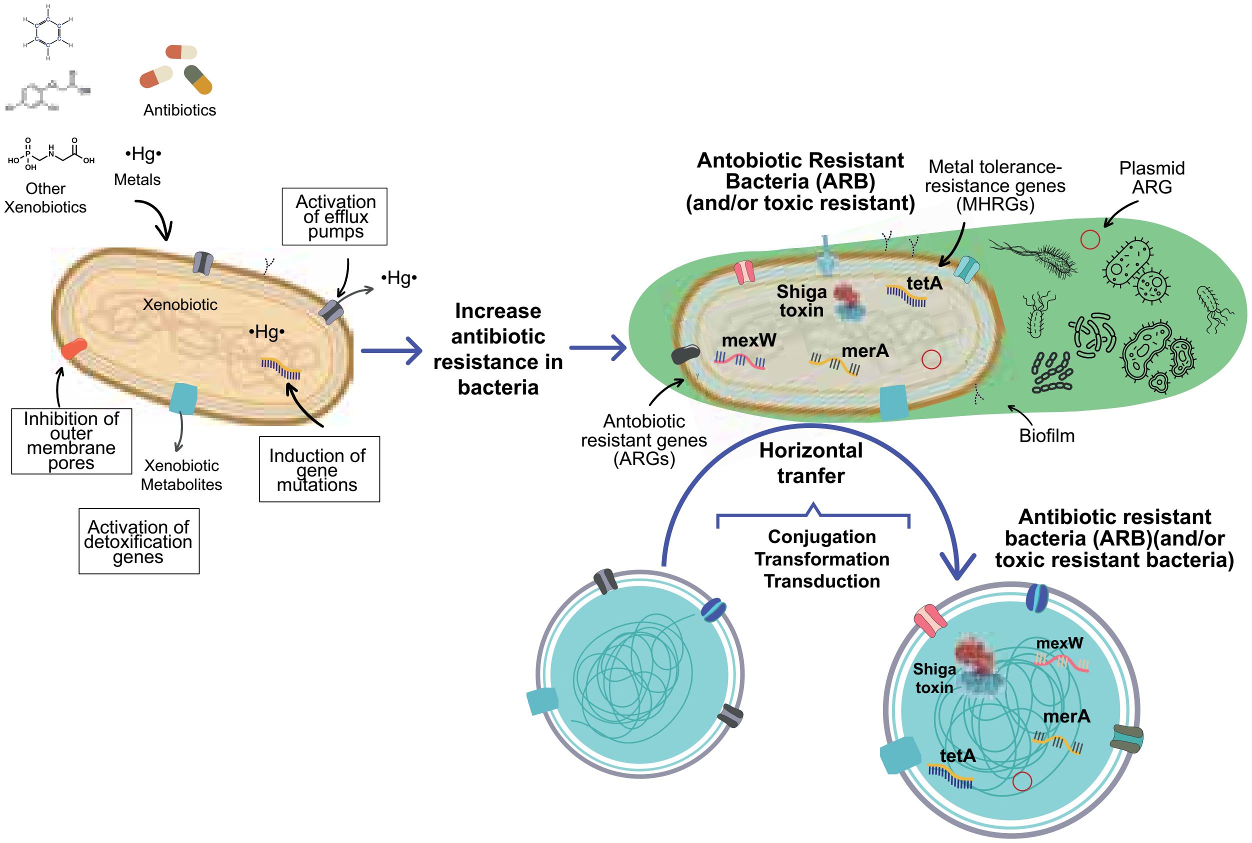


Fig. 2. Metabolic activity and gene mutations are used by bacteria as mechanisms to survive in toxic environments, thus generating organisms resistant to chemical challenges, like pharmaceutical drugs, natural and synthetic chemical compounds, and metals. Central to resistance dissemination is the horizontal transfer taking place between organisms of the same or different species, either directly or via free DNA or plasmids, and it can occur either inside an organism or in an adequate niche like a biofilm, a pond, a plastic bag, a microparticle or in the sediments of aquatic bodies, or else, on wounds, epithelia and other tissues. A biofilm is a matrix composed of carbohydrates where organisms of different origins adhere, staying in close proximity and avoiding the effects of antibiotics or antiseptics.

Tang et al. (2021) found antibiotic resistance in wastewater from pharmaceutical and food processing industries, as well as from a slaughterhouse and a wastewater treatment plant (WWTP), containing bacitracin, fluoroquinolone, chloramphenicol, tetracycline, aminoglycosides, beta-lactams, tigecycline, penicillin, and sulfonamides. Additionally, resistance to ampicillin via synthetic plasmids has even been observed in samples from six rivers in China, with higher concentrations in rivers receiving untreated industrial discharges (Brown et al. 2015).

Wastewater treatment plants

Regarding WWTPs, Mutuku et al. (2022) proposed that they create an ideal environment for antibiotic concentration and interaction with bacteria and resistance genes, facilitating horizontal transmission of ARGs. As a result, WWTP effluents contribute to the spread of both commensal and pathogenic bacteria in receiving environments, a finding supported by several authors (Novo et al. 2013, Rizzo et al. 2013, Martí et al. 2014, Khan et al. 2016, de la Cruz et al. 2024, Yadav et al. 2024, Bustamante et al. 2025). Rodríguez-Mozaz (2015) also found that beyond the dissemination of resistant organisms and genes, incompletely eliminated antibiotics can leak from poorly maintained or aging plants, perpetuating resistance in water bodies. Tang et al. (2021) found similar pathogen levels in industrial effluents and WWTP discharges, further confirming that most conventional water purification plants fail to remove chemical compounds. Additionally, methods used to eliminate pathogens, such as chlorine, UV light, and ozone, contribute to the development of resistance in many of these organisms. Water regulation practices can also alter microbial community dynamics and increase the abundance of ARGs and ARB (Ding et al. 2024).

Hence, antibiotics are not the sole contributors to ARGs dissemination; various compounds play a role, including pesticides (Qiu et al. 2022), flame retardants (Wu et al. 2024), perfluorooctanoic acid (Wang et al. 2024), metals (McArthur and Tuckfield 2000, Lucious et al. 2013, Castillo 2014, Mittal et al. 2019, Gupta et al. 2022), along with all the other previously mentioned compounds (Aishwarya et al. 2021). Areas containing these rich mixtures of synthetic compounds, such as in domestic and industrial wastewater, are considered hot spots for ARG formation (Tang et al. 2021), fostering pathogen prevalence and diversification in the environment.

To contextualize this issue, health agencies in a significant number of countries recognize antibiotic resistance as a serious and growing public health issue. A 2016 review (O'Neill 2016) estimated that it could lead to 10 million deaths annually by 2050.

Pollution by plastics

Plastics—both macro and micro—are particularly relevant because, in addition to the toxins released from additives during production, such as bisphenol-A (BPA), brominated flame retardants, phthalates, residual monomers, and dyes, they provide microhabitats, acting as reservoirs and transporters of communities to distant sites. Resistant and pathogenic organisms can travel within these toxic reservoirs.

Microplastics enriched the presence of *Acinetobacter*, *Legionella*, and *Mycobacterium*, although other pathogens were more prevalent in river water (Silva et al. 2024). Similarly, Guruge et al. (2024) found an enrichment of *Exiguobacterium* and *Eubacterium* in a Japanese river. They also observed that polyethylene (PE), polyethylene terephthalate (PET) (Silva et al. 2024), and polypropylene fibers (Guruge et al. 2024) provided a more favorable environment for these pathogens compared to natural sand particles. Moreover, Zhou et al. (2024) found that biofilms in PE enhanced the frequency of ARG conjugative transfer by a factor of 12. This was attributed to an increased collision frequency between donor and recipient bacteria in biofilms, leading to the upregulation of outer membrane protein genes *ompA*, *ompC*, and *ompF*, which improve membrane permeability for gene transfer, as well as increased expression of genes related to pili synthesis, conjugation pairing, and DNA replication. Guruge et al. (2024) found that the abundance of ARGs conferring resistance to antibiotics, biocides, arsenic (As), and mercury (Hg) was three times higher, along with an increase in MGEs. Yan et al. (2024) confirmed these findings and further observed that contaminants, including metals, organic pollutants, antibiotics, and radionuclides, are also enriched on microplastic surfaces.

Macroplastic waste, such as abandoned plastic bags in landfills, serves as reservoirs that become breeding grounds and are subsequently transported to water bodies by rainfall and runoff, or wind. Additionally, they contribute to the air microbiota, which, like that of water, contains a greater number of pathogens in highly polluted sites (Agarwal et al. 2024). These pathogens are associated with particles and aerosols, particularly $PM_{2.5}$ and PM_{10} (Liu et al. 2018). Such particles create an ideal environment for mutations, resistance acquisition, and conjugation to occur.

As can be seen, toxic substances in the environment can move through water and air currents, dispersing across all environmental matrices where they interact with microorganisms and other living beings. The importance of these interactions lies in the fact that microorganisms have significantly shorter life cycles than multicellular organisms and adapt more rapidly to exposure. They transmit mutations and changes efficiently not only to other microorganisms within their own species but also across species, giving them a survival advantage over other organisms within the same ecosystem. Humans, by contrast, lack this adaptive efficiency. Furthermore, microbiota have been identified in every multicellular organism, from cnidarians to humans, inhabiting every organ of the body (Kuziel and Rakoff-Nahoum 2022). Although microbiota can confer extraordinary capacities to their host organisms, they are subject to transformations similar to those occurring in open environments such as water, air, and soil when exposed to toxic agents or medicinal products.

WHAT ARE THE RISKS TO HUMAN HEALTH FROM POLLUTED RIVERS?

Polluted rivers have sadly become reservoirs of ARB and ARGs. People can be infected through direct consumption of contaminated water, engaging in sports, recreational, or religious activities in rivers or lakes, or consuming food irrigated with such water (Pereira et al. 2013, Contreras et al. 2020, Purohit et al. 2020, Chibwe et al. 2023, Ram et al. 2024; **Fig. 3**). Even a simple walk along the banks of a polluted river can expose individuals to aerosol droplets or fog carrying these organisms (Hu et al. 2018, Chibwe et al. 2023, Cangola et al. 2025), with respiratory and digestive tract infections being the most likely

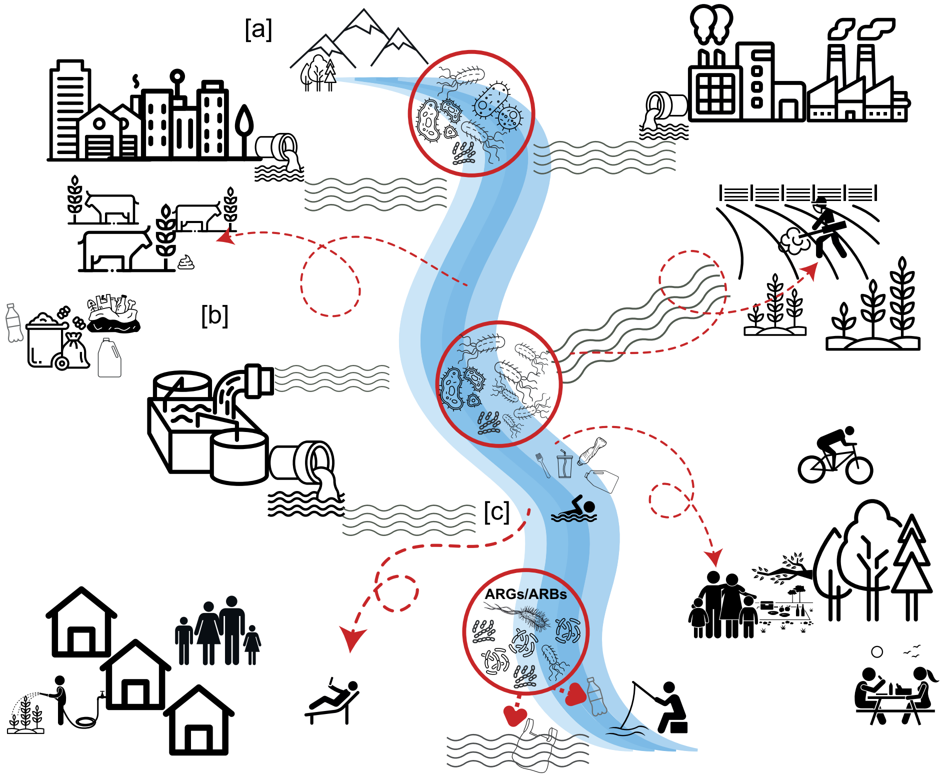


Fig. 3. (a) The natural microbiota of rivers is altered by pesticide runoff and discharges of chemical pollutants from urban or industrial sources. Mutations occur, plus the activation of molecular functions that provide microorganisms with advantages for their survival. (b) Rivers receive agrochemicals and antiseptics from farms, as well as the feces of animals or humans, along with runoff, debris, and leachate from open-air dumps. This causes the microbiota to accumulate more changes, which become manifest when living beings are colonized or infected, making them more virulent and resistant to antibiotics. Treatment plants do not completely eliminate microorganisms, and the most resistant ones survive. Activities near the river become a health risk due to the possibility of infection through the water, from food irrigated with that water, from droplets or fog, or from the transport of microorganisms in air currents. (c) Eventually, the microbiota also decrease in variety, and only those that have developed resistance or acquired it remain (antibiotic resistance bacteria [ARB] with their antibiotic resistance genes [ARGs]). This is happening in lakes, lagoons, rivers, and oceans around the world, where they develop resistance to pollutants, which often coexist with drug resistance, and is already a global health problem. Notation: wavy lines represent runoff into the river and arrows on dotted lines represent air emissions (drawing by Regina Montero and Rocío López Vargas).

diseases. Additionally, the interaction of ARGs and ARB with the normal microbiota of the gut or lungs can induce significant changes, leading to alterations that further negatively impact health.

In healthy individuals, microbiota is a community of bacteria, fungi, and viruses, estimated to include about 1500 species coexisting in a population equilibrium. The microbiome is the set of genomes of microorganisms coexisting with the host, with an encoding capacity 150 times greater than that of the human genome alone. This provides the latter with functional capacities that it has not developed through its own evolution. Its normal functions within the organism include stimulating the immune system maturation, promoting tissue differentiation, protecting against pathogens, and forming a biochemical, molecular, and cellular interface between the external environment and the organism (Li et al. 2021). Furthermore, microbiota has been linked to brain cognitive functions and epigenetic modifications in the genome (Cresci and Bawden 2015, Fackelman and Sommer 2019). Eubiosis refers to this state of balance.

Air, which carries moisture from water bodies and is the medium in which all terrestrial organisms exist, also carries micro- and nanoparticles from soil, landfills, and other sources. These particles, to which microorganisms adhere, can easily enter the respiratory and digestive systems (Mousavi et al. 2022, Qiu et al. 2022), creating a continuity between the environment and the internal space of the body. Particles carry microorganisms and all kinds of pollutants (Li et al. 2021), while plastic particles can accumulate these compounds within organisms, magnifying their effects (Fackelman and Sommer 2019), and leading to dysbiosis—a state in which the balance is disrupted and the relationship between microbiota species and their host is altered—along with its secondary health consequences.

Just as in rivers, the presence of xenobiotic compounds within organisms induces bacterial metabolic activity (**Fig. 2**), potentially leading to the production of toxic metabolites. Once inside the host, these metabolites can damage organs, causing local or systemic chronic inflammation and associated diseases, such as asthma, irritable bowel syndrome, autism, multiple sclerosis, and allergies (Tralau et al. 2015). This means the issue extends beyond the risk of antibiotic-resistant infections to chronic non-communicable diseases that severely impact quality of life.

As stated, the intestinal tract is an open system with a continuous influx of microbes from the surrounding environment. The diversity found in the environment is as extensive as that within organisms, where the phyla Bacillota (formerly known as Firmicutes, **Table I**), Bacteroidota, and Pseudomonadota predominate, with Actinobacteriota present to a lesser extent in the normal microbiota (Arumugam et al. 2011, Almeida et al. 2019). River pollution generates ARB and ARGs that eventually re-enter organisms—including humans—establishing a cycle of infection and re-infection with an intermediate period of mutation-conjugation-resistance that poses significant dangers to human communities worldwide.

THE UPPER ATOYAC RIVER BASIN: A HIGH HEALTH RISK AREA IN THE MEGALOPOLIS

The Atoyac River Basin is a heavily polluted region affected by industrial, agricultural, and urban waste. It encompasses the Atoyac, Zahuapan, and Alseseca rivers, which cross the metropolitan areas of Puebla and Tlaxcala. It is one of the most populated and industrialized areas in the country and serves as an example of how severe environmental problems can escalate, affecting larger regions. This basin is situated near the Valley of Mexico, home to Mexico City and its Metropolitan Area, and shares an atmospheric basin with them. Together they form part of the so-called Megalopolis, an urban and socio-economic oddity facing numerous problems, including the one described here. The aforementioned rivers form the river network of the Alto Atoyac Basin (CAA, acronym in Spanish), which is designated as a Region of Sanitary and Environmental Emergency (RESA, acronym in Spanish) due to heavy pollution and its severe effects on human health (CONAHCYT 2023, **Fig. 4**).

Numerous studies have examined this basin's toxic pollution and its biological and health effects (Montero et al. 2006, 2020, Greenpeace 2018; López-Vargas et al. 2018). The exposure of residents to various toxic agents, including metals, persistent pesticides, PCBs, phthalates, and VOCs, has also been documented (CONAHCYT 2023). In 2011, a formal declaration was issued regarding these rivers (CONAGUA-SEMARNAT 2011), but it failed to stop the deterioration process. At the same time, numerous studies indicate that the rivers of the CAA have become reservoirs for a wide variety of microorganisms (Rivera-Tapia et al. 2006, Rodríguez-Tapia and Morales-Novelo 2017, CONAGUA 2018, Pérez-Castresana et al. 2018, Mora et al. 2021) that enter the aquatic environment through municipal and hospital wastewater, contributing to bacterial resistance (Rivera-Tapia and Cedillo-Ramírez 2005, Castillo-Díaz 2014, Bairán 2017, Tejeda-Hernández 2021, Gómez et al. 2023). **Table V** summarizes several studies assessing whether pathogens in the basin's water currents exhibit antibiotic resistance.

Only 40% of the municipalities in the CAA treat municipal wastewater (CONAGUA 2024). However, operational WWTPs fail to remove toxic chemicals (Castillo-Díaz 2014, Mejía-Morales et al. 2020, Pacheco-Torres 2022) and, as previously mentioned, they instead provide an environment conducive to ARG and ARB generation while selecting for highly pathogenic bacteria, such as *E. coli*, *Enterobacter aerogenes*, and *Pseudomonas aeruginosa* (Rodríguez-Tapia and Morales-Novelo 2017, Pérez-Castresana et al. 2019, Mejía-Morales et al. 2020). These bacteria have been detected in the effluent of a hospital WWTP, eventually reaching the sewage system of Puebla. Castillo-Díaz (2014) found similar results in effluents that had undergone primary and secondary treatments, revealing a correlation between metal contamination tolerance and antibiotic resistance, as observed in other studies (McArthur and Tuckfield 2000, Lucious et al. 2013, Mittal et al. 2019).

Additionally, *K. pneumoniae* (Rivera-Tapia and Cedillo-Ramírez 2005) is among the bacteria responsible for a significant number of deaths linked to antimicrobial resistance (ARC 2022). They have also been identified in well water designated for

Fig. 4. Atoyac Basin in Central Mexico. The line delimits the basin between the volcanoes Matlalcueitl to the east and Popocatepetl and Iztaccihuatl to the west, formed by the runoff of the latter. The rivers run south, towards the Valsequillo Dam at the southern end of the basin. Within the basin, there is a process of conurbation between the city of Puebla and several cities of Tlaxcala (state boundaries in dotted lines). Mexico City and other smaller towns can be seen outside the basin, as part of the Megalopolis, and they have their own pollution problems. (Image taken from Google Earth in April 2024).

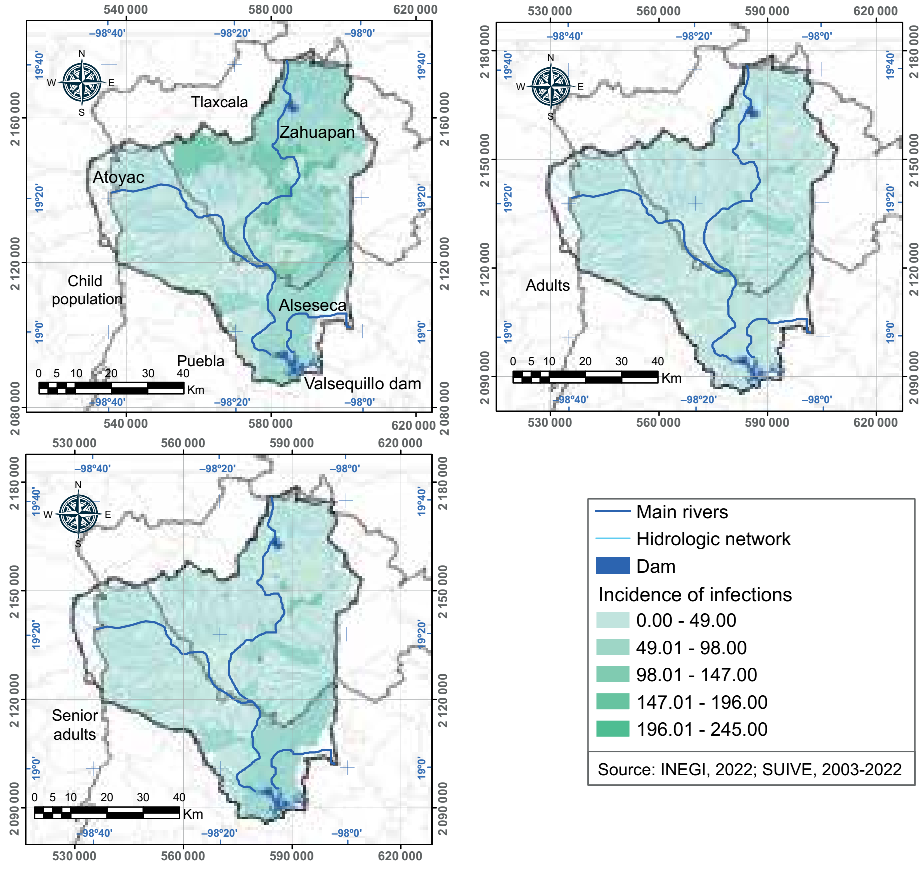
TABLE V. ANTIBIOTIC RESISTANCE IN GENERA OF PATHOGENIC BACTERIA ISOLATED FROM WATER SAMPLES FROM THE UPPER ATOYAC RIVER BASIN.

River in the Basin	Pathogens identified	Resistance to:	Authors
Atoyac River, city of Puebla metropolitan area	*Bacillus* spp. *Salmonella* spp. *Escherichia* spp. *Pseudomonas* spp. *Staphylococcus* spp. *Streptococcus* spp.	- Beta-lactam - Amoxicillin - Amoxicillin - Ampicillin - Clindamycin - Dicloxacillin	Gómez et al. (2023)
Santa Elena River	*Edwardsiella* spp. *Salmonella* spp.	- Sulfamethoxazole - Sulfasalazine - Sulfacetamide - Sulfanilamide - Sulfadiazine	Bairán (2017)
Alseseca River	*Escherichia* spp. *Klebsiella* spp. *Serratia* spp. *Enterobacter* spp.	- Carbenicillin - Ampicillin - Cefotaxime - Trimethoprim - Chloramphenicol	Rivera-Tapia (2005)
Alseseca River	*Salmonella* spp.	- Trimethoprim - Sulfamethoxazole - Carbenicillin	Tejeda-Hernández (2021)
Alseseca River	*Escherichia* spp.	- Cefotaxime - Fluoroquinolones - Nalidixic acid - Aminoglycoside	Castillo (2014)

human consumption as well as irrigation canals (Pérez-Castresana et al. 2019).

The ESKAPE group of bacteria should also be mentioned: *Enterobacter cloacae*, *Staphylococcus aureus*, *K. pneumoniae*, *Acinetobacter baumannii*, *P. aeruginosa*, and *Enterococcus faecium*, which are also considered the primary etiological agents of infections of this kind in Mexico (Giono-Cerezo et al. 2020, Guevara 2021). They are highly virulent and antibiotic-resistant, and have been included in the list of 12 bacteria for which new antibiotics or treatment strategies are urgently needed (Tacconelli et al. 2018). The risk of exposure to these organisms remains high, as the most contaminated stretches of the CAA are located in densely populated areas, and river water continues to be used for farming in some rural communities (Castro-González et al. 2017, 2019, Pérez-Castresana et al. 2019).

A spatiotemporal analysis of morbidity from gastrointestinal and acute respiratory diseases, along with their relationship to socio-environmental factors in this basin, revealed a significant positive correlation between the density of higher-order rivers within urban areas and the incidence of intestinal infections by other organisms and poorly defined ones, which are numerically dominant among acute intestinal diseases in children (A04 and A08-A09 according to the SUIVE [Spanish acronym] classification [SSA 2021], and the International Classification of Diseases [CIE-10; PAHO 2018]). River density is influenced by temperature, salinity, and the presence of dissolved or suspended substances. It is higher in urban areas, and the highest incidences of gastrointestinal infections occur in municipalities where major rivers flow (**Fig. 5**). Furthermore, Rodríguez-Tapia and Morales-Novelo (2017) found



Source: INEGI, 2022; SUIVE, 2003-2022

Fig. 5. Incidence rate per 10 000 inhabitants of intestinal infections by other organisms and those not specified at the municipal level in the Atoyac Basin. Median rates for the period 2003-2022 are shown. Children are the most affected in riverside communities. This distribution of infections is also observed in senior adults, although with less severity. The Atoyac River is the most affected, with the most polluted stretches. (INEGI: Instituto Nacional de Geografía y Estadística [National Institute of Statistics and Geography]; SUIVE: Sistema Único de Información para la Vigilancia Epidemiológica [Single Information System for Epidemiological Surveillance].)

a correlation between bacteriological pollution in the Atoyac River and the incidence of gastrointestinal diseases in a study using environmental models. The risk of infection is higher in river sections that flow through communities where homes are situated just 2-3 m from the water.

According to the aforementioned analysis of infectious diseases, the incidence of acute intestinal and respiratory diseases in the CAA population has been higher than the national average in recent years (**Fig. 5**). While the nationwide average incidence was 2460.67 per 100 000 inhabitants, in Tlaxcala it was nearly double, at 4490.82 per 100 000 inhabitants. Additionally, the incidence of intestinal infections caused by other organisms and by unspecified organisms ranked second at the national level, due to the high value recorded in 2022, the most recent year of registration.

In addition to the exposure routes outlined in **figure 3**, another critical one is provided by the irrigation canals that carry water from the Atoyac, Xochiac, Zahuapan, and other rivers to farmland. The use of river water has not been replaced by well water, as its levels have dropped due to the drought affecting the entire country. Moreover, dams, such as Atlangatepec in the northern part of the basin, also show bacteriological and toxic pollution, according to the diagnostic report by the official water agency (SEMARNAT-CONAGUA 2022). This situation poses a significant health risk for gastrointestinal diseases, as many of these infections are spread through the consumption of contaminated food (Guzmán et al. 2015, Gómez-Duarte 2018, Lara and García 2019).

DISCUSSION

This review presents substantial evidence that pollution from toxic chemicals, plastic residues, microplastics, and biological waste in rivers and other freshwater bodies creates conditions that foster bacterial resistance to antibiotics, biocides, metals, and various other chemicals. This resistance is horizontally transmitted to other bacteria, while simultaneously inducing additional protective mechanisms, such as biofilm formation and virulence factors. These resistant organisms can infect humans, domestic and wild animals, and contaminate agricultural products.

In places like the CAA and countless rivers worldwide that receive industrial waste, human communities find themselves trapped in environmental degradation, resulting in precarious living conditions and heightened health risks. Exposure to toxic pollutants can result in neoplasms, endocrine disruption, reproductive problems, congenital malformations, and metabolic, pulmonary, renal, hepatic, and neurological diseases (WHO 2016a, Landrigan 2018, 2020). Concurrently, infections from antibiotic-resistant microorganisms pose a growing threat, as antibiotics remain our only defense against them (WHO 2016b, 2021, CSG 2018). These infections may not only tend to be persistent and more virulent, but they can also trigger gut dysbiosis, with far-reaching health consequences.

In its 2022 review, the Collaborative Consortium on Antimicrobial Resistance estimated that 1.27 million deaths worldwide in 2019 were attributable to microbial antibiotic resistance. In Mexico, during the same year, the standardized death rate from this cause was estimated at 70 per 100 000 inhabitants (ARC 2022).

Boelee et al. (2019) proposed a conceptual framework to simultaneously and comprehensively address the environmental and health challenges posed by water pollution, which causes both non-communicable and communicable diseases. The starting point is directives of a political-economic nature. For example, one directive may aim to establish industries to create jobs and produce consumable goods. However, this initiative creates environmental pressures by altering land use in previously undeveloped areas or those designated for different activities. From this point, a series of societal consequences arise that must be addressed at all levels to prevent environmental degradation while safeguarding health and society (**Fig. 6**).

Responses to environmental problems in developed countries have led to the implementation of local laws and international agreements (**Table VI**), alongside efforts to regulate the cross-border transport of toxic substances. However, these measures have not been sufficient to mitigate the impact of toxic chemical compounds on the environment, which are gradually being understood through costly scientific research in the public sector. In contrast, the design and synthesis of new compounds continue to be developed and released industry-wide every year, generating substantial profits.

Meanwhile, during their development, countries in the Global South did not consider the experiences and environmental and health protection measures established by developed countries. As a result, they have seriously compromised their natural resources and environmental quality. Consequently, there has been a rise in chronic non-communicable diseases, affecting the development of new generations,

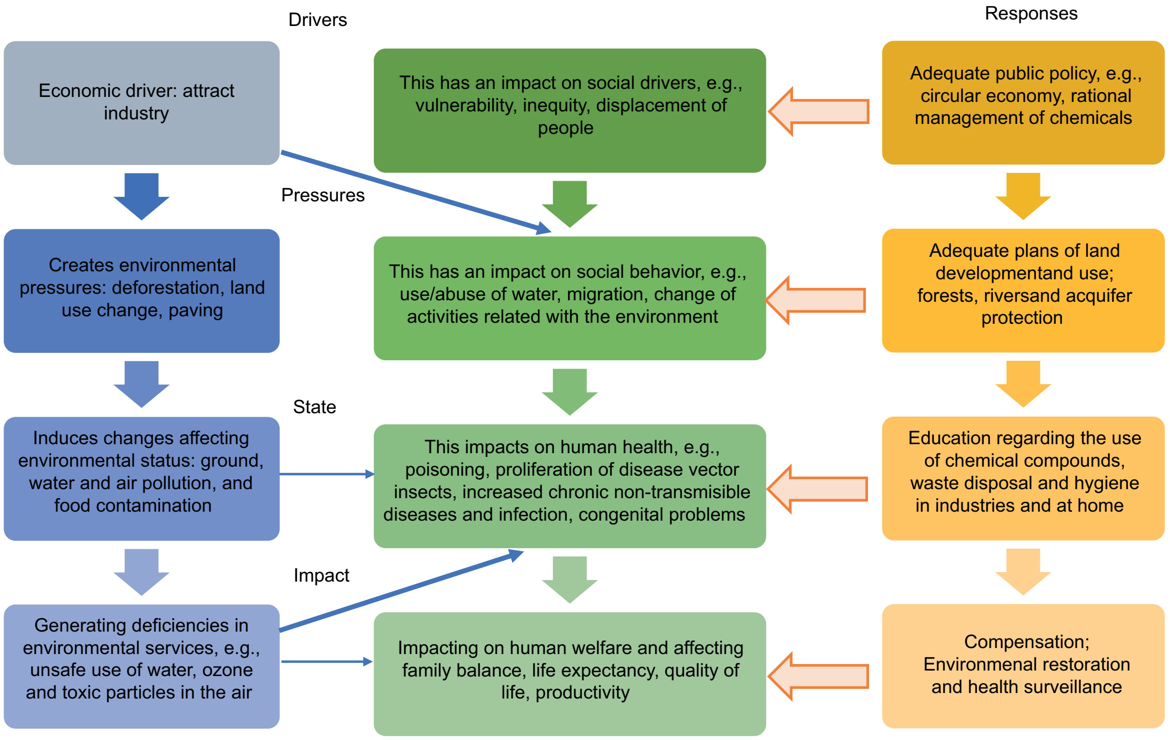


Fig. 6. Conceptual framework for analyzing and designing solutions to complex problems caused by environmental pollution applied to the Atoyac Basin (according to the model of Boelee et al. [2019]).

challenges for which their health systems were unprepared (Vineis and Xun 2009), along with infections caused by super-resistant ARB.

Given the severe health risks posed by chemical contamination and fecal pollution in water bodies, with unforeseen consequences, strategies must be designed to save these sources that nourish life on Earth, not only for human beings, but also for the global ecosystem (**Fig. 7**). While this review focused on bacterial modifications, similar threats arise from viruses, phages, and fungi.

In the approaches adopted, the objective set by the Global Framework on Chemicals (UNEP 2024) —formerly known as Strategic Approach to International Chemicals Management (SAICM) and promoted by the WHO—must undoubtedly prevail, in terms of the comprehensive management of materials to ensure their traceability from origin, whether through extraction or industrial synthesis, to final reuse, recycling, renovation, or controlled biodegradation. In addition, transitioning from highly polluting energy production to methods that do not generate greenhouse gases or toxic emissions at current levels must be planned and implemented, particularly in developing countries, alongside efforts to eliminate plastic waste.

CONCLUSIONS

Development reached the countries of the Global South, introducing a production model characterized by technological deficiencies and resource overuse and waste, which impacts the environment across all its matrices. The destruction of forests and entire ecosystems due to the demands of this development, along with pollution from extractive and productive activities, has impacted air quality and severely compromised rivers and aquifers that sustain continental life, favoring the formation and survival of ARB.

The health effects of this model have emerged swiftly, and these countries are now suffering an epidemic of cancer and chronic non-communicable diseases. Additionally, infections caused by super-ARB continue to rise, causing more deaths globally each year. This crisis has become a major environmental problem, impacting the global economy and deepening social stress.

TABLE VI. EXAMPLES OF PUBLIC POLICIES ADOPTED IN RESPONSE TO ENVIRONMENTAL PROBLEMS THAT AFFECT HUMAN HEALTH.

Environmental problem	Response from authorities or international agencies.
Extensive wildlife death and reproductive alterations due to pesticide use	Creation of the US Environmental Protection Agency to protect human health.
Visible air pollution in major cities of the USA, with a deep increase in respiratory problems in the population	The Clean Air Act was established to introduce standards of air quality and a monitoring program.
Polluted sources of drinking water in the USA, both by microorganisms and chemicals, generate health problems	Safe Drinking Water Act to establish standards that drinking water for human use must comply with.
A hidden toxic-waste dumpsite at Love Canal that provoked clusters of cancer cases	Comprehensive environmental response, Compensation and Liability Act (CERCLA) to assist victims and to financially compensate for their losses.
Toxic air emissions from the explosion at a pesticide factory in Italy, with loss of life, and numerous cases of cancer and malformations in offsprings	European Union Seveso Directive, warranting the right to know about chemical dangers due to industrial activities.
Extensive global distribution and health effects to wildlife and humans of persistent organic pollutants	Stockholm (international) Convention to control and eliminate the use of persistent organic pollutants.
A hole is discovered in the stratospheric ozone layer due to the reaction of chlorofluorocarbon aerosols with ozone	The Montreal Protocol is adopted to phase out the use of these compounds and halons from products.
Central nervous system alterations and skeletal malformations in mammals and humans in the town of Minamata	Minamata Agreement to eliminate the use of mercury from industrial activities and any kind of use.
Accumulation of waste in the environment poses a continuous health hazard to marginalized communities around the world	Strategic Approach to International Chemicals Management (SAICM), today known as Global Framework on Chemicals, for countries to implement a sound management of chemicals and chemical waste to protect the environment and human health.

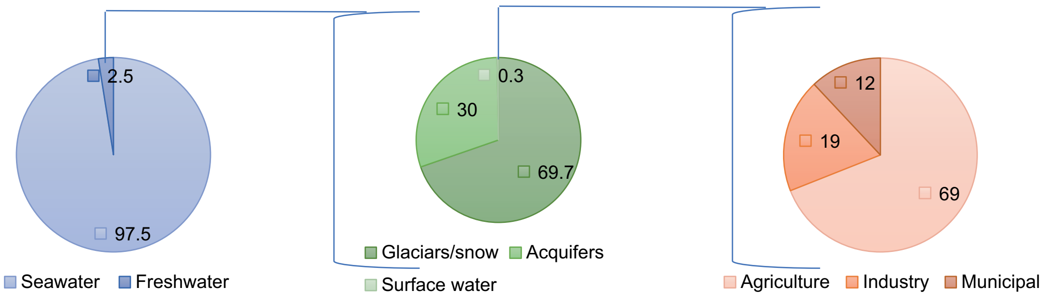


Fig. 7. Water for human use: 2.5% of the planet's total water is freshwater. Of this, 0.3% is surface water for recreational activities and, in general, for human consumption in most countries (information taken from Mullen [2023]). Some of these countries, including Mexico, extract groundwater with high mineral content, at very high cost, for human use; however, industry, mining, and extensive agriculture are hoarding the use of this water, polluting and dumping it into surface waters.

It is imperative for societies to take action and implement rational measures that prioritize social well-being and the protection of natural resources, supported by scientific and innovative technical solutions that are necessary to halt a process that has pushed us further away from solving poverty and inequality.

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