



GLOBAL PATTERNS OF ANTIMICROBIAL RESISTANCE ACROSS MAJOR BACTERIAL PATHOGENS

Dr.Reet Arora¹, Dr Gokula krishnan B²

¹Junior Resident, Department of Naturopathy, MD in clinical Naturopathy, Swami Vivekanand Subharti University, Uttar Pradesh, India, Email Id: reet.arora1412@gmail.com, ORCID ID: 0009-0008-6559-3915

²PG Scholar, Maharishi Aurobindo Subharti College & Hospital of Naturopathy & Yogic Sciences, Swami Vivekananda Subharti University, Naturopathy & yoga, MD - Clinical Naturopathy, Pincode: 250002, Email id: doctor.gk14@gmail.com, ORCID ID: 0009-0005-1791-8664

Corresponding Author: Dr.Reet Arora

ABSTRACT

Antimicrobial resistance (AMR) has become a major global public health concern, threatening the effective prevention and treatment of bacterial infections. This study investigated global patterns of antimicrobial resistance across major bacterial pathogens using multicountry surveillance data collected between 2018 and 2023. A quantitative secondary data analysis was conducted using publicly available datasets comprising 138 resistance observations from 20 countries representing six World Health Organization regions. Descriptive statistics, one-way analysis of variance, Kruskal–Wallis testing, linear trend analysis, and correlation analyses were performed to evaluate pathogen-specific, regional, and country-level resistance patterns and their association with selected healthcare indicators. The findings revealed significant variation in antimicrobial resistance among bacterial pathogens, with *Acinetobacter* spp. exhibiting the highest pooled resistance, while *Escherichia coli* accounted for the greatest number of resistant isolates. Increasing resistance trends were observed across most WHO regions, whereas stronger healthcare systems and higher surveillance quality were generally associated with lower resistance levels. These findings highlight the importance of continuous global surveillance, strengthened antimicrobial stewardship, improved diagnostic capacity, and coordinated public health strategies to mitigate the growing burden of antimicrobial resistance and preserve the effectiveness of existing antimicrobial agents.

Keywords: Antimicrobial resistance, Bacterial pathogens, Global surveillance, Antibiotic stewardship, Public health.

Article History:

Article Type: **Research**

Received Date:**05/05/2026** | Revised Date:**06/06/2026** | Accepted Date:**14/06/2026** | Published Date:**21/06/2026**

© 2026 Authors, Licensing under CC-BY-NC-ND 4.0 [Read More.](#)

1. Introduction

One of the biggest threats to global public health today is the rise of antimicrobial resistance (AMR) – a phenomenon that is undermining the ability of antibiotics to treat infections which have been managed effectively for decades. The development and spread of resistant bacterial pathogens has led to more cases of treatment failure, longer hospital stays, higher health care costs as well as significant morbidity and mortality globally (Aljeldah, 2022; Okeke et al., 2024). The spread and emergence of resistant microorganisms in different ecological environments is further aggravated by the use of antimicrobials in human medicine, agriculture and food production, which is often inappropriate. (Samtiya et al., 2022; Hou et al., 2023) Maintaining the effectiveness of current antimicrobial drugs is a huge problem for health care systems and international health organizations, as bacterial pathogens continue to acquire and spread resistance determinants.

Recent studies have shown significant geographical, species and antibiotic class variability in antimicrobial resistance, highlighting the need for coordinated monitoring systems that can provide reliable, comparable epidemiological data (Mendelsohn et al., 2023; Rahbe et al., 2023). International reporting has been improved, with global initiatives, such as the Global Antimicrobial Resistance and Use Surveillance System (GLASS) by the World Health Organization (WHO), providing standardized information on antimicrobial resistance patterns and consumption among countries participating in these initiatives (Bertagnolio et al., 2023; Ajulo & Awosile, 2024). Continual surveillance is needed to guide evidence-based antimicrobial stewardship and public health interventions, as these surveillance efforts have identified increased resistance among clinically important pathogens such as *Escherichia coli*, *Klebsiella pneumoniae*, *Acinetobacter* species, and methicillin-resistant *Staphylococcus aureus* (Wise et al., 2024; Luo et al., 2024).

The problem of antimicrobial resistance is not limited to the clinical sphere and is a major biological, environmental and socioeconomic issue. Large scale regional studies have shown high variability in burden of resistance across Europe and other global regions, related to differences in antimicrobial stewardship, infection prevention strategies, surveillance and healthcare infrastructure overall (Mestrovic et al., 2022, Li et al., 2022). Environmental reservoirs are also important reservoirs for the persistence and dissemination of resistance genes, and there have been many examples of antimicrobial resistance determinants in wastewater and sewage systems throughout the world identified by genomic investigations (Munk et al., 2022). In addition,

of pathogens to acquire resistance via horizontal gene transfer, chromosomal changes and the presence of mobile genetic elements which enable the rapid spread of resistance between microbial populations (Darby et al., 2023).

Although significant advances have been made in global surveillance, there are still key areas of knowledge that remain lacking on the distribution of antimicrobial resistance (AMR) for multiple bacterial pathogens, across geographical areas and in healthcare settings, using integrated secondary datasets. Often, existing studies have concentrated on a single pathogen or infection or only a small geographic area and not offered a broad overview of resistance trends across several pathogens in a single analytical framework (Lewnard et al., 2024). These comparative analyses are useful for identifying high risk pathogens, identifying regional differences, antimicrobial stewardship programs, and future surveillance priorities. To investigate the global antimicrobial resistance trends in major bacterial pathogens and understand their regional and temporal variation, the present study analysed multicountry surveillance data from 2018 to 2023.

Research Objectives

- To evaluate global antimicrobial resistance patterns across major bacterial pathogens using multicountry surveillance data collected between 2018 and 2023.
- To compare antimicrobial resistance across bacterial pathogens, World Health Organization regions, countries, and antibiotic classes using descriptive and inferential statistical analyses.
- To examine the relationships between antimicrobial resistance and selected country-level healthcare and socioeconomic indicators to identify factors associated with global resistance variation.

2. Methodology

2.1 Study Design

Identify the study as quantitative, observational and retrospective and a secondary data analysis. Point out that the aim was to analyse antimicrobial resistance trends in the major bacterial pathogens around the world based on publicly available surveillance data from 2018 to 2023.

2.2 Data Source and Study Variables

Identify that the primary data set included 138 observations from 20 countries in 6 WHO regions. Describe briefly variables included: country, year, WHO region, bacterial pathogen, antibiotic class, antibiotic, infection type, resistance percentage, tested isolates, resistant isolates, antibiotic consumption, GDP per capita, health expenditure, physician density, hospital beds, universal health coverage and surveillance quality score. Define % antimicrobial resistance as the main outcome variable (Mamoon, 2025).

2.3 Data Pre-processing

Describe how you extracted the ZIP file in Google Colab and imported all the datasets with Python. To ensure data integrity for analysis, indicate that variable types were checked, any missing data was assessed, categorical data was standardized, any numerical data was converted to the correct data type and reported resistance percentages were checked against the number of reported resistant and tested isolates.

2.4 Statistical Analysis

Describe that descriptive statistics have been used to describe the features of a data set. Describe how there were pooled resistance rates calculated for the bacterial pathogens, countries, and WHO regions. State that differences between the groups of pathogens were analyzed by one-way ANOVA and Kruskal–Walli's test. Simple linear regression was used to describe trends in those regional temporal trends (2018-2023), and Spearman's rank correlation was used to evaluate the relationships between pooled resistance and country-level indicators, including GDP per capita, consumption of antibiotics, number of physicians, hospital beds, health expenditure, universal health coverage, and the quality of surveillance. Pearson correlation was also performed to determine the relationship between GDP per capita and combined antimicrobial resistance. Statistically significant differences between the two sides were set at a p of < 0.05 .

2.5 Data Visualization

Explain how graphical output was developed to aid in the interpretation of the results. Explain that a bar chart showed pooled resistance across bacterial pathogens, a line graph showed resistance trends over time across regions and a country–pathogen heatmap showed geographical differences in resistance, whereas a scatter plot with a regression line showed the relationship between GDP per capita and antimicrobial resistance.

3. Results

3.1 Dataset Characteristics and Overall Resistance Burden

The pooled antimicrobial resistance (AMR) data set was used to obtain international surveillance data from 20 countries in all six World Health Organization (WHO) regions. A total of 138 observations were available in the primary resistance data from 2018 to 2023, encompassing six groups of bacteria pathogens, four antibiotic classes, five specific antibiotics, and three broad categories of infections. A total of 2,414,950 bacteria were detected and of those 799,033 were considered resistant. The overall pooled antimicrobial resistance was 33.09% and the arithmetic mean resistance for each individual observation was 34.15% with a standard deviation of 19.46%. The median resistance level was 32.80%, which showed that there was significant variation in resistance between countries, pathogens, and antimicrobial agents. Table 1 shows the main features of the analytical data set.

Table 1. Overall Characteristics of the Antimicrobial Resistance Dataset

Characteristic	Value
Resistance observations	138
Countries represented	20
WHO regions represented	6
Study period	2018–2023
Bacterial pathogen groups	6
Antibiotic classes	4
Individual antibiotics	5
Infection types	3
Total isolates tested	2,414,950
Resistant isolates	799,033
Overall pooled resistance	33.09%
Mean resistance	34.15%
Median resistance	32.80%
Standard deviation	19.46%

3.2 Resistance Patterns Across Bacterial Pathogens

A significant difference in antimicrobial resistance was seen among the six groups of bacterial pathogens. *Acinetobacter* spp. had the highest pooled resistance rate (57.57%) with 33,219 resistant isolates out of 57,700 tested. This pathogen also had the highest mean resistance of

59.51%. The next highest pooled resistance rate was observed in *Staphylococcus aureus* (38.37%), *Escherichia coli* (36.11%) and *Shigella* spp. (33.01%). Pooled resistance rate was lower for *Klebsiella pneumoniae* (20.09%) and *Salmonella* spp. (18.54%). The highest proportional resistance burden was seen for *Acinetobacter* spp., while the highest absolute number of resistant isolates was *E. coli*. Of 1,363,650 tested *E. coli* isolates, 492,471 were resistant (accounting for more than half of all resistant *E. coli* isolates in the data set). A high level of variation was also observed in the *E. coli* data (with a standard deviation of 21.75 percentage points). Estimates of pathotype-specific resistance are shown in Table 2.

Table 2. Antimicrobial Resistance Across Major Bacterial Pathogens

Bacterial pathogen	Records	Countries	Isolates tested	Resistant isolates	Mean resistance (%)	SD	Median resistance (%)	Pooled resistance (%)
<i>Acinetobacter</i> spp.	12	2	57,700	33,219	59.51	7.78	59.30	57.57
<i>Staphylococcus aureus</i>	24	4	392,800	150,724	31.36	13.04	35.60	38.37
<i>Escherichia coli</i>	48	8	1,363,650	492,471	38.91	21.75	45.00	36.11
<i>Shigella</i> spp.	6	1	15,900	5,249	31.47	10.49	30.45	33.01
<i>Klebsiella pneumoniae</i>	42	7	576,700	115,850	25.75	16.28	23.85	20.09
<i>Salmonella</i> spp.	6	1	8,200	1,520	18.03	4.14	17.85	18.54

The Kruskal–Wallis test indicated that resistance levels differed significantly among bacterial pathogen groups, ($H=32.04$), ($p<0.001$). A one-way analysis of variance produced a comparable result, ($F=9.34$), ($p<0.001$), confirming substantial between-pathogen differences. As illustrated in Figure 1, the pathogen profile was dominated by the elevated resistance rate observed for *Acinetobacter* spp., while *Salmonella* spp. exhibited the lowest pooled resistance.

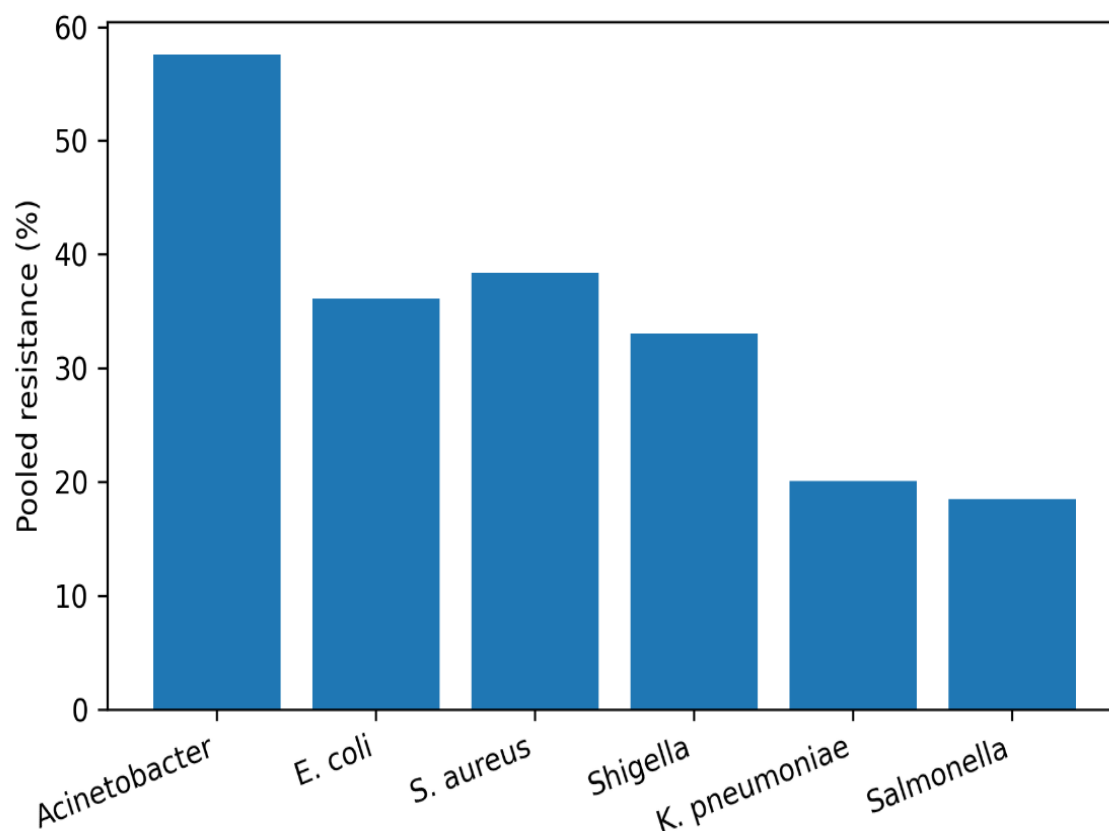


Figure 1. Pooled Antimicrobial Resistance by Bacterial Pathogen

3.3 Regional and Temporal Trends in Antimicrobial Resistance

During the study period (2018-2023), regional resistance levels fluctuated irregularly. The region with the highest average level of resistance was South-East Asia with 28.50% in 2018, followed by Eastern Mediterranean with 26.10%. In 2023 the average resistance was 33.30% for both regions. The biggest absolute gains were recorded in the Eastern Mediterranean region (+7.20 percentage points or +27.59% in relative terms). The Americas and South-East Asia each saw a rise by 3.00 percentage points and 4.80 percentage points, respectively. Moderate increases occurred in the Western Pacific (1.90 percentage point) and African (1.80 percentage point) areas. The only region that saw a decrease was Europe, from 11.20% in 2018 to 10.00% in 2023. This was a 1.20 percentage point decrease, or a 10.71% decrease from the previous year. The changes across the region are summarised in Table 3.

Table 3. Changes in Antimicrobial Resistance Across WHO Regions, 2018–2023

WHO region	Region name	Resistance 2018 (%)	Resistance 2023 (%)	Absolute change (percentage points)	Relative change (%)	Countries reporting in 2023
SEARO	South-East Asia	28.50	33.30	4.80	16.84	11
EMRO	Eastern Mediterranean	26.10	33.30	7.20	27.59	14
WPRO	Western Pacific	19.80	21.70	1.90	9.60	20
AFRO	Africa	18.20	20.00	1.80	9.89	26
AMRO	Americas	16.50	19.50	3.00	18.18	22
EURO	Europe	11.20	10.00	−1.20	−10.71	46

All 6 WHO regions had statistically significant annual changes in linear trend analysis. The increase in average resistance was strongest in the Eastern Mediterranean region, where the average is now just over 1.36 points higher than it was on average yearly. South-East Asia had an estimated annual increase of 1.04 percentage points. Some of the other regions with substantial positive annual trends were the Americas, Africa, and Western Pacific. Europe showed a negative slope of about 0.23 percentage points per year; this was statistically significant. Figure 2 demonstrates the regional disparities between the resistance trajectories over the six-year period, especially the ones in the Eastern Mediterranean and South-East Asian regions.

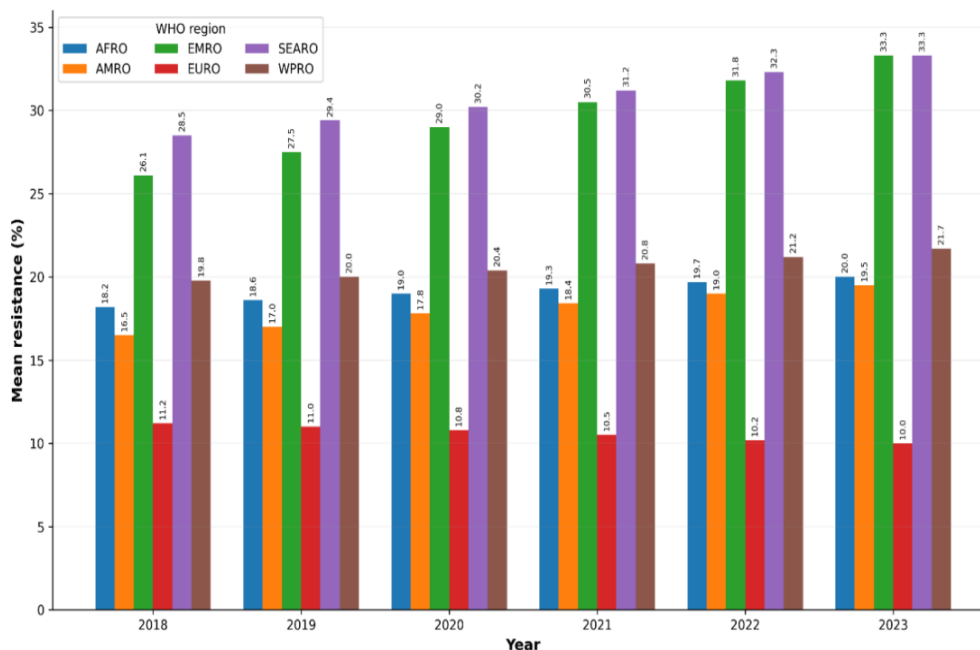


Figure 2. WHO Regional Trends in Antimicrobial Resistance, 2018–2023

3.4 Country–Pathogen Distribution of Resistance

Geographical heterogeneity in the levels of resistance was evident in the country–pathogen matrix. Several LMICs had high levels of resistance, especially to *E. coli*, *K. pneumoniae* and *Acinetobacter* spp. Pooled resistance rate was highest in Egypt ($\approx 66.78\%$), followed by India (58.03%), DSA (57.60%), Pakistan (54.88%), Brazil (52.87%) and Nigeria (52.29%). France, Sweden, Australia and the United States on the other hand had comparatively low pooled resistance levels. The distribution also revealed in Figure 3 that within the same country resistance was not even among bacterial species. The resistance in some countries was also higher for one particular pathogen–antibiotic combination, while other countries had lower values for all the combinations. If a pathogen–country combination was not reported in the dataset, then blank cells in the heatmap indicated that the combination, not the absence of resistance, and not the absence of the pathogen or the absence of the country. Blank cells in the heatmap represented pathogen–country combinations that were not reported in the dataset, rather than confirmed absence of resistance, absence of the pathogen or absence of the country.

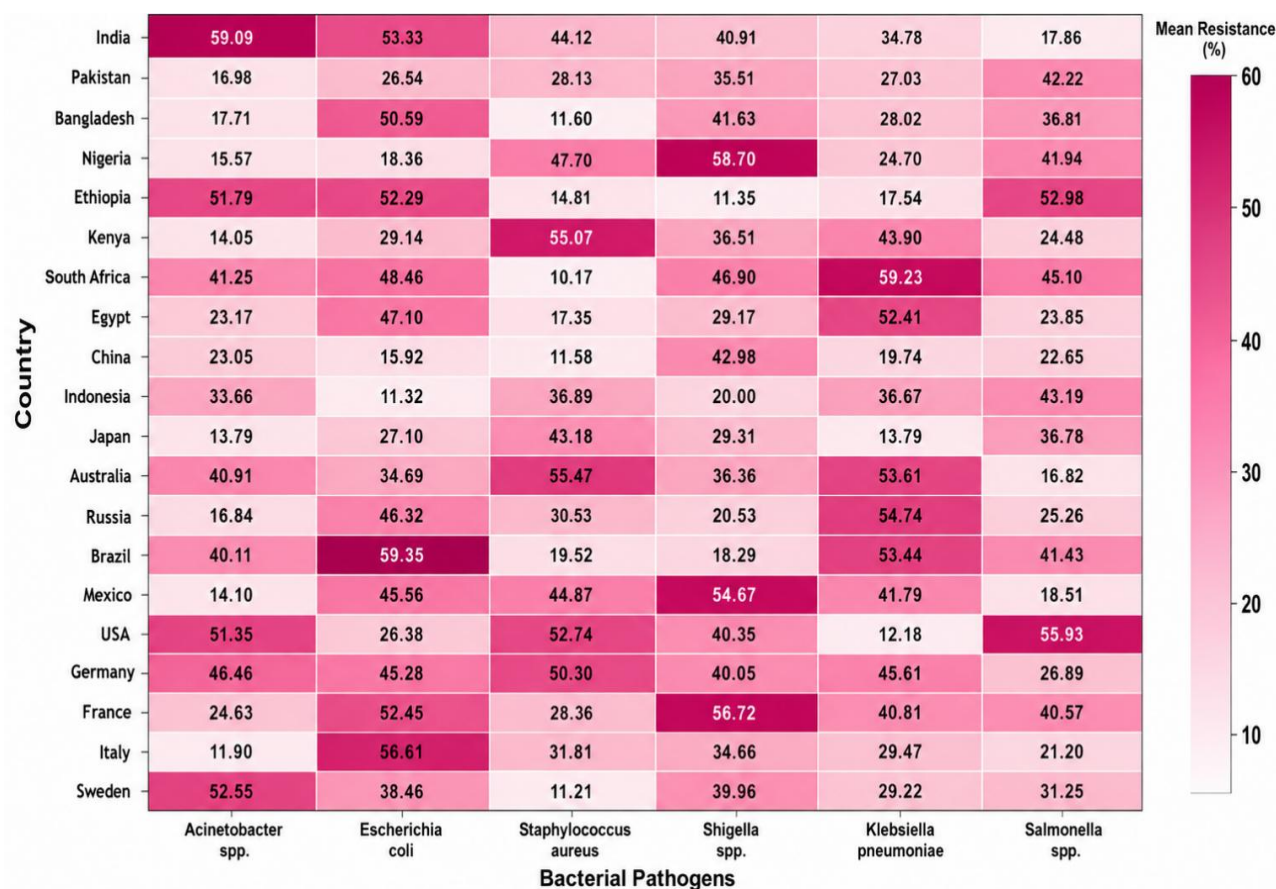


Figure 3. Country-Pathogen Antimicrobial Resistance Matrix

3.5 Country-Level Health-System Correlates of Resistance

At the country level, multiple relationships were found to be significant and negative between the health-system indicators and the pooled antimicrobial resistance. GDP per capita had the highest correlation, with higher national income being associated with lower resistance levels, Spearman's $\rho = -0.576$ ($p=0.0079$). Pooled resistance was also found to be negatively associated with universal health coverage ($\rho=-0.500$), ($p=0.0248$). Benelux countries, which had the highest level of health expenditure per capita, had the fewest physicians per capita and the lowest quality of surveillance. Similarly, there was a negative correlation between the number of hospital beds per 1000 population and resistance, but this was not statistically significant ($\rho=-0.379$), ($p=0.0990$). Pooled resistance at the country level, ($\rho=-0.125$), ($p=0.6001$), was not significantly associated with the antibiotic consumption in terms of defined daily doses (DDD) per 1,000 population per day. These estimated associations are provided in Table 4.

Table 4. Associations Between Country-Level Indicators and Pooled Antimicrobial Resistance

Country-level indicator	Spearman's rho	p-value
Antibiotic consumption, DDD/1,000/day	-0.125	0.6001
GDP per capita, USD 2022	-0.576	0.0079
Universal health coverage index	-0.500	0.0248
Health expenditure as percentage of GDP	-0.492	0.0274
Hospital beds per 1,000 population	-0.379	0.0990
Physicians per 1,000 population	-0.486	0.0297
Surveillance quality score	-0.463	0.0400

Figure 4 shows the scatter plot of the GDP per capita and pooled resistance, which shows an inverse relationship. Generally countries with higher per-capita incomes were in the lower end of the resistance distribution, while some of the countries with lower or middle-income levels showed significantly higher resistance. Pooled resistance was also statistically significantly correlated with GDP per capita ($r=-0.712$, $p=0.0004$).

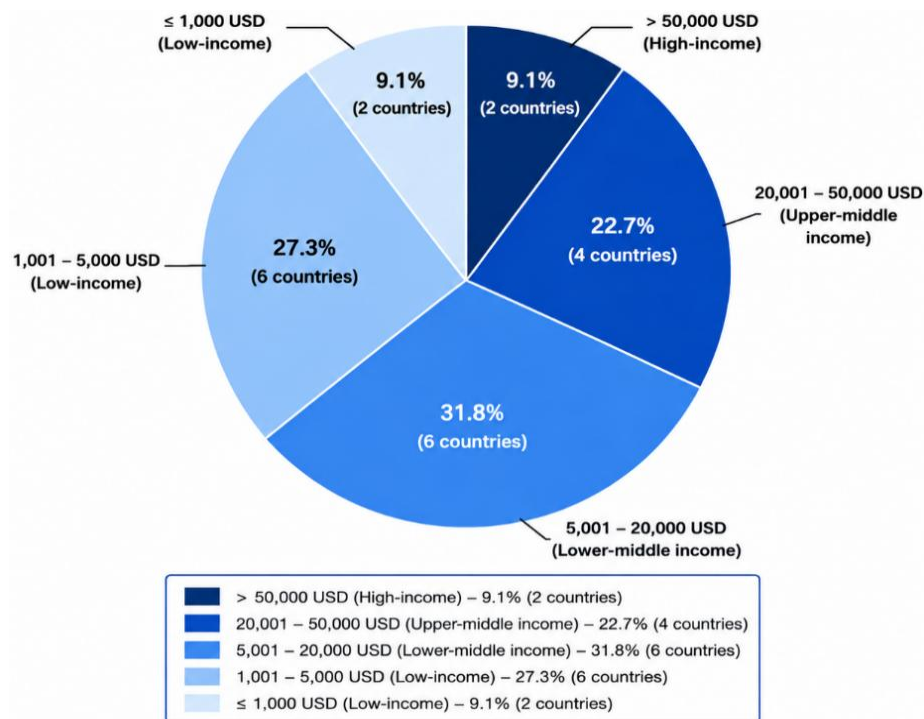


Figure 4. Association Between National Income and Antimicrobial Resistance

4. Discussion

This study assessed the global trend in antimicrobial resistance (AMR) of key bacterial pathogens through surveillance data from multiple countries from 2018 to 2023. Results showed significant differences in resistance across various bacteria, geographic region, and country health care features. *Acinetobacter* spp. were the most resistant, while *Escherichia coli* was the most numerous as a result of being found most frequently. The large variations between the bacterial pathogens and the high level of resistance in all WHO regions shows that AMR is still a multi-faceted problem on the global health agenda that needs coordinated monitoring and evidence-based interventions. This is in line with recent literature on how antimicrobial resistance (AMR) is an increasing threat to society due to the misuse of antimicrobials, pathogen evolution and inequities regarding access to health care services in countries (Walsh et al., 2023; Aggarwal et al., 2024).

This is due to their ability to develop several resistance mechanisms and survive in the healthcare setting, which has been well recognized for *Acinetobacter* spp. and other clinically relevant pathogens. They are commonly responsible for health care associated infections and are becoming resistant to multiple antibiotics. Comparable findings have been noted in cross-country studies of the WHO Africa Region, with Gram-negative pathogens with resistance playing a significant role in the disease burden in this region (Sartorius et al., 2024). Similarly, surveys of the susceptibility of underlying bacterial pathogens of CA-UTI have consistently shown growing resistance, reflecting the need for ongoing monitoring of susceptibility for empirical treatment and to minimize treatment failure (Silva et al., 2022; Alhazmi et al., 2023). The high proportion of *E. coli* in the present study further emphasizes its role as the most common bacterial pathogen causing community or HAI.

Regional comparisons revealed an increase of resistance in most WHO regions and comparatively lower resistance levels in Europe with a slight decrease. The differences could be due to differences in antimicrobial stewardship programmes, infection prevention activities, laboratory capacity and healthcare investment. The level of effort and the practice of stewardship in the country is generally associated with the level of surveillance. By contrast, areas with already constrained health care services tend to have the latest diagnosis, no restriction on antimicrobial access, and poor surveillance, which helps maintain the transmission of resistance. Recent international evaluations have shown the disproportionate burden of AMR in lower-resource settings, and continued upward trends in AMR if coordinated interventions are not intensified (Sartorius et al., 2024; Naghavi et al., 2024).

The inverse association with antimicrobial resistance with their respective measures of health system strength indicates that healthcare systems could play a role in slowing the spread of antimicrobial resistance, such as through better infection prevention, antimicrobial stewardship, lab capacity and access to appropriate clinical care. Antibiotic use, per se, was not correlated with pooled resistance in the current data set, but there are other factors that are interconnected, which are important in the development of resistance. Similarly, prior reviews have shown that effective control of AMR requires comprehensive strategies, including the surveillance of AMR, stewardship of antibiotics, rapid AMR diagnostics, regulatory AMR policies, public awareness, and coordinated international action; rather than individual interventions (Walsh et al., 2023; Aggarwal et al., 2024).

The results also indicate that antimicrobial resistance is not confined to hospital/clinical settings. Resistant bacteria and antimicrobial resistance genes persist and spread between environmental, animal and human populations with reservoirs in environmental, agricultural soils, wastewater, livestock production systems and manure amended ecosystems. All these transmission pathways underscore the need for use of a One Health approach that involves environmental, human and veterinary surveillance to gain a better understanding of resistance emergence and dissemination (Zhu et al., 2022). In addition, the changes in resistance patterns have been observed in hospital-based studies before and following the coronavirus disease 2019 (COVID-19) pandemic, indicating that alterations in antimicrobial use and infection prevention measures can significantly impact resistance trends over time (Taleb et al., 2023). Similarly, community-based surveillance studies have also identified continued resistance of common bacterial pathogens, which underscores the need for ongoing surveillance beyond the tertiary healthcare system (Islam et al., 2022).

The study has several strengths: The use of multicountry surveillance data, multiple bacterial pathogens, data capturing temporal observations and data capturing contextual healthcare indicators in the same analytical framework. However, the analyses used secondary surveillance data on an aggregate level only and were not able to adjust for patient level clinical characteristics and outcomes. Also, specific bacterial pathogens and antibiotic combinations were selected and might not necessarily reflect the extent of global antimicrobial resistance.

The overall results showed that antimicrobial resistance is still a heterogeneous global phenomenon with microbiological, geographical and healthcare related factors all playing a role. In the future,

antimicrobial resistance will continue to affect the impact of antimicrobial use and will require strengthening surveillance systems, responsible antimicrobial stewardship, improvements in diagnostic capacity, better infection prevention measures, and coordinated international public health policies to limit its impact and to support sustainable management of bacterial infections globally.

5. Conclusion

This study aimed to examine antimicrobial resistance trends in the most commonly reported bacterial pathogens worldwide from 2018 to 2023 based on surveillance data from multiple countries. The results showed that there was significant inter-country, inter-region and inter-species differences in resistance where *Acinetobacter* spp. had the highest pooled resistance and *Escherichia coli* the largest number of resistant isolates. Increasing trends in resistance were identified across the majority of the WHO regions in the regional analyses, and better healthcare systems and enhanced surveillance capacity were generally associated with lower levels of resistance. These findings highlight that there are complex interactions between microbiological, geographical and healthcare factors that impact on antimicrobial resistance, not just antimicrobial consumption. The research underscores the importance of integrated surveillance data for the identification of high-risk pathogens and differences between regions that can guide antimicrobial stewardship and public health interventions. Continued investment in strengthening surveillance systems, laboratory capacity, rational use of antimicrobials and infection prevention and control programmes is needed to help limit the spread of resistant bacterial pathogens. In the future, clinical data at the isolate level, genotypic resistance data and a more comprehensive geographical representation should be integrated into research to better understand resistance dynamics and evidence-based policy making. Together, these findings add to the evidence to help guide coordinated global action to maintain antimicrobial effectiveness and minimise the long-term burden of antimicrobial resistance.

References

1. Aggarwal, R., Mahajan, P., Pandiya, S., Bajaj, A., Verma, S. K., Yadav, P., ... & Johri, A. K. (2024). Antibiotic resistance: a global crisis, problems and solutions. *Critical Reviews in Microbiology*, 50(5), 896-921.
2. Ajulo, S., & Awosile, B. (2024). Global antimicrobial resistance and use surveillance system (GLASS 2022): Investigating the relationship between antimicrobial resistance and antimicrobial consumption data across the participating countries. *PloS one*, 19(2), e0297921.

3. Alhazmi, A. H., Alameer, K. M., Abuageelah, B. M., Alharbi, R. H., Mobarki, M., Musawi, S., ... & Dhayhi, N. (2023). Epidemiology and antimicrobial resistance patterns of urinary tract infections: a cross-sectional study from Southwestern Saudi Arabia. *Medicina*, 59(8), 1411.
4. Aljeldah, M. M. (2022). Antimicrobial resistance and its spread is a global threat. *Antibiotics*, 11(8), 1082.
5. Bertagnolio, S., Suthar, A. B., Tosas, O., & Van Weezenbeek, K. (2023). Antimicrobial resistance: strengthening surveillance for public health action. *PLoS Medicine*, 20(7), e1004265.
6. Darby, E. M., Trampari, E., Siasat, P., Gaya, M. S., Alav, I., Webber, M. A., & Blair, J. M. (2023). Molecular mechanisms of antibiotic resistance revisited. *Nature Reviews Microbiology*, 21(5), 280-295.
7. Hou, J., Long, X., Wang, X., Li, L., Mao, D., Luo, Y., & Ren, H. (2023). Global trend of antimicrobial resistance in common bacterial pathogens in response to antibiotic consumption. *Journal of Hazardous Materials*, 442, 130042.
8. Islam, M. A., Islam, M. R., Khan, R., Amin, M. B., Rahman, M., Hossain, M. I., ... & Riley, L. W. (2022). Prevalence, etiology and antibiotic resistance patterns of community-acquired urinary tract infections in Dhaka, Bangladesh. *Plos one*, 17(9), e0274423.
9. Lewnard, J. A., Charani, E., Gleason, A., Hsu, L. Y., Khan, W. A., Karkey, A., ... & Laxminarayan, R. (2024). Burden of bacterial antimicrobial resistance in low-income and middle-income countries avertible by existing interventions: an evidence review and modelling analysis. *The Lancet*, 403(10442), 2439-2454.
10. Li, X., Fan, H., Zi, H., Hu, H., Li, B., Huang, J., ... & Zeng, X. (2022). Global and regional burden of bacterial antimicrobial resistance in urinary tract infections in 2019. *Journal of clinical medicine*, 11(10), 2817.
11. Luo, Q., Lu, P., Chen, Y., Shen, P., Zheng, B., Ji, J., ... & Xiao, Y. (2024). ESKAPE in China: epidemiology and characteristics of antibiotic resistance. *Emerging microbes & infections*, 13(1), 2317915.
12. Mamoon, H. (2025). Global Antibiotic Resistance 2018–2023 | GLASS [Data set]. Kaggle. <https://www.kaggle.com/datasets/hussnainmamoon1/global-antibiotic-resistance-2018-2024-glass>
13. Mendelsohn, E., Ross, N., Zambrana-Torrel, C., Van Boeckel, T. P., Laxminarayan, R., & Daszak, P. (2023). Global patterns and correlates in the emergence of antimicrobial resistance in humans. *Proceedings of the Royal Society B: Biological Sciences*, 290(2007), 20231085.
14. Mestrovic, T., Aguilar, G. R., Swetschinski, L. R., Ikuta, K. S., Gray, A. P., Weaver, N. D., ... & Naghavi, M. (2022). The burden of bacterial antimicrobial resistance in the WHO European region in 2019: a cross-country systematic analysis. *The Lancet Public Health*, 7(11), e897-e913.

15. Munk, P., Brinch, C., Møller, F. D., Petersen, T. N., Hendriksen, R. S., Seyfarth, A. M., ... & Aarestrup, F. M. (2022). Genomic analysis of sewage from 101 countries reveals global landscape of antimicrobial resistance. *Nature Communications*, 13(1), 7251.
16. Naghavi, M., Vollset, S. E., Ikuta, K. S., Swetschinski, L. R., Gray, A. P., Wool, E. E., ... & Dekker, D. M. (2024). Global burden of bacterial antimicrobial resistance 1990–2021: a systematic analysis with forecasts to 2050. *The Lancet*, 404(10459), 1199-1226.
17. Okeke, I. N., de Kraker, M. E., Van Boeckel, T. P., Kumar, C. K., Schmitt, H., Gales, A. C., ... & Laxminarayan, R. (2024). The scope of the antimicrobial resistance challenge. *The Lancet*, 403(10442), 2426-2438.
18. Rahbe, E., Watier, L., Guillemot, D., Glaser, P., & Opatowski, L. (2023). Determinants of worldwide antibiotic resistance dynamics across drug-bacterium pairs: a multivariable spatial-temporal analysis using ATLAS. *The Lancet Planetary Health*, 7(7), e547-e557.
19. Samtiya, M., Matthews, K. R., Dhewa, T., & Puniya, A. K. (2022). Antimicrobial resistance in the food chain: trends, mechanisms, pathways, and possible regulation strategies. *Foods*, 11(19), 2966.
20. Sartorius, B., Gray, A. P., Weaver, N. D., Aguilar, G. R., Swetschinski, L. R., Ikuta, K. S., ... & Naghavi, M. (2024). The burden of bacterial antimicrobial resistance in the WHO African region in 2019: a cross-country systematic analysis. *The Lancet Global Health*, 12(2), e201-e216.
21. Silva, A., Costa, E., Freitas, A., & Almeida, A. (2022). Revisiting the frequency and antimicrobial resistance patterns of bacteria implicated in community urinary tract infections. *Antibiotics*, 11(6), 768.
22. Taleb, M. H., Elmanama, A. A., Taleb, A. H., & Tawfick, M. M. (2023). Pre-and post-COVID-19 antimicrobial resistance profile of bacterial pathogens, a comparative study in a tertiary hospital. *The Journal of Infection in Developing Countries*, 17(05), 597-609.
23. Walsh, T. R., Gales, A. C., Laxminarayan, R., & Dodd, P. C. (2023). Antimicrobial resistance: addressing a global threat to humanity. *PLoS medicine*, 20(7), e1004264.
24. Wise, M. G., Karlowsky, J. A., Mohamed, N., Hermsen, E. D., Kamat, S., Townsend, A., ... & Sahm, D. F. (2024). Global trends in carbapenem-and difficult-to-treat-resistance among World Health Organization priority bacterial pathogens: ATLAS surveillance program 2018–2022. *Journal of global antimicrobial resistance*, 37, 168-175.
25. Zhu, L., Lian, Y., Lin, D., Huang, D., Yao, Y., Ju, F., & Wang, M. (2022). Insights into microbial contamination in multi-type manure-amended soils: The profile of human bacterial pathogens, virulence factor genes and antibiotic resistance genes. *Journal of hazardous materials*, 437, 129356.