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A systematic review of sources, occurrence, behavior and risks of global marine antibiotics

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The widespread use of antibiotics has resulted in their significant release into the environment, with the ocean becoming a major sink for antibiotics and antibiotic resistance genes (ARGs). This review synthesizes global data on marine antibiotic contamination, covering sources, occurrence, behavior, and associated ecological and human health risks. Sulfonamides, fluoroquinolones, macrolides, and tetracyclines dominate, with sulfamethoxazole most frequently detected (71.1% in seawater, 30.4% in sediment, 47.6% in biota). Peak levels reached 332,440 ng L^{-1} in seawater, 1515 ng g^{-1} in sediment, and 3341 ng g^{-1} in organisms, the highest in coastal China. Antibiotics with low direct toxicity may still drive ARG development. Coexisting contaminants (e.g., heavy metals, microplastics) may enhance impacts. Seafood-related health risks, especially in adolescents, merit attention. Monte Carlo analysis confirms ecological, antimicrobial resistance, and health risks remain significant under realistic exposure scenarios. These findings support global efforts in marine antibiotic pollution control and risk governance.

Environmental pollution from emerging contaminants is becoming increasingly severe with the growth of the population and the development of industry and agriculture[1]. Among these contaminants, antibiotics are widely used in human and veterinary medicine to treat infectious diseases, as well as in livestock as growth promoters[2]. Among pharmaceutical active compounds (PhACs) monitored worldwide, antibiotics are the most frequently detected in both aquatic environments and wastewater. However, the widespread use of antibiotics, along with limited wastewater treatment rates, has led to their frequent detection and persistence across various environmental phases[3]. Antibiotics in aquatic environments can easily enter surface water, groundwater, and even seawater due to the mobility of water and their "pseudo-persistent" nature, ultimately contaminating drinking water sources[4]. The concentration of antibiotics in water typically falls within the range of ng L^{-1} to μg L^{-1} [5], with sulfamethoxazole (SMX), trimethoprim (TMP), ciprofloxacin (CIP), erythromycin (ETM), and clarithromycin (CLM) being the main antibiotics detected. Despite their relatively low concentrations, they can pose considerable ecological and human health risks[6]. Bioaccumulation of antibiotics in aquatic organisms can induce toxicological effects, potentially disrupting physiological functions and ecosystem stability[7]. Through trophic transfer, accumulated antibiotics may ultimately enter the human body, contributing to adverse health outcomes[8]. Furthermore, the persistence of antibiotic residues in the environment exerts selective pressure on microbial communities, accelerating the proliferation of antibiotic-resistant bacteria (ARBs) and the horizontal transfer of antibiotic resistance genes (ARGs). This process enhances pathogen resistance, undermines the efficacy of antimicrobial therapies, and complicates disease management[9]. The dissemination of ARBs and ARGs has emerged as a critical global public health concern, necessitating urgent intervention[10].

The ocean represents a vast and intricate ecosystem, harboring billions of microbial populations within each liter of seawater[11]. It provides abundant food resources for organisms on the Earth and is pivotal in regulating the global climate and maintaining environmental health[12]. Antibiotics originating from industrial activities, livestock farming, aquaculture, pharmaceuticals, and domestic sewage are capable of both local and transboundary transport and ultimately accumulate in marine ecosystems, particularly in ecologically sensitive zones such as estuaries, coastal waters, and semi-enclosed bays[6]. Marine microbial communities are fundamental to the functioning of marine ecosystems, serving as the basis of the marine food web and contributing to global biogeochemical cycles, including those

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of carbon, nitrogen, and sulfur[13]. Even at low concentrations, antibiotics can interfere with microbial metabolic activities and alter community structures, posing threats to ecological integrity[4]. The widespread microbial populations in the marine environment act as global reservoirs for ARBs and ARGs, facilitating their migration, dissemination, and propagation within biological communities[13]. However, current research on antibiotic contamination in the global marine environment remains limited in several important respects. Most existing studies are geographically restricted to specific regions or focused on individual environmental media, lacking a comprehensive global perspective. Moreover, systematic risk assessments are still rare, particularly with regard to ARGs. The processes governing the transport and transformation of antibiotics across different environmental compartments, the influence of unique marine conditions on these processes, and the interactions between antibiotics and coexisting contaminants, such as microplastics (MPs) and heavy metals, have not yet been comprehensively reviewed. These knowledge gaps constrain our ability to fully understand and address the ecological and human health risks posed by antibiotics in marine environments.

To address these challenges, this study provides a comprehensive analysis of antibiotics in the global marine environment, encompassing their sources, pollution levels, environmental behaviors, ecological effects, and associated health risks. Drawing on an extensive literature review, we systematically summarize the migration and transformation of antibiotics across various environmental compartments, with particular attention to the distinct characteristics of marine ecosystems. The ecological and human health impacts of antibiotic contamination are also examined, including the potential synergistic effects arising from co-occurring pollutants. Furthermore, we conduct an integrated environmental risk assessment that combines ecological risk, antimicrobial resistance (AMR) development, and human health risk, based on a quantitative analysis of global data. Based on the above summarization and analysis, future research directions and control measures to support the protection and management of marine ecosystems were discussed. Overall, the review is structured into six sections: (1) emission sources; (2) occurrence characteristics; (3) environmental behavior; (4) environmental effects; (5) risk assessment; and (6) conclusions and implications.

Results

Sources

Antibiotics used by humans and animals are not completely metabolized, and most are released into the environment in the form of excreta[14]. Marine environments receive antibiotic contaminants from various sources, including activities across different industries. The emergence and rapid expansion of these pollution sources pose potential threats to marine ecosystems. Therefore, identifying the primary sources of marine antibiotics is of significant importance for reducing antibiotic contamination at its origin. As illustrated in Fig. 1, the sources of antibiotics in the marine environment can be categorized into direct and indirect sources.

The direct sources of antibiotics in the marine environment primarily include atmospheric deposition, discharge from mariculture, and offshore sewage. Atmospheric activity over the ocean is significant[15]. Thus, atmospheric deposition can serve as a potential source of antibiotics in the marine environment[16]. Although atmospheric antibiotic concentrations are relatively low, resulting in a limited direct contribution of atmospheric deposition to marine antibiotic loads[17], this process remains an important pathway for the long-range transport and global dissemination of antibiotics and their associated ARGs[9].

The increasing global demand for aquatic products has driven the expansion of mariculture, making it a significant sector within the aquaculture industry[18]. To mitigate disease outbreaks and enhance growth rates, antibiotics are frequently incorporated into feed, resulting in their direct release into the surrounding marine environment[19]. Mariculture farms, predominantly situated in coastal regions, introduce antibiotics into the marine environment primarily through the excreta of farmed animals, following their ingestion via medicated feed. This process represents a significant pathway for antibiotic contamination in coastal waters[20]. Coastal regions, characterized by high population densities and ecologically sensitive marine ecosystems, are particularly susceptible to the adverse effects of

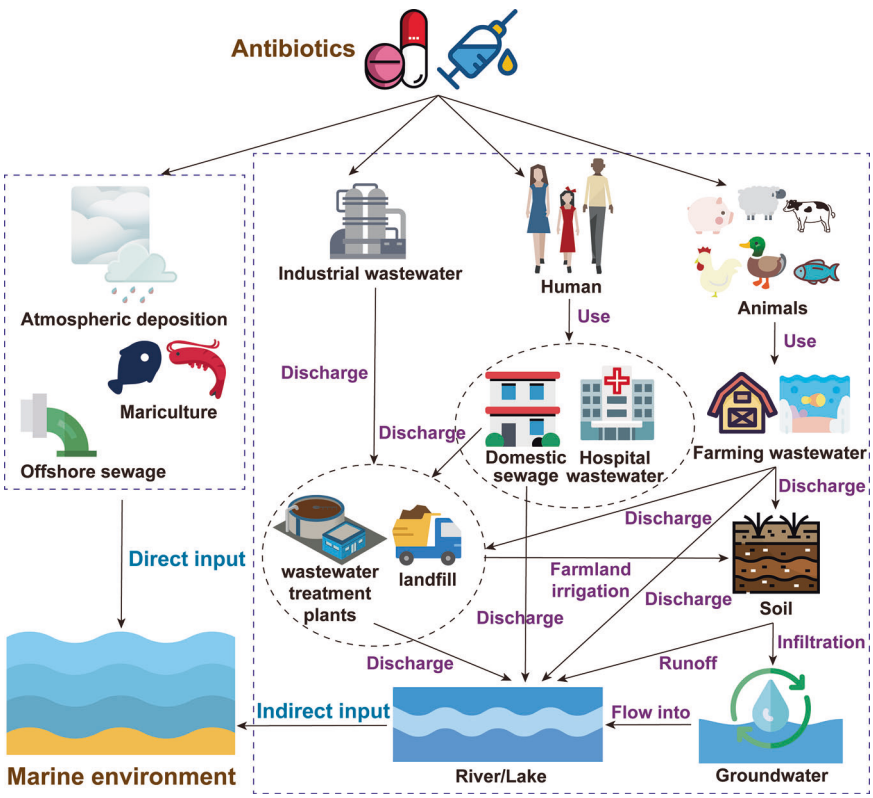

Fig. 1 | The sources of antibiotics in the marine environment.

antibiotic contamination[6,21]. Moreover, nearshore waters are significantly influenced by human activities, with antibiotics from various sources being frequently released directly into these areas along with sewage, thereby intensifying antibiotic contamination[22].

Indirect sources of antibiotics are their discharge into marine environments through various land-based activities. These sources include domestic sewage, hospital effluent, industrial discharges, and wastewater from livestock and aquaculture[22]. Domestic sewage originates from both urban and rural areas[23]. In urban areas, sewage is typically directed to wastewater treatment plants (WWTPs), yet the treatment processes often fail to completely remove antibiotics, resulting in their persistence in the effluent[24]. In contrast, wastewater treatment infrastructure in rural areas is limited or even absent, and untreated sewage containing antibiotics is often discharged directly into water bodies[25].

Hospital effluent is another significant contributor, containing high concentrations of antibiotics due to pharmaceutical waste, drug production, and excreta from patients[26]. Industrial activities, especially those within the pharmaceutical sector, also discharge wastewater contaminated with antibiotics[27]. The highest residues of antibiotics (mg L^{-1}) have been detected in wastewater from pharmaceutical manufacturing. In addition, the removal of these compounds remains incomplete in many pharmaceutical wastewater treatment plants (PWWTPs). Limitations in pharmaceutical and industrial wastewater treatment processes, combined with persistently high emissions, lead to the continuous discharge of residual pollutants into the surrounding environment[28].

In agriculture, the primary pathways through which antibiotics enter the environment are livestock farms and aquaculture systems[29]. Livestock production stands out as a significant contributor, with up to 90% of administered veterinary antibiotics being excreted by animals[30]. Many farms, especially small-scale ones, often lack adequate wastewater treatment facilities, leading to the release of untreated or inadequately treated wastewater into nearby water bodies[31]. Moreover, animal waste is frequently utilized as fertilizer, inadvertently introducing antibiotics into the soil[32].

Overall, the antibiotics discharged into the environment predominantly accumulated in soil and water[33]. The reuse of wastewater and sludge from various sources can contribute to the accumulation of antibiotics in the soil[34]. In soil, these compounds may be washed into marine waters via rainfall, infiltration into groundwater systems, and other processes[22]. In water, antibiotics are transported both locally and over long distances through surface runoff and groundwater circulation, eventually reaching the marine environment. Due to its vast volume, complex ecosystems, extensive pollutant inputs, and role as the ultimate sink in the global water cycle, the ocean has accumulated antibiotic contamination from land-based sources over the long term, ultimately serving as a significant reservoir for both antibiotics and ARGs.

Occurrence

Status of antibiotic contamination in various environmental phases. Statistics on the global marine pollution by antibiotics over the last two decades are presented in Supplementary Tables 6–9, alongside the detection rates of individual antibiotics are shown in Fig. 2. Monitoring antibiotics in the atmosphere remains challenging due to their low concentrations and detection difficulty, which is why studies typically focus on environmental phases such as seawater, marine sediments, and marine biota. However, some studies have reported the presence of ARBs in the atmosphere, highlighting the potential health risks due to the high mobility of airborne contaminants and the possibility of direct human inhalation[35,36].

As detailed in Fig. 2a, seawater is the most extensively studied marine environment, with 72 antibiotics detected. Concentrations ranged from non-detectable (ND) to 332,440 ng L^{-1}, with most falling in the level of ng L^{-1}, although some areas showed levels reaching μg L^{-1} [37–39]. The most frequently detected antibiotics were SAs, FQs, and MAs, with SMX having the highest detection rate (71.1%), followed by TMP at 65.8%, CLM at 44.8%, and both ofloxacin (OFX) (34.2%) and norfloxacin (NFX) at 31.6%. SMX, a widely used antibiotic in medicine and livestock production, is often used in combination with TMP[40]. The highest concentration of TMP observed was 332,440 ng L^{-1}, recorded near the mariculture zone of Laizhou Bay in the Bohai Sea. In this area, the concentrations of other antibiotics, such as sulfamethazine (SMZ), sulfadimethoxine (SDM), enrofloxacin (EFX), doxycycline (DC), and oxytetracycline (OTC), also reached μg L^{-1} levels. These elevated concentrations largely result from the discharge of mariculture wastewater[37]. Remote regions like the Antarctic have also been affected by antibiotic contamination, with CIP detected at concentrations ranging from 4 ng L^{-1} to 218 ng L^{-1} [41], highlighting the long-range transport and environmental persistence of antibiotics in seawater.

Antibiotics released into the marine environments can adsorb onto suspended solids and subsequently deposit in marine sediments[42]. A total of 56 antibiotics were identified in sediments. The concentrations range from ND to 1515 ng g^{-1}, with most at the ng g^{-1} level. As shown in Fig. 2b, SAs, FQs, and TCs were the predominant antibiotic classes detected in sediments. Among the specific antibiotics identified, TMP (39.1%), tetracycline (TC) (39.1%), SMZ (34.8%), SMX (30.4%), EFX (30.4%), and CIP (30.4%) were the most frequently observed. The highest concentration observed was for OTC, with a value of 1515 ng g^{-1} in sediments from the Southern Baltic Sea, an area influenced by agricultural runoff and tourism[43]. Even sediments in the Arctic region have shown substantial contamination, with CIP concentrations reaching 685 ng g^{-1}, likely due to the extensive use of CIP in Norway[44]. The proximity to pollution sources plays a crucial role in determining antibiotic levels in sediments, with higher concentrations commonly observed in areas near densely populated regions, mariculture activities, and WWTPs[42,43,45]. Besides, the physicochemical properties of antibiotics, particularly their hydrophobicity, influence their interaction with sediments. Antibiotics with higher hydrophobicity (log $K_{OW} > 2$) tend to exhibit a stronger tendency to adsorb to sediments[46].

Marine organisms are capable of adsorbing and accumulating antibiotics, which may subsequently enter the food chain and pose potential health risks to humans[47]. A comprehensive understanding of antibiotic bioconcentration in marine biota is fundamental for evaluating these risks. Current research has primarily focused on Asian regions, where 45 different antibiotics have been identified in marine organisms, with concentrations varying from ND to 3341 ng g^{-1}. As illustrated in Fig. 2c, SMX (47.6%), TMP (38.1%), sulfadiazine (SDZ) (33.3%), SMZ (28.6%), EFX (28.6%), and CIP (28.6%) were the most frequently detected compounds. FQs exhibited higher concentrations than other antibiotic classes, likely due to their strong bioaccumulation potential in marine organisms[48]. Among the FQs detected, oxolinic acid (OA) had the highest concentration, reaching 3341 ng g^{-1} at a mariculture farm in South Korea, where several other antibiotics also reached μg g^{-1} levels[49]. Antibiotic accumulation in organisms appears to be tissue-specific. Specifically, FQs predominantly accumulate in muscle, while MAs tend to concentrate in the liver[47].

Comparison of antibiotic contamination among countries. Based on the highest detected concentration, the antibiotic contamination in different marine areas across countries was compared (Fig. 3), with specific references in Supplementary Table 6. In global seawater, China (0.06–322,440 ng L^{-1}, mean 2247 ng L^{-1})[37,39,42,45,50–60] and Costa Rica (2–7425 ng L^{-1}, mean 1281 ng L^{-1})[61] showed the highest antibiotic concentrations. The East China Sea had the largest variety of antibiotics detected, with 43 types, including SAs, FQs, MAs, TCs, and βLs[42]. In China, the highest antibiotic concentration was found in the Laizhou Bay of the Bohai Sea, where TMP reached 322,440 ng L^{-1} and SDM reached 42,550 ng L^{-1} in the seawater, generally higher than other marine areas by 2–5 orders of magnitude[37]. This is likely due to the proximity of mariculture areas. Similarly, a high level of OTC (15,163 ng L^{-1}) was also detected in the South China Sea[39]. Costa Rica exhibited high levels of DC (5509 ng L^{-1}) and oxacillin (OXA) (7425 ng L^{-1}), with OXA being detected only in this region, likely due to the presence of sources including WWTPs[61]. High concentrations of antibiotics were also detected in South Korea (0.196–1626 ng L^{-1}, mean 231 ng L^{-1})[38,46], South

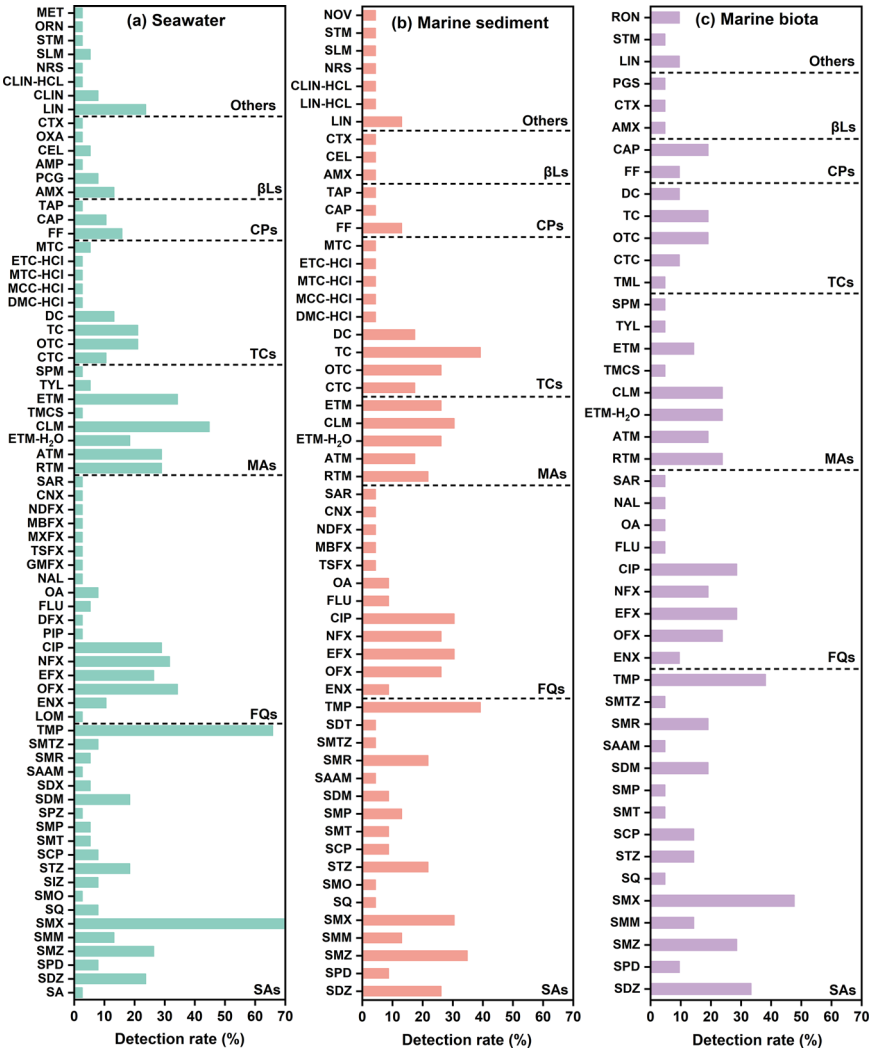

Fig. 2 | The detection rate of each antibiotic in the global marine environment. a Seawater, **b** marine sediment, and **c** marine biota.

Africa (9.5–1167 ng L^{-1}, mean 278 ng L^{-1})[62,63], Fiji (6.3–760 ng L^{-1}, mean 244 ng L^{-1})[64], and Ireland (870 ng L^{-1} for TMP)[65]. The lowest antibiotic concentrations were found in Singapore (0.24–6.26 ng L^{-1}, mean 2.98 ng L^{-1}), where mangrove ecosystems, a unique transitional coastal ecosystem, are located[66]. Despite the low concentration, antibiotics might accelerate mangrove loss as they are vulnerable to stressors like chemical contamination (including antibiotics).

In marine sediments, China (0.02–1260 ng g^{-1}, mean 23.3 ng g^{-1})[37,39,42,45,50,53,57,58,60,67], Iran (2.28–119 ng g^{-1}, mean 27.9 ng g^{-1})[68], Norway (only CIP was detected with a concentration of 685 ng g^{-1})[44], and Poland (1.33–1515 ng g^{-1}, mean 191 ng g^{-1})[43,69–72] exhibited high levels of antibiotic contamination. The highest concentrations of antibiotics were observed in the adjacent marine embayment of Jin River in southeastern China, with SMX ranging from 38.3 ng g^{-1} to 1260 ng g^{-1}, due to the impacts of mariculture wastewater[45]. In Iran, elevated NFX levels (119 ng g^{-1}) in the Persian Gulf are linked to runoff discharges from WWTPs[68]. In Arctic Norway, CIP was detected in sediments, with its persistence supported by low temperatures and slow degradation rates, posing long-term risks to the Arctic ecosystem[44]. In Poland, the major antibiotic contaminants are SMX (276 ng g^{-1}), OTC (1515 ng g^{-1}), and TC (449 ng g^{-1}) in the southern Baltic Sea[43,71] and OTC (625 ng g^{-1}) in the Gulf of Gdańsk[72].

For marine biota, South Africa showed the highest mean concentrations (272–689 ng g^{-1}, mean 481 ng g^{-1}), although SMX was the only antibiotic detected[62,73]. Interestingly, SMX was also the sole antibiotic found in South African seawater[62], underscoring the cross-phase migration of antibiotics from seawater to biota. Significant antibiotic contamination in marine biota was also observed in other countries, including China (0.01–336 ng g^{-1}, mean 25.2 ng g^{-1})[37,47,50,53,57,59,74,75], the United States (US) (0.1–430 ng g^{-1}, mean 92 ng g^{-1})[76,77], and South Korea (0.174–3341 ng g^{-1}, mean 289 ng g^{-1})[46,49]. Notably, high levels of NFX (256 ng g^{-1}) and spectinomycin (STM) (366 ng g^{-1}) were found in the Pearl River Delta of China[50], and EFX reached 270 ng g^{-1} in the Laizhou Bay of the Bohai Sea[47]. The SMZ detected on the California coast of the US reached 430 ng g^{-1}, 1–2 orders of magnitude higher than other antibiotics detected in the US[77]. South Korea reported the highest concentration in biota, with OA at 3341 ng g^{-1} in Korean bullheads, far exceeding the maximum residue limit of Korean veterinary drugs (100 ng g^{-1})[49]. A concerning observation was the detection of ronidazole (RON) (ND-2.26 ng g^{-1}) in Spain, despite its ban in 1993 due to its genotoxic and carcinogenic properties[78], which underscores the persistence of this antibiotic in marine sediments.

China's marine environments have been the subject of extensive research on antibiotic contamination, with increasing numbers of antibiotics being detected across the country's four major marine areas (Bohai Sea, Yellow Sea, East China Sea, and South China Sea). As one of the largest producers and consumers of antibiotics[79], China exhibited higher detection frequencies and concentrations of antibiotics in its marine environments compared to other countries, underscoring the severe antibiotic contamination in these marine areas. Although considerable progress has been made in assessing antibiotic contamination and associated risks in many parts of the world, significant research gaps remain in regions such as South America, Africa, and polar areas. These regions are under-represented,

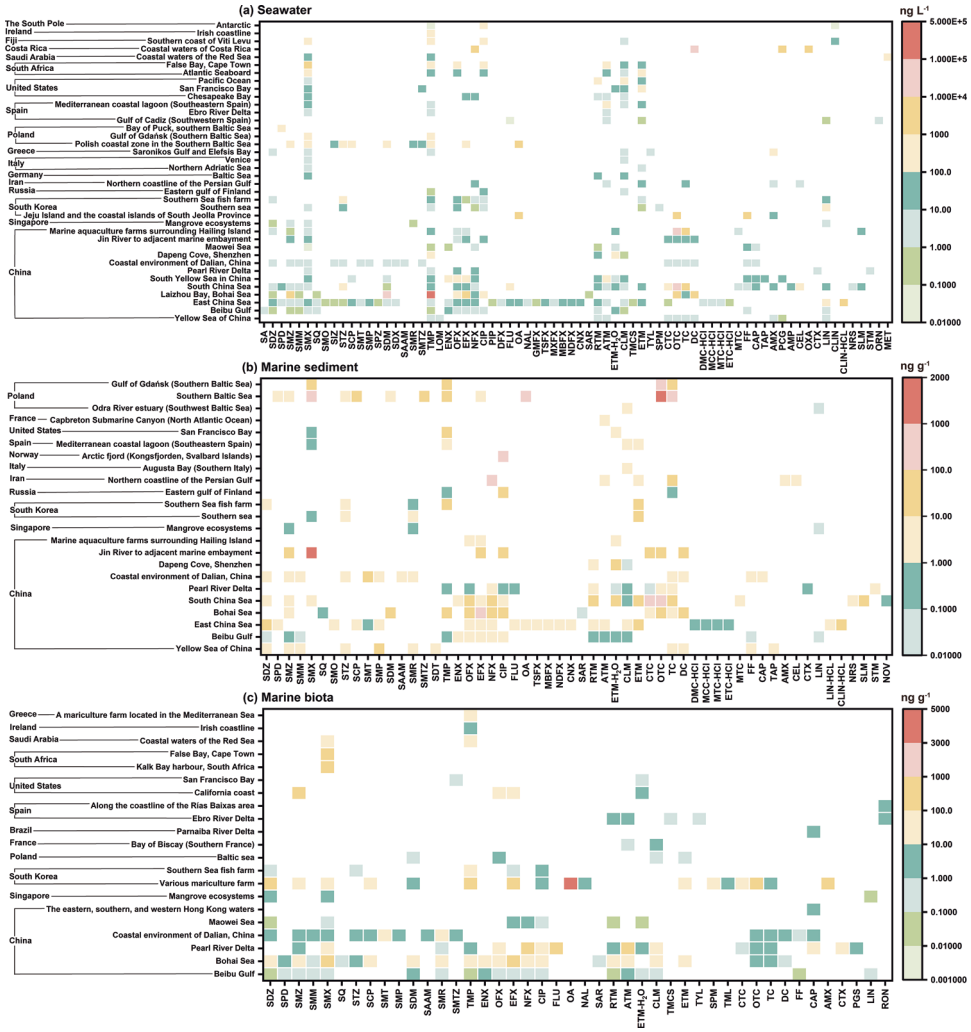

Fig. 3 | Antibiotic contamination across marine areas of different countries. a Seawater, **b** marine sediment, and **c** marine biota.

possibly due to limited research funding and infrastructure, less frequent data publication, weaker regulatory frameworks, and logistical challenges associated with sampling in remote or harsh environments. The scarcity of monitoring data from these regions limits our understanding of the global distribution and ecological impacts of antibiotics. Environmental conditions, antibiotic usage patterns, and ecosystem sensitivities may differ substantially in these areas, potentially leading to unique risks that are currently overlooked. Therefore, future studies should conduct comprehensive monitoring and risk assessment in these understudied regions to achieve a more complete and accurate global evaluation.

Due to the lack of continuous and systematic long-term monitoring data, this study is limited in its ability to analyze temporal trends in antibiotic concentrations. Future research should aim to collect and integrate temporally continuous monitoring data, particularly through comparative analyses of the same marine regions across different years or seasons, to better characterize the temporal dynamics of antibiotic contamination and identify potential driving factors. Moreover, data for certain environmental compartments, such as deep-sea sediments and marine biota, remain limited. These compartments should be prioritized in future targeted monitoring efforts. The absence of such data has contributed to a geographic bias in the spatial distribution of antibiotic concentrations in marine biota, which are primarily concentrated in Asian seas. This reflects a broader geographic imbalance in global marine monitoring. Similar biases are also evident in seawater and marine sediment data, with some regions lacking any available information. Such geographic gaps may affect the representativeness of the results at the global scale. Nonetheless, the coastal waters of Asia, characterized by the highest levels of antibiotic production, use, and environmental contamination[79,80], serve as a critical reference for high-risk marine areas. To enhance the global relevance and comparability of findings, future research should advance integrated, multimedia monitoring across diverse marine regions.

Environmental behavior

Cross-phase migration and transformation of antibiotics. In marine ecosystems, antibiotics undergo migration and transformation across multiple environmental phases, including the atmosphere, seawater, sediments, and biota (Fig. 4). This cross-phase behavior is governed by a range of physicochemical and biological factors, such as temperature, salinity, and pH value. These factors collectively modulate the partitioning, degradation, and bioavailability of antibiotics, thereby shaping their persistence and potential ecological consequences.

Antibiotics present in seawater can exist in particulate form, enabling their diffusion into the marine atmosphere, where they may contribute to aerosol formation and subsequently return to the ocean through atmospheric deposition[16]. This deposition occurs via two primary mechanisms: dry deposition, in which airborne contaminants settle onto surfaces in the absence of precipitation, and wet deposition, where pollutants are scavenged by atmospheric precipitation (e.g., rain and snow) and deposited onto the surface[81]. These processes facilitate the exchange of antibiotics between the atmosphere and seawater.

Antibiotics in seawater can migrate to marine sediments through diffusion and sedimentation processes[82]. Meanwhile, antibiotics retained in

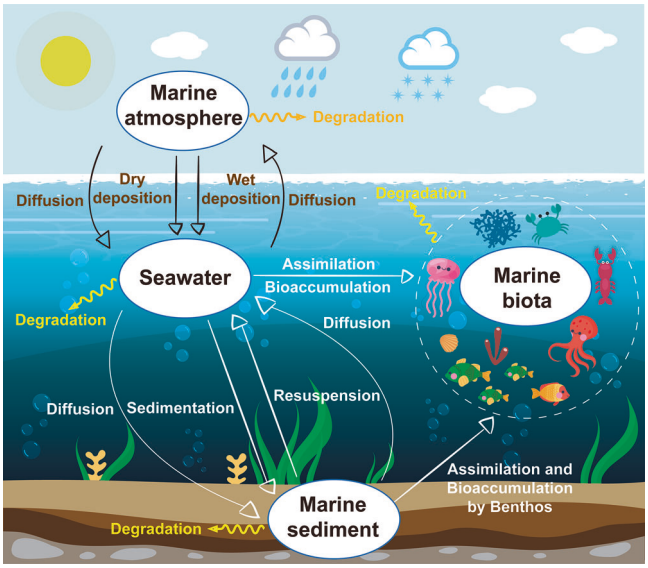

Fig. 4 | Cross-phase migration and transformation of antibiotics in the marine environment.

sediments can be resuspended into seawater under environmental disturbances, such as changes in hydrodynamic conditions, temperature, and pH[83]. Although antibiotic concentrations in seawater often vary over time, they tend to remain relatively stable in sediments, which serve as a major reservoir in the marine environment[78]. The extent of antibiotic retention in sediments is strongly influenced by molecular properties, with FQs, for instance, exhibiting a high adsorption affinity due to their capacity to chelate metal cations and associate with particulate matter[4].

The migration of antibiotics between seawater and marine biota is governed by processes of absorption, bioaccumulation, and metabolic transformation[84]. Marine organisms, including plankton, nekton, and benthic species, support a variety of microbial communities and enzymatic systems capable of breaking down antibiotics[85]. Antibiotics that enter the organism, if rapidly metabolized into various metabolites that reduce their toxicity, will exhibit a biodilution effect[86]. However, antibiotics are not always completely degraded, resulting in a potential biomagnification effect with higher concentrations in organisms of higher trophic levels[47]. Additionally, benthic organisms can absorb antibiotics from sediments, promoting the transfer of these compounds from sediments to living organisms[86].

In regions with high antibiotic concentrations and dense microbial populations, the biodilution effect is likely to prevail, as microbes are capable of efficiently degrading large quantities of antibiotics[87]. Antibiotics that resist degradation tend to accumulate within organisms over time, resulting in a predominance of biomagnification[53]. The extent of these effects depends on the particular antibiotic type and the physiological and ecological traits of the organisms involved, including factors such as lifestyle, age, body size, and osmoregulation[53,73]. Generally, SAs are more prone to biomagnification, while FQs and MAs are often subject to dilution[86]. The trophic magnification factor (TMF) is a critical metric used to quantify these phenomena, with TMF values greater than 1 indicating biomagnification and values less than 1 indicating biodilution[88].

Plastics are capable of adsorbing antibiotics, fostering microbial colonization, and providing both habitats and nutrients for algae[89]. Therefore, the prevalence of plastic in the ocean may contribute to the increased accumulation of antibiotics in algae. Given that algae are primary producers, the presence of antibiotics in these organisms could result in a wider dispersal of these compounds across the marine ecosystem[90]. Nevertheless, the effects of plastics and other pollutants on the behavior of antibiotics in marine environments remain an area that requires further research.

In general, antibiotics experience intricate processes of migration and transformation across various marine environmental phases, eventually accumulating in sediments[91]. As a result, marine sediments may serve as potential reservoirs for antibiotics[92], whereas seawater functions as a medium that facilitates the movement and transformation of these compounds within the marine ecosystem.

The adsorption and degradation of antibiotics. Adsorption and degradation are key processes determining the migration and transformation of antibiotics in the marine environment[93]. Adsorption can be either physical or chemical[22]. Physical adsorption takes place when intermolecular forces create adsorption sites on the surfaces of particulate matter, whereas chemical adsorption involves the formation of chemical bonds between antibiotic molecules and environmental molecules[93]. For example, antibiotic molecules can form complexes or chelate with organic matter, metal ions, or other substances present on the sediment surface[94]. The efficiency of adsorption depends on the specific type of antibiotic. FQs and TCs tend to have a stronger affinity for adsorption, whereas SAs and MAs are less likely to adsorb[95].

Degradation can reduce the concentration and toxicity of antibiotics. It includes hydrolysis, photolysis, and biodegradation[50]. Hydrolysis often occurs alongside other degradation processes, increasing the polarity and hydrophilicity of antibiotics, thus promoting further biodegradation[20]. Hydrolysis occurs when water molecules interact with specific hydrolyzable groups in antibiotic molecules, leading to bond cleavage and the formation of new products[96]. Hydrolysis can be either biological or chemical. Chemical hydrolysis forms new compounds by replacing functional groups with $H+$ or $OH-$ ions in water[97]. In contrast, biological hydrolysis is the breakdown of complex organic compounds by water, catalyzed by biological catalysts, such as enzymes[97]. Antibiotics like TCs, MAs, and βLs are highly susceptible to hydrolysis[98,99], while SAs exhibit low hydrolytic activity, and FQs resist hydrolysis[93].

Photolysis is driven by light, and it breaks down antibiotics by altering their chemical structure and reducing their activity[100]. Photolysis usually requires specific light sources and environmental conditions, such as ultraviolet (UV) light or the presence of photocatalysts[101]. In the ocean, photolysis mainly happens in surface waters where UV light is strongest, but it rarely occurs in deeper waters or sediments[102]. The susceptibility of antibiotics to photolysis depends on their structure. For example, TCs are highly susceptible to photolysis, while FQs are much less affected by this process[95].

Biodegradation is more common than hydrolysis or photolysis, occurring when microbial metabolism triggers chemical reactions that deactivate antibiotics[103]. Antibiotics containing short-chain or unsaturated aliphatic groups are generally more biodegradable than those with long-chain or aromatic structures[104]. FQs are more resistant to biodegradation compared to other antibiotics due to their fluorine atoms and aromatic structure[105].

In short, adsorption and degradation play key roles in determining the fate of antibiotics in the marine environment[93]. Adsorption helps retain antibiotics on particulate matter, while degradation is crucial for lowering antibiotic concentrations and reducing their potential toxicity[20]. These processes collectively affect the migration, transformation, and ecological impact of antibiotics in marine ecosystems.

Unique characteristics of the marine environment and their impacts. The marine environment differs significantly from freshwater systems, due to its unique physicochemical and ecological properties, such as salinity, temperature, pH, dissolved oxygen (DO) levels, oxidation–reduction potential (ORP), electrical conductivity, biodiversity, and hydrodynamic conditions[106]. These interconnected factors collectively influence the transport, transformation, and ultimate fate of antibiotics in marine ecosystems, shaping their bioavailability, degradation pathways, and persistence.

High salinity in marine environments can lead to osmotic stress in microbial cells, resulting in water loss, suppressed enzyme activity, and hindered antibiotic degradation[107,108]. High salinity may also promote the

adsorption of cations onto sediment surfaces, thereby reducing the binding sites available for antibiotics[109]. For instance, the adsorption of TC by marine sediments has been reported to decrease with rising pH and salinity, potentially altering its partitioning between seawater and sediments[110]. However, some studies have also reported a positive correlation between salinity and the adsorption of SMX by marine sediments[111], indicating that antibiotic structure influences its interaction with salinity and sediments.

Salinity also impacts the solubility of antibiotics in seawater[112]. Increased salinity can lower solubility, leading to the aggregation of antibiotics into larger particles, which are less accessible for microbial degradation[113]. Salinity may also affect the hydrolysis rate of antibiotics[20], though additional research is needed to fully understand this relationship. MPs in marine environments can adsorb antibiotics and ARGs, but studies have shown that the concentration of antibiotics and ARGs on MPs declines as salinity increases[114]. This phenomenon may be attributed to the inhibitory effect of high salinity on hydrogen bond formation[115].

Additionally, salinity can influence pH levels. Increased concentrations of salt ions may lead to a decrease in pH, thereby accelerating ocean acidification[116,117]. Such acidification may impede antibiotic degradation by decreasing their bioavailability and modifying the composition of dissolved organic matter (DOM)[118,119]. It has been reported that the uptake and bioaccumulation of pharmaceuticals in aquatic organisms increases with rising pH levels[47,120]. Therefore, a decline in pH could limit the transfer of antibiotics from seawater or sediments to aquatic organisms.

Marine ecosystems typically exhibit higher biodiversity than terrestrial freshwater systems[121]. High biomass levels consume DO, while elevated salinity reduces oxygen solubility, collectively leading to lower DO concentrations in seawater compared to terrestrial freshwater systems[122]. Numerous studies have shown that reduced DO levels could hinder the degradation of antibiotics[52,123,124]. ORP is a key parameter influencing the redox reactions of antibiotics[125], with high ORP generally promoting antibiotic degradation[126,127]. A decrease in DO is generally accompanied by a reduction in ORP[128]. In deeper seawaters and sediments, reduced DO and ORP may facilitate anaerobic biodegradation, but it occurs at a much slower rate compared to aerobic biodegradation, leading to the accumulation of antibiotics in these environments[129].

The temperature and light exposure in seawaters exhibit considerable variation with depth. Surface seawaters are typically warmer and receive more light than deeper seawaters[112]. Although increased precipitation during summer enhances seawater flow, facilitating the dilution and dispersal of antibiotics[52], antibiotic concentrations were generally higher in winter than in summer due to the accelerated degradation driven by stronger sunlight and higher temperatures in summer[33]. Thus, it can be inferred that the lower temperatures and reduced light availability at greater depths may hinder the biodegradation of antibiotics, potentially contributing to their accumulation in deeper seawaters and sediments. These environmental gradients may lead to depth-dependent variations in the behavior of antibiotics with notable differences in concentration among surface waters, deeper waters, and sediments[112].

Overall, the unique marine environments shape distinct antibiotic dynamics. However, the complex interaction among various environmental factors makes it difficult to establish direct relationships between antibiotic behavior and any single factor. Therefore, systematic research is needed to comprehensively understand the impact of marine-specific environmental conditions on antibiotic behavior.

Ecological and human health effects

Adverse effects on marine organisms. Antibiotics released into the marine environment can be toxic to aquatic organisms, interfering with essential biological functions such as algal growth, photosynthesis, and reproduction in species like *Daphnia magna*[28]. These lower trophic level organisms are essential for primary production and nutrient cycling, contributing to the overall stability of the marine ecosystem[121]. For instance, antibiotics such as levofloxacin (LVX) and NFX could significantly suppress the growth and enzymatic activity of microalgae[130]. The introduction of exogenous antibiotics and ARGs in regions like the Bohai Sea could alter the bacterial community composition, altering microbial-mediated sedimentary processes[91]. Antibiotic contamination combined with ocean acidification could lead to neurological disorders in marine organisms such as scallops[131].

Antibiotics can also cause genetic damage and interfere with larval development. For instance, antibiotics like SMX and CLM could compromise the immune system of zebrafish (*Danio rerio*), increasing their susceptibility to viral infections[132]. Antibiotics such as SMZ, EFX, DC, and FF could impair lipid metabolism in zebrafish larvae[133]. Ocean acidification and the naturally high salinity of marine environments may enhance the toxicity of antibiotics to marine organisms[134]. For example, antibiotic contamination and ocean acidification collectively could induce apoptosis of scallop (*Argopecten irradians*) cells[135].

Marine organisms can absorb antibiotics both directly and indirectly, such as through the consumption of phytoplankton or small organisms that have assimilated these compounds[136]. It has been reported that the bioaccumulation factors (BAFs) of NFX, dehydrated erythromycin (ETM-H_2O), and roxithromycin (RTM) could exceed 5000 L kg^{-1} for certain offshore fishes, indicating significant bioaccumulation potential[137]. Trophic amplification of enoxacin (ENX) has also been observed in coastal coral reef fish food webs, with a TMF of 2.75[137]. These indicate that antibiotics can bioaccumulate through marine food chains and webs, potentially endangering higher trophic level organisms.

Marine ecosystems host a diversity of microorganisms, and the presence of antibiotics can drive the emergence of ARBs and the dissemination of ARGs. This poses a global public health challenge by complicating the treatment of previously manageable infections and increasing healthcare costs[138]. The increasing prevalence of antibiotic resistance raises concerns that the development of new antibiotics may fail to keep up, potentially undermining infection treatment efforts[139]. It has been reported that the ARGs of βLs, TCs, and multiple other antibiotics are widespread in marine environments, especially in mariculture areas, with approximately 20% of them posing emerging risks[140]. Beyond antibiotic discharge, human activities can also affect the expression of ARGs by altering nitrogen, phosphorus levels, and seawater temperature[13], highlighting the role of anthropogenic factors in shaping ARG dynamics in marine environments.

Negative impacts on human health. Antibiotics in marine ecosystems pose significant health risks to humans, primarily through two pathways: dietary exposure and the dissemination of ARBs and ARGs. The consumption of seafood has been identified as a critical pathway for human exposure to antibiotic residues[141]. It has been reported that some antibiotics can transfer and bioaccumulate through the food chain, increasing the human exposure risk when consuming contaminated seafood[50]. It was estimated that about 4.02 kg of antibiotics are transferred annually via marine fishery catches for human consumption[142]. It was found that the HQ in Hailing Bay could reach 3.1% due to exposure to ETM through shrimp consumption (considerable health risk: $1\% < HQ \leq 5\%$)[83].

The human microbiome consists of a diverse array of beneficial microorganisms and plays a vital role in sustaining human health[143]. Exposure to antibiotics via seafood, desalinated seawater, or marine aerosol may disturb the human microbiome, leading to potential digestive and immune system issues[143,144]. Microbiota imbalances can promote the overgrowth of harmful bacteria and opportunistic pathogens, leading to a range of diseases[145]. The presence of ARBs and ARGs can worsen these problems by making infections harder to treat[146]. The emergence of "superbugs" has become a major global public health challenge[147]. It was estimated that 4.95 (3.62–6.57) million deaths in 2019 were associated with bacterial AMR[148].

Synergistic environmental risks of antibiotics and coexisting contaminants. In marine environments, antibiotics frequently coexist with other contaminants, including heavy metals[149] and plastics[114], as well as phage viruses[150]. These coexisting contaminants can interact through

complex physicochemical and biological processes, potentially leading to synergistic effects that exacerbate both ecological disturbances and human health risks[151]. Heavy metals, for instance, can promote the spread of antibiotic resistance by co-selecting ARGs, thereby increasing the risk of multidrug-ARBs[149,152]. This has been demonstrated by the positive correlation between the abundance of ARGs and metals revealed in previous studies[153–155].

MPs are now widely distributed in global marine environments[156]. They can selectively adsorb and enrich antibiotics, ARGs, and microorganisms, acting as carriers for these contaminants[114]. It has been demonstrated that MPs can increase the accumulation of antibiotics in marine organisms and alter microbial community structures[157]. The coexistence of MPs and antibiotics has been found to promote the growth of antibiotic-resistant pathogens, such as *Pseudomonas aeruginosa* (*P. aeruginosa*), and cause severe infections in humans[158]. Additionally, MPs can exacerbate the toxic effects of antibiotics by inducing oxidative stress, resulting in cellular damage in marine organisms[115].

Phages are among the most abundant microorganisms in marine environments[159]. They can regulate bacterial populations and influence microbial community dynamics[160]. Phages can carry certain ARGs, facilitate the horizontal transfer of these ARGs between bacteria through transduction[161], and accelerate the spread of plasmid-encoded antibiotic resistance[162], thereby promoting the spread of resistance. Phages can also create selective pressure on bacteria in combination with antibiotic contamination, leading to a more rapid emergence and propagation of resistant strains[150].

In summary, the combined effects of antibiotics and other contaminants create a complex pollution issue in marine ecosystems. The interactions between these pollutants require further investigation, as their collective impact may pose a greater threat to both ecological systems and human health than individual contaminants alone. Understanding and addressing these synergistic effects is crucial for protecting marine biodiversity and ensuring public health.

Risk assessment

Ecological risk. The ecological risk of antibiotics in seawater and marine sediments was assessed by examining three trophic levels of organisms (algae, invertebrates, and fish). The RQ values of antibiotics for these trophic levels in seawater are shown in Supplementary Fig. 2. The ecological risk posed to marine ecosystems is influenced by various factors, including their toxicity, physicochemical properties, and persistence[134]. Based on existing data, antibiotics tend to be more toxic to organisms at lower trophic levels, such as algae, than to those at higher trophic levels, like fish[2]. As a result, algae face significantly higher ecological risks from antibiotic contamination compared to invertebrates or fish. However, uncertainty remains due to potential long-term effects and possible biomagnification through food chains and webs, which may lead to higher levels of exposure and increased toxicity over time for higher-level predators.

In seawater, 41.7% of antibiotics posed a moderate or higher risk to algae, with 29.2% classified as high risk. SMX, SDM, TMP, OFX, EFX, NFX, CIP, OA, RTM, ETM-H_2O, CLM, ETM, spiramycin (SPM), CTC, OTC, TC, DC, amoxicillin (AMX), penicillin G (PCG), ampicillin (AMP), and salinomycin (SLM) were of particular concern, with CIP in False Bay, Cape Town ($RQ_{Water\text{-}Algae}$ = 92.4) presenting the highest risk. For invertebrates, 23.6% of antibiotics posed a moderate or higher risk, with 6.94% (SMX, TMP, NFX, DC, and SLM) identified as high risk. The antibiotic with the highest risk to invertebrates was DC in the coastal waters of Costa Rica ($RQ_{Water\text{-}Invertebrate}$ = 11.1). Similarly, for fish, 15.3% of antibiotics posed a moderate or higher risk, and 5.56% posed a high risk, with NFX in the coastal waters of Costa Rica again showing the highest risk ($RQ_{Water\text{-}Fish}$ = 15.1). The Costa Rican coastal waters demonstrated a particularly severe ecological risk, where multiple antibiotics simultaneously posed high risks to algae, invertebrates, and fish, underscoring the urgent need for targeted management in this region[61]. In marine sediments, as shown in Supplementary Fig. 3, the ecological risk was notably lower than in seawater. For algae, 9.62% of antibiotics posed moderate or high risk, with 5.77% categorized as high risk, including SMX, OTC, and OA. The highest-risk regions for sediment pollution include the Southern Baltic Sea in Poland (OA and OTC posed high risk)[43,71] and the Jin River estuary in China (SMX posed high risk)[45], where stricter antibiotic controls are necessary. For invertebrates, 3.85% of antibiotics posed a moderate risk, but no antibiotics presented a high risk. Fish were exposed to minimal risks from sediment-bound antibiotics, with only NFX and chlortetracycline (CTC) posing low risks.

The mixed ecological risk assessment, illustrated in Fig. 5a, b, was conducted to evaluate the synergistic pollution caused by multiple antibiotics coexisting in the same marine environment. The mixed risk quotient (RQ) values ($MRQ_{MEC/PNEC}$ and MRQ_{STU}) in seawaters ranged from 0.02 to over 178, indicating that the majority of marine areas (81.6%) faced high mixed ecological risk, particularly in 12 countries and regions, including China, Korea, Russia, and the Antarctic. In marine sediments, the mixed ecological risks were considerably lower, with $MRQ_{MEC/PNEC}$ and MRQ_{STU} values ranging from 0 to 3.49. Approximately 39.1% of marine areas faced moderate or higher risk, notably in the Jin River estuary[45] and the Southern Baltic Sea[43,71].

While this assessment offers valuable insights into the ecological risks of marine antibiotic contamination, it does not fully consider the potential long-term cumulative effects of continuous antibiotic exposure[163]. The potential amplification of ecological impacts due to the coexistence of other contaminants, such as MPs and heavy metals[164], was also not included. Future research should focus on chronic exposure and the interactive effects of multiple contaminants. This is essential for gaining a more comprehensive understanding of the long-term ecological risks of antibiotic contamination.

Risk of developing AMR. Globally, the concentrations of most antibiotics in seawater remain below the AMR-PNEC values. However, in some regions, concentrations of certain antibiotics surpassed the AMR-PNEC threshold, indicating a potential risk for AMR development (Fig. 5c). Twelve antibiotics, including SMX, TMP, EFX, CIP, azithromycin (ATM), TYL, OTC, TC, DC, cefalexin (CEL), OXA, and metronidazole (MET), posed a risk for AMR development across 13 marine areas spanning 10 countries or regions, such as China, South Korea, Poland, Spain, South Africa, and Antarctica. Notably, the risk of AMR development due to TMP in Laizhou Bay of the Bohai Sea in China was the most severe, followed by the risk associated with OTC in the Marine aquaculture farms surrounding Hailing Island and in the South China Sea.

Importantly, certain antibiotics with relatively low ecological risk, such as ATM, CEL, and MET, still show potential to promote AMR. This highlights that even antibiotics posing minimal threats to marine ecosystems from a toxicity perspective may contribute to the rise of AMR, underscoring the need for comprehensive risk assessments for antibiotic contamination that integrate both ecological and AMR-related risks.

Traditional ecological risk assessments that rely on RQ methods do not fully address the risks due to the development of AMR[165]. However, the emergence of AMR is a major risk associated with antibiotic contamination[166]. It has been reported that many AMR genes can persist even in low antibiotic concentrations, indicating that even sub-lethal doses of antibiotics in marine environments may still contribute to the development of resistance[167]. Therefore, it is essential to integrate various assessment approaches to better understand and identify high-risk antibiotics, enabling the development of more effective environmental management and regulatory policies.

Health risk. The human health risk assessment was conducted by integrating exposure parameters and the ADI values for each antibiotic across different age groups—children, adolescents, and adults—based on seafood consumption patterns (Supplementary Fig. 4). For most of the antibiotics assessed, health risks were relatively low. However, 11.4% of

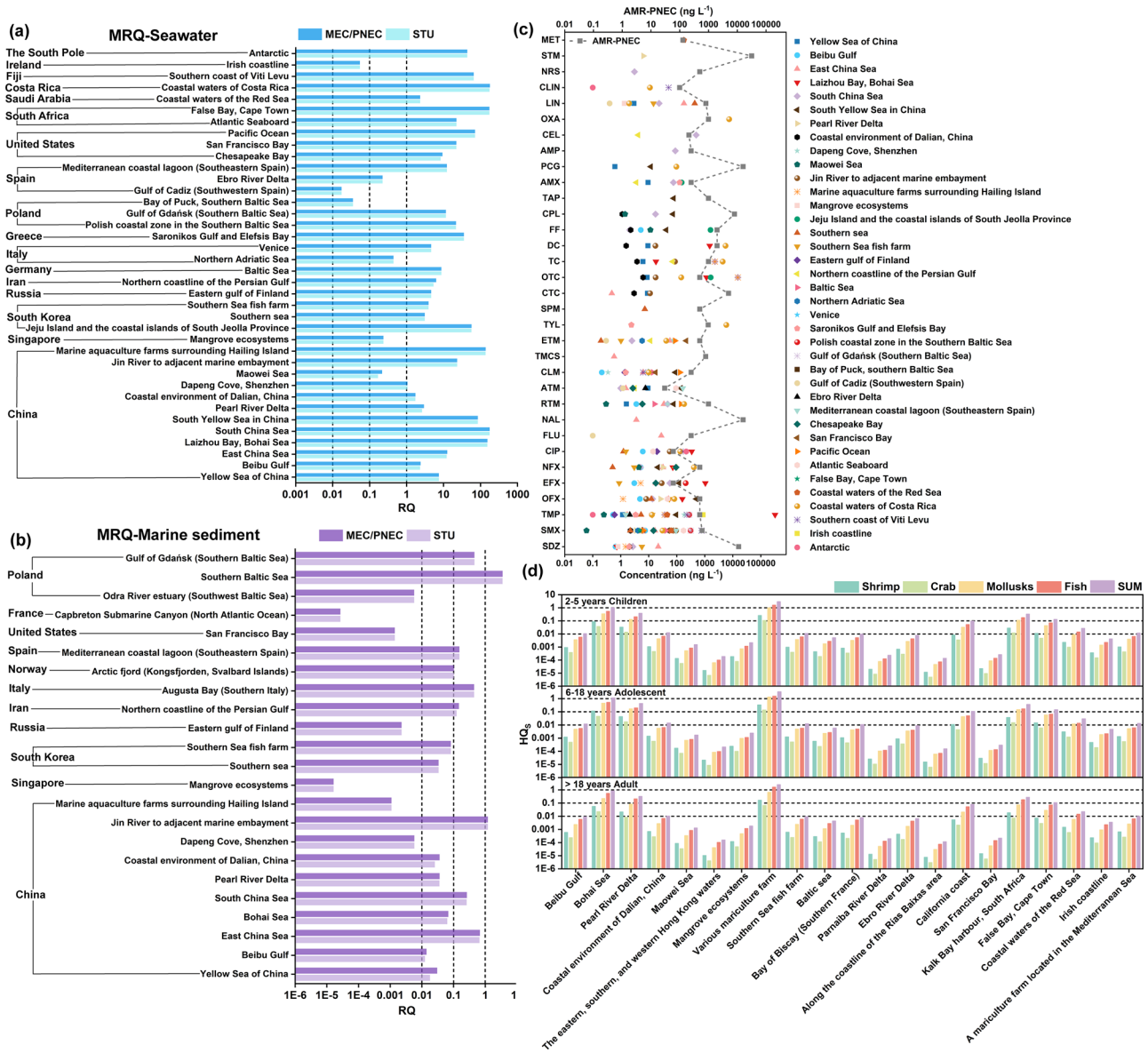

Fig. 5 | Environmental risk of antibiotics in the global marine environment. **a** Mixed ecological risk in eawater (low risk: MRQ < 0.1, moderate risk: 0.1 <MRQ < 1, and high risk: MRQ < 1), **b** mixed ecological risk in marine sediment, **c** risk of AMR development, and **d** the combined health risk (low risk: HQ_S < 0.), moderate risk: 0.1 < HQ_S < 1, and high risk: HQ_S > 1).

the antibiotics, including SMX, EFX, OA, RTM, and CLM, presented moderate or higher health risks. Notably, OA posed a high health risk to all age groups. These antibiotics require stringent control measures to mitigate potential health risks.

Further analysis of health risks based on seafood consumption across different age groups (Fig. 5d) revealed that adolescents (6–18 years) had the highest health risk, followed by children (2–5 years), and lastly, adults. This finding contrasts with other studies that have reported increasing health risks with age. The discrepancy arises from the differences in the food items analyzed. While other studies focused on drinking water or edible fish[168,169], this study specifically investigated seafood consumption. Children aged 2–5 years consume less seafood on average (29.05 g day^{-1}) compared to adolescents (80.55 g day^{-1}) and adults (91.6 g day^{-1}). Additionally, while the seafood consumption between adolescents and adults is relatively close, adolescents' lower body weight (mean 40.1 kg) makes them more vulnerable to higher antibiotic exposure compared to adults (mean 60.6 kg). Thus, adolescents, particularly in high-risk marine areas, should be prioritized for health risk mitigation.

It is worth noting that in recent years, 60% of the areas with $HQ_{S\text{-}SUM}$ greater than 0.1 (moderate or higher risk) were predominantly in Asian seas. In high-risk areas such as the Bohai Sea[37,47] and Pearl River Delta[50] in China, as well as various mariculture farms in South Korea[49], the overall seafood consumption risk ($HQ_{S\text{-}SUM}$) reached or approached high-risk levels across all age groups. Among these regions, South Korean marine farms[49] exhibited the highest combined health risk, with the consumption of all seafood types, except crab, reaching a moderate risk, while the overall combined health risk from consuming all types of seafood reached a high risk level. This is because the extensive use of veterinary antibiotics in these regions has led to significant residues in both seawater and seafood, which are subsequently transferred to humans through seafood consumption[134]. These highlight the urgent need for strict regulation of antibiotic use in aquaculture and marine farming. The health risks associated with different seafood types are ranked as follows: fish > mollusks > shrimp > crab. This suggests that reducing the consumption of fish and mollusks could be an effective strategy for minimizing human exposure to antibiotic residues in high-risk areas.

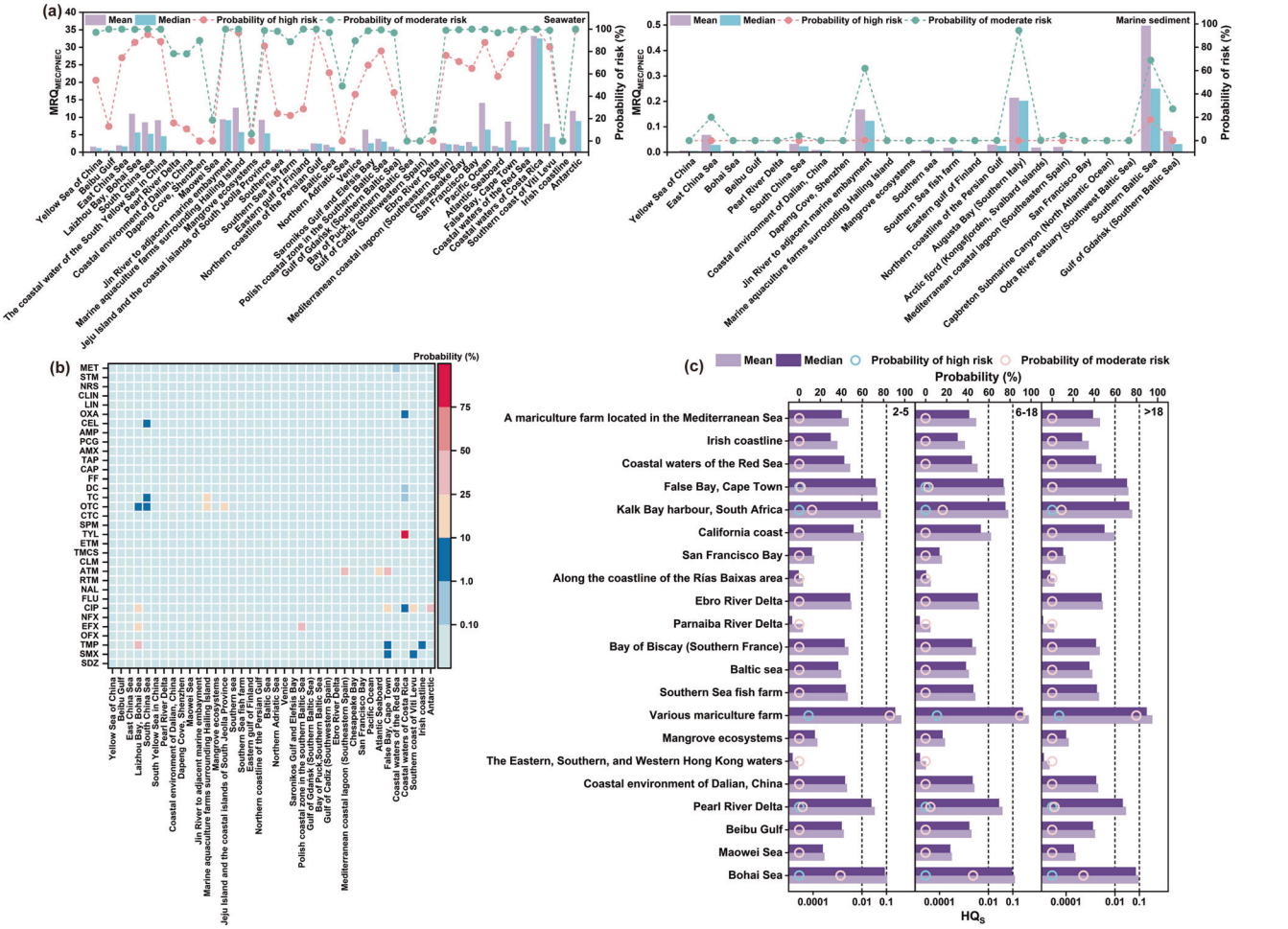

Fig. 6 | Uncertainty analysis of environmental risk in the global marine environment. a Mixed ecological risk of antibiotics (low risk (MRQ < 0.1), moderate risk (0.1 < MRQ < 1), and high risk (MRQ > 1)); **b** probability of generating risk of AMR development; and **c** the combined health risk of antibiotics in three age groups (2–5-years-old: children, 6–18-years-old: adolescent, and >18-years-old: adult) (low risk (HQ_S < 0.1), moderate risk (0.1 < HQ_S < 1), and high risk (HQ_S > 1)).

In light of these risks, strict national standards on residue limits must be enforced, and effective withdrawal periods should be established to ensure antibiotics in seafood reach safe levels before consumption[49]. Public health campaigns should educate consumers on avoiding seafood species with high antibiotic residues. More importantly, more regulated antibiotic use and stricter emission controls are needed to reduce antibiotic contamination in seafood at its source.

Uncertainties. Although the RQ of individual antibiotics decreased compared to the "worst-case scenario", most reductions were within one order of magnitude (Supplementary Figs. 5–8). In seawater, 81.6% of marine areas were classified as high risk under the worst-case MRQ, while this proportion dropped to 63.2% and 57.9% for the mean and median MRQs, respectively (Supplementary Table 11). Similarly, areas categorized as moderate risk declined by about 10%. The 95% confidence interval for MRQ in global seawater ranged from 0 to 29.2 at the lower bound and from 0.145 to 59.4 at the upper bound. Approximately 60% of marine areas exhibited a > 50% probability of high risk, and the probability of moderate risk exceeded 80% in most regions (Fig. 6a). These findings indicate that the underlying risk remains substantial in many locations. In marine sediments, the 95% confidence interval for global MRQ ranged from 9.77×10^{-9} to 8.84×10^{-3} at the lower limit and from 7.68×10^{-6} to 2.02 at the upper limit. The proportion of areas with a medium risk classification declined markedly, from 39.1% under the worst-case assumption to 13% under the uncertainty-based estimate. High-risk probabilities were virtually absent in most areas, with the exception of the Southern Baltic Sea (Poland), which showed a high-risk probability of approximately 17%. These results suggest that ecological risks in sediments are generally lower than in seawater but may still be significant in localized hotspots. Therefore, marine regions with relatively high MRQs and a substantial probability of high risk should be prioritized for ecological risk control and monitoring.

In most regions, the majority of antibiotics posed very low AMR risks (<0.1%) (Fig. 6b and Supplementary Table 12). However, certain antibiotics in ten regions exhibited AMR development probabilities exceeding 10%. Notably, TYL in the coastal waters of Costa Rica showed a 75% probability of AMR risk, indicating a high likelihood of promoting AMR. Other antibiotics with elevated AMR risk probabilities included TMP in Laizhou Bay (Bohai Sea), EFX in the Southern Baltic Sea (Poland), ATM in the Mediterranean coastal lagoon (Southeastern Spain) and False Bay (Cape Town), and CIP in Antarctic waters. Interestingly, CEL, which posed a negligible ecological risk under both assessment approaches, showed an 8.26% probability of AMR development in the South China Sea, highlighting the importance of AMR-specific risk assessment. These antibiotics and associated regions should be identified as AMR-priority control areas. Moreover, even compounds with low environmental concentrations and minor ecological risks should not be dismissed, as they may still contribute to resistance selection and dissemination.

For human health risk (Fig. 6c and Supplementary Table 13), only mariculture farms in South Korea showed a non-negligible probability (10%) of high health risk. Several other regions exhibited moderate risk, ranked by probability as follows: mariculture farms (South Korea) > Bohai

Sea (China) > Kalk Bay Harbour (South Africa) > Pearl River Delta (China) > False Bay (Cape Town). HQs based on the mean and median values were significantly lower than those estimated under the "worst-case scenario", only 4.68–46.4% of the worst-case HQs. The 95% confidence interval for HQs ranged from the lowest levels observed in Eastern, Southern, and Western Hong Kong waters (1.57×10^{-6} to 9.16×10^{-5}) to the highest values in South Korean mariculture farms (0.0693–2.05). Most regions showed low HQs based on mean and median values, indicating generally low health risks. Only the mariculture zones in South Korea and the Bohai Sea reached moderate risk levels. Importantly, the probability of moderate health risk (HQs > 0.1) for children and adolescents, especially the latter, was substantially higher than for adults. These findings underscore the necessity for age-specific strategies in seafood consumption guidelines.

Discussion

This study provides a comprehensive review of the sources, pollution levels, environmental behavior, and risks of antibiotics in marine environments worldwide. SAs, FQs, MAs, and TCs were identified as the most prevalent antibiotic classes, with SMX and TMP being the most frequently detected compounds in seawater and biota. Antibiotic concentrations in seawater ranged from ND to 332440 ng L^{-1}, with TMP reaching the highest levels. In sediments, concentrations ranged from ND to 1515 ng g^{-1}, with TMP and TC most commonly detected, while OTC exhibited the highest levels. In biota, concentrations ranged from ND to 3341 ng g^{-1}, with OA showing the highest measured concentration. China accounted for the majority of studies on marine antibiotic contamination, indicating severe pollution in its coastal areas. Antibiotics in the marine environment migrate and transform across the atmosphere, seawater, sediments, and biota. Marine-specific conditions influence antibiotic behavior differently compared to terrestrial systems. Coexisting contaminants, such as heavy metals, plastics, and phages (as coexisting viruses), further exacerbate environmental risks.

Antibiotics negatively impact marine organisms, promoting ARGs expression and posing risks to human health. Ecological risk assessments revealed that 29.2%, 6.94%, and 5.56% of antibiotics globally posed high risks to algae, invertebrates, and fish, respectively, with the coastal waters near Costa Rica presenting the greatest ecological risk. Despite the lower RQ observed for higher trophic level organisms, attention should still be given to their potential long-term effects and the risk of bioaccumulation through food chains and food webs. Thirteen antibiotics, including ATM, CEL, and MET, were identified as potential drivers of AMR despite their low ecological risk. Health risk assessments showed that adolescents (6–18 years) faced the highest health risk. Across all age groups, SMX, SCP, EFX, RTM, and CLM posed moderate risks, while OA presented a high risk. High health risks were observed in the Bohai Sea and Pearl River Delta in China, as well as in mariculture farms in South Korea. This study uses a dual assessment strategy for environmental risk, compared to the "worst-case scenario", high mixed ecological risks decreased by 20% under uncertainty analysis, yet 60% of marine areas still had >50% probability of high risk. Several regions showed >10% AMR risk, and South Korea's mariculture farms posed notable health risks, especially for children and adolescents.

To address the growing global challenge of antibiotic contamination and the associated emergence and spread of ARBs and ARGs in the marine environment, future research should prioritize several key areas. These include (1) investigating the sources of antibiotics, such as industrial, agricultural, and domestic origins, along with their distribution, migration, and transformation across different marine regions and depths; (2) examining the risks associated with the co-occurrence of antibiotics and other contaminants, such as plastics and heavy metals, particularly how these interactions influence antibiotic behavior and promote the spread of resistance; (3) exploring the mechanisms and distribution of ARGs, particularly their transport, transformation, and reproduction in relation to antibiotic concentrations; (4) comprehensive monitoring and assessment of the occurrence and risk of antibiotics in the marine environment in under-studied regions to improve the global assessment system; (5) Strengthening research on the toxicity of understudied antibiotics to marine organisms to improve the accuracy of ecological risk assessments in marine ecosystems; (6) developing advanced monitoring technologies, such as high-precision biomarkers and remote sensing, to detect low-concentration antibiotics and ARGs and enable intelligent environmental monitoring; (7) integrating environmental, hydrological, and meteorological data to construct predictive models that consider the effects of climate change on antibiotic and ARGs distribution; (8) assessing the ecological impacts of antibiotics on biodiversity, food webs, and ecosystem functions, incorporating broader chronic exposure effects to inform risk management; and (9) designing environmentally friendly and cost-effective technologies to remove antibiotics and ARGs from marine environments.

Effective mitigation of antibiotic contamination requires integrating scientific research, policy, and technological innovation. Key strategies include (1) targeting antibiotics with severe pollution and high risks, such as SAs and MAs in seawater, FQs and TCs in sediments, and bioaccumulative FQs in biota; (2) reducing emissions at the source by promoting sustainable agricultural practices like green farming and enforcing stringent standards on antibiotic use and discharge; (3) establishing national and international monitoring networks to regularly track antibiotic contamination in marine areas and provide reliable data for policy formulation; (4) strengthening environmental regulations, such as implementing stricter water quality and discharge standards with penalties for violations; (5) upgrading wastewater treatment facilities, particularly for mariculture wastewater and rural sewage, to improve the removal efficiency of antibiotics and ARGs; and (6) considering future human activities, including the impacts of climate change, on antibiotic contamination and ARGs expression, integrating these factors into comprehensive mitigation plans.

Effective management should prioritize regions and antibiotics with elevated environmental risks. Future research should focus on robust methods for monitoring and predicting antibiotic behavior in marine environments. Coordinated efforts across monitoring, prediction, and control strategies are essential to mitigate antibiotic contamination effectively.

Methods

Data collection and preprocessing

The review process of this study is illustrated through the PRISMA (Preferred Items for Reporting Systematic Reviews and Meta-analyses) flow chart (Supplementary Fig. 1 and Supplementary Table 1). The literature search focused on themes related to the occurrence, environmental behavior, and ecological effects of antibiotics in marine ecosystems. Searches were conducted across databases, including Web of Science, Scopus, PubMed, and China National Knowledge Infrastructure (CNKI). The review includes both original research and review articles published over a span of 15 years, from 2010 to 2025. Keywords used in the search strategy combined the term "*antibiotic*" with terms such as *marine*, *ocean*, *seawater*, *sediment*, *seafood*, *organism*, *biota*, *offshore*, *gulf*, *coastal*, or *coastline*. Various combinations and permutations of these terms were employed across the different databases. All retrieved articles were systematically organized and manually screened. Reference lists were reviewed to identify additional relevant studies, and duplicates were subsequently removed. Data included in the review were extracted directly from the original studies, encompassing information on sources, pollution levels, environmental behavior, ecological impacts, and human health risks of antibiotics in the global marine ecosystem.

To evaluate the extent of antibiotic contamination in marine ecosystems globally, studies reporting measured antibiotic concentrations were selected based on the following three criteria:

(1) The study provided actual monitoring data on antibiotic concentrations in seawater, marine sediments, or marine organisms.
(2) Sampling locations were clearly recorded, with geographic specificity to a particular country or region.
(3) Sampling and analytical methods were scientifically robust and clearly described. Samples were collected from various marine environments, including coastal zones, offshore waters, estuaries, and bays. Samples

were promptly transported to laboratories for concentration analysis after collection. Quality assurance and quality control (QA/QC) were implemented, and detection methods included liquid chromatography (LC) and gas chromatography (GC) coupled with mass analyzers (such as LC-MS/MS, GC-MS/MS, and LC-MS/qTOF).

The review covers data on 80 antibiotics across 50 marine areas in 20 countries or regions. These antibiotics belong to various classes, including sulfonamides (SAs), fluoroquinolones (FQs), macrolides (MAs), tetracyclines (TCs), chloramphenicols (CPs), β-lactams (βLs), and others. A detailed summary of the antibiotics considered is provided in Supplementary Table 2. Although studies using LC-MS/MS, GC-MS/MS, and LC-MS/qTOF were considered during the literature selection process, all included studies ultimately employed LC-MS/MS for antibiotic quantification, ensuring methodological consistency. Extracted data were systematically categorized by antibiotic class, environmental medium, and geographic location to create a database for further analysis (Supplementary Table 6). The mean, median, and range of antibiotic concentrations in the global marine environment, as well as the limit of detection (LOD) and limit of quantitation (LOQ), are presented in Supplementary Tables 7–9. Supplementary Table 10 summarizes the instruments for the determination of antibiotic concentration in each study.

Environmental risk assessment

The ecological risk of antibiotics in seawater and marine sediments was evaluated using toxicity data derived from three trophic levels of aquatic organisms: algae, invertebrates, and fish[52]. This assessment followed the framework outlined in the EU technical guidance document on risk assessment, employing the RQ approach as a quantitative metric to characterize ecological risk[10]. RQ is obtained by dividing the measured concentration by the predicted no-effect concentration (PNEC) (Eq. (1)). PNEC is calculated based on toxicity data of antibiotics on organisms, but due to the lack of toxicity data, the PNEC of some antibiotics is predicted by the ECOSARv2.0 software developed under the supervision of the United States Environmental Protection Agency[42]. Based on established classification criteria, risk levels were categorized as low risk (RQ < 0.1), moderate risk (0.1 < RQ < 1), and high risk (RQ > 1)[6].

$$RQ = \frac{MEC}{PNEC} \quad (1)$$

Where MEC is the measured concentration of antibiotics in seawater (ng L^{-1}) or marine sediments (ng g^{-1}). In accordance with the "worst-case scenario" principle defined by the European Chemicals Agency in the Guidance on Information Requirements and Chemical Safety Assessment in 2016[134], the maximum detected concentration within a given dataset was selected as the MEC value. $PNEC_{Water}$ (ng L^{-1}) is derived by dividing acute toxicity values (LC50, EC50) or chronic toxicity values (NOEC, ChV) by an appropriate assessment factor (AF). Standard AF values of 1000 and 100 were applied for acute and chronic toxicity data, respectively[33]. $PNEC_{Sed}$ was estimated by $PNEC_{Water}$ (Eqs. (2 and 3)). The PNEC values are summarized in Supplementary Table 3.

$$PNEC_{Sed} = (K_{susp-water}/RHO_{susp}) \times PNEC_{Water} \times 1000 \times 4.6 \quad (2)$$

$$K_{susp-water} = F_{water-susp} + F_{solid-susp} \times F_{oc-susp} \times (K_{OC}/1000) \times RHO_{solid} \quad (3)$$

Where RHO_{susp} and RHO_{solid} were densities of wet suspended matter and the solid phase, valued 1150 and 2500 in kg $(m^3)^{-1}$, respectively. $F_{water\text{-}susp}$ and $F_{solid\text{-}susp}$ were the volume fractions of water and solid in suspended matter, defined as 0.9 and 0.1 in m^3 $(m^3)^{-1}$. $F_{oc\text{-}susp}$ was the mass fraction of organic carbon in suspended matter, with an assigned value of 0.1 in kg kg^{-1}. K_{OC} was the partition coefficient of organic carbon-water (L kg^{-1}), as shown in Supplementary Table 2.

In addition, a mixing concentration model was employed for ecological risk assessment of mixed toxicity to account for the synergistic effects of multiple antibiotics[28]. The mixed RQ $MRQ_{MEC/PNEC}$ and MRQ_{STU} for all detected antibiotics in each marine area are determined in Eqs. (4 and 5). The risk level definition for MRQ is the same as for RQ.

$$MRQ_{\frac{MEC}{PNEC}} = \sum_{i=1}^{n} \frac{MEC_i}{PNEC_i} = \sum_{i=1}^{n} \frac{MEC_i}{\min(PNEC_{Algae}, PNEC_{Inverterbrate}, PNEC_{Fish})} \quad (4)$$

$$MRQ_{STU} = \max\left(\sum_{i=1}^{n} \frac{MEC_i}{PNEC_{Algae}}, \sum_{i=1}^{n} \frac{MEC_i}{PNEC_{Inverterbrate}}, \sum_{i=1}^{n} \frac{MEC_i}{PNEC_{Fish}}\right) \quad (5)$$

A standardized assessment framework, established by the AMR Industry Alliance, has been adopted to evaluate the potential risk of AMR emergence[10]. This approach involves a comparative analysis between the PNEC for AMR selection (AMR-PNEC) and the measured environmental concentrations of antibiotics (MEC). The lower of the PNEC-environment (PNEC-ENV) and the PNEC-minimum inhibitory concentration (PNEC-MIC) was selected as the AMR-PNEC value. The AMR-PNEC values for various antibiotics, as detailed in Supplementary Table 2, serve as reference thresholds. When MEC levels surpass the corresponding AMR-PNEC, the likelihood of AMR development is considered significant, necessitating further investigation.

Estimating human dietary exposure to antibiotics through seafood consumption is crucial for assessing health risks[169]. Four types of seafood, including shrimp, crab, mollusks, and fish, were selected for this analysis[60]. The daily intake of antibiotics was estimated based on the concentrations detected in marine biota and the daily seafood consumption of different age groups. The three age groups included were children (2–5 years), adolescents (6–18 years), and adults (>18 years). The health hazard quotient (HQ) was calculated by dividing the estimated daily intake (EDI, ng (kg bw d)$^{-1}$) by the acceptable daily intake (ADI, ng (kg bw d)$^{-1}$) of antibiotics (Eqs. (6 and 7)). ADI is designated as a dose that can be consumed by humans on a daily basis without adverse health effects (Supplementary Table 4). This is derived based on toxicological and pharmacological action data[73,170], noting that some data are calculated by LTD (lowest therapeutic dose of pharmaceuticals)[171]. HQ was classified into three risk levels: low risk (HQ < 0.1), moderate risk (0.1 < HQ < 1), and high risk (HQ > 1). The coexistence of multiple antibiotics in the environment may pose a synergistic risk to human health[172]. Therefore, the combined health HQ_S was employed to assess the overall health risk of different age groups (Eq. (8)). HQs uses the same risk level definition as HQ.

$$EDI = \frac{MEC_{Marine\ biota} \times M_{Seafood}}{bw} \quad (6)$$

$$HQ = \frac{EDI}{ADI} \quad (7)$$

$$HQ_S = \sum_{i=1}^{n} HQ_i \quad (8)$$

Where $MEC_{Marine\ biota}$ is the measured concentration of antibiotics in marine biota (ng g^{-1}) that considers the worst case, using the maximum value for each antibiotic, in order to effectively identify high-risk antibiotics and to understand the safety of consuming seafood[60,142]. $M_{Seafood}$ is the daily consumption of seafood by different age groups (g d^{-1}), and bw is the body weight (kg) (Supplementary Table 5).

Uncertainty analysis

To comprehensively assess the environmental risks of antibiotic contamination in the global marine environment, a dual-assessment strategy was employed in this study. First, a "worst-case scenario" approach was adopted using the maximum observed concentrations of antibiotics for risk estimation. Second, uncertainty analysis was conducted based on the

statistical distribution of observed concentrations (median and range). Assuming a log-normal distribution, Monte Carlo simulations (10,000 iterations) were performed to derive probabilistic indicators, including the mean, median, risk probabilities, and confidence intervals. This dual approach enables a more systematic evaluation of risk variability and provides insight into the probability of high-risk scenarios.

Data availability

All data generated or analyzed during this study are included in this published article and its supplementary information files.

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Yuru Chen: methodology, investigation, data curation, writing—original draft, and writing—review and editing. Ye Huang: conceptualization, writing—original draft, writing—review and editing and funding acquisition. Yangmin Chen: investigation and validation. Ying Li: investigation and writing—review and editing. Nazupar Sidikjan: investigation and writing—review and editing. Nan Lin: conceptualization. Ye Li: conceptualization. Xingpan Guo: writing—review and editing. Guofeng Shen: writing—review and editing. Min Liu: conceptualization, funding acquisition, and supervision.

Competing interests

The authors declare no competing interests.

Additional information

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