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Evaluating the relationship between Antimicrobial resistance and climate through the evaluation of different countries and regions: A Literature Review

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Abstract

This study investigates the connection between antimicrobial resistance (AMR) and climate change across diverse global regions. The study focuses on Mexico, Southeast Asia, and Canada. By analyzing how regional climatic conditions such as temperature, humidity, and seasonal weather patterns influence AMR dynamics, the research can address the critical question of how to tackle AMR. Based on the global escalation of AMR and its profound implications for public health, our study is vital in highlighting the necessity for integrated climate change mitigation strategies within AMR management. The findings emphasize the urgency of surveillance, targeted research, and enforcing strict antimicrobial stewardship to counteract the rising threat of AMR, thereby informing more effective global health responses and policy-making in an era of significant environmental change.

Introduction

Antimicrobial resistance (AMR) is a near unsurmountable issue in the global healthcare landscape. Microorganisms characterized by the ability to withstand the effects of medications designed to eradicate them not only significantly hinder the treatment of infections but also elevate the disease spread, severity of the illness, and mortality rate. Various factors, including misuse and overuse of antibiotics in human medicine, agriculture, and animal treatment, bolster AMR resistance. As these microbes evolve, the misuse of these drugs accelerates the selection of resistant strains by removing those susceptible to the drugs. The ever-escalating crisis of AMR

demands innovative solutions that encompass prudent antibiotic use, enhanced surveillance, and the development of new antimicrobials. Antimicrobial resistance (AMR) and climate change presents a complex challenge that is gaining attention from researchers across all fields. Researchers are investigating how various climate-related factors such as temperature, precipitation, extreme weather events, humidity, etc, influence the spread of antimicrobial-resistant pathogens. Additionally, the impact of climate change on antimicrobial use in agriculture, human health, and environmental reservoirs, as well as how changes in the structure and logistics of an environment may affect the transmission dynamics of AMR. In a country's case, evaluating the economic status, the countries advancements in technology, and the proximity of the population to a hospital could all be various factors in AMR resistance. By altering ecosystems and disease vector distribution, ever-changing climates may further influence microbial resistance dynamics, making it a potential accelerant of AMR. Understanding the intricate connection between various climates and AMR is vital for creating thorough strategies to mitigate the threat posed by drug-resistant pathogens. This paper explores the relationship between antimicrobial resistance and climate by surveying various countries and regions to unravel the complexities of AMR in the face of a changing climate.

Methods

When compiling our literature review, we searched various databases such as Pubmed and the WHO for research and data published between 2010 and 2024 with the keywords and phrases such as “AMR” or “Antibiotic resistant” or “Antibiotics-Climate” or “AMR in Asia” or “Mexico AMR”. This allowed for the searches to remain as relevant to material as possible while allowing room for a broadened, more thorough, understanding of the subject.

Each report was reviewed and confirmed for relevance. The reports included in the literature review were limited by several constraints including but not limited to: i) English language ii) Peer-reviewed journal publications and iii) Geographical Diversity. In cases where the eligibility of an article could not be determined simply by the title or abstract, the full text was examined. This search strategy yielded a total of 3 publications per area, evenly divided between Mexico, South Asia, and Canada.

Results

Southeast Asia

Southeast Asia is known for its year-round hot and humid climate, containing various tropical and subtropical environments with the high precipitation levels it receives annually. This enriching environment has fostered a biodiverse range of wildlife and cultured many viruses and infections that have increased mortality. Many government and health organizations in the Southeast Asian region have worked rigorously to combat the evolving viruses and infections, but they have recently been met with antimicrobial resistance. This obstacle has easily put the years of cumulative work to waste. Not only has antimicrobial resistance caused higher mortality rates, but it has also led to significant economic loss for many countries. So far, antimicrobial resistance will contribute to more deaths than viruses like malaria, predicted at 389,000 from WHO risk assessment surveys. Antimicrobial resistance has caused higher mortality rates and adverse economic loss across 12 Southeast Asian countries.

Data from The Lancet Regional Health helps us visualize how antimicrobial resistance has caused more deaths than HIV, AIDS, or Malaria itself. In 2019, the Southeast Asian region

had 4 million deaths caused by bacterial infections; 1.41 million were caused by antimicrobial resistance. The World Health Organization compiled data regarding infection-related deaths in the Southeast Asian region. A small sample of the accumulated data would be Bangladesh, which had 161,192 deaths caused by bacterial infection; out of that total, 98,779 deaths were associated with antimicrobial resistance, and 26,193 were solely caused by it. From this data sample alone, we can infer that approximately 50% of the cumulative deaths from bacterial infection have a strong relationship with antimicrobial resistance. However, out of that total research, we can only deem approximately 20% of those cases directly caused by antimicrobial resistance. Looking at the bigger picture, this distribution can be found throughout all other Southeast Asian countries. A similar example would be a data sample from Myanmar, with a total cumulative bacterial-associated death count of 78,905. Out of that cumulative total, 40,233 are associated with antimicrobial resistance, while 11,170 deaths were caused. Comparing the two data samples, a typical pattern that you will see is the distribution that approximately 50% of cases were associated with antimicrobial resistance while 20% were caused by it.

Mexico

Understanding how different countries, including Mexico, are addressing antimicrobial resistance (AMR) is crucial due to its significant impact it has on global health. By analyzing the prevalence and study of infections such as Nontyphoidal Salmonella and UTIs, we can gain insight into how AMR affects Mexico. As Mexico is classified as a low-middle-income country, comprehending its approach to addressing antimicrobial resistance is crucial for shaping future strategies, understanding its influence on global efforts to combat AMR, and as well as

understanding the extent of antimicrobial resistance and its potential connection to climate change.

Non-typhoidal Salmonella is among the leading causes of foodborne diseases according to the WHO, and Multi-drug resistant (MDR) Non-Typhoidal Salmonella has caused public concern on a global scale; MDRs are hard to treat and expensive. The presence of multidrug-resistant Salmonella has raised significant public concern and debate due to the link between antibiotic use in farming and growing resistance issues. (2) This heightened awareness stems from potential risks posed by antibiotic-resistant bacteria in food production systems, including the spread of resistant strains to humans through contaminated food products. As antibiotic resistance becomes an increasingly urgent public health issue worldwide, the role of livestock in contributing to the problem has generated attention and calls for enhanced surveillance, regulation, and mitigation strategies to address antimicrobial resistance in agricultural settings

The surge in antimicrobial resistance (AMR) has also complicated the management of urinary tract infections (UTIs). Given that UTIs are one of the most common reasons for consultations that involve the prescription of an antibiotic, they are a re

In this study, *Genomic surveillance links livestock production with the emergence and spread of multi-drug resistant non-typhoidal salmonella in Mexico*; they used a subset of 44 NTS isolated from a prior study for which antibiotic susceptibility data was accessible. These isolates represented seven different serovars and were collected across various stages of beef production and diverse locations throughout Mexico. This diverse panel of strains facilitated a comprehensive analysis of the resistome of non-clinical bovine-associated NTS. Non-clinical

bovine associated NTS refers to non-typhoidal Salmonella (NTS) strains that are found in cattle but are not directly linked to clinical cases of disease in humans or animals. These strains are typically isolated from sources such as feces, carcasses, cuts, or ground beef in the context of an agricultural setting rather than from individuals presenting symptoms of salmonellosis. This is what the study had done there; every isolate that was collected was taken from different samples of feces, carcasses, cuts, or ground beef and some were obtained on different dates.

The literature describes findings showing a higher prevalence and variety of antimicrobial resistance (AMR) genes in Salmonella isolates linked to meat production compared to those from other sources in Mexico. Aminoglycoside resistance genes were notably common, present in 97% of isolates, with meat-related isolates displaying greater diversity. Additionally, meat-associated isolates were more likely to carry genes that were resistant to multiple antibiotic classes. These findings stress the importance of addressing AMR in meat production to combat the spread of multidrug-resistant Salmonella. The literature also reveals a concerning prevalence of multi-drug resistant Salmonella among isolated sources from various non-clinic; bovine origins in Mexico. This MDR prevalence surpasses rates reported in similar studies conducted 5-7 (more from when paper is out) years ago in Africa, Asia, and Latin America. Despite expected variations in AMR over time and across regions, these results show that there needs to be continued effort for its control and continuance to address this issue.

The diverse tropical climates in Mexico are a significant factor to consider in the context of AMR. The abundance of land and favorable climates in Mexico supports a large population of cattle and other food animals, which are prone to infection. This agricultural setting creates conditions conducive to the spread of AMR among livestock, highlighting the importance of

addressing antimicrobial use in animal husbandry practices to mitigate the emergence and transmission of resistant pathogens, therefore it is important to consider how the environment and climate change as a possible reason to high prevalence of AMR.

Canada

In Canada's efforts to monitor and follow climate change and its impact on Antimicrobial Resistance, honey bees are a remarkable biomarker of both heavy metals in the environment, air pollutants, pesticides, plant pathogens, bacteria resistance within themselves, and bacteria resistance within the surrounding environment. The symbiotic relationship between honey bees, their surrounding environment, and the determinants of environmental health create a model of the interaction between Antimicrobial Resistance and climate change. Similarly, the positive feedback loop between the terrestrial surface temperature and the spread of honey bee disease models indicates the importance of regulating the Earth's temperature. Simultaneously, the negative feedback loop between the spread of honey bee diseases and the efficacy of antimicrobials in treating pathogens and pests has become equally concerning. The literature describes many findings concerning monitoring the European honey bee, *Apis mellifera* (*A. mellifera*), the *A. mellifera* honey, wax, stored pollen, and *Paenibacillus larvae* (*P. larvae*), a bacterium found in the honey bees in Saskatchewan, Canada.

The studies concerning *A. mellifera*, gene expression, microbiome profiling, and many high-throughout methodologies to study dose-dependent exposure measure contaminant accumulation. Smith measured concentrations of Al, Cu, Cr, Pb, Cd, and measured isotopic compositions in of PB in honey from different sample sectors within the Greater Vancouver

Regional District in British Columbia, Canada. These heavy metals can have many isotopes that have some responsibility for air pollution. These elements were elevated in urban areas such as Vancouver compared to rural and suburban areas. *A. mellifera* and their hive matrices also accumulated persistent chemicals and particulate matter (PM), particularly on the bodies of *A. mellifera*. The study measures the Polychlorinated Biphenyls (PCB) and Polycyclic Aromatic Hydrocarbons (PAH) classes of persistent organic pollutants (POP) that occur due to environmentally poor practices such as organochlorine chemicals excreting from damaged electrical equipment and pollute the air due to the burning of things such as coal, crude oil, and gasoline. Using electron microscopy and x-ray spectroscopy the study found airborne PM heavily concentrated correlates with the particle matter in the region's soil. Particulate matter was found in higher concentrations in urban areas, while suburban and rural areas were comparable, likely due to the distribution by wind.

In the study concerning *Paenibacillus* larvae, 718 samples were collected containing spore suspensions, and *P. larvae* isolates derived from the 718 pooled, extracted honey samples used to represent the 52 commercial beekeeping operations in SK. The samples were cultured in MYPGP medium 18 as well as 3mm L-tyrosine and 3mm uric acid in order to increase the germination of *P. larvae* spores. The samples were divided into two groups determined by whether the sample contained greater or less than three spores. 284 samples contained more than 3 spores and 434 samples did not.

The studies concerning *A. mellifera* determined that honey bees containing Enterbacteriaceae detected Antimicrobial resistance. In particular, the presence of amoxicillin or clavulanic acid

interests scientists because it is not used in beekeeping, but in human and veterinary applications. This indicated that AMR genes found in *A. mellifera* could have environmental origin, supporting the utility of honey bees as indicators of environmental Antimicrobial Resistance.

In the study concerning *P. larvae*, the prevalence of Oxytetracycline, an antibiotic used to metaphylaxis the honey bee population in response to American foulbrood (AFB), an infectious disease of honey bee brood is observed. Of the 718 *P. larvae* sampled, 645 (89.8%) were susceptible to OTC, 8 (1.1%) isolates had intermediate resistance to OTC, and 65 (9.0%) were resistant to OTC based on minimum inhibitory concentrations. Most OTC-resistant isolates were identified in 6 beekeeping operations in the Northeast of SK and the remaining 5 OTC-resistant isolates were found in the Northwest region of SK.

The climate of Canada plays a pivotal role in shaping the habitat and behavior of honey bees across the country. With its vast expanse and diverse landscapes, ranging from the temperate Pacific coast to the frigid Arctic, Canada experiences a wide range of climatic conditions. Honey bees, essential pollinators for many crops and wildflowers, are influenced by these variations. In the warmer months, bees thrive in regions with abundant floral resources, such as the prairies and the southern provinces. However, in colder climates like the northern territories, bee activity is limited to a shorter season, impacting both honey production and pollination services. Climate change further exacerbates these dynamics, altering flowering patterns and challenging bee populations with unpredictable weather events. Thus, understanding the intricate connection between Canada's climate and honey bees is crucial for effective conservation efforts, sustainable agricultural practices, and the future of monitoring Antimicrobial Resistance.

Discussion

The research data shows that antimicrobial resistance is starting to affect society heavily. The world is going through climate change with our rising sea levels and overall increase in global climate. Southeast Asia has a humid and hot climate that causes bacteria to evolve. Still, climate change has expedited this process, and where they are evolving faster than our medicine can keep up with. That, along with the constant misuse and abuse of antibiotics, caused the bacteria to evolve in ways we can't fathom. Overall, the government has to invest a lot of effort into preventing this issue. In other words, many governments have implemented policies to restrict the purchase and usage of antibiotics to mediate this issue.

Antimicrobial resistance (AMR) poses a significant threat to public health worldwide, exacerbated by factors such as antibiotic misuse and climate change. Climate change influences environmental conditions like temperature and humidity which can impact the spread and evolution of AMR. Understanding AMR dynamics in Latin American countries, including Mexico, is pivotal due to their diverse climates. By studying AMR across these regions, we can unravel the relationship between AMR and climate, shedding light on its global implications.

Despite the global impact of AMR, many countries lack comprehensive surveillance systems, leading to gaps in understanding. This hampers our ability to understand AMR's surveillance, spread and response strategies effectively.

Our proposed approach involves conducting surveys collecting data from various countries through research articles published which is limited to the amount of data taken by countries and the amount of funding that goes into it. Despite the potential benefits, we acknowledge challenges such as data availability and resource constraints different countries have. Although many countries may not have enough data on AMR, this data-driven approach can offer insights

into geographic patterns and environmental influences on AMR. Additionally, understanding the complex interactions between microbes and environmental factors present inherent limitations to our study, as not every country has the same data on similar microbes.

In conclusion, studying AMR in Mexico and Latin American countries and its correlation with climate changes offers valuable insights into addressing these pressing global health challenges. By prioritizing research and intervention strategies, we can work towards a healthier and more sustainable future.

Canada's diverse climates, spanning from the Arctic to temperate regions, each face unique challenges posed by climate change that intersect with the issue of antimicrobial resistance (AMR). Recent research underscores the profound impact of rising temperatures on bacterial infections and the development of antibiotic resistance, particularly among vulnerable populations. In the Canadian North, Indigenous communities bear a disproportionate burden of invasive bacterial diseases and *H. pylori* infections, highlighting the intricate link between poverty and resistance risk. Moreover, MRSA infections among the homeless population underscore the nuanced relationship between behavioral factors and AMR.

Various factors, including soil quality, agricultural practices, waste management, and food safety, contribute to Canada's antimicrobial resistance landscape. Soil, for instance, acts as a reservoir for antibiotic resistance genes, with agricultural practices like manure and sewage sludge application exacerbating this issue. Additionally, water quality, sanitation practices, and hygiene standards play pivotal roles in shaping the emergence and spread of resistant pathogens.

As we explore the connections between climate, climate change, and AMR, it's imperative to consider the disparate impacts and address the underlying inequities. Socioeconomic disparities influence susceptibility to resistant infections, with higher-income individuals often afforded greater protection. Conversely, lower-income groups face heightened health risks and increased vulnerability to resistant pathogens. Central to the AMR challenge is the rampant overuse and misuse of antibiotics, fueling a global epidemic of resistance. The intricate interplay between human health, veterinary medicine, and agricultural practices further complicates efforts to combat AMR.

Addressing these challenges requires a comprehensive approach, including enhanced surveillance, standardized protocols, and coordinated interventions. Strengthening our understanding of key pathogens, bolstering surveillance capabilities, and fostering collaborative, multisectoral efforts are essential steps in tackling Canada's antimicrobial resistance crisis.

Conclusion

In conclusion, this literature review goes through and evaluates the multifaceted relationship between antimicrobial resistance (AMR) and climate across various global regions, highlighting the urgent need for a swift and comprehensive strategy to approach this challenge. The findings from Mexico, Southeast Asia, and Canada illustrate the pervasive impact of AMR, which is further exacerbated by the various climate factors in the region. The data presented showcases the critical role of environmental conditions, agricultural practices, and human behavior in the development and spread of AMR, emphasizing the importance of integrating climate change mitigation strategies into public health planning. Moreover, the study reveals the significant gaps

in surveillance and data availability, which threatens to undermine decades of progress in the fight against infectious diseases. By fostering a deeper understanding of the complex interactions that occur between climate and AMR, we can pave the way for more successful and sustainable health systems capable of withstanding the challenges of the 21st century.

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