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Summary of Recent Research on Antibiotic-Resistant Microbial Pollutants in Mangrove Wastewater Ecosystems: Public Health and Environmental Risks

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Abstract

This literature review brings together in a single document all the knowledge on the phenomenon of antibiotic resistance in the water compartment of mangrove ecosystems. Several articles have been browsed in order to highlight the main sources of antibiotic resistance. Several articles were reviewed in order to highlight the main sources of antibiotic resistance in this part of the mangrove ecotone. Our results show that the sources of antibiotic-resistant bacteria (ARB) and antibiotic resistance genes (ARG) in mangrove waters are either natural or anthropogenic. Many phenotypes and genotypes of antibiotic resistance have already been identified in this environment. Phenotypes such as Gram-negative bacteria (*Aeromonas* sp.; *Serratia* sp.; *Klebsiella* sp.; *Pseudomonas* sp.; *E. coli* or *Vibrio* sp.) resistant to Augmentin (AUG) and Gentamicin (GEN) or *Enterococcus faecalis* resistance to vancomycin. Furthermore, β-lactam resistance genes (*bla*TEM-1 and *bla*CTX-M-8) may be associated with Mobile Genetic Elements (MGEs) such as the IncI1 plasmid. This confirms that anthropogenic pressures contribute to amplifying the reservoir of antibiotic resistance in mangrove waters, which may pose a threat to human health. Finally, much work remains to be done in these environments, particularly in African countries and in monitoring seasonal changes in ARGs and MGEs in ecosystems.

Keywords: Wastewater; Mangroves; ARBs; ARGs; Antibiotic resistance; Human health

Introduction

Mangroves are coastal ecosystems located at the interface between marine and terrestrial environments and distributed across 123 countries [1]. These ecosystems have considerable economic value thanks to the diversity of ecosystem services they provide, such as provisioning, regulating, supporting and cultural services [1,3]. The ecological importance of these ecotones also extends to human health, as these areas can provide natural resources on which coastal inhabitants depend for their survival and livelihoods [5]. Despite the economic benefits mangroves provide to surrounding communities, this ecosystem is not considered an attractive environment, mainly due to the perception of mangroves as a hostile, foul-smelling, and muddy environment [1,6]. It remains one of the most threatened ecosystems due to several human activities, including urban development, aquaculture, agriculture,

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overexploitation of resources, and pollution [7]. High population density in and around mangroves has led to their contamination. Oil spills and wastewater discharges are among the main sources of mangrove pollution [8]. As a result, a quarter of the world's mangroves have disappeared due to human activity [9] and human populations are exposed to all kinds of contamination [7,10]. Emerging contaminants such as antibiotic-resistant genes and bacteria pose the most alarming global threat to human health due to the overuse of antibiotics in healthcare and livestock farming [11,12]. They are responsible for hundreds of thousands of deaths each year [11,13] and, to a lesser extent, pose a risk to the ecological balance of ecosystems [14].

Given that the problem of antibiotic-resistant bacteria is a growing phenomenon in mangrove environments, a meticulous analysis of mangrove ecosystems is essential to determine the incidence, transmission routes, and impacts of these clinically important bacteria on these vital environments. It is therefore necessary to summarize the distribution and abundance of antibiotic-resistant bacteria and genes in the different compartments of these ecosystems. In addition, there are few studies on changes in the abundance of antimicrobial resistance genes and the risk of transfer of these genes in wastewater from mangrove ecotones. Consequently, the main content of this study presents systematic and comprehensive research on the presence and abundance of antibiotic-resistant bacteria and genes in mangrove wastewater.

Materials and Methods

Carrying out this work on the phenomenon of antibiotic resistance in the water compartment of mangrove ecosystems around the world required a precise research strategy. This consisted of first selecting articles from Google Scholar, PubMed, and CrossRef databases, as they contain the largest number of publications on our subject. Articles and other scientific publications dealing mainly with the following keywords: “mangrove wastewater”; “antibiotic resistance genes in mangrove waters”; “antibiotic-resistant bacteria in mangrove waters”; “antibiotic resistance phenotypes or genotypes in mangrove waters”; “antibiotic resistance in mangrove waters” were all taken into account. The articles included in this review were published over the last 20 years up to October 2025, mainly in English. A single inclusion criteria was used: scientific publications dealing with antibiotic resistance in mangrove waters, not in the soil, sediment, or fauna of the ecosystem. This approach allowed us to stay focused on our objective, which was to identify recent trends in antibiotic resistance in wastewater from mangrove ecotones and the risks they pose to human health.

Results and Discussion

Sources of antibiotic resistance in mangrove waters

Antibiotic resistance is a natural and ancient phenomenon that predates human activity. Mangroves naturally contain bacteria such as Pseudomonas that naturally produce antibiotics, although the phenomenon takes on other proportions with human pressures. Manivasagan et al. [17], who studied the seasonal distribution of antibiotic resistance heterotrophic bacteria in mangroves, report that marine forms resistant to commercial antibiotics may have developed certain resistance proteins in order to adapt to extreme marine conditions [17]. Ghosh and other studies found that the abundance of antibiotic resistance genes was low in one of the stations studied, suggesting that this could be due to limited human interference in this region (perhaps due to the pristine nature of the Sundarbans) [16,17]. The absence of human activities does not completely rule out the presence of ABRs or AGRs and mobile genetic elements in these aquatic environments. A study on the prevalence of β-lactam resistance in *Escherichia coli* in water and sediment samples from urban mangrove ecosystems in Kerala (India), showed that of the three sampling stations selected for the study, the Vallarpadam station (station 3), due to its proximity to anthropogenic inputs, had the highest ABRs values [18]. This confirms that domestic activities amplify the reservoir of antibiotic resistance in mangrove waters [5,18,19]. This occurs indirectly, i.e., through the release of drug residues into these environments. It is known that antibiotic residues in aquatic environments such as mangroves are likely to lead to the development and maintenance of antibiotic resistance in bacterial populations [20,21]. On the other hand, ABRs and ARGs can be directly discharged into mangrove waters through hospital, household, and aquaculture waste [18]. According to Jalal et al. [22] and Manivasagan [15], high levels of antibiotic resistance in marine bacteria could result from terrestrial bacteria possessing antibiotic-resistant plasmids entering the ecosystem. This makes sense when we consider that wastewater is recognized as one of the most common routes of distribution for emerging contaminants linked to antibiotic resistance (antibiotic residues, ARBs, and ARGs) [23]. Finally, it should be noted that the phenomenon of antibiotic resistance in mangrove wastewater can be influenced by several factors. For example, it has been found that microbial biomass causes significant differences in the absolute and relative abundance of ARG genes and is a key factor influencing their distribution [17]. Furthermore, environmental factors accounted for 61.8% of the variation in ARG in mangrove water [17]. This could be a combination of factors such as temperature, tidal flow, surface runoff, agricultural and aquaculture waste, and other anthropogenic activities [19].

Occurrence of antibiotic-resistant bacteria in mangrove wastewater

Authors report that just over 50% of bacterial microflora was resistant to antibiotics used in clinical settings [15,24]. This demonstrates the impact of human pressures on these

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crucial ecosystems. As confirmed by Kümmerer et al. [25], differences in the percentage of bacteria resistant to various antibiotics may reflect the history of antibiotic use. A study in the Muthupettai mangroves (India), indicates that the population of antibiotic-resistant bacteria has been influenced by several parameters, including significant seasonal freshwater input, agricultural runoff, and wastewater pollution [15]. In Nigeria, ABR levels were found to be higher in the rainy season than in the dry season [26]. In the urban mangroves of Kerala (India), the authors report that in water samples, they observed a very wide diversity of antibiotic resistance profiles in E. coli isolates from station 3. This station is described in the study as being close to domestic effluents [18]. This means that hospital, household and aquaculture discharges in these ecosystems increase likelihood of these ecotones harboring [18]. Furthermore, it has been confirmed that mangrove environments, which act as reservoirs for bacteria resistant to several clinically used antimicrobial drugs, pose a risk to human health [27-29]. In Nigeria, isolates of Gram-negative bacteria (*Aeromonas sp.*; *Serratia* sp.; *Klebsiella sp.*; *Pseudomonas sp.*; *E. coli* ou *Vibrio sp.*) from mangrove wastewater samples collected during the rainy season were 100% resistant to augmentin and gentamicin. In contrast, 100% of Gram-positive (*Staphylococcus sp.*; *Micrococcus sp.*) isolates showed no resistance to gentamicin [26]. This could lead to a health impasse, given that augmentin remains one of the most widely used antibiotics in clinical practice, particularly in the treatment of respiratory tract infections [30]. In Brazil, *Enterococcus faecalis* resistance to vancomycin (≥64µg/mL) (named UFSEfl) was detected in a water sample. This strain also showed resistance to teicoplanin (≥32 µg/mL), tetracycline (≥64 µg/mL), ciprofloxacin (≥ 64 µg/mL), erythromycin (≥64 µg/mL), chloramphenicol (16 µg/mL), and gentamicin, as reported in Table 1 [5]. Vancomycin-resistant enterococcal infections are of great importance to public health due to limited treatment options [31]. These phenotypes are nosocomial bacteria classified as high priority by the World Health Organization [5], hence the interest in paying particular attention to them. The same applies to ampicillin, as the emergence of resistance to this antibiotic is very worrying. Ampicillin-resistant Enterococcus species are among the most common causes of nosocomial infections [32]. Isolates of *V. cholerae* and *V. parahaemolyticus* both showed the highest resistance to ampicillin (> 89.1%) in the waters of southeast Asian mangroves [18]. Finally, although several studies do not mention it, it is clear that the percentage of ABR is not the same at low tide as it is at high tide. Li et al. [23] found that bacterial resistance was higher at low tide than at high tide, particularly resistance to ampicillin (HT: 29.17%; LT: 66.18%), cefepime (HT: 20.84%; LT: 66.18%), and trimethoprim (HT: 29.17%; LT: 54.41%).

Multidrug resistance in mangroves wastewaters

It is common to find MDR bacteria in mangrove wastewater. Environmental contamination by multidrug-

Table 1: Summary of Studies on ARGs in Mangrove ecosystems.

Antibiotics	Bacteria and groups of bacteria	MPR (%)	CMI and Inhibition Area	Sources
Ampicillin (AMP)	*Vibrio parahaemolyticus*	38.5 – 43.70	2 µg/mL	[24]
	Vibrio parahaemolyticus	89.1		[33]
	Escherichia Coli (Ec 4Ge)	R		[34]
	Enterococcus faecalis	R		[5]
	Vibrio Chlorea	94.1		[33]
Gentamycin (GEN)	*Escherichia Coli (Ec 4Ge)*	R	not specified	[34]
	Vibrio parahaemolyticus	10.70 –17.50		[24]
	Gram-	0–100		[26]
	Gram+	00		[26]
	Escherichia Coli (Ec 4Ga1)	R		[34]
Aztreonam (ATM)	*Escherichia Coli (Ec 4Ge)*	R	not specified	[34]
Chloramphenicol (CHL)	*Vibrio parahaemolyticus*	25.40 – 31.70		[24]
	Enterococcus faecalis	R	16 µg/mL	[5]
	Escherichia Coli (Ec 4Ge)			[34]
	E. coli (NBRC 102203 and U 5/41)	R	< 5 mm	[35]
Piperacillin (PIP)	*Vibrio Chlorea*	70.5	not specified	[33]
	Vibrio parahaemolyticus	84.7		[33]
Ceftriaxone (CAX)	Gram+	12.5	32 µg/mL	[26]
	E. Coli (ECEST9)	R		[36]
	Escherichia Coli (Ec 4Ge)	R		[34]
Cefixime (CXM)	Gram-	50 – 100	not specified	[26]
	Gram+	100		
Cefuroxime (*CRX*)	*Escherichia Coli (Ec 4Ge)*	R	not specified	[34]
	Gram-	50 – 100		[26]
	Gram+	56.25 – 100		[26]
Penicillin (P)	*Vibrio parahaemolyticus*	60.60 – 65.70		[24]
	E. coli (NBRC 102203 and U 5/41)	R	< 5 mm	[35]

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Rifampicin (RIF)	*Vibrio parahaemolyticus*	33.80 – 40.90		[24]
Tetracycline (TET)	*Escherichia Coli (Ec 4Ge)* *Vibrio parahaemolyticus* *Enterococcus faecalis* *Escherichia Coli (Ec 4Ga1)*	R 28.50 – 35.7 R R	64 µg/mL	[34] [24] [5] [34]
Nitrofurantoin (NIT)	Gram+ Gram-	75 50 – 75	not specified	[26] [26]
Nalidixic acid (NAL)	*Vibrio parahaemolyticus* *E. Coli (ECEST9)*	74.40 – 85.10 R	4 µg/mL	[24] [36]
Ceftazidime (CZ)	Gram+ *Vibrio Chlorea* *Vibrio parahaemolyticus* Gram- *E. coli (ECEST9)* *Escherichia Coli (Ec 4Ge)*	75 64.7 78.2 50 – 75 R R	32 µg/mL	[26] [33] [33] [26] [36] [5]
Cefotaxime (CTX)	*Vibrio Chlorea* *E. coli* (ECEST9) *Escherichia Coli (Ec 4Ge)*	64.7 R R	32 µg/mL	[33] [36] [5]
Augmentin (AUG)	Gram+ Gram-	12.5 – 100 100	not specified	[26]
Ofloxacin (OFL)	Gram- Gram+	0 – 50 0 – 6.25	not specified	[26] [26]
Cloxacin (CXC)	Gram+	25	not specified	[26]
Novobiocin (NVB)	*Vibrio parahaemolyticus*	52.80 – 60.50	not specified	[24]
Streptomycin (S)	*Vibrio parahaemolyticus* *E. coli* (NBRC 102203 and U 5/41)	28.50 – 37.50 R	>5mm	[24] [35]
Kanamycin (KAN)	*Vibrio parahaemolyticus* *Escherichia Coli (Ec 4Ge)*	45.60 – 52.70 R	not specified	[24] [34]
Erythromycin (ERY)	Gram+ *Enterococcus faecalis* *E. coli* (NBRC 102203 and U 5/41)	12.5 R R	64 µg/mL < 5 mm	[26] [5] [35]
Ciprofloxacin (CPR)	*Enterococcus faecalis* *E. coli* (NBRC 102203 and U 5/41) *Escherichia Coli (Ec 4Ge)*	R R R	64 µg/mL >5mm	[5] [35] [34]
Vancomycin (VAN)	*Enterococcus faecalis*	R	64 µg/mL	[5]
Cefepime (CPM)	*Escherichia Coli (Ec 4Ge)*	R	not specified	[34]

Note: R (Resistant); Gram- involves *E. coli*; Pseudomonas sp; Klebsiella sp Serratia sp; Micrococcus sp; Vibrio sp; Aeromonas sp and Gram+ involves Alcaligene sp; Staphylococcus sp; Bacillus sp.

resistant bacterial pathogens has raised public health concerns worldwide [5], making these environments ones ecosystems to be monitored. The high frequency of *E. coli* phylotypes B2 and D in the tropical estuary of Cochin (India) indicates that *E. coli* bacteria carrying multidrug-resistant genes could pose a threat to populations that depend on these aquatic ecosystems for their livelihoods [18]. It is said that multidrug-resistant enterobacteria strains in the environment can cause serious opportunistic infections [34]. In Brazil, Sacramento [33] reported that the ECEST9 strain had a multidrug-resistant (MDR) profile with resistance to amoxicillin/clavulanic acid, ceftriaxone (MIC = 32 µg/mL), cefotaxime (MIC = 32 µg/mL), ceftazidime (MIC = 32 µg/mL), cefepime (MIC = 32 µg/mL), ciprofloxacin & levofloxacin, nalidixic acid, trimethoprim and colistin (MIC = 4 µg/mL). In addition, one study reports a profile of *Enterococcus faecalis* multi-resistant to vancomycin (≥64µg/mL), teicoplanin (≥32 µg/mL), tetracycline (≥64 µg/mL), ciprofloxacin (≥ 64 µg/mL), erythromycin (≥64 µg/mL), chloramphenicol (16 µg/mL) and high-level gentamicin [5]. It goes without saying that it is important to monitor these multi-resistance profiles in mangrove waters, when rates of multi-resistance profiles to drugs used specifically in healthcare facilities have been found to reach 37% [34].

Prevalence and diversity of ARGs in wastewater from mangrove ecosystems

Mangrove ecosystems are potential reservoirs of ARGs [19]. Several studies show that β-lactam resistance genes are the most frequently detected, ahead of those belonging to other families. For example, an Indian study showed that in mangrove water samples, a total of 26 Vibrio isolates harboured the CTX-M-group 1 gene (*V. cholerae* - 14.2% and *V. parahaemolyticus* - 26.9%) [33]. Preliminary genome sequencing of an *Escherichia coli* (ECEST9) isolated from a polluted mangrove ecosystem in north-eastern Brazil revealed the presence of several genes, including β-lactam resistance genes (*bla*TEM-1 et *bla*CTX-M-8) [36]. Similarly, in Guanabara Bay [34], demonstrated the presence of β-lactam resistance genes in strains of *Klebsiella pneumoniae*

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subsp., *K. pneumoniae subsp. ozaenae* and *Escherichia coli*. Several studies have reported the presence of genes encoding β-lactamases. In addition, the CTX-M-15 and CTX-M-14 genes encoding the CTX-M family of ESBL enzymes have been reported in Vibrio spp., by White et al. [33]. In the XinCun lagoon in China, one of the main ARGs detected in mangrove environments (water compartment) was β-lactamase (blaSHV, blaPSE-1) [17]. Nevertheless, there are very few studies in which β-lactam resistance genes have not been detected. This is the case in the mangroves of north-eastern Brazil, where resistome analysis has shown the presence of genes conferring resistance to streptogramin B [euh(B)], streptogramin A [Isa (A)], tetracycline [et(M)], glycopeptide [vanHAX] and phenicols [chat] [5]. It is also worth noting the coexistence of beta-lactam resistance genes with quinolone resistance genes (aac(6′)-Ibcr; (*qnrS1*) [17,36]; trimethoprim (dfrA5), colistin (mcr-1) [36] and Macrolide-Lincosamide-Streptogramin B (MLSB) (macB, mphA-01), sulfonamides (sul1), aminoglycosides (aadA-01, aadA-02, strB), tetracyclines (tetG), chloramphenicol (floR, cmlA1-01, cmlA1-02) [17]. Point mutations in the gyrA gene (S83L) have been detected, conferring resistance to fluoroquinolones [36]. This distribution of AGR genes in mangrove ecosystem waters sometimes indicates anthropogenic influence. Analysis of samples from the Sundarbans mangroves led the authors to conclude that the abundance of ARGs in the studied stations suggests a potential increase in pollution levels in the Sundarbans [16], confirming that the widespread distribution of the *bla*TEM gene indicates anthropogenic influence on the environment [16].

Mobile Genetic Elements (MGEs) involved in the dissemination of ARGs

Antibiotic resistance involves genes and biochemical mechanisms, including horizontal gene transfer (HGT), which enable bacteria to rapidly become resistant by integrating new genetic material into their genomes [38,39]. The involvement of plasmids in the resistance of heterotrophic bacteria, for example in mangrove ecosystems, has already been well documented [24]. Sacramento [33] showed that the *bla*CTX-M-8 gene was associated with the IncI1 plasmid, while the mcr-1 gene was associated with the *Inc*X4 plasmid. Also, IncX4 plasmids carrying the mcr-1 gene have been associated with the spread of the mcr-1 gene in Enterobacteriaceae, mainly in Brazil. This reinforces the idea that MGEs, such as plasmids and integrons, facilitate HGT, thereby increasing the risk of ARG dissemination in microbial communities [40]. Ghosh [16] identified two MGEs, other than plasmids, in the eleven stations studied in the Sundarbans mangrove forest (South Asia). These were transposons and integrons, whose abundance was less than 0.1% and low in all study areas, respectively. Genomic analysis of a vancomycin-resistant Enterococcus faecalis strain isolated from a heavily impacted mangrove ecosystem in northeastern Brazil confirmed the presence of the Tn1546-vanA transposon and clinically relevant antimicrobial resistance genes, such as streptogramins, tetracycline, phenicols, and fluoroquinolones [5]. Associated MGEs, including integrase, recombinase, and transposase, were also widely distributed across all study sites, with transposase being the most abundant [16] (Table 2, Figure 1).

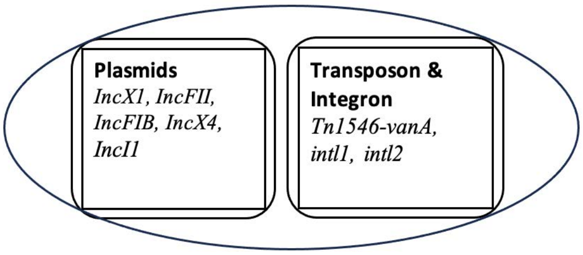

Figure 1: Repertoire of mobile genetic elements identified in mangrove wastewater.

Environmental and human risks related to antibiotic resistance in mangrove wastewater

It is clear from all the studies reviewed that the prevalence of ARB, ARG, and all the elements involved are likely to pose risks to both humans and aquatic life in mangrove ecosystems. This has been demonstrated by Wu et al. [16], who found that ARGs proliferating in mangrove environments via MGEs increase the risk of pathogens becoming multi-resistant, which could lead to a health impasse. This is supported by Gonçalves et al. [36] when they state that the release of *E. coli* into the environment carrying the mcr-1 gene, which confers resistance to polymyxins, is a public health problem, as this genotype is versatile and could persist in environmental ecosystems, exposing humans and animals to a potential risk of infection. Another issue is that ARBs and ARGs present in water and sediments could be transferred through trophic levels via the food chain and have a negative impact on human health [33]. It has also been proven that the presence of ARGs in these environments may be linked to the presence of metals [41], given the danger to which we may be exposed in the event of heavy metal pollution. In Ghana and elsewhere, human and animal infections caused by multidrug-resistant *E. coli* pathogens have been documented [42]. In addition, a previous study found that all isolates from mangroves had an Multiple antibiotic resistance (MAR) indices greater than 0.2 and were high-risk sources of environmental contamination [18].

Prospects for combating antibiotic resistance in mangrove waters

So far, it is clear that work on the phenomenon of antibiotic resistance in mangrove wastewater is well advanced, especially in countries such as India, China, and Brazil. Nevertheless, much work remains to be done to fill in the gaps in our knowledge [1]. For example, it is known that MGEs proliferate ARGs in estuaries such as Haihe in China and increase the risk of pathogens becoming multi-resistant. It would therefore be important to monitor changes in ARGs and MGEs on a seasonal basis in ecosystems. One of the problems associated with monitoring and detecting the emergence of antibiotic-resistant bacteria is cost and accessibility [19]. Some authors say that to better understand antibiotic resistance in mangrove ecosystems, further research focused on ESBL resistance in bacterial isolates is needed. This could help track changes in antibiotic resistance patterns [18]. A study by Palacios et al. [1] asserts that there is a lack of knowledge about these emerging contaminants (ABR, ARG) in mangroves, particularly regarding physiology and functionality. This reinforces the fact that much remains to be done in this area within these ecosystems, whose importance is well established.

Table 2: Summary of Studies on ARGs in Mangrove ecosystems.

Studies	Location	ARGs detected	Strains	Bacteria	Family of antibiotics
[36]	Brazil	*bla*CTX-M-8 and *bla*TEM-1	ECEST9	*E. coli*	β-lactam
[17]	China	blaSHV, blaPSE-1		not specified	
[34]	Brazil	aacC2 / blaTEM / blaCTX-M-1/ qnrB	Ec 4Ge	E. coli	
[17]	China	aadA-01, aadA-02, strB	not specified	not specified	Aminoglycoside
[18]	India	*CTX-M-group 1*	not specified	*V. cholerae* and *V. parahaemolyticus*	β-lactam
[36]	Brazil	*dfrA5*	ECEST9	*E. coli*	Trimethoprim
[16]	India	*tetABDJLMNPQRTW, otrABC, tet34, tet35, tet36, tet39 and tet41*	not specified	*Pseudomonas*	Tetracycline
[5]	Brazil	*tet* (M)		*E. coli*	
[17]	China	macB, mphA-01	not specified	not specified	MLSB
[17]	China	sul1	not specified	not specified	Sulfonamide
[36]	Brazil	*gyr*A	S83L	*E. coli*	Fluoroquinolon
[5]		*gyr*A	S83R		
[5]		*par*C	S80I		
[16]	India	*van*ABCDEGHBKILMNRSTUWXYZ *van*HB, *van*KI, *van*RI, *van*SD, *van*TG, vanTrL and vanYG1	not specified	not specified	Glycopeptides
[36]	Brazil	[vanHAX]		E. *coli*	
[36]	Brazil	*qnrS1*	not specified	*E. coli*	Quinolones
[17]	China	aac(6′)-Ib-cr		not specified	
[5]	Brazil	tet(M)	not specified	E. coli	Tetracycline
[17]	China	tet(G)		not specified	
[5]	Brazil	[lsa (A)]	not specified	E. *coli*	Streptogramine A
		[euh(B)]			Streptogramine B
[5]	Brazil	[cat]	not specified	*E. coli*	Phenicol
[17]	China	floR, cmlA1-01, cmlA1-02		not specified	Chloramphenicol

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Conclusion

In conclusion, mangrove waters constitute a natural reservoir of antibiotic resistance that is amplified by human activities. Several antibiotic resistance genotypes have been identified worldwide in these environments. The same is true for antibiotic resistance phenotypes that are dangerous to human health. Therefore, if MDR profiles or *Klebsiella sp*. and *Pseudomonas sp*. resistant to AUG are not monitored, this can very quickly lead to a therapeutic impasse. This is especially true given that amoxicillin + nalidixic acid (AUG) remains one of the most widely used antibiotics in clinical practice, particularly in the treatment of respiratory tract infections. Learning more about the reservoir of antibiotic resistance that mangrove waters represent can therefore help us better circumvent the public health threats to which human populations may be exposed.

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