Climate Change Potential to Accelerate the Dispersal of Antimicrobial Resistance (AMR) Bacteria in Animals, Humans, and the Environment

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Abstract

Antimicrobial resistance (AMR) is a serious public health challenge. There is an increasing trend in the emergence of resistant pathogens have been detected due to the misuse and overuse of antimicrobial agents. The different sectors of the ecosystem are equally affected by this threat, and it could also easily traverse through different species and ecosystems. Climate change (CC) alters the different ecosystems, and hence it promotes the survival and spread of resistant microbes because it favors the proliferation of microbes. This phenomenon becomes a major concern in human and veterinary medicine. To address this critical challenge, there is need of a one health approach. It requires global coordinated efforts such as the implication of the use of antimicrobial guidelines, the implementation of strong surveillance systems and collaboration between different sectors. There should also be a worldwide adaption of guidelines for agriculture practices and waste disposal. Additionally, the new technologies such as artificial intelligence (AI), nanotechnology, and the use of genomic tools should be used to tackle AMR.

Keywords: Antimicrobial Resistance, Climate change, Pathogens resistance, One Health, Public Health

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Introduction

With the passage of time, some microbes evolve to a point where the antimicrobial drugs ultimately become ineffective against them. This phenomenon is called antimicrobial resistance (AMR) (Algammal et al., 2021). In the year 2019, about 1.27 million deaths were estimated due to AMR. Nowadays, AMR becomes a major challenge to all countries because it is contributing to health complications, increased healthcare expenses, and an increasing number of deaths (Allel et al., 2023). A report published in 2017 from the World Health Organization (WHO) had stated that if the use of existing drugs and microbial modification continues, the whole world would suffer as the existing antibiotics would ultimately become useless (Garoy et al., 2019). A report from the European Commission estimated that about 33000 deaths per year in the European Union were due to AMR. They also mentioned that this costs around 1.5 billion per year in terms of healthcare costs (Meinen et al., 2023). A report on antibiotic resistance published in 2019 from the Center for Disease Control and Prevention reported that AMR cases were estimated to be more than 2.8 million per year in the United States (US), which includes around 35000 cases of deaths (Punchihewage-Don et al., 2022).

Climate change (CC) is the consequence of human activities like fossil fuel burning, forest cutting, and different industrial procedures that affect natural climate patterns (Yarzábal et al., 2021). There are many results of CC, like the rise of sea levels, high temperature, severe and frequent storms, alterations in ocean currents (Fox et al., 2015). There are many microbes that are sensitive to climate change. A change in temperature and other environmental conditions may cause an increase in the dispersal of these microbes. The increased prevalence of diseases could lead to the use of more and imbalanced use of antimicrobial agents, which ultimately develop and exacerbate the AMR. For instance, large-scale outbreaks of helminth parasites are increasing in human and livestock populations due to the climate crisis (Fox et al., 2015).

The understanding of the relation between CC and AMR is crucial for the development of strategies to integrate the human, animal, and environmental health (Reddy et al., 2022). The exploration of the mechanisms of AMR due to CC will help in the information about regional and global risk assessment (Fox et al., 2015). The topics like food security, environmental reservoirs like water bodies and soil, public health security, and policy development would be better addressed with the knowledge of the relation between CC and AMR. This chapter describes the importance of change in the climatic factors and explains these factors push up the AMR.

2.1 Mechanisms Linked to Climate Change and AMR Spread

2.1.1 Changes Derived due to High Temperature

In recent years, it has become clear that temperature is important in cellular, physiological, ecological, and evolutionary processes that

determine bacterial survival. Antibiotic-temperature linkages are investigated using three types of responses: physiological, genetic, and large-scale.

Latest studies relate the antibiotic resistance spread to the increase in temperature because bacterial duplication time is accelerated, thus multiplying the chance of mutations (Ibáñez et al., 2023). In warmer countries, where mean temperature is 10°C higher than the overall mean temperature in European countries, an increased rate of change of AMR by 0.33% per year for aminoglycoside -resistant *E. coli* and 0.55% per year for third-generation cephalosporin-resistant *E. coli* was observed. For fluoroquinolone-resistant *E. coli*, an increase of 0.57% per year was found after accounting for other recognized resistance drivers including antibiotic consumption and population density (Meinen et al., 2023).

2.1.2 Horizontal Gene Transfer and Expression of Resistant Gene

In the presence of increased temperature, the bacterial duplication time would be fastened and the horizontal transfer of genes (some of them related to antibiotic resistance) and infectivity would also thus increase. Temperature is one of the strongest drivers of bacterial reproduction and can also modulate aspects of horizontal gene transfer through which resistance genes can be exchanged (Ibáñez et al., 2023).

2.2 Extreme Events of Weather

Rising temperatures are strongly associated with flooding, population displacement, and overpopulation induced by storms and precipitation (Burnham, 2021).

2.2.1 Contamination of Water with Resistant Bacteria due to Flooding

Extreme weather events resulting in flooding that could strongly disrupt weak sanitation infrastructure, increase crowding in already crowded areas, and spread antibiotic resistance from dissemination of sewage, a known reservoir for antibiotic-resistance genes (Burnham, 2021). Sewage is another significant source of antibiotics in the aquatic environment, antibiotics enter into the water cycle as parent compounds as well as their metabolites, when they are partially metabolized and subsequently excreted (Allel et al., 2023). Nitrogen fertilizers increase antibiotic resistance and therefore, floodwater pollution by nitrogen fertilizers during severe flooding due to climate change would increase antibiotic resistance. Eutrophication, which can be worsened by flooding, increases antibiotic resistance and can lead to dissemination of resistant pathogens and antibiotic-resistance genes (Sun et al., 2020).

Instances linking catastrophic floods to AMR have been observed in Asia, where surface and groundwater samples were analyzed after a major flood event in Chennai, India, in December 2015. The floods contaminated wells with sewage, leading to elevated bacterial counts and chemical ion levels beyond recommended limits. Worryingly, bacteria found in the groundwater exhibited resistance to medically important antimicrobials, highlighting the third-generation cephalosporin ceftriaxone (Crook et al., 2003). Similar findings were observed in urban areas affected by hurricanes in North America. In August 2017, Hurricane Harvey, a Category 4 storm, inundated the Houston metropolitan area in the United States with rainfall equivalent to an entire year's worth, causing severe flooding in numerous wastewater treatment plants and damaging thousands of homes. Scientific reports have shown that AMR genes were more prevalent in samples collected shortly after the flooding compared to those taken much later (Moniruzzaman et al., 2023).

2.2.2 The Link between drought and Increased Antibiotic Concentrations in Water Sources

Furthermore, extreme weather events can cause drought, which, along with food deprivation and a decrease in the healthcare system, increases the chance of acquiring antibiotic-resistant enteric bacteria (Reddy et al., 2022). Interestingly, diarrheal pathogens such as Campylobacter, Salmonella, and cholera survive better in warmer temperatures, explaining the recent re-emergence of these diarrheal infections (Cambaza et al., 2019). Food and water scarcity are closely related, which may lead to poorer nutrition in addition to an increase in diarrheal illnesses. Malnutrition, overcrowding, and inadequate sanitation all increase a child's risk of contracting antibiotic-resistant enteric infections (Crook et al., 2003). This inevitably results in more severe diarrhea and increased fatality rates, especially if antibiotic resistance increases and prevents appropriate medication from being administered (Garoy et al., 2019).

2.2.3 The Spread of Resistant Microbes through air by Hurricanes

The role of hurricanes is very significant in the spreading of AMR microbes. The floods caused by hurricanes produce a mixture of untreated wastewater, agriculture runoff and natural water. This could contaminate the drinking water sources and produce AMR (Swift et al., 2018). The overwhelmed wastewater treatment facilities and runoff from livestock farms and aquaculture could further increase the magnitude of AMR (Zdanowicz et al., 2020). High winds have the potential to contaminate the natural water bodies. It could be done by the aerosolization of resistant bacteria. It can also displace soil particles having resistant bacteria. The hurricanes also displace populations of humans and animals and these results in an increased interaction of human, animal and environment (Meyer et al., 2014).

2.3 Changes in the Ecosystems

2.3.1 The Relationship between Wildlife Habitat Alteration and an Increased Risk of AMR Transmission

When the habitats of wildlife animals are disturbed due to CC, the wildlife would have more chances of contact with humans and domesticated animals (Swift et al., 2018). In this way, the resistant bacteria would get a chance to share between animals and environment (Reddy et al., 2022). Vittecoq et al. (2016) suggest that the habit losses such as the deforestation, urbanization and the expansion of agriculture have the ability to introduce resistant genes in the ecosystem. The loss of habitats of wildlife animals force them to migrate. It would also facilitate the dispersal of resistant bacteria. This stressed condition also compromises the immunity of wildlife animals. It would make then susceptible for the colonization of resistant bacteria (Meyer et al., 2014).

2.3.2 Risk of the Migration of Resistant Bacteria with the Migration of Carrier Animals

The migratory carrier animals play a major role in the dispersal of resistant bacteria. The resistant bacteria get a chance to spread in various geographical regions (Vittecoq et al., 2016). The migratory birds, fish and other animals would act as reservoirs of resistant bacteria. Their migration could disperse these pathogens to new locations (Swift et al., 2018). The stopover points in their migratory tracks have to potential to spread these pathogens in other animals because at these points the animals had a close contact with other species (Meyer et al., 2014).

2.4 The Link between Soil and Agricultural Practices

2.4.1 Alteration of Soil Microbiota and the AMR Gene Pool

The alteration in the composition of soil microbiota occurred due to CC. It influences the AMR gene pool due to the change in quantity, diversity and mechanisms of transfer of AMR genes (ARGs) in the soil (Henriot et al., 2019). The soil is a natural reservoir of antibiotics and ARGs. But more antibiotics got a chance to be added through manure, irrigated water and runoffs (Lu et al., 2019). It would exacerbate the prevalence and spread of these genes. The climate change-induced factors like the altered precipitation patterns, temperature fluctuations and salinity changes have the potential to significantly modify the soil microbial communities (Kim et al., 2010). For example, the salinity in beach soils shapes the distribution of the soil resistome. The changes in the rhizosphere could increase the dissipation of ARGs. Furthermore, the landfills could act as significant reservoirs for antibiotics and ARGs (Kathi, 2019).

2.4.2 How Climate Stress could Intensify Agricultural Practices?

In response to climate stress, sometimes, farmers need to intensify the agricultural practices such as the use of manure and increased livestock farming. The manure of livestock used for this purpose to enhance soil fertility (Kim et al., 2010). It introduces antibiotics coming with the manure into the soil that increases the abundance and transfer of resistance genes. Intensive livestock farming also contribute to the groundwater contamination with antibiotics (Lu et al., 2019). The continuous discharge of these compounds into soil and water systems extends their bioavailability. These practices would alter the microbial communities of soil and promote the persistence and dissemination of ARGs (Kathi, 2019).

3. How could Climate Change Boost Antimicrobial use?

3.1 The link of Rising Infectious Disease Incidences and Climate Conditions

The infectious diseases incidences are raising due to climate change are due to an increase in the AMR (Henriot et al., 2019). Because it creates conditions that favor the spread of infections and the misuse of antibiotics. Climate change shifts the distribution and behavior of disease vectors like mosquitoes and ticks, and it also promotes the emergence of new pathogens (Yarzábal et al., 2021). Warmer temperatures, flooding, and extreme weather events create a stress on both animal and human populations that leads to a higher incidence of infections. In its response the antibiotics are often overprescribed, either as a precautionary measure or to treat diseases that are more difficult to diagnose (McEwen et al., 2018). This misuse accelerates the development of resistant bacteria. Moreover, the changes in land use, urbanization and agricultural practices are linked to CC. They can introduce antimicrobial-resistant bacteria into the environment and increasing the risk of resistance across populations. This interaction between rising infectious diseases and climate change thus creates a vicious cycle that would exacerbate the AMR crisis (Mareş et al., 2020).

3.2 An Increased Dependence on Antibiotics

The increased dependence on antibiotics in human and veterinary medicine has significantly contributed to the rise of antimicrobial resistance (AMR) due to several interconnected factors (Yarzábal et al., 2021). Overuse and misuse of antibiotics, for example prescribing them for viral infections in humans and veterinary medicine or their use for growth promotion and prophylaxis would create a selection pressure. It would allow the resistant microbes to survive and proliferate (Holzbauer et al., 2016, Mareş et al., 2020). The resistant strains of microbes could also spread through foodborne pathogens, environmental contamination from animal waste and horizontal gene transfer among microbes. This could further be amplified by the global trade of animal products and human travel (McEwen et al., 2018). The frequent use of broad-spectrum antibiotics disrupts beneficial microbiota. It would enhance the survival of resistant pathogens. The inadequate diagnostic practices and reliance on empirical treatments would also exacerbate the issue. Additionally, the unmetabolized antibiotics in waste streams could also contribute to resistance in environmental microbes (Holzbauer et al., 2016).

3.3 The Prophylactic use of Antibiotics in Livestock

The prophylactic antibiotics use in livestock which involves the administration of antibiotics to healthy animals to prevent disease rather than to treat existing infections. It contributes significantly to AMR (Holzbauer et al., 2016). This practice is very common in industrial farming where the antibiotics are often used routinely to prevent illness in overcrowded and unsanitary conditions or to promote growth in healthy animals. When antibiotics are used in such a way, the bacteria are exposed to sub-lethal doses (Singh et al., 2013). These antibiotics do not kill them but can select for resistant strains. These resistant bacteria can then multiply and spread, either within the livestock population (Mareş et al., 2020). They also spread to humans through direct contact, consumption of contaminated meat, or through environmental transmission. With time as these resistant pathogens accumulate, they would pose a serious threat to both veterinary and human medicine. The presence of antimicrobial-resistant genes in the livestock environment could spread to other bacteria, thus further exacerbating the AMR crisis (Holzbauer et al., 2016, McEwen et al., 2018).

4. Evidences of AMR Outbreaks in Human Populations due to Climatic Conditions

Climate-driven antimicrobial resistance (AMR) outbreaks in human populations are increasingly recognized as a public health threat due to the interplay between environmental factors, microbial evolution, and human activity (Singh et al., 2013). Here are some examples and mechanisms illustrating this phenomenon (Table 1):

Fable 1: Human Histor	y outbreaks of AMR	microbes due	to Climate Change
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Sr.	Examples of	History	Climatic Cause	Mechanism	Reference
No.	Outbreaks of AMR in				
	Humans				
1	Vibrio spp. Infections	In 2014, a Vibrio vulnificus outbreak	Unusual warm	This bacterium thrive in the warmer	(Yu et al., 2018)
		occurred along the Swedish coat.	summer	water and infect swimmers through	
				open wounds or by ingestion	
2	Methicillin-Resistant	In 2005, crowded living conditions	Climate induced	Hurricanes disrupt healthcare	(Garoy et al.,
	Staphylococcus	in shelters and compromised	natural disaster:	infrastructure, increase human-to	2019)
	aureus (MRSA)	hygiene led to an increase in skin	Hurricane	human contact and create	
		and soft tissue infections caused by		environments where resistant bacteria	
		MRSA.		spread rapidly.	
3	Salmonella	During heat waves in Europe in	Improper food	Elevated temperatures promote	(Crook et al.,
	Outbreaks	2000 the outbreaks of Salmonella	storage under high	bacterial growth in food, increasing the	2003)
			temperatures	risk of exposure to resistant strains.	
4	AMR in Flood-	In Bangladesh, recurrent flooding	Contamination of	Floodwater spreads resistant bacteria	(Moniruzzaman
	Affected Populations	has been associated with outbreaks	water sources.	from livestock farms, healthcare	et al., 2023)
		of multidrug resistant Escherichia		facilities and untreated sewage into	
		coli and other enteric pathogens.		drinking water supplies.	
5	Tuberculosis (TB) in	In sub-Saharan Africa, where	Droughts	Climate change drives migration and	(Kalu et al.,
	Post-Drought Areas	overcrowded conditions contribute		urbanization, facilitating the spread of	2015)
		to the spread of multidrug resistant		drug resistant pathogens in densely	
		TB (MDR-TB).		populated areas.	
6	Cholera Outbreaks	In Mozambique (2019), a cholera	Cyclone Idai.	Extreme weather events cause the	(Cambaza et al.,
	after Extreme	outbreak that included strains		collapse of infrastructure allowing the	2019)
	Weather Events	resistant to tetracycline and other		mixing of antibiotic resistant bacteria	
		antibiotics.		through waterborne pathways.	
7	Klebsiella	In Italy, heat waves have been	Increased weather	Heat stress during extreme weather	(Henriot et al.,
	pneumoniae in	correlated with increased hospital	temperature	conditions may promote the	2019)
	Hospitals After Heat	admissions for infections caused by		transmission of resistant pathogen.	
	Waves	carbapenem-resistant Klebsiella			
		pneumonia.			

5. Evidences of AMR outbreaks in livestock and aquaculture due to climatic conditions

Below are examples and mechanisms (Table 2) illustrating how climate-driven AMR outbreaks affect these sectors:

7. One Health Perspective

7.1 The Interconnection of Human, Animal and the Environment in the AMR Dynamics

AMR exemplifies the complex interaction between humans, animals and the environment. The widespread use and misuse of antimicrobial drugs in the human healthcare, veterinary medicine and agriculture fuels the emergence of resistant microbes (Henriot et al., 2019). These resistant organisms can easily be transferred between species and environments (Shah et al., 2016). It creates a shared risk for all sectors. Antibiotics and resistant microbes when released into the environment through wastewater, animal manure and agricultural runoff act as reservoirs, they could re-enter human and animal populations through contaminated water, food or direct contact (Louis et al., 2005). The food chain further amplifies this interconnectedness because the resistant bacteria from livestock can reach humans through meat and dairy products. To Address AMR, it requires a holistic One Health approach that would integrates human, animal and environmental health to mitigate shared risks effectively (Mursalim et al., 2022, Mzula et al., 2019).

7.2 Complications of One Health Interventions due to Climate Change

The climate change significantly complicates the efforts need to address AMR within a One Health framework (Cambaza et al., 2019). Factors such as rising global temperature, changing weather pattern and extreme climatic events are constantly creating such conditions that favor the survival and proliferation of resistant pathogens and their vectors (Skarżyńska et al., 2020). These changes alter the distribution of hosts and pathogens. It would lead to the emergence of new disease dynamics that challenge existing antimicrobial stewardship measures (Singh et al., 2013). Additionally, the stress induced by the climate on healthcare and veterinary systems that is further worsen with resource scarcity, undermines the enforcement of proper antibiotic use and infection control (Brightling et al., 2009). In agriculture, food insecurity due to climate change can encourage the farmers to excessively use antimicrobials to sustain livestock production. It would further exacerbate the resistance. The scarcity of clean water that is critical for hygiene and sanitation would strengthen the risks of pathogen spread and contamination. It would complicate the intervention strategies aimed at AMR mitigation (Reddy et al., 2022).

7.3 A Unified Global Approach is needed to Mitigate AMR

Addressing the dual threats of AMR and climate change necessitates a unified global approach. AMR transcends through borders with

resistant pathogens and genes. It spread through international travel, trade and environmental pathways (Ruhoollah at al., 2021). It makes the coordinated actions essential. A global strategy enables the pooling of resources, making of harmonized policies and integrated surveillance systems that could monitor AMR trends and climate impacts in real time (Scicchitano et al., 2024). It also ensures the equitable distribution of financial, technological and human resources. This would allow the low-income and climate vulnerable regions to strengthen their healthcare and veterinary systems (Mzula et al., 2019). Harmonizing antimicrobial use guidelines and waste management practices across nations promotes the consistency and it also amplifies the impact of interventions (Singh et al., 2013). Furthermore, global collaboration could foster the innovation in research and development for alternative treatments, diagnostics and vaccines. It would provide scalable solutions to combat AMR amidst climate related challenges (Kalu et al., 2015).

<u>Cn</u>	Examples of Outbrooks	History	Climatic	Machaniam	Deference
51. N-	examples of Outbreaks	History	Cimiatic	Mechanism	Reference
NO.	of AMR in livestock and		Cause		
	Aquaculture				<u> </u>
1	Vibrio spp. Outbreaks in Aquaculture	In shrimp farms along the coasts of Southeast Asia, the outbreaks of <i>Vibrio</i> <i>harveyi</i> and <i>Vibrio parahaemolyticus</i> . These pathogens are often resistant to tetracyclines and other antibiotics that are widely used in aquaculture.	f Warming o ocean . temperatures	Rising sea temperatures create optimal conditions for Vibrio spp. proliferation, leading to higher antibiotic use in aquaculture and subsequent selection of resistant strains.	(Liu et al., 2023)
2	AMR Salmonella in Poultry During Heat Waves	In the United States, an increase in multidrug resistant Salmonella outbreaks occurred in poultry farms.	a Prolonged a heat waves	Heat stress weakens the immune response of birds. It makes them more susceptible to infections. This often results in overuse of antibiotics, which selects for resistant strains of pathogens.	(Punchihewage- Don et al., 2022)
3	<i>E. coli</i> Outbreaks in Dairy Cattle Post-Flooding	In South Asia, the outbreaks of multidrug-resistant <i>Escherichia coli</i> in dairy cattle were observed.	f Heavy monsoons and flooding	Floodwaters spread antibiotic residues and resistant bacteria from livestock manure into the environment.	(Shah et al., 2016)
4	Aeromonas spp. in Freshwater Aquaculture	Freshwater fish farms in Africa and South Asia have experienced outbreaks of <i>Aeromonas hydrophila</i> resistant to sulfonamides and fluoroquinolones.	l Elevated s water o temperatures	Warmer water temperatures encourage the growth of pathogenic bacteria, which are already exposed to antibiotics in aquaculture systems.	(Mursalim et al., 2022, Mzula et al., 2019)
5	<i>Streptococcus</i> in Nile Tilapia Farms	In tilapia farms , outbreaks of <i>Streptococcus iniae</i> resistant to macrolides occurred.	f Unusual high water temperatures	Stress induced by suboptimal water temperature fluctuations increases disease prevalence and antibiotic use.	(Mzula et al., 2019)
6	Mastitis in Cattle During Droughts	In Australia, increased cases of mastitis caused by resistant <i>Staphylococcus</i> <i>aureus</i> were observed.	s Prolonged s droughts	Water scarcity and poor hygiene practices in cattle farms increases the bacterial infections and reliance on antimicrobials.	(Brightling et al., 2009)
7	Parasitic Infections in Goats and Sheep Post- Floods	In the regions of Pakistan and India, post-flood conditions have increased the incidence of <i>Haemonchus contortus</i> infections in small ruminants. There are reports of its resistance to commonly used anthelmintics.	, Floods G	Floods disrupt grazing patterns, forcing animals into confined spaces where parasites spread easily. This encourages the overuse of antiparasitic drugs.	(Ruhoollah at al., 2021, Singh et al., 2013)
8	AMR Pathogens in Intensive Pig Farming	In Europe, there was a spread of resistant <i>Actinobacillus</i> <i>pleuropneumoniae</i> in intensive pig farms.	f Warmer 5 winters 5	Warmer conditions alter pathogen survival and transmission dynamics. It potentially increases the infections and antibiotic treatments.	(Scicchitano et al., 2024)
9	Antibiotic-Resistant <i>Edwardsiella tarda</i> in Fish Farms	Fish farms reported outbreaks of <i>Edwardsiella tarda</i> , a pathogen resistant to quinolones.	f Prolonged warm seasons	Elevated water temperatures facilitate pathogen growth and biofilm formation. It reduces the antibiotic efficacy and promote resistance.	(Algammal et al., 2021)
10	Campylobacter in Poultry Post-Storm Events	In the UK, <i>Campylobacter jejuni</i> resistant to fluoroquinolones was detected in poultry farms.	i Severe s storms	Storms and heavy rainfall redistribute resistant bacteria from contaminated water sources to poultry.	(Louis et al., 2005)

Table 2: livestock and Aquaculture History outbreaks of AMR microbes due to Climate Change

8. Policy Making and Future Research Directions

8.1 Coordination of International Efforts

• There should be established a unified global framework for antimicrobial use that would integrate sustainable practices and climate

adaptation strategies.

• There should be an encouragement of international agreements to regulate over-the-counter antibiotic sales and regulations should be made to promote sustainable agricultural practices.

• There should be the development of funding mechanisms to support low-income nations in building capacity for surveillance, infrastructure and education to promote AMR awareness.

• There should be a promotion of cross-sector collaboration between healthcare, agriculture and environmental departments under the One Health approach.

8.2 Sustainability of Agricultural Practices

• Transition from antibiotic dependent farming to sustainable practices should be considered. For example, the use of probiotics, vaccines and improved animal husbandry techniques.

• Strategies should be made to implement the effective manure management systems. For example, composting and biogas production to reduce environmental contamination by resistant bacteria.

8.3 Enhancement of a Global Surveillance System

• A robust surveillance system should be made that is capable to integrate climate data to monitor and address threats linked to climate.

• The provision and education of standardize protocols and diagnostic tools globally to facilitate real time data sharing on the development of resistance patterns and pathogen prevalence.

• An international partnership should be established to create a comprehensive database that is a combination of human, animal and environmental health information.

8.4 Key Gaps in the Understanding of Climate and AMR Nexus

There is a need to research how climate variables influence the dynamics of AMR.

• There is a need to study the role of ecosystems, for example the soil and rivers acting as reservoirs for resistance genes and antibiotic residues.

There is a need to conduct long-term and globally coordinated studies in order to predict the impact of climate change on AMR patterns.

8.5 Interdisciplinary Research

• There is a need to foster the collaboration among climate scientists, microbiologists and public health experts in order to address the climate-AMR nexus.

• There is a need to investigate the effects of climate-induced phenomena, for example the flooding and droughts on the transmission of AMR in different ecosystems.

There is a need to promote the interdisciplinary education to equip the researchers with the skills in order to address this multifaceted issue.

8.6 Emerging Technologies

• There is a need to utilize the advanced genomic tools, for example the metagenomics and CRISPR, in order to analyze the resistance genes in different dynamic environments.

There is a need to leverage the machine learning and AI for the prediction of modeling of AMR trends.

• There is a need to explore the nanotechnology to target the antimicrobial agents and vaccines in order to reduce reliance on traditional antibiotics.

Conclusion

Climate change (CC) significantly exacerbates the spread of antimicrobial resistance (AMR) by the alteration of ecosystems, disruption of microbial balances, and acceleration of the transfer of resistance genes in humans, animals, and the environment. Factors, such as global warming, extreme weather events, and shifts in agricultural practices would create certain conditions that would favor the survival and spread of resistant pathogens. This makes AMR a growing threat in a warming world. This threat underscores the need to view climate change not just as an environmental crisis but also as a critical driver of the public health challenge. To address this, several adaptation measures such as the establishment of a sustainable farming with an improved waste management protocol, and a robust surveillance system must be integrated into the national and global AMR action plans. The requirements to tackle the dual challenge of climate change and AMR are the coordinated global cooperation between governments, researchers, policymakers, and industries across borders and disciplines to develop unified and scalable solutions. Only a shared commitment and collective action can safeguard the health of humans, animals, and the environment for future generations.

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