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Convergence Crises: Climate Change as an Accelerant of the Global Antibiotic Resistance Crisis

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ABSTRACT

Background. Global health security is seriously threatened by syndemic created by antibiotic resistance and climate change, each crisis exacerbating the other.

Methodology. This review collected data from peer-reviewed literature published between 2000 and 2025 on the intersection of climate change and Antimicrobial Resistance (AMR). Data was extracted for climate drivers, resistance mechanisms health outcomes, and geographical patterns, with findings synthesized narratively.

Results. The feedback loop (vicious cycle) disproportionately impacts vulnerable populations and pushes healthcare systems towards collapse while reducing the efficacy of advanced medicines.

Conclusion. The study argued that the climate-AMR nexus necessitates a paradigm shift from independent interventions towards integrated "One Health" policies. Transcending this cycle requires urgent, synergistic efforts that link climate change mitigation with enhanced AMR stewardship, new drugs, and effective global surveillance. A coordinated response to this interconnected crisis is urgently needed; if the relevant measures are not taken timely, foreseeable future risks serious weakening of environmental protections.

Keywords: antibiotic resistance, climate change, feedback loop, global health, one health, Vicious Cycle

Highlights

- Antibiotic resistance accelerated by climate change by 14% by 1^0C rise in temperature.
- Flood, drought, and heat, creating a self-sustained vicious cycle with antibiotic resistance.
- One health policy required urgently to break the climate-AMR feedback loop.

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1. INTRODUCTION

Human-induced climate change, characterized by rising temperature and extreme weathers, is a basic global threat [1]. The study comprehensively reviewed global climate change impacts. Furthermore, it also reported that rise in temperature and climate change directly contributes to spread infectious diseases burden, forcing to increase antibiotic use. Resultantly, this drives microbial resistance rate across multiple ecosystems. Climate change affects agricultural systems beyond crops and livestock management (Figure 1). Antibiotic use in human beings and livestock contributes to antibiotic resistance, contaminating the environment and food sources [2]. Their widespread use has lowered mortality rates. However, their extensive usage has led to antibiotic resistance, posing significant challenges to healthcare. Sir Alexander Fleming's Nobel-winning penicillin discovery extended life expectancy by three decades. His warnings against antibiotic misuse were disregarded, leading to rising drug-resistant bacteria. Consequently, once-treatable infectious diseases resurfaced, posing severe health threats [3,4].

In the upcoming decades, an increase in global temperature is expected due to global warming [5]. Moreover, temperature affects bacterial survival, spanning cellular, physiological, ecological, and evolutionary aspects. Responses occur at various biological levels, including physiological and genetic. Physiological changes due to temperature alterations enhance antibiotic tolerance and persistence. Heat stress induces mutations, promoting antibiotic resistance and its spread globally [6]. Supporting this relationship, Zeng et al. [64] examined Antimicrobial Resistance (AMR) surveillance data collected from 31 Chinese provinces (2014-2020). It was reported that each 1°C rise in annual average temperature was associated with a 10.7% increase in the detection rate of carbapenem resistant *K. pneumoniae.* This suggests a potential climate-AMR link, the observational nature of the data precludes causal conclusions.

Beyond genetic makeup, bacteria can gain tolerance against antibiotics by slowly downing the growth temporarily under antibiotic stress [8] and persistence where subpopulation survive with antibiotics in a dormant state**.** Environmental factors including temperature and pH further modulate antibiotic efficacy [9]. Its impact extends to medical procedures requiring efficient antibiotic support, such as organ transplantation and invasive surgeries. Lack of effective antibiotics heightens risks in hospitals, leading to increased morbidity, mortality, and challenges in managing infections. World Health Organization (WHO) warns of advanced procedures becoming risky or impossible without effective antibiotics, exacerbating healthcare complications [10].

Antibiotic resistance and climate change are interconnected crises that multiply the threats to human health and ecosystems. Climate change accelerates the spread of infectious diseases [16], which may increase antibiotic use and as a result contribute to resistance [62]. Geographical range of disease vectors, such as ticks and mosquitoes expand due to rising temperatures [16], potentially increasing antibiotic demand. Extreme weather events including droughts, floods, and hurricanes can disrupt healthcare facilities. This complicates infection control and provides favorable conditions for the spread of antibiotic-resistant pathogens [11]. The Sustainable Development Goals (SDGs) promote a framework to mitigate the dual challenges. SDG 13 (climate action)

directly targets the drivers of resistance by promoting emission reductions and health system resilience. At the same time, SDG 3 (good health and well-being) focuses to control antibiotic resistance as a pillar of healthcare. Information-based integrated polices are essential to minimize the dual threat [12].

2. ANTIBIOTIC RESISTANCE: A GLOBAL HEALTH CRISIS

Antibiotic resistance is a global health crisis, causing an estimated 1.27 million deaths globally every year, with projections suggesting severing economic and clinical unintended consequences by 2050 if unattended [13].

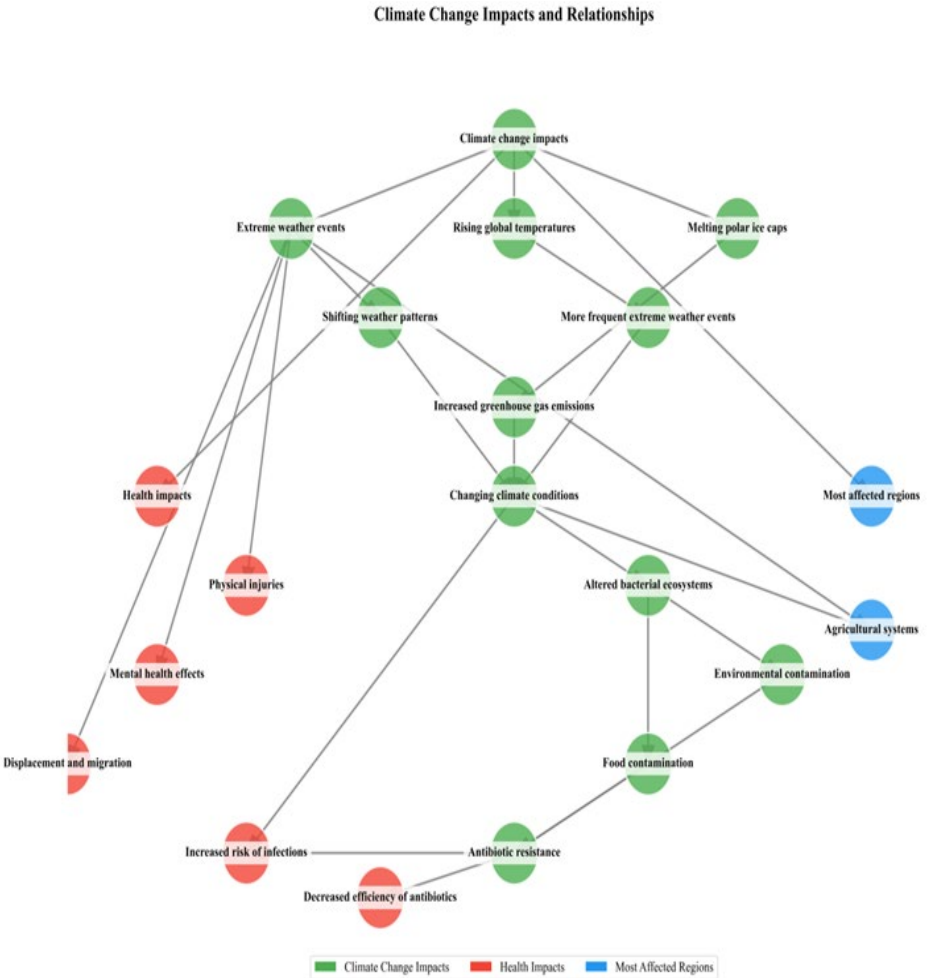


Figure 1. The Interconnected Pathways Linking Climate Change Impacts, Including Increased Greenhouse Gas Emissions, Extreme Weather Events, and Changes in Agricultural Systems, to Antibiotic Resistance, Emphasizing its Central Role in the Health Consequences of Climate Change

Table 1. Environmental Factors, Antibiotic Resistance, and Health Impacts Across Global Regions

Country/ Region	Climatic Parameters	Resistance Patterns	Health Impacts	References
United States	Humid subtropical regions	Methicillin-resistant *Staphylococcus aureus* (MRSA)	Increased hospital-acquired infections	[22,23]
Zambia	Tropical savanna climate regions	Extended-spectrum beta-lactamase (ESBL) producing *Enterobacteriaceae*	Respiratory infections	[24]
India	Tropical monsoon climate regions	Metallo-B-lactamase 1 and Cephalosporin Resistance Genes Among Carbapenem-Resistant *Enterobacteriaceae*	Rise in sepsis-related mortality	[25]
China	Humid sub-tropical, subtropical monsoon, humid continental regions	Fluoroquinolone-resistant *Escherichia coli*	Increased urinary tract infections (UTIs)	[26]
Russia	Subarctic and tundra regions	Vancomycin-resistant *Enterococci* (VRE)	Higher rates of nosocomial infections	[27]
Australia	Arid and temperate regions	Multidrug-resistant *Acinetobacter* baumannii	Prolonged hospital stays due to infections	[28,29]
Bangladesh	Tropical monsoon, tropical savanna and humid subtropical	Chloramphenicol-resistant *Salmonella typhi*	Rising cases of typhoid fever	[30]
Kuwait	Hot desert climate	Penicillin-resistant *Streptococcus pneumoniae* (PRSP)	Increased incidence of pneumonia and prevalence of (PRSP) in upper respiratory tract	[31]
Japan	Humid subtropical climate	Methicillin-resistant *S. aureus* (MRSA) and fluoroquinolone-resistant *E. coli*	Deaths due to blood stream infection	[32]
South Africa	Arid, temperate, and subtropical	Extended-spectrum beta-lactamase (ESBL) producing *Klebsiella pneumoniae*	Higher mortality rates in ICU patients	[33]
Middle East and North Africa	Hot desert and hot semi-arid regions	Multidrug-resistant *Pseudomonas aeruginosa*	Increased risk of postoperative wound infections and life-threatening infections	[34]
United Kingdom	Temperate oceanic climate	Methicillin-resistant *Staphylococcus aureus* (MRSA)	Elevated rates of bloodstream infections	[35]
Egypt	Hot desert climate	Carbapenem-resistant *Acinetobacter baumannii*	Surge in ventilator-associated pneumonia	[36]
Nepal	Monsoon influenced humid subtropical	Extended-spectrum beta-lactamase (ESBL) producing *Escherichia coli*	Rising incidence of UTIs	[37]
Senegal	Tropical savanna and arid desert	Extended-spectrum beta-lactamases producing *Enterobacteriaceae*	Increased bloodstream infections and UTIs	[38]

2.1. Mechanisms and Causes of Antibiotic Resistance

The mechanisms by which the bacteria can be enabled to evade the antibiotic effects, and, thus, the antibiotic resistance arises, are not limited to genetic mutations, horizontal gene transfer, and the over expression of efflux pumps [14]. The research confirmed that efflux pumps alone can confer resistance to multiple antibiotic classes simultaneously. Moreover, temperature extremes up-regulate these pumps, linking climate change directly to antibiotic resistance mechanism at molecular level. Additionally, extreme weather conditions, such as floods compromise sanitation and promote antibiotic misuse which leads towards the microbial resistance [15]. Rise in temperature due to climate change supports the survival and growth of *Vibrio cholera* [16], *Salmonella s*pp. *and campylobacter* spp. [17], *E.coli*, *Staphylococcus aureus, klebsiella pneumoniae* [18], *Candida auris* [19], and *Plasmodium falciparum*[20], pose unprecedented threat to healthcare systems.

2.2. Prevalence of Antibiotic-resistant Bacteria

The presence of antibiotic-resistant bacteria is common in both developed and developing countries, with resistance levels varying significantly across regions because of the patterns of antibiotic use and the healthcare infrastructure. However, emerging resistant pathogens have become more prevalent over recent decades, severely compromising the ability to treat previously-treatable infections (Table 1). This makes many first line antibiotics less effective, forcing to use last-resort antibiotics with higher cost and side effects [21].

2.3. Trends and Implications

2.3.1. Climate Resistance Correlation.

- The data in the table revealed that areas with high humidity (Zambia, Bangladesh, and Japan) showed dominance of extended spectrum beta-lactamase (ESBL) producing Enterobacteriaceae and Methicillin resistant Staphylococcus (MRSA), linked to enhanced plasmid stability and biofilm formation in moist environment.
- Hot climate/arid mainly including Kuwait and Egypt favor Multi Drug Resistant (MDR) *Pseudomonas aeruginosa* and carbapenem resistant *Acinetobacter baumannii* due to gene activation under the stressing environment.
- Cold climate, including mainly Russia, exhibits Vancomycin-resistant *Enterococci*, may be due to indoor healthcare load during winter season.

2.3.2. Health Impact Patterns.

- In India, Nepal, and Spain (Tropical regions), ESBL pathogens correlate with UTIs.
- In temporal zones including US, UK, and Japan, bloodstream infections are connected with hospital-associated MRSA/VRS.

Penicillin-resistant *Streptococcus pneumoniae and Klebsiella* pneumoniae respiratory pathogens surge in arid transitional climate (South Africa and Kuwait)

2.3.3. Climate Change Projections. Warming may expand range of MDR strains northward, and intensified monsoon could intensify ESBL-linked species in

South Asia [39–42].

2.4. Vicious Cycle Model for Climate Change and Antibiotic Resistance

The Vicious Model describes how climate change supports the spread and persistence of antibiotic resistance. Each climate driver triggers cascade of linked effects including environmental, biological, and socio-economic that mutually reinforce each other in a self-perpetuating loop (Figure 2). For instance, rising temperatures speed up bacterial mutation rates and horizontal gene transfer, as demonstrated by external studies [6,43]. The study experimentally explained that a 4-degree Celsius increase in temperature speeds up the evolution of antibiotic resistance in E.coli by increasing plasmid conjugation frequency. Even moderate warming directly increases the genetic mechanism underlying antibiotic resistance. In addition, flooding is suspected of facilitating the spread of antibiotic resistance genes. While, drought may concentrate resistant bacteria and pollutants within the limited water resource [4, 5]. On the other hand, agriculture increases reservoirs for resistant genes using antibiotics and runoff [45]. These activities not only enhance the occurrence of resistant infections and rice dependency on antibiotics but also impose economic and health costs that undermine the ability of communities and health systems to adapt. This makes them more vulnerable to climate shocks [46]. Climate change increases global antibiotic resistance by 2.4%. The data given in Table 2 provides evidences to establish a close relationship between these two threats. Break of this cycle is essential to reduce the development of antibiotic resistance as well as to prevent healthcare systems and economy. Research-based interconnected solutions are required to address these challenges [47,48].

The connection of climate change and antimicrobial resistance creates a self-sustained, reinforcing cycle instead of a linear path. For instance, floods are responsible for contaminating water bodies with farm waste and sewage and also damage infrastructures including healthcare facilities. Transfer of antibiotic resistant genes (blaCXT-M-15) among bacteria is accelerated by the contaminated environment. This condition also increases the frequency of waterborne diseases, especially in vulnerable communities. Furthermore, it also increases treatment costs, pressure on healthcare system, and economy; this completes the feedback loop.

This makes infrastructures, economy, and societies more vulnerable to future climate shocks and results in wastage of resources. As shown in Figure 2, each crisis enlarges the other which, in turn, decreases global health stability [44]. The study clearly reported that large scale flood events are involved in the dissemination of beta-lactamase genes across large geographical areas. This provides the evidence that climate-induced flooding introduces previously-unknown pathways for antibiotic resistance propagation beyond hospital setting.

2.5. Burden of Antibiotic Resistance on Economy Due to Climate Change

The rising threat of antibiotic resistance puts huge pressure on global healthcare systems, and climate change fuels this financial pressure. Treating resistant infections requires longer hospitalization, which incurs greater costs compared with treatable strains. This disproportionately affects vulnerable communities in climate-affected areas.

Table 2. Climate-antibiotic Resistance Vicious Cycle: Mechanism and Pathways

Step 1 Climate Drivers	Step 2 Direct Impact	Step 3 Mechanism for Antibiotic Resistance Amplification	Step 4 Economic/Health Consequences	Step 5 Feedback Loop	Evidence
Rising Temperatures	-Geographical range of vectors is expanding (mosquitoes). -Heat stress in hospitals	-Increased rate of bacterial mutation[6]. -Reported elevated rates of Plasmid conjugation in *E.coli, Klebsella*[50] -Carbapenem resistant *K. Pneumoniae* increased 14% per 1°C[7]	-Rise in previous rare infections (*Vibrio cholera* and fungal infections) -Increase in morbidity/mortality. -Increase in healthcare costs.	-Vulnerable populations are more at risk to next heatwave. -Loss to economy diverts resources from public health and climate adaptation technologies	[16]
Floods and Heavy Rainfall	-Mixing of sewage and agricultural runoff to freshwater sources. -Disruption of sanitation systems.	-Horizontal gene transfer of ARGs (blaCTX-M-15) in water [44]. -Distribution of antibiotic-resistant bacteria from hospitals and farms to environment.	-Spread of waterborne diseases (resistant *E.coli* and *Salmonella*) -Enhanced antibiotic use especially in displaced populations.	-Week and damaged infrastructure remain vulnerable to next disasters (floods etc). -Economic losses due to floods restrict investment in clean water and sanitation.	[11,44]
Drought	-Water shortages, contamination of water. -Impact on livestock health	-Presence of antibiotics and antibiotic-resistant bacteria scarce water sources. -Boost in antibiotic use in agriculture in stressed livestock to prevent diseases.	-More transfer of resistant infections in populations sharing the limited water. -Entrance of resistant pathogens to food chain	-Shortage of nutrients/poor, quality food, and water-borne illnesses impact community resilience. -Poverty increase due to economic loss in agriculture	[45]
Livestock Farming (as driver of both)	-Enhances antibiotic use. -Use of manure as fertilizer	-Selection of antibiotic-resistant bacteria in animal guts. -Presence of antibiotic-resistant bacteria in runoff and soil[47].	-Infections in humans due to the resistant bacteria (e.g. ESBL *E.coli).* -Contaminated environment	-Environmental contamination increases diseases burden in humans. -Emissions of methane (greenhouse gas) worsening climate change.	[2,50]

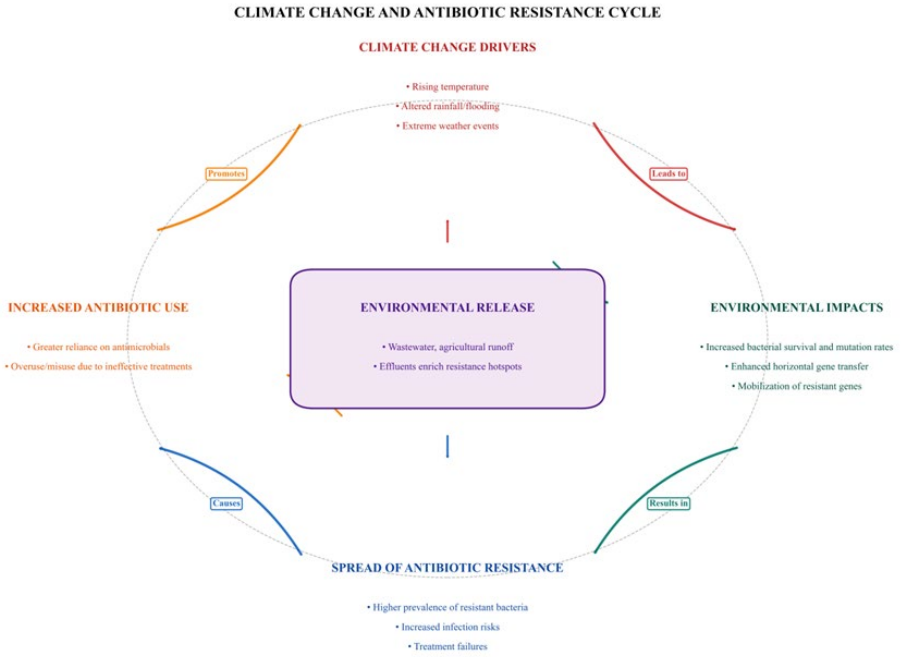


Figure 2. Antibiotic Resistance and Climate Change (The Vicious Cycle)

Economic burden escalates further due to lengthy treatments and additional medical complications. The development of new antibiotics to combat resistance further adds to the economic burden on healthcare systems and pharmaceutical companies [51–53]. In this study, the analysis of the US healthcare data revealed that treatment costs for antibiotic resistant illnesses have doubled since 2002 (exceeding 2 billion annually). Financial burden on patients in climate vulnerable regions drives repeated hospitalizations.

2.6. Twin Challenges of Climate Change and Antimicrobial Resistance: From Microbial Ecology to Global Policy

The transboundary nature of antibiotic resistance exacerbated by climate driven pathogen (Table 1) demands global cooperation, with governments, medical institutions, and pharmaceutical companies collaborating to develop innovative solutions [54]. Global Action Plan on antibiotic resistance promotes monitoring, scientific research, and equitable access to antibiotics, with recent amendments emphasizing monitoring the resistance in flood and drought prone regions [57]. Organizations, such as the European Centre for Disease Prevention and Control facilitate information sharing on emerging resistance patterns linked to extreme climates, such as ESBL outbreaks post-flooding. Despite these efforts, very few countries (about 30%) have aligned their policies on antibiotic resistance and climate change adaptation strategies, highlighting the need for binding targets [56].

Recent studies correlate warming with higher fluoroquinolones resistant *E.coli* in

tropical regions. An increase in the incident of post-surgical infections has also been reported due to methicillin-resistant *Staphylococcus aureus* in heat-stressed hospitals [57,58]. Rising temperatures supporting vector-borne disease increase antibiotic use and as a result the resistance. Deforestation also increases gene transfer, and communities with limited resources due to poor economy face the harshest tool. Therefore, timely collective action at global scale is required to reduce the impacts of these climate stresses [59]. For long-term benefits, bold steps are needed to shift from fossil fuel to renewable energy, encourage sustainable farming, connect human, animal, and environmental health under One Health concept at global scale [60]. Individual communities' action would not be fruitful, to achieve the targets, agreements at global scale are indispensable [53]. Partial or selective measures are no longer enough; only bold policies can answer these dual threats.

2.7. Engaging Stakeholders and Fostering Innovations and Research Frontiers in Addressing the Dual Challenges

Multi stakeholder strategy is required to efficiently manage interlinked crises of climate change and antibiotic resistance [61]. It can include evidence-based prescribing behaviors to reduce unnecessary use of antibiotics [62]. Compulsory reporting of antibiotic use should be implemented by policy makers. Furthermore, researchers should be encouraged and facilitated to hasten innovation in climate resilient therapy, that is, phase-based therapies and narrow spectrum antibiotics [63]. Through incorporation of climate-consciousness in antimicrobial resistance stewardship, the stakeholders can turn systemic weaknesses into opportunities for long-term health resilience [64]. Perfect storm, antibiotic resistance, and climate change come together in ways that risk undermining decades of medical innovation [59]. In the new scenario, drug-resistant microbes are adapting new means of transmission, prompting researchers to rethink entirely containment strategies. In the search of new ways to fight super bugs (multi drug resistant bacteria), scientists are turning to some unexpected sources, such as forests, plants, and marine sponges, as well as genetic engineering [52,59].

Real-time monitoring of antibiotic resistance is now possible with digital tools, and even prediction of emerging risks is also possible with the help of AI-based diagnostics. However, this alone is not the solution. There is also a need for sustainable development of antibiotics, to speed up the search of new treatment methods by developing effective international collaboration, such as CARB-X, and control on misuse of antibiotics in agriculture and pharmaceutical pollution by proper implementation of strict policies. It is not only the issue of public health but is also the test of our ability as to how effectively we join the science and economics to address the issue [44,53].

2.8. One Health, Climate Change, and Global Distribution Antibiotic Resistant Bacteria: A Multi-sectoral Environmental Threat

Resistant bacteria and antibiotic resistance use multiple pathways to enter the environment, including municipal and industrial wastewater, agricultural run-off, and improper medication disposal (Figure 3). The figure explaining the spread of contamination in water, soil, and air with airborne transmissions originated from agricultural, industrial, residential areas, and hospital air. Resistant genes develop

and spread in wastewater facilities and agricultural settings, then transfer through crop exposure and dust. This increases antibiotic resistance in different ecosystems and poses risk to food safety and microbiota [65]. Climate change acts as a booster by changing wind pattern and expanding wind storms. This makes possible the spread of air-borne resistant pathogens to long-distances. Vulnerable groups including immune-compromised population, children (under five), and elderly can face elevated health risks due to biological susceptibility and system inequities.

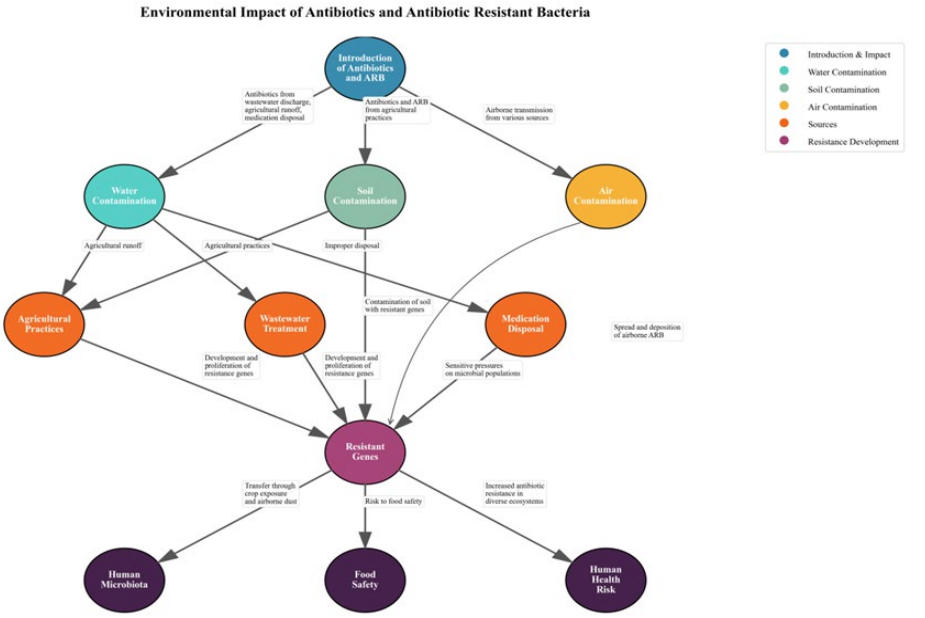


Figure 3. Pathways of Antibiotics and Antibiotic-resistant Bacteria in the Environment

One Health approach can be used to address the interconnected threats as described through a concept in Figure 4. This concept integrates human health, animal health, and environmental health through centralized surveillance, genetic monitoring, and data normalization at local, national, and global levels. Initiatives, such as Global Antimicrobial Resistance and Use Surveillance System and the European Surveillance Network support these efforts [60,53]. The study argued that antibiotic resistance is a global problem requiring coordinated integrated actions. Moreover, the study also provided evidence that new pathways develop due to the change in climatic conditions and the pathways transcend national borders. This makes One Health surveillance not optional but essential. However, many developing countries lack funding and trained staff, limiting surveillance capabilities [20,46]. Policy solutions aligned with Global Antimicrobial Action Plan and the Paris Agreement emphasize climate-smart agriculture, resilient healthcare systems, and global cooperation as essential to addressing the dual crises of antibiotic resistance and climate change [43].

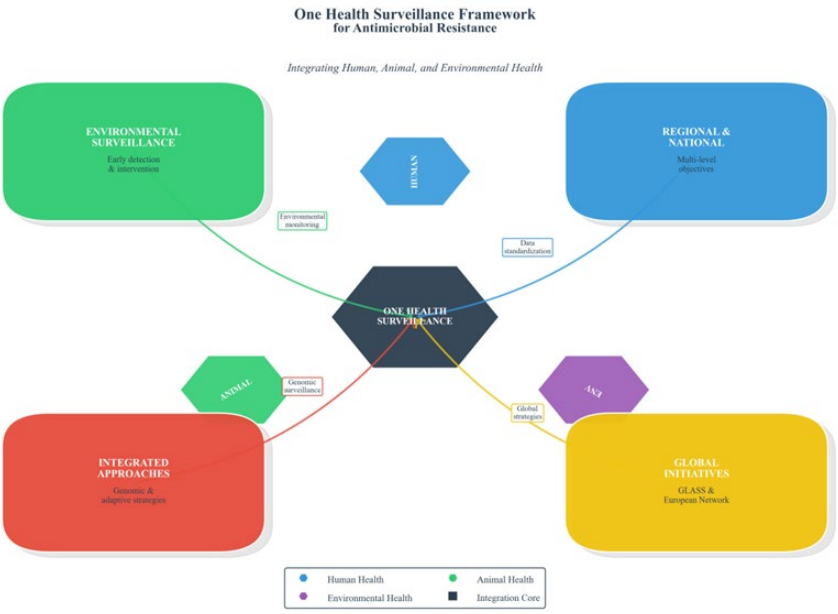


Figure 4. Global Surveillance Strategies and Collaborative Efforts to Combat Antibiotic Resistance

3. CONCLUSION

The synergetic effects of antibiotic resistance and climate change pose health threats that can undo years of medical achievements. The reviewed evidence suggested that an interconnected global approach is needed to address the growing issue instead of isolated actions. For this, i) the trans-boundary spread of AMR reported in this review supported the need of "One Health" surveillance system that should connect multi-sectoral data (climate, health and environmental monitoring) to predict and prevent antimicrobial resistance[63,43]; ii) climate resilience strategies should be integrated into antimicrobial resistance plans to prevent the healthcare systems and agriculture from climatic stress without increasing antibiotic use; as explained by the flood and drought-related transmission pathways given above[16,45]; iii) the gap in the antibiotic research, highlighted by the emergence of carbapenem resistance reviewed here, underscores the need of global fund to support research and development to evolve new antibiotics and rapid diagnostics systems[65,21]. Laws and regulations are equally important to prevent industries and farms from antibiotic pollution. International organizations should work together to align policies and responsibilities across sectors[56]. Finally, technologies, such as AI and IOT tools should be used to predict trends in antimicrobial resistance and to develop procedures for antibiotic use by real-time data analysis.

Author Contribution

Maqsood Ahmad: Conceptualization, investigation, formal analysis. **Faheem Nawaz:** methodology. **Anila Bahadur:** data curation,

resources. **Fouzia Bahadur:** writing, reviewing & editing. **Sadaf Aslam Ghori:** writing, reviewing & editing. **Hafiza Hina Irfan:** writing, reviewing & editing. **Imran Ali Sani:** data curation. **Sobia Faisal:** formal analysis. **Muhammad Farhan:** writing, reviewing & editing. **Syed Ali Raza:** writing, reviewing & editing.

Conflict of Interest

The authors have no financial or non-financial conflict of interest in the subject matter or materials discussed in the manuscript.

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Data Availability Statement

The data supporting the findings of this study is available within the manuscript.

Generative AI Disclosure Statement

The authors did not use any type of generative artificial intelligence (AI) software for this research.

REFERENCES

1. Abbass K, Qasim MZ, Song H, Murshed M, Mahmood H, Younis I. A review of the global climate change impacts, adaptation, and sustainable mitigation measures. *Environ Sci Pollut Res Int.* 2022;29(28):42539–42559. https://doi.org/10.1007/s11356-022-19718-6
2. Van Boeckel TP, Gandra S, Ashok A, et al. Global antibiotic consumption 2000 to 2010: An analysis of national pharmaceutical sales data. *Lancet Infect Dis.* 2014;14(8):742–750. https://doi.org/10.1016/S1473-3099(14)70780-7
3. Huemer M, Mairpady Shambat S, Brugger SD, Zinkernagel AS. Antibiotic resistance and persistence—implications for human health and treatment perspectives. *EMBO Rep.* 2020;21(12):e51034. https://doi.org/10.15252/embr.202051034
4. Talebi Bezmin Abadi A, Rizvanov AA, Haertlé T, Blatt NL. World Health Organization report: Current crisis of antibiotic resistance. *BioNanoScience.* 2019;9(4):778–788. https://doi.org/10.1007/s12668-019-00658-4
5. Sajjad W, Ilahi N, Haq A, et al. Bacteria populating freshly appeared supraglacial lake possess metals and antibiotic-resistant genes. *Environ Res.* 2024;247:e118288. https://doi.org/10.1016/j.envres.2024.118288
6. Sajjad W, Rafiq M, Din G, et al. Resurrection of inactive microbes and resistome present in the natural frozen world: Reality or myth? *Sci Total Environ.* 2020;735:139275. https://doi.org/10.1016/j.scitotenv.2020.139275
7. Wong C. Antibiotic resistance is a growing threat—is climate change making it worse? *Nature.* Published online January 8, 2024. https://doi.org/10.1038/d41586-023-04077-0
8. Sajjad W, Ali B, Niu H, et al. High prevalence of antibiotic-resistant and metal-tolerant cultivable bacteria in remote glacier environment. *Environ Res.* 2023;239(Pt 2):117444. https://doi.org/10.1016/j.envres.2023.117444
9. Kester JC, Fortune SM. Persisters and beyond: Mechanisms of phenotypic drug resistance and drug tolerance in bacteria. *Crit Rev Biochem Mol Biol.* 2014;49(2):91–101. https://doi.org/10.3109/10409238.2013.869543
10. World Health Organization. *Overcoming Antimicrobial Resistance.* World Health Organization; 2000. Accessed April 26, 2026. https://iris.who.int/items/ba46fa94-adda-42c8-b6d2-

a2253b79b776

11. Kouadio IK, Aljunid S, Kamigaki T, Hammad K, Oshitani H. Infectious diseases following natural disasters: Prevention and control measures. *Expert Rev Anti Infect Ther.* 2012;10(1):95–104. https://doi.org/10.1586/eri.11.155

12. Lee BX, Kjaerulf F, Turner S, et al. Transforming our world: Implementing the 2030 Agenda through Sustainable Development Goal indicators. *J Public Health Policy.* 2016;37(suppl 1):13–31. https://doi.org/10.1057/s41271-016-0002-7

13. Alara JA, Alara OR. An overview of the global alarming increase of multiple drug resistant: A major challenge in clinical diagnosis. *Infect Disord Drug Targets.* 2024;24(3):e250723219043. https://doi.org/10.2174/1871526523666230725103902

14. Blair JM, Webber MA, Baylay AJ, Ogbolu DO, Piddock LJ. Molecular mechanisms of antibiotic resistance. *Nat Rev Microbiol.* 2015;13(1):42–51. https://doi.org/10.1038/nrmicro3380

15. Lin D, Du S, Zhao Z, et al. Climate warming fuels the global antibiotic resistome by altering soil bacterial traits. *Nat Ecol Evol.* 2025;9(8):1512–1526. https://doi.org/10.1038/s41559-025-02740-5

16. Semenza JC, Menne B. Climate change and infectious diseases in Europe. *Lancet Infect Dis.* 2009;9(6):365–375. https://doi.org/10.1016/S1473-3099(09)70104-5

17. Sajjad W, Kang S, Yin X, et al. Depth-resolved transcriptional activity of antibiotic resistance genes in deep permafrost of the Qinghai–Tibet Plateau. *Commun Biol.* Published online June 30, 2026. https://doi.org/10.1038/s42003-026-10593-2

18. Kaba HE, Kuhlmann E, Scheithauer S. Thinking outside the box: Association of antimicrobial resistance with climate warming in Europe—a 30 country observational study. *Int J Hyg Environ Health.* 2020;223(1):151–158. https://doi.org/10.1016/j.ijheh.2019.09.006

19. Arora P, Singh P, Wang Y, et al. Environmental isolation of *Candida auris* from the coastal wetlands of Andaman Islands, India. *mBio.* 2021;12(2):e03181-20. https://doi.org/10.1128/mBio.03181-20

20. Chaves LF, Koenraadt CJM. Climate change and highland malaria: Fresh air for a hot debate. *Q Rev Biol.* 2010;85(1):27–55. https://doi.org/10.1086/650284

21. O'Neill J. *Tackling Drug-Resistant Infections Globally: Final Report and Recommendations.* Review on Antimicrobial Resistance; 2016. Accessed April 26, 2026. https://amr-review.org/sites/default/files/160518_Final%20paper_with%20cover.pdf

22. Rzymski P, Gwenzi W, Poniedziałek B, Mangul S, Fal A. Climate warming, environmental degradation and pollution as drivers of antibiotic resistance. *Environ Pollut.* 2024;346:e123649. https://doi.org/10. 1016/j.envpol.2024.123649

23. Klein EY, Sun L, Smith DL, Laxminarayan R. The changing epidemiology of methicillin-resistant *Staphylococcus aureus* in the United States: A national observational study. *Am J Epidemiol.* 2013;177(7):666–674. https://doi.org/10.1093/aje/kws 273

24. Blanco N, Perencevich E, Li SS, et al. Effect of meteorological factors and geographic location on methicillin-resistant *Staphylococcus aureus* and vancomycin-resistant enterococci colonization in the US. *PLoS One.* 2017;12(5):e0178254. https://doi.org/10.1371/journal.pone.0178254

25. Basikolo L. *Occurrence of Extended-Spectrum Beta-Lactamase-Producing Enterobacteriaceae and Bacterial Loads in Dust From Poultry Farms in Lusaka-Zambia* [doctoral thesis]. University of Zambia; 2023. Accessed April 26, 2026. https://dspace.unza.zm/handle/123456789/8502

26. Kalasseril SG, Krishnan R, Vattiringal RK, Paul R, Mathew P, Pillai D. Detection of New Delhi metallo-β-lactamase 1 and cephalosporin resistance genes among carbapenem-resistant Enterobacteriaceae in water bodies adjacent to hospitals in India. *Curr Microbiol.* 2020;77(10):2886–2895. https://doi.org/10.1007/s00284-020-02107-y

27. Zhao Q, Shen Y, Chen G, Luo Y, Cui S, Tian Y. Prevalence and molecular characterization of fluoroquinolone-resistant *Escherichia coli* in healthy children. *Front Cell Infect Microbiol.* 2021;11:e743390. https://doi.org/10.3389/fcimb.2021.743390

28. Makarov DA, Ivanova OE, Pomazkova AV, et al. Antimicrobial resistance of commensal *Enterococcus faecalis* and *Enterococcus faecium* from food-producing animals in Russia. *Vet World.* 2022;15(3):611–619. https://doi.org/10.14202/vetworld.2022.611-619

29. Gordon LG, Elliott TM, Forde B, et al. Budget impact analysis of routinely using whole-genomic sequencing of six multidrug-resistant bacterial pathogens in Queensland, Australia. *BMJ Open.* 2021;11(2):e041968. https://doi.org/10.1136/bmjopen-2020-041968

30. Moriel DG, Beatson SA, Wurpel DJ, et al. Identification of novel vaccine candidates against multidrug-resistant *Acinetobacter baumannii. PLoS One.* 2013;8(10):e77631. https://doi.org/10.1371/journal.pone.0077631

31. Mina SA, Hasan MZ, Hossain AKMZ, Barua A, Mirjada MR, Chowdhury AMMA. The prevalence of multi-drug resistant *Salmonella Typhi* isolated from blood sample. *Microbiol Insights.* 2023;16:e11786361221150760. https://doi.org/10.1177/11786361221150760

32. Mokaddas EM, Rotimi VO, Albert MJ. Implications of *Streptococcus pneumoniae* penicillin resistance and serotype distribution in Kuwait for disease treatment and prevention. *Clin Vaccine Immunol.* 2008;15(2):203–207. https://doi.org/10.1128/CVI. 00277-07

33. Tsuzuki S, Matsunaga N, Yahara K, et al. National trend of blood-stream infection attributable deaths caused by *Staphylococcus aureus* and *Escherichia coli* in Japan. *J Infect Chemother.* 2020;26(4):367–371. https://doi.org/10.1016/j.jiac.2019.10.017

34. Founou RC, Founou LL, Allam M, Ismail A, Essack SY. Whole genome sequencing of extended spectrum β-lactamase (ESBL)-producing *Klebsiella pneumoniae* isolated from hospitalized patients in KwaZulu-Natal, South Africa. *Sci Rep.* 2019;9:e6266. https://doi.org/10.1038/s41598-019-

42672-2

35. Al-Orphaly M, Hadi HA, Eltayeb FK, et al. Epidemiology of multidrug-resistant *Pseudomonas aeruginosa* in the Middle East and North Africa region. *mSphere.* 2021;6(3):e00202-21. https://doi.org/10.1128/mSphere.00202-21

36. Edgeworth JD, Batra R, Wulff J, Harrison D. Reductions in methicillin-resistant *Staphylococcus aureus*, *Clostridium difficile* infection and intensive care unit-acquired bloodstream infection across the United Kingdom following implementation of a national infection control campaign. *Clin Infect Dis.* 2020;70(12):2530–2540. https://doi.org/10.1093/cid/ciz764

37. Mohamed A, Daef E, Nafie A, Shaban L, Ibrahim M. Characteristics of carbapenem-resistant gram-negative bacilli in patients with ventilator-associated pneumonia. *Antibiotics (Basel).* 2021;10(11):e1325. https://doi.org/10.3390/antibiotics10111325

38. Kayastha K, Dhungel B, Karki S, et al. Extended-spectrum β-lactamase-producing *Escherichia coli* and *Klebsiella* species in pediatric patients visiting International Friendship Children's Hospital, Kathmandu, Nepal. *Infect Drug Resist.* 2020;13:e1178633720909798. https://doi.org/10.1177/1178633720909798

39. Ndir A, Diop A, Ka R, et al. Infections caused by extended-spectrum beta-lactamases producing Enterobacteriaceae: Clinical and economic impact in patients hospitalized in 2 teaching hospitals in Dakar, Senegal. *Antimicrob Resist Infect Control.* 2016;5:e13. https://doi.org/10.1186/s13756-016-0114-7

40. Purwaningrum D, Pratama A. Climate change and antimicrobial resistance: A global public health crisis at the environmental nexus. *Pharmacy Reports.* 2024;4(1):e94. https://doi.org/10.51511/pr.94

41. Chowdhury MSR, Hossain H, Rahman MN, et al. Emergence of highly virulent multidrug and extensively drug resistant *Escherichia coli* and *Klebsiella pneumoniae* in buffalo subclinical mastitis cases. *Sci Rep.* 2025;15:e11704. https://doi.org/10.1038/s41598-025-95914-x

42. Kain MJ, Reece NL, Parry CM, Rajahram GS, Paterson DL, Woolley SD. The rapid emergence of hypervirulent *Klebsiella* species and *Burkholderia pseudomallei* as major health threats in Southeast Asia: The urgent need for recognition as neglected tropical diseases. *Trop Med Infect Dis.* 2024;9(4):e80. https://doi.org/10.3390/tropicalmed9040080

43. Alhassan MY, Ahmad AA. Antimicrobial resistance in a changing climate: A One Health approach for adaptation and mitigation. *Bull Natl Res Cent.* 2025;49:e26. https://doi.org/10.1186/s42269-025-01318-2

44. Yang JW, Nam JH, Lee KJ, Yoo JS. Effect of temperature on carbapenemase-encoding plasmid transfer in *Klebsiella pneumoniae.* *Microorganisms.* 2024;12(3):e454. https://doi.org/10.3390/microorganisms12030454

45. Furlan JPR, Sellera FP, Lincopan N, Debone D, Miraglia SGEK, Tavella RA. Catastrophic floods and antimicrobial resistance: Interconnected threats with wide-ranging impacts. *One Health.* 2024;19:e100891. https://doi.org/10.1016/j.onehlt.2024.100891

46. Pinto Jimenez CE, Keestra S, Tandon P, et al. Biosecurity and water, sanitation, and hygiene (WASH) interventions in animal agricultural settings for reducing infection burden, antibiotic use, and antibiotic resistance: A One Health systematic review. *Lancet Planet Health.* 2023;7(5):e418–e434. https://doi.org/10.1016/S2542-5196(23)00049-9

47. Zhang MS, Li W, Zhang WG, Li YT, Li JY, Gao Y. Agricultural land-use change exacerbates the dissemination of antibiotic resistance genes via surface runoffs in Lake Tai Basin, China. *Ecotoxicol Environ Saf.* 2021;220:e112328. https://doi.org/10.1016/j.ecoenv.2021.112328

48. Rehman M, Sajjad W, Kang S, Rafiq M, Zhao Y. Mobilization of the ancient resistome from thawing permafrost. *Crit Rev Microbiol.* Published online July 9, 2026:1–21. https://doi.org/10.1080/1040841X.2026.2698958

49. Okoth D. Climate change fuels drug resistance in poor countries. *SciDev.Net.* Published May 1, 2025. Accessed April 26, 2026. https://www.scidev.net/global/news/climate-change-fuels-drug-resistance-in-poor-countries/

50. Pruden A, Larsson DGJ, Amézquita A, et al. Management options for reducing the release of antibiotics and antibiotic resistance genes to the environment. *Environ Health Perspect.* 2013;121(8):878–885. https://doi.org/10.1289/ehp.1206446

51. Czatzkowska M, Harnisz M, Korzeniewska E, et al. The impact of antimicrobials on the efficiency of methane fermentation of sewage sludge, changes in microbial biodiversity and the spread of antibiotic resistance. *J Hazard Mater.* 2021;416:e125773. https://doi.org/10.1016/j.jhazmat.2021.125773

52. Thorpe KE, Joski P, Johnston KJ. Antibiotic-resistant infection treatment costs have doubled since 2002, now exceeding $2 billion annually. *Health Aff (Millwood).* 2018;37(4):662–669. https://doi.org/10.1377/hlthaff.2017.1153

53. Bell BG, Schellevis F, Stobberingh E, Goossens H, Pringle M. A systematic review and meta-analysis of the effects of antibiotic consumption on antibiotic resistance. *BMC Infect Dis.* 2014;14:13. https://doi.org/10.1186/1471-2334-14-13

54. Roope LSJ, Smith RD, Pouwels KB, et al. The challenge of antimicrobial resistance: What economics can contribute. *Science.* 2019;364(6435):eaau4679. https://doi.org/10.1126/science.aau4679

55. Alkorta I, Garbisu C. Expanding the focus of the One Health concept: Links between the Earth-system processes of the planetary boundaries framework and antibiotic resistance. *Rev Environ Health.* 2025;40(1):159–173. https://doi.org/10.1515/reveh-2024-0013

56. World Health Organization. *Global Action Plan on Antimicrobial Resistance.* World Health Organization; 2015.

57. Semenza JC, Paz S. Climate change and infectious disease in Europe: Impact, projection and adaptation. *Lancet Reg Health Eur.* 2021;9:e100216. https://doi.org/10.1016/j.lanepe.2021.100216

58. Rzymski P, Gwenzi W, Poniedziałek

B, Mangul S, Fal A. Climate warming, environmental degradation and pollution as drivers of antibiotic resistance. *Environ Pollut.* 2024;346:e123649. https://doi.org/10.1016/j.envpol.2024.123649

59. Magnano San Lio R, Favara G, Maugeri A, Barchitta M, Agodi A. How antimicrobial resistance is linked to climate change: An overview of two intertwined global challenges. *Int J Environ Res Public Health.* 2023;20(3):e1681. https://doi.org/10.3390/ijerph20031681

60. Laxminarayan R, Duse A, Wattal C, et al. Antibiotic resistance—the need for global solutions. *Lancet Infect Dis.* 2013;13(12):1057–1098. https://doi.org/10.1016/S1473-3099(13)70318-9

61. Zeng Y, Li W, Zhao M, et al. The association between ambient temperature and antimicrobial resistance of *Klebsiella pneumoniae* in China: A difference-in-differences analysis. *Front Public Health.* 2023;11:e1158762. https://doi.org/10.3389/fpubh.2023.1158762

62. Godman B, Fadare J, Kwon HY, et al. Evidence-based public policy making for medicines across countries: Findings and implications for the future. *J Comp Eff Res.* 2021;10(12):1019–1052. https://doi.org/10.2217/cer-2020-0273

63. Piddock LJV, Alimi Y, Anderson J, et al. Advancing global antibiotic research, development and access. *Nat Med.* 2024;30(9):2432–2443. https://doi.org/10.1038/s41591-024-03218-w

64. Ventola CL. The antibiotic resistance crisis: Part 1: Causes and threats. *P T.* 2015;40(4):277–283.

65. Sun J, Jin L, He T, et al. Antibiotic resistance genes (ARGs) in agricultural soils from the Yangtze River Delta, China. *Sci Total Environ.* 2020;740:e140001. https://doi.org/10.1016/j.scitotenv.2020.140001