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Changing climate and socioeconomic factors contribute to global antimicrobial resistance

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Climate change poses substantial challenges in containing antimicrobial resistance (AMR) from a One Health perspective. Using 4,502 AMR surveillance records involving 32 million tested isolates from 101 countries (1999–2022), we analyzed the impact of socioeconomic and environmental factors on AMR. We also established forecast models based on several scenarios, considering antimicrobial consumption reduction, sustainable development initiatives and different shared socioeconomic pathways under climate change. Our findings reveal growing AMR disparities between high-income countries and low- and middle-income countries under different shared socioeconomic pathway scenarios. By 2050, compared with the baseline, sustainable development efforts showed the most prominent effect by reducing AMR prevalence by 5.1% (95% confidence interval (CI): 0.0–26.6%), surpassing the effect of antimicrobial consumption reduction. Key contributors include reducing out-of-pocket health expenses (3.6% (95% CI: −0.5 to 21.4%)); comprehensive immunization coverage (1.2% (95% CI: −0.1% to 8.2%)); adequate health investments (0.2% (95% CI: 0.0–2.4%)) and universal access to water, sanitation and hygiene services (0.1% (95% CI: 0.0–0.4%)). These findings highlight the importance of sustainable development strategies as the most effective approach to help low- and middle-income countries address the dual challenges of climate change and AMR.

Antimicrobial resistance (AMR) is a main threat to global health. The current estimate shows that bacterial AMR is responsible for approximately 1.14 million deaths in 2021, with an expected increase to 1.91 million deaths in 2050 (ref. 1). It disproportionately affects low- and middle-income countries (LMICs)[1–3], and goes beyond increasing healthcare costs by undermining patient care outcomes[4]. Extensive research has identified several factors contributing to AMR, with the overuse and misuse of antimicrobials being a primary driver. However, addressing AMR in healthcare alone is not enough[5,6]; agricultural practices[7], animal husbandry[8] and wastewater treatment[9] also play a role. This highlights the need for a comprehensive AMR management strategy that integrates these various factors.

Climate change is believed to substantially worsen the AMR crisis[10–12]. Environmental events associated with climate change such as rising ambient temperatures[13–16], air pollution[17,18] and extreme weather events such as floods[19–21], have increasingly concerning impacts on the development and spread of AMR. However, the complex nature of climate change effects and uncertainty surrounding future scenarios make it challenging to quantify the exact influence of climate change on AMR[22].

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Table 1 | Policy summary

Background	AMR poses a substantial threat to global health. At the 79th UNGA HLM on AMR, global leaders committed to reduce human deaths from AMR by 10% by 2030. However, little research has explored the evolving nature of AMR in the broader context of climate change and socioeconomic conditions, particularly in LMICs.
Main findings and limitations	We identified several factors associated with global AMR, including air pollutant fine particulate matter ($PM_{2.5}$), surface and subsurface runoff, health expenditures, out-of-pocket healthcare payments, immunization coverage and AMC. By 2050, sustainable development efforts are projected to reduce AMR prevalence by 5.1% (95% CI, 0.0–26.6%), surpassing the effect of reducing AMC (2.1% (95% CI, 0.1–6.7%)). Key drivers of this reduction include lowering out-of-pocket health expenses, increasing health investments, ensuring universal access to WASH services and expanding immunization coverage. However, long-term climate change impacts are expected to continue influencing AMR dynamics. Under the worst-case scenario, compared with a sustainable low-emission pathway, AMR prevalence is projected to increase by 0.9% to 4.1% by 2050 in different income-level countries. Limitations of this study include the inability to establish causal relationships due to the use of ecological models, the exclusion of certain potential AMR influencers, variability in AMR surveillance data quality, and the complex interactions between climate change, socioeconomic development and the COVID-19 pandemic.
Policy implications	Particular attention should be directed toward LMICs, which bear substantial AMR burdens but have limited economic resources. Efforts should prioritize supporting these regions in implementing effective AMR control measures through a One Health approach, recognizing the health of people, animals and the wider environment, including ecosystem, are closely linked. Addressing the complex interplay between climate change, human activities and AMR demands sustained research, informed policy development and the implementation of targeted interventions.

Studies emphasize the importance of mitigating AMR risks through measures such as improving environmental sanitation, ensuring access to clean water, promoting effective antibiotic stewardship, increasing public health funding, improving microbiological testing infrastructure, enhancing AMR surveillance and implementing stricter regulation of the private health sector[1,23,24]. LMICs face unique challenges in the fight against AMR due to issues such as poverty, corruption, inadequate sanitation and poor testing infrastructure, which exacerbate AMR compared with their high-income country (HIC) counterparts[25–27]. Additionally, LMICs often face the difficult choice between investing in infrastructure and combating AMR[28], further complicated by limited expertise, low public awareness, insufficient monitoring, restrictive regulatory environments and fragile healthcare systems[29,30]. Developing effective AMR intervention strategies within the resource and infrastructure constraints of LMICs is crucial.

Given the disparities between LMICs and HICs in addressing AMR challenges, it is essential to expand AMR response strategies beyond infection control and new antimicrobial development[31]. This is particularly important considering the disproportionate impact of climate change on LMICs, despite their lower contribution to climate change. Overemphasizing a single driver of AMR can hinder a comprehensive assessment of how various factors, particularly climate change, influence the development of AMR. In this study, we analyzed global surveillance data on the World Health Organization (WHO) critical priority drug-resistant bacterial strains to investigate potential climate and socioeconomic determinants of AMR[32]. Table 1 summarizes our main findings and policy implications.

Results

Spatiotemporal distribution of AMR

Our study collated 4,502 records from 101 countries, using data from ResistanceMap, the Global Antimicrobial Resistance and Use Surveillance System (GLASS), the European Antimicrobial Resistance Surveillance Network (EARS-Net), the Central Asian and European Surveillance of Antimicrobial Resistance (CAESAR) network and the China Antimicrobial Resistance Surveillance System (CARSS)[33–37]. These datasets encompassed over 32 million tested isolates of six AMR profiles, including third-generation cephalosporin-resistant *Escherichia coli* (3GCREC), *Klebsiella pneumoniae* (3GCRKP) and carbapenem-resistant *E. coli* (CREC), *K. pneumoniae* (CRKP), *Acinetobacter baumannii* (CRAB) and *Pseudomonas aeruginosa* (CRPA) (Supplementary Table 1-1). However, the available data were not proportionally represented across countries or regions (Supplementary Table 1-2). In some regions, a large proportion of countries did not report data: 83.3% in Latin America and the Caribbean, 70.8% in Sub-Saharan Africa and 57.9% in East Asia and the Pacific. Other regions with some data gaps included the Middle East and North Africa (31.8%), Europe and Central Asia (29.3%), and South Asia (25.0%). Countries marked in gray in Fig. 1 indicate those lacking relevant data.

We observed higher average AMR prevalence in regions such as South Asia (33.5%), the Middle East and North Africa (30.7%), and Sub-Saharan Africa (19.6%). Countries like India, Iran and Egypt exhibited an average AMR prevalence exceeding 50% (Fig. 1a). Regarding the annual growth of AMR, the Middle East and North Africa (4.3% annual growth rate) and Latin America and the Caribbean (1.9% annual growth rate) showed notable increases, with countries such as Malawi, Oman and Bahrain leading this trend—all exceeding annual growth rates of 5%. In contrast, countries including Georgia, the Philippines, Myanmar, Jordan, Egypt and China demonstrated a gradual decline in AMR prevalence (Fig. 1b). The distribution and progression of various AMR profiles are presented in Extended Data Figs. 1 and 2, showing similar patterns.

Overall, there was an increase in the prevalence of AMR since 2000 in countries across all income groups, despite varying growth rates (0.4% annual growth rate (95% confidence interval (CI), −3.2% to 4.1%)) and even declining AMR in 20 countries. HICs showed a slower rate (0.3% (95% CI, −0.5% to 3.8%)) of increase in AMR prevalence compared with LMICs (0.4% (95% CI, −0.7% to 4.1%)) (Fig. 2a).

Substantial variations in AMR prevalence across different profiles were observed: 3GCREC, 3GCRKP and CRAB were notably higher, averaging above 20%, compared with CREC and CRKP. With the exception of CRPA, there was an increasing trend of AMR in all other resistance profiles, with 3GCREC exhibiting the most rapid growth rate (Fig. 2b).

Factors associated with AMR

Multivariable analyses identified several socioeconomic and environmental factors associated with AMR (Supplementary Table 2). Average AMR prevalence was correlated positively with air pollutant fine particulate matter ($PM_{2.5}$, $\mu g\ m^{-3}$) (0-year lag) (odds ratio (OR) = 1.02; 95% CI, 1.01–1.04), surface runoff (100 mm) (2-year lag) (OR = 1.22; 95% CI, 1.05–1.40), out-of-pocket health costs (percentage of health expenditures) (3-year lag) (OR = 1.02; 95% CI, 1.01–1.03) and antimicrobial consumption (AMC) (defined daily doses (DDD) $1{,}000^{-1}\ day^{-1}$) (2-year lag) (OR = 1.02; 95% CI, 1.00–1.03). In contrast, average AMR prevalence was associated negatively with subsurface runoff (100 mm) (2-year lag) (OR = 0.84; 95% CI, 0.76–0.93), health expenditure (percentage of gross domestic product (GDP)) (4-year lag) (OR = 0.93; 95% CI, 0.87–1.00) and immunization coverage (percentage of eligible population) (2-year lag) (OR = 0.99; 95% CI, 0.98–1.00). Further analyses of specific AMR profiles and lag years confirmed these associations, with a few exceptions: the prevalence of CRAB (3-year lag) was associated positively with temperature change (°C) (OR = 1.23; 95% CI, 1.06–1.43), the prevalence of 3GCREC (3-year and 1-year lag) was associated positively with international tourism

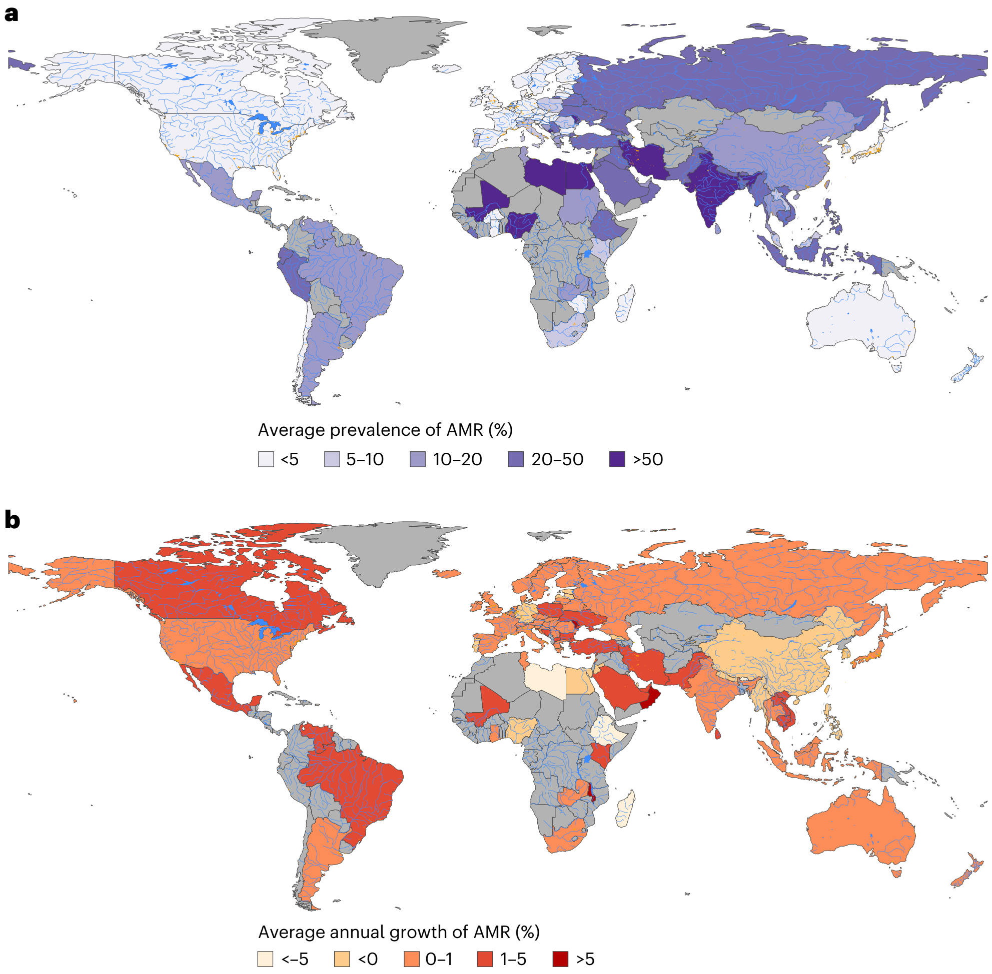


Fig. 1 | Global distribution and annual changes in AMR. a, Average prevalence of AMR across different countries and regions. **b**, Average annual growth of AMR prevalence across different countries and regions. Average values were derived from the slopes of linear fits between AMR rates and time. Gray areas, regions with no available data.

(log(persons)) (OR = 1.04; 95% CI, 1.01–1.07) and population density (log(persons km^{-2})) (OR = 1.51; 95% CI, 1.17–1.97) and the prevalence of 3GCRKP (4-year lag) (OR = 0.99; 95% CI, 0.98–0.99) and CRPA (0-year lag) (OR = 0.99; 95% CI, 0.98–0.99) showed negative associations with the corruption perceptions index (CPI) (Fig. 3).

Sensitivity analysis based on the EARS-Net further validated the results, confirming significant effects of subsurface runoff (OR = 0.80; 95% CI, 0.70–0.91), health expenditure (OR = 0.94; 95% CI, 0.89–0.99), out-of-pocket health costs (OR = 1.02; 95% CI, 1.01–1.04) and immunization coverage (OR = 0.97; 95% CI, 0.95–0.99) on AMR prevalence. However, it did not reveal significant effects of surface runoff or AMC, possibly due to insufficient differentiation in geographical location and income levels among the participating countries (Extended Data Fig. 3).

We extended the original multivariable regression models by incorporating additional factors with limited monitoring data to assess their potential contributions to AMR. These factors included the consumption of different classes of antimicrobial agents, educational attainment and animal AMC. The results indicated a positive relationship between AMR prevalence and AMC (DDD 1,000^{-1} day^{-1}), driven primarily by the use of other beta-lactam antibiotics and fluoroquinolones. In contrast, tetracyclines (OR = 0.86; 95% CI, 0.78–0.94), sulfonamides and trimethoprim (OR = 0.77; 95% CI, 0.62–0.96) and aminoglycosides (OR = 0.19; 95% CI, 0.07–0.51) seemed to be correlated negatively with AMR prevalence (Fig. 4a). Regarding educational attainment, secondary school enrollment (percentage of school-age population) (OR = 1.00; 95% CI, 1.00–1.01) was associated positively with average AMR prevalence, but this relationship was not observed in any specific AMR profiles (Fig. 4b). Regarding animal AMC (mg kg^{-1}), the use of fluoroquinolones (OR = 1.06; 95% CI, 1.01–1.12) seemed to contribute to the increasing prevalence of average AMR, whereas cephalosporins (OR = 0.43; 95% CI, 0.24–0.76) had the opposite effect. However, CREC was associated positively with antibiotic consumption, while 3GCREC showed a negative correlation with the consumption of several types of animal antibiotics. The consumption of cephalosporins in animals was correlated negatively with many AMR profiles (Fig. 4c).

Forecasts of AMR under different scenarios

To assess the impact of climate change and socioeconomic development on AMR, we combined varying levels of socioeconomic development, AMC and shared socioeconomic pathways (SSPs) to construct a series of AMR development scenarios until 2050 (Extended Data Fig. 4). SSPs are a set of global development scenarios that integrate socioeconomic trends with climate change outcomes, providing a framework to assess how different societal choices—such as economic growth, inequality and environmental policies—shape future climate risks and adaptation challenges[22].

The results indicated that a 50% reduction in AMC could lower AMR by an average of 2.1% (95% CI, 0.1–6.7%) by 2050. However, this reduction was smaller than the potential benefits of sustainable development

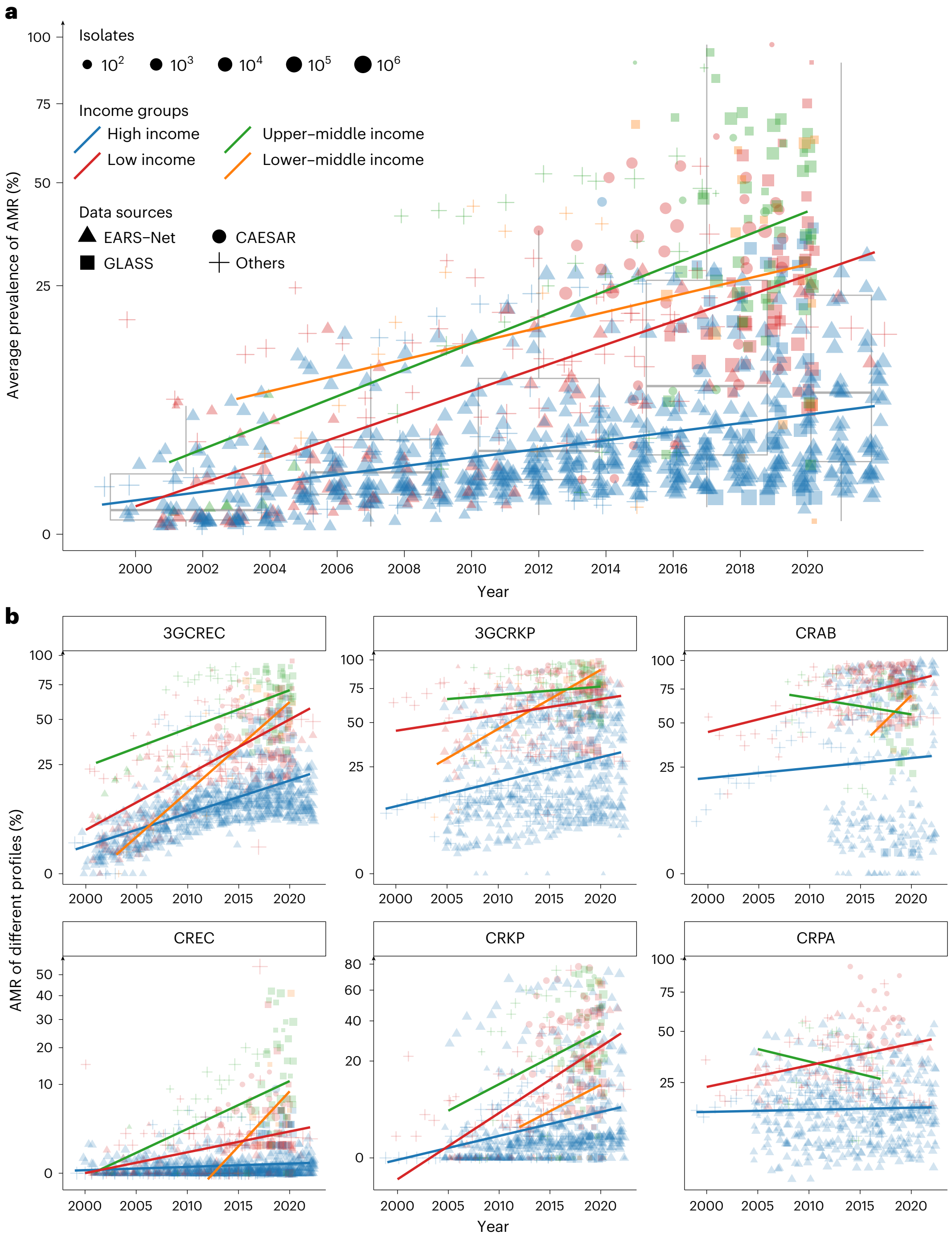


Fig. 2 | Changing trends in AMR across different income groups. a, Average prevalence of AMR. **b**, Prevalence of six AMR profiles. Income levels were classified by the World Bank Atlas method, which categorizes economics based on gross national income per capita.

efforts, which could reduce AMR by 5.1% (95% CI, 0.0–26.6%) (Fig. 5a). For different resistant profiles, the decrease in the prevalence of 3GCREC, CREC and CRAB seem to be more dependent on sustainable development efforts, whereas 3GCRKP, CRKP and CRPA seem to be more dependent on reduced AMC (Extended Data Fig. 5).

Across all four SSPs scenarios, AMR prevalence was generally lowest under the sustainable low-emission pathway scenario (SSP1-2.6 in Fig. 5a). By 2050, under the worst-case scenario (SSP5-8.5 in Fig. 5a), AMR was projected to increase by 2.4% (95% CI, −2.9% to 14.3%). Specifically, the projected increases were 0.9% (95% CI, −0.9% to 5.5%) in HICs, 1.6% (95% CI, −3.9% to 7.1%) in upper-middle-income countries, 4.1% (95% CI, −5.2% to 22.3%) in LMICs and 3.3% (95% CI, −0.7% to 13.8%) in low-income countries (Fig. 5a).

Among the four specific intervention measures for sustainable development—increased health investment; reduced out-of-pocket expenses; access to water, sanitation and hygiene (WASH) services; and full immunization coverage—reducing out-of-pocket expenses was associated with the greatest reduction of AMR by 3.6% (95% CI, −0.5% to 21.4%). This was followed by full immunization coverage (1.2% (95% CI, −0.1% to 8.2%)). Increased health investment (0.2% (95% CI, 0.0–2.4%)) and WASH coverage (0.1% (95% CI, 0.0–0.4%]) seemed to have minimal effects on AMR (Fig. 5b). In contrast to the resistant *E. coli*

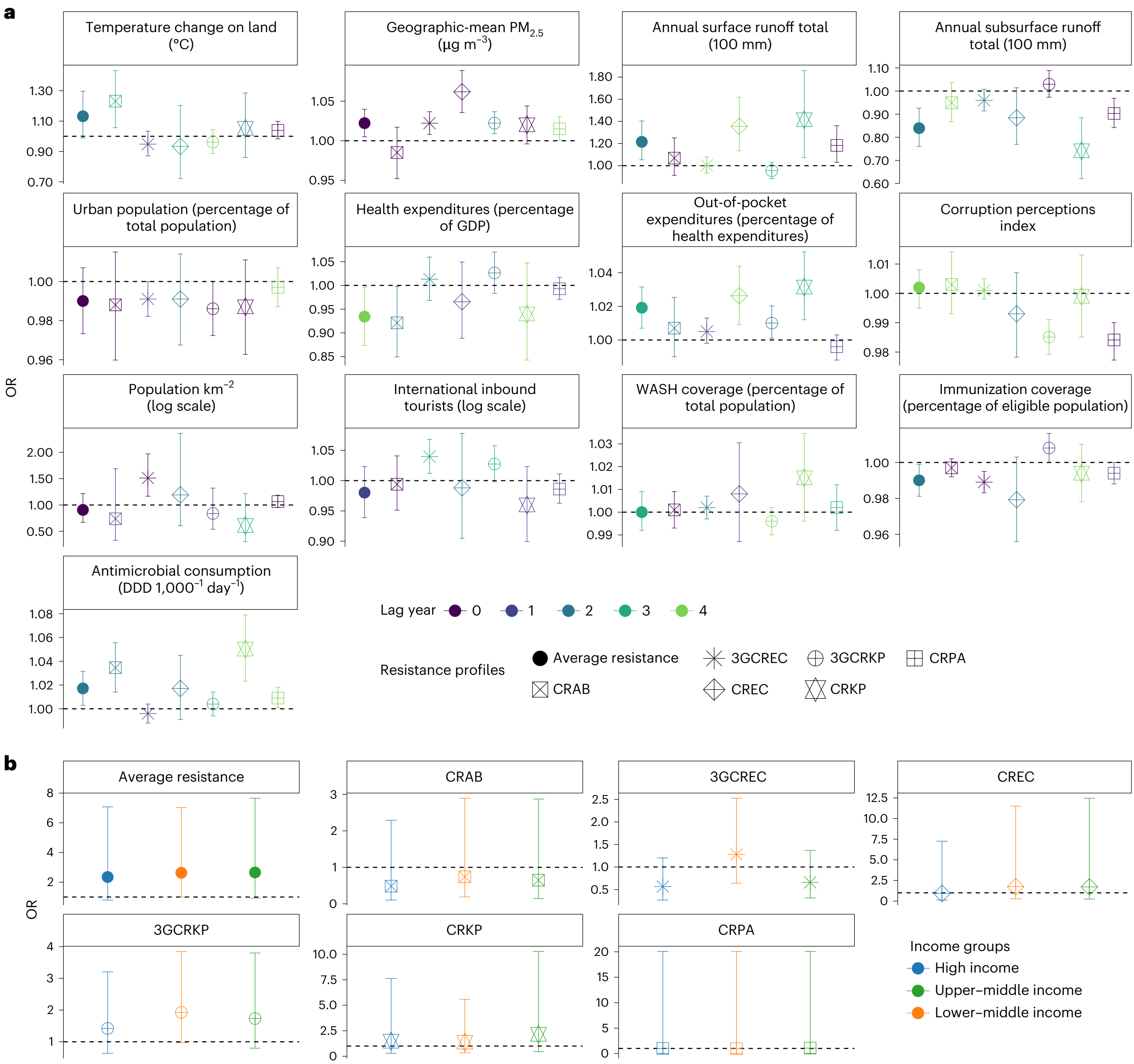


Fig. 3 | Adjusted ORs of predictors of AMR prevalence on average and for specific AMR profiles and lag years. Spatial–temporal mixed-effects models with structured random effects were fitted independently for each AMR profile. Results are presented as adjusted ORs (points) with 95% CIs (error bars). The analysis included 975 independent biological observations for average AMR, with specific profiles comprising 945 (3GCREC), 805 (3GCRKP), 870 (CREC), 774 (CRKP), 510 (CRAB) and 598 (CRPA) observations, respectively. Each observation represents a distinct country–year geographical unit. The optimal lag year for each predictor was determined by selecting the model with the minimum DIC value. **a**, Effects of quantitative variables, including environmental and socioeconomic factors. **b**, Influence of income group, demonstrating no statistically significant effect of income classification on AMR patterns after adjusting for potential confounding factors.

and *K. pneumoniae* strains, whose decrease showed greater benefits from reduced out-of-pocket expenses, the reduction in CRAB was more affected by access to WASH services, while CRPA was more affected by full immunization coverage (Extended Data Fig. 6).

Discussion

Understanding the multifaceted influence of socioeconomic and environmental determinants on the spread of AMR is an important step in formulating and implementing strategies to combat AMR. Through an approach involving ignoring the heterogeneity between surveillance networks, our research has found that air pollutant PM$_{2.5}$, surface runoff, subsurface runoff, health expenditures, out-of-pocket healthcare payments, immunization coverage and AMC are associated with global AMR. Rising ambient temperatures are also associated with an increasing prevalence of CRAB. The forecast modeling underscores the disparate trajectories of AMR in countries distinguished by different development policies and economic tiers. Particularly, it accentuates the challenges LMICs face in combating AMR in the context of climate change, underscoring the critical need for integrating AMR management within the sustainable development framework.

Our quantitative analysis connects AMR with a range of environmental factors associated with climate change. Previous studies have demonstrated that these factors probably have direct or indirect effects on the proliferation of drug-resistant bacteria and the horizontal transmission of AMR genes[18,38–41]. Rising temperatures are among the most tangible effects of climate change, and the impact of ambient temperature on AMR was first observed in studies conducted in the United States and Europe[14–16]. However, some researchers have suggested that this association may be confounded by socioeconomic factors[42]. In this study, we confirmed a positive association between ambient temperature and prevalence of CRAB. This finding contrasts with our previous results, which demonstrated a positive association between ambient temperature and CRKP and CRPA, but not CRAB[13]. This discrepancy underscores the existence of species-specific responses to temperature elevation among bacterial pathogens. For instance, in *A. baumannii*, low temperatures upregulate resistance genes (for example, *adeJ*, *oxa-51* and *oxa-23*) and enhance meropenem stress tolerance[43], whereas in *P. aeruginosa*, elevated temperatures inactivate genes such as *PA3242* and *PA0011*, leading to outer membrane destabilization and increased carbapenem susceptibility[44,45]. These pathogen-specific mechanisms highlight the complex, temperature-dependent nature of AMR evolution. Of particular concern is the potential for sustained warming to reduce the fitness cost associated with resistance mutations, thereby enabling resistant bacterial populations to persist without evolutionary trade-offs[10,46]. This phenomenon could lead to the establishment of persistent AMR reservoirs in the context of ongoing climate change, emphasizing the importance of identifying temperature-sensitive pathogens for the development of targeted mitigation strategies.

We observed an association between $PM_{2.5}$ and AMR, consistent with a previous study[17]. As a common air pollutant, $PM_{2.5}$ can penetrate deep into the lungs and enter the bloodstream, which could lead to cardiovascular (ischemic heart disease), cerebrovascular (stroke) and respiratory impacts[47]. The mechanisms through which $PM_{2.5}$ may influence AMR development are multifaceted. First, $PM_{2.5}$ particles can serve as vectors for drug-resistant bacteria or genetic material, thereby facilitating their transmission between environmental reservoirs and human hosts[17,18]. Second, $PM_{2.5}$ exposure may indirectly promote AMR development by exacerbating respiratory conditions, consequently increasing the demand for antibiotic treatments. This mechanistic pathway is supported by empirical evidence demonstrating that short-term exposure to air pollution correlates with elevated antimicrobial usage following primary care consultations for acute respiratory symptoms in the general population[48]. Although antibiotic pollutants and AMR genes have been detected in various aquatic environments, little is known about the factors influencing the transmission of resistant microorganisms between humans and the environment[49]. Although many studies have highlighted the AMR risks associated with flooding[19–21], our study provides evidence that runoff is correlated with AMR.

Socioeconomic factors are critical determinants of AMR, with AMC being one of the most concerning contributors. Previous ecological studies have reported inconsistent correlations between AMC and AMR, raising questions about the effectiveness of limiting AMC as a standalone strategy for AMR containment[23,50,51]. One possible confounding factor is the dynamics of AMR transmission among hosts, which may not be fully addressed by simply reducing antimicrobial usage[5]. Using a spatial–temporal mixed-effects model, we observed a positive association between AMC and AMR, with particularly strong impacts from certain classes of antibiotics, including beta-lactams and fluoroquinolones. These findings suggest that optimizing antimicrobial usage patterns could help curb AMR crisis. This optimization could involve increasing the use of less frequently prescribed antibiotics, such as tetracyclines, sulfonamides, trimethoprim and aminoglycosides. Additionally, expanding immunization coverage and improving WASH initiatives could be effective strategies to reduce AMR by lowering the need for antimicrobial treatments for infectious diseases[52–54]. Even after adjusting for AMC, we observed an independent effect of immunization that extends beyond reducing antimicrobial usage. This finding potentially highlights the role of vaccines in preventing pathogen colonization[52].

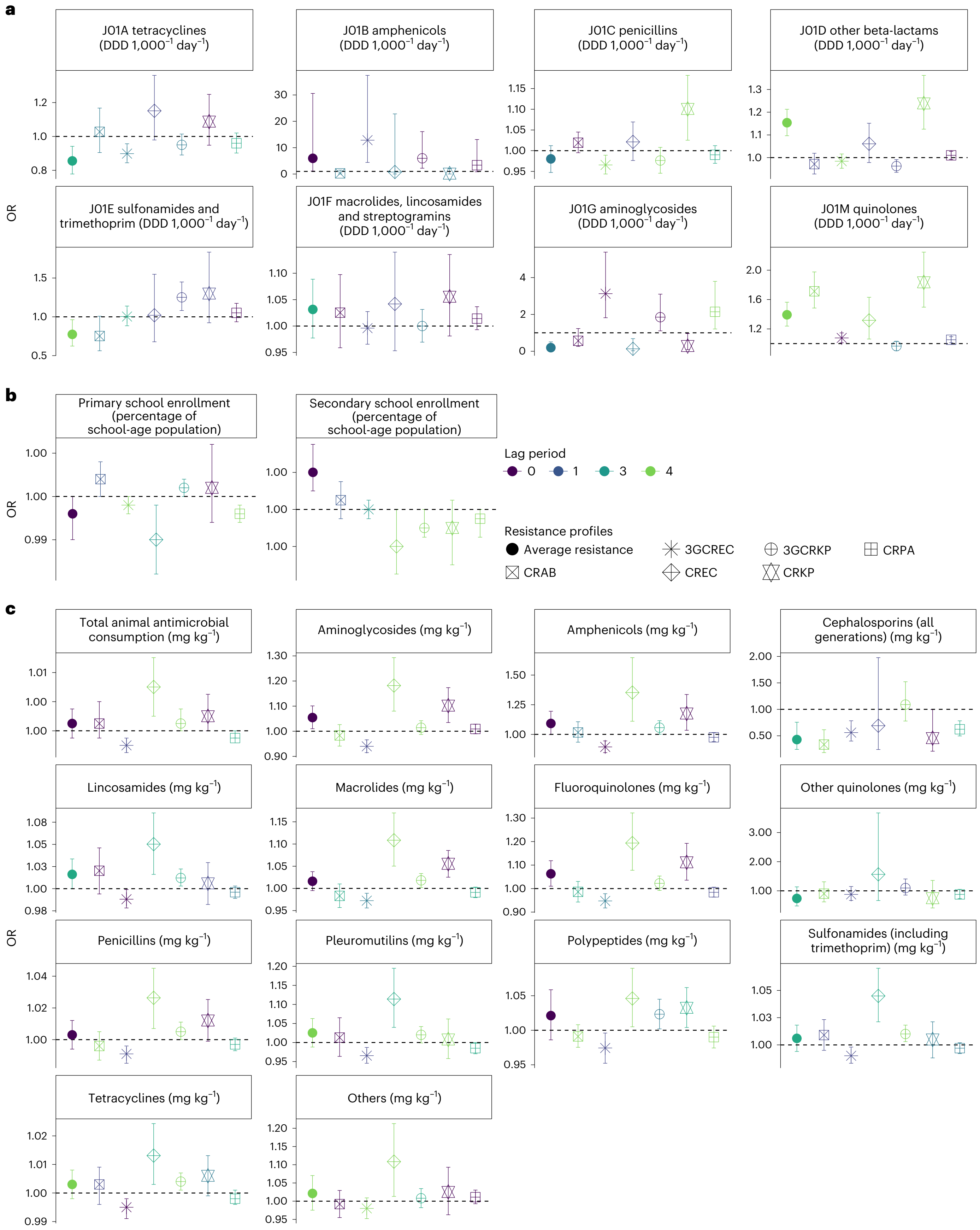
In addition to AMC, demographic factors also warrant attention. Our analysis found that high population density was positively associated with prevalence of 3GCREC, as previous studies have correlated this with increased AMR[55]. In areas with underdeveloped social systems, increased population density may be a main factor contributing to elevate pathogen transmission. In more developed regions, factors such as high immunization coverage and access to WASH facilities could mitigate the potential impact of population density on AMR[56]. Moreover, our findings highlight the role of human mobility in shaping certain AMR profiles, such as 3GCREC. Human mobility, particularly driven by the growing international tourism industry, has emerged as a critical factor in the global spread of AMR[57]. Travelers visiting regions with high levels of resistance are at increased risk of encountering resistant bacteria, which they may carry back to their home countries, thereby potentially contributing to the worldwide dissemination of these pathogens[58,59].

In our analysis, economic factors were found to be correlated with the development of AMR that was just as comparable as AMC. Higher out-of-pocket health costs and lower health expenditures were both associated with increased AMR. High out-of-pocket expenses, in particular, reflect excessive prescriptions and reduced quality standards[60]. Increasing investment in health funding for new medicines, diagnostic tools, vaccines, and other interventions remains a cornerstone of the global action plan on AMR[61]. Furthermore, our findings revealed a negative correlation between poor governance—measured by the CPI—on the prevalence of 3GCRKP and CRPA. This underscores the critical role of effective government regulations in curbing irrational antibiotic prescriptions[27].

Scenario simulations further highlight the impacts of socioeconomic factors on AMR. Specifically, compared with limiting AMC, sustainable development efforts that emphasize universal access to WASH services, comprehensive immunization coverage, adequate health investments and affordable out-of-pocket healthcare costs can help LMICs better address AMR challenges. Additionally, our analysis suggested the impact of the COVID-19 pandemic on socioeconomic factors, such as the decline in international travel, increased AMC and higher out-of-pocket health expenditures. These interconnected factors introduce further uncertainty regarding the future trajectory of AMR, especially in LMICs. Therefore, considering the diverse resource availability, needs and priorities in LMICs, focusing on foundational health measures may be a more practical approach than allocating limited resources to the development of new antibiotics and diagnostic strategies[31].

At the 2024 United Nations General Assembly (UNGA) High-Level Meeting (HLM) on AMR, member states adopted a political declaration to address AMR through a 'One Health' approach[62]. This declaration

Fig. 4 | Adjusted ORs of additional predictors of AMR on average and for specific AMR profiles and lag years. Spatial–temporal mixed-effects models with structured random effects were fitted independently for each AMR profile. Results are presented as adjusted ORs (points) with 95% CIs (error bars). The analysis included 975 independent biological observations for average AMR, with specific profiles comprising 945 (3GCREC), 805 (3GCRKP), 870 (CREC), 774 (CRKP), 510 (CRAB) and 598 (CRPA) observations, respectively. Each observation represents a distinct country–year geographical unit. The optimal lag year for each predictor was determined by selecting the model with the minimum DIC value. **a**, Impact of consumption of different classes of antimicrobial agents on AMR prevalence. **b**, Influence of educational factors on AMR prevalence. **c**, Effect of animal AMC on human AMR prevalence.


a
OR
J01A tetracyclines (DDD 1,000^{-1} day^{-1})
0.8
1.0
1.2
J01B amphenicols (DDD 1,000^{-1} day^{-1})
0
10
20
30
J01C penicillins (DDD 1,000^{-1} day^{-1})
0.95
1.00
1.05
1.10
1.15
J01D other beta-lactams (DDD 1,000^{-1} day^{-1})
1.0
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1.2
1.3
J01E sulfonamides and trimethoprim (DDD 1,000^{-1} day^{-1})
0.5
1.0
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J01F macrolides, lincosamides and streptogramins (DDD 1,000^{-1} day^{-1})
0.95
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1.10
J01G aminoglycosides (DDD 1,000^{-1} day^{-1})
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2
4
J01M quinolones (DDD 1,000^{-1} day^{-1})
1.2
1.6
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b
OR
Primary school enrollment (percentage of school-age population)
0.99
1.00
1.00
Secondary school enrollment (percentage of school-age population)
1.00
1.00
1.00
Lag period
0
1
3
4
Resistance profiles
Average resistance
3GCREC
3GCRKP
CRPA
CRAB
CREC
CRKP
c
OR
Total animal antimicrobial consumption (mg kg^{-1})
1.00
1.00
1.01
Aminoglycosides (mg kg^{-1})
0.90
1.00
1.10
1.20
1.30
Amphenicols (mg kg^{-1})
1.00
1.25
1.50
Cephalosporins (all generations) (mg kg^{-1})
0.50
1.00
1.50
2.00
Lincosamides (mg kg^{-1})
0.98
1.00
1.03
1.05
1.08
Macrolides (mg kg^{-1})
0.95
1.00
1.05
1.10
1.15
Fluoroquinolones (mg kg^{-1})
0.90
1.00
1.10
1.20
1.30
Other quinolones (mg kg^{-1})
1.00
2.00
3.00
Penicillins (mg kg^{-1})
1.00
1.02
1.04
Pleuromutilins (mg kg^{-1})
0.95
1.00
1.05
1.10
1.15
1.20
Polypeptides (mg kg^{-1})
0.95
1.00
1.05
Sulfonamides (including trimethoprim) (mg kg^{-1})
1.00
1.03
1.05
Tetracyclines (mg kg^{-1})
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Others (mg kg^{-1})
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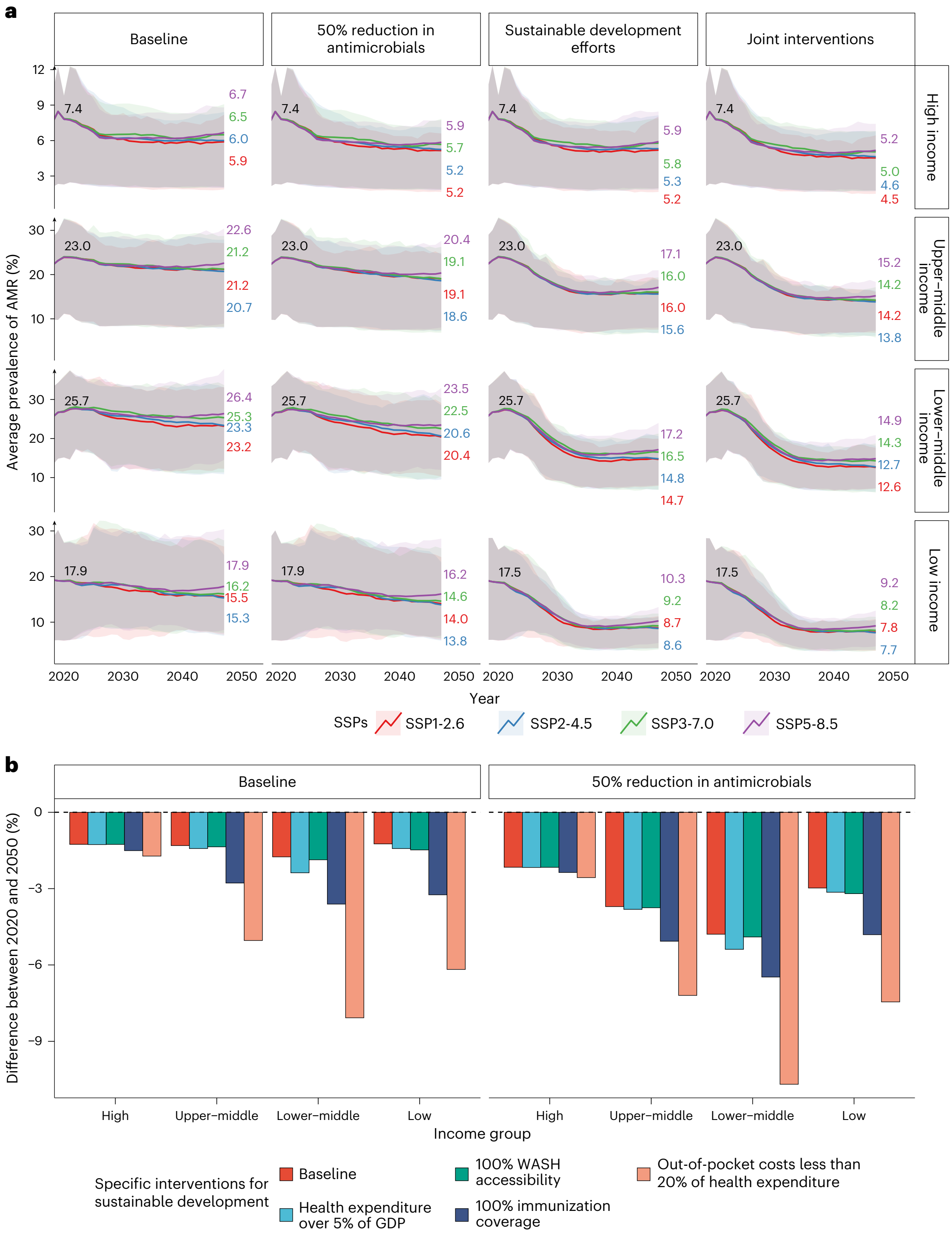

Fig. 5 | Forecasting AMR across different countries under various scenarios. We used mixed-effects models to perform linear extrapolation forecasts of the outcomes. **a**, Trends in average AMR under different scenarios. Results are presented as mean estimates (lines) with interquartile ranges (shaded areas). Sustainable development efforts refer to four specific intervention measures to curb AMR. **b**, Impact of individual intervention measures on AMR development.

sets targets, including a 10% reduction in AMR-related deaths by 2030, and the allocation of US$100 million in catalytic funding to achieve at least 60% of countries having national action plans on AMR by 2030. Crucially, it emphasizes multisectoral coordination across human health, agriculture and environmental sectors—a framework that aligns closely with our findings on the interconnected roles of socioeconomic, environmental and healthcare determinants in driving AMR.

Our findings provide evidence to operationalize the 2024 UNGA declaration on AMR in guiding LMICs' prioritization of interventions. Although reducing AMC yields modest AMR reductions (2.1% by 2050), sustainable development strategies—emphasizing equitable healthcare access and climate resilience—offer 2.4-fold greater benefits (5.1% reduction). This aligns with the declaration's call for multisectoral action, as our future scenario analyses reveal that SSP1-2.6 (sustainable pathway) minimizes AMR burden by synergistically addressing socioeconomic disparities. LMICs face disproportionate risks: under SSP5-8.5 (high emissions/inequality), LMICs may experience up to 22.3% AMR increases. To maximize effects, LMICs should prioritize (1) reducing out-of-pocket health expenses, which curbs irrational antibiotic use driven by unaffordable diagnostics; (2) scaling immunization, particularly for CRPA-prone regions and (3) context-specific WASH investments, crucial for curbing CRAB transmission. These measures directly support the UNGA's funding targets for national action plans. By embedding these priorities within climate adaptation frameworks (for example, flood-resistant WASH systems) and governance reforms (for example, anticorruption measures), LMICs can transform the 'One Health' approach into localized interventions.

Although the immediate effects of climate change on AMR may not be as evident as those driven by sustainable development efforts or reductions in AMC, the long-term impact of climate change on AMR presents a considerable challenge[10]. Climate change can exacerbate AMR through several pathways. Extreme weather events, such as heavy rainfall and floods, critically challenge AMR prevention efforts in LMICs. These events not only increase the risk of AMR spread but also threaten to destabilize already vulnerable health infrastructure, complicating antimicrobial stewardship and infection prevention efforts[63]. Furthermore, climate change, in combination with human activities, is altering animal habitats and natural microbial ecosystems, which increases the likelihood of zoonotic and vector-borne diseases[11,12]. Environmental degradation, particularly air pollution and changes in surface runoff due to urbanization and the spread of impermeable surfaces, further exacerbates these risks by disrupting urban hydrological cycles and potentially facilitating the wider spread of AMR[64]. These challenges highlight the urgent need for global cooperation in developing and implementing strategies to address the interconnected and evolving threats posed by climate change and AMR[65].

This study has several limitations that warrant attention. First, our ability to draw causal inferences is limited due to the lack of a clear causal sequence. The study relies on ecological models, which limits the establishment of definitive causal links between the factors studied and AMR. For instance, it remains challenging to determine whether AMC drives the development of AMR or whether increased AMR leads to greater AMC. Consequently, when highlighting the effects of interventions, we relied on factors validated by existing evidence and grounded in hypothesized causal mechanisms, rather than exclusively on data-driven variables. However, we explored the lagged associations between important covariates and current AMR prevalence to provide further context.

Second, some variables that have been reported as potential influencers of AMR dynamics, such as education, antimicrobial use in food production and animal husbandry[66], were not included in our primary model. However, where feasible, some of these factors were incorporated into supplementary analyses to assess their potential impacts. This study does not include analyses or reporting related to sex or gender, as it relies on aggregated national and annual-level data that do not necessitate gender-specific analysis.

Third, the variability in the quality and standards of AMR surveillance data across different networks presents a challenge to comparability[67,68]. This limitation undermines the robustness of data analyses, as it constrains our ability to make meaningful comparisons between regions or over time. Moreover, relying solely on patient data for passive surveillance may lead to an overestimation of AMR in the community, as these data may not fully represent the broader population. This limitation should be considered when interpreting the findings and generalizing to the wider community. Given the scarcity of surveillance data in LMICs, careful interpretation and generalization of the model estimation results are necessary.

Finally, climate change and socioeconomic development are intertwined, rather than independent factors, as assumed in our forecast modeling. Specifically, environmental and socioeconomic changes are mutually influential. Additionally, the COVID-19 pandemic has simultaneously impacted various socioeconomic factors, particularly international tourist numbers and antibiotic consumption data[69], underscoring the need for ongoing monitoring and periodic reassessment. Despite these complexities, the ecological model remains a valuable tool for assessing factors that affect AMR transmission[70].

In conclusion, our study underscores the potential substantial impact of climate change on AMR through various pathways, including air pollution, surface runoff and subsurface runoff. In addition to AMC, socioeconomic factors—health investment, out-of-pocket health costs, access to WASH services and immunization coverage—also contribute to the rise of AMR. Whereas short-term sustainable development initiatives and efforts to reduce AMC can help mitigate the rapid growth of AMR, it is important to recognize that the long-term consequences of climate change and human activities will continue to influence AMR dynamics. Therefore, comprehensive evaluation and management strategies are essential and must involve global collaboration. Particular attention should be given to LMICs that face substantial AMR burdens but have limited economic resources. Efforts must focus on supporting these regions in implementing effective AMR control measures and improving healthcare infrastructure. Addressing the complex relationship between climate change, human activities and AMR requires ongoing research, policy development and the implementation of targeted interventions. A multifaceted and collaborative approach is critical to effectively managing AMR and safeguarding global public health.

Online content

Any methods, additional references, Nature Portfolio reporting summaries, source data, extended data, supplementary information, acknowledgements, peer review information; details of author contributions and competing interests; and statements of data and code availability are available at https://doi.org/10.1038/s41591-025-03629-3.

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Methods

Study design and data source

In this global longitudinal observatory study, we analyzed a dataset of AMR profiles covering 101 countries from 1999 to 2022, alongside a range of associated climate and socioeconomic variables. The six AMR profiles on the WHO priority list include 3GCREC, 3GCRKP, CREC, CRKP, CRAB and CRPA[32]. The AMR data were derived primarily from ResistanceMap, a collection of tools summarizing national and subnational data on antimicrobial use and resistance around the world. The primary sources of data are public and private laboratory networks that routinely collect AMR test results[33]. This was supplemented by several original data sources, including GLASS, EARS-Net, the CAESAR network and CARSS. The antibiotic susceptibility testing mainly followed the guidelines and quality control requirements specified in the Clinical and Laboratory Standards Institute and European Committee on Antimicrobial Susceptibility Testing[71].

GLASS, launched by WHO in October 2015, is the first global initiative to standardize AMR surveillance. Initially focused on bacteria causing common human infections, it now also tracks AMC, invasive fungal infections and implements a One Health surveillance model that integrates human health[34].

EARS-Net, coordinated by the European Center for Disease Prevention and Control, is Europe's largest publicly funded AMR surveillance system. It requires all European Union/European Economic Area countries to report data annually[35]. The CAESAR network—a joint initiative involving WHO/Europe, the European Society of Clinical Microbiology and Infectious Diseases and the Dutch National Institute for Public Health and the Environment—covers all countries in the WHO European Region not included in EARS-Net[36].

CARSS, established in 2005, is China's national initiative for monitoring and addressing AMR. It was launched by the Ministry of Health, with leadership from the Chinese Hospital Association and Peking University's Clinical Pharmacology Institute. The system currently covers over 4,000 hospitals across all 31 provinces and cities in China[37].

AMC data were sourced from GLASS, the ESAC-Net and the GRAM project.

ESAC-Net is a Europe-wide network providing reference data on AMC. It collects and analyzes consumption data from European Union/European Economic Area countries, covering both community and hospital sectors[72].

GRAM estimates antibiotic consumption using data from sources like IQVIA, WHO and ESAC-Net, along with sociodemographic and health covariates, to model total antibiotic use[73].

Additionally, data on antimicrobial use in animals were obtained from the Animal Antimicrobial Use Global Database (ANIMUSE). ANIMUSE was established by the World Organisation for Animal Health in September 2022. This automated system covers nearly 80% of global geography and 65% of the world's total animal biomass[74].

Historical environmental data were obtained from the European Center for Medium-Range Weather Forecasts Reanalysis v5 (ERA5), the Atmospheric Composition Analysis Group[75] and Agriculture Organization Statistics (FAOSTAT). Scenario-forecast data were acquired from the Coupled Model Intercomparison Project Phase 6 (CMIP6) and SSPs public database. We calculated the average value of each variable for each country and year based on the high-resolution spatiotemporal data provided by those datasets.

ERA5, produced by the Copernicus Climate Change Service (C3S) at European Center for Medium-Range Weather Forecasts, offers hourly estimates of atmospheric, land and oceanic climate variables from January 1940 to the present. The dataset covers the Earth on a 31 km grid, with 137 vertical levels extending up to 80 km (ref. 76). FAOSTAT provides food and agriculture data for over 245 countries and territories, spanning from 1961 to the latest available year[77].

CMIP6 is an international collaboration focused on climate model simulations to better understand climate change. It provides a framework for comparing models from various research institutions, assessing the impact of factors like greenhouse gas emissions, aerosols and land-use changes[78]. A key component is its integration with SSPs, which describe different global development scenarios based on varying socioeconomic development, technology and policy responses. And the SSP public database includes scenario data from integrated assessment models, quantifying factors like population, economic growth, land use and energy consumption[79].

Socioeconomic data were sourced from the DataBank and International Transparency. DataBank is a tool for analyzing and visualizing time series data on various topics. The World Development Indicators is the World Bank's main collection of development indicators, sourced from officially recognized international sources. It provides the most current and accurate global development data, including national, regional and global estimates[80], as well as country classification by region and income (Extended Data Fig. 7).

Transparency International is a global nongovernmental organization dedicated to fighting corruption, promoting transparency and enhancing civil society participation. Its CPI is a widely recognized tool that measures the perceived level of corruption in the public sector of countries. Based on surveys from experts and business leaders, the CPI is scored from 0 (highly corrupt) to 100 (corruption-free)[81].

All data sources and corresponding URLs are now provided in the Supplementary Table 3.

Dependent variable

To provide a general overview of AMR, we computed the average prevalence of AMR for each country by employing country-level annual geometric averaging across six AMR profiles (equation (1)). This approach served two purposes: it (1) effectively captured minor variations in low resistance rates while mitigating the influence of larger fluctuations in high resistance rates and (2) provided a comprehensive representation of the sigmoidal progression in AMR development[82]. Employing geometric means allowed for a more integrated analysis of the development stages of diverse antimicrobial-resistant profiles.

We then applied logit transformation to the average prevalence of AMR (equation (2)), which was designed to broaden the range of ratios within our model.

$$R_{\text{average}} = \sqrt[6]{R_{\text{3GCREC}} \times R_{\text{3GCRKP}} \times R_{\text{CREC}} \times R_{\text{CRKP}} \times R_{\text{CRAB}} \times R_{\text{CRPA}}} \quad (1)$$

$$\text{logit}\,(R) = \log\left(\frac{R}{1-R}\right) \quad (2)$$

Independent variable

Independent variables were selected according to three principles:

(1) Environmental or socioeconomic factors previously identified in the literature as influencing AMR in humans.
(2) Available from the national-level comprehensive monitoring data.
(3) Minimal correlations with each other to preclude multicollinearity.

This resulted in measurements of air quality (for example, $PM_{2.5}$), water conditions (surface and subsurface runoff) and ambient temperature representing environmental factors, economic growth, healthcare resources (for example, health expenditures, out-of-pocket expenditures, immunization coverage), sanitation (for example, WASH coverage), population structure (for example, population density, urban population, international tourism) and governance (for example, CPI) representing socioeconomic factors, and AMC representing human behaviors.

We transformed the skewed data into ratio forms, such as the proportion of health expenditure to GDP and the share of out-of-pocket payments in total health expenditure. The variables exhibiting exponential changes, such as population density and international tourists, were logarithmically transformed (Supplementary Table 2). Extended Data Fig. 8 illustrates the evolving trends of the variables used in the multivariable analysis.

Statistical analysis

Our analysis encompassed both descriptive analysis and multivariable analysis. The primary results were calculated based on the average prevalence of AMR, along with the results of specific AMR profiles.

Descriptive analysis included global distribution maps illustrating the average prevalence of AMR and its average rate of annual change. The average annual growth rate was calculated as the slope of the linear regression between the year and AMR prevalence. Scatter plots were used to describe the trends of specific AMR profiles within each country group classified by income.

We employed Pearson tests to test the correlations between the dependent variable and each independent variable (Extended Data Fig. 9). Multivariable analyses were performed using a spatial–temporal mixed-effects model with structured random effects. Given the spatiotemporal nature of the dependent variable, 'year' and 'country' were incorporated as structured random effects in the model (equation (3)), with 'year' modeled using a random walk (RW1) process and 'country' modeled using a Besag–York–Mollié (BYM) approach[83] based on a spatial adjacency matrix W (Extended Data Fig. 7a).

$$\begin{aligned}\operatorname{logit}(R) &= \beta_0 + \beta_1 x_1 + \ldots + \beta_i x_i + \text{IncomeGroup}\\ &+ f(\text{year}, \text{model} = \text{“}rw1\text{”}) + f(\text{country}, \text{model} = \text{“BYM”}, \text{graph} = W)\end{aligned} \tag{3}$$

Where R is the prevalence of AMR and x_i denotes the various independent variables. Exponential transform β_i signifies the OR for the risk of AMR relative to non-AMR, corresponding to a unit increase in a given independent variable. Furthermore, we created lag variables with a maximum lag of 4 years for each predictor, selected based on the statistical model's deviance information criterion (DIC) to identify the optimal lag period (Extended Data Fig. 10). For sensitivity analysis, we conducted separate modeling for each specific AMR profile.

Considering the heterogeneity across different surveillance networks, we conducted a subgroup analysis based on the EARS-Net, which contributed 2,891 observations covering six AMR profiles, accounting for 64.2% of our whole dataset. Additionally, given the limited number of observations for some variables that might still have a significant impact on AMR, we included them as supplementary covariates in our primary model. These additional variables included the consumption of different classes of antimicrobial agents, education factors and animal AMC. The effects of these covariates on AMR were evaluated carefully.

All analyses were conducted in R v.4.4.1 (R Foundation for Statistical Computing) with the 'INLA' (integrated nested laplace approximation) package[84]. Because INLA uses efficient Bayesian inference, it does not provide traditional P values for parameter significance. Instead, it estimates confidence intervals for the model parameters, which serve as a measure of uncertainty in the estimates.

Scenarios

We projected AMR trends up to 2050, utilizing predictive datasets under various scenarios (Supplementary Table 4). Our environmental factor projections included temperature, runoff and $PM_{2.5}$ under four SSPs: SSP1-2.6, SSP2-4.5, SSP3-7.0 and SSP5-8.5.

SSPs were developed based on representative concentration pathways (RCPs), which are part of the coupled model intercomparison project phase 5 (CMIP5). Whereas RCPs focus primarily on quantifying greenhouse gas concentration trajectories and their radiative forcing effects on the climate system, SSPs extend this by integrating socioeconomic dimensions such as population growth, technological advancements and economic development. The differences among SSPs reflect these varying societal trajectories, providing a more comprehensive analysis of how global climate change may unfold under different socioeconomic scenarios[22].

SSP1-2.6 merges a sustainable development pathway (SSP1) with a low greenhouse gas concentration trajectory (RCP2.6), envisioning a future oriented towards sustainability, with substantial investments in education, health and renewable energy, targeting low emissions and striving to limit global warming to well below 2° C. This pathway emphasizes environmental protection and social equity.

SSP2-4.5 pairs a moderate development pathway (SSP2) with an intermediate greenhouse gas concentration trajectory (RCP4.5), depicting a future that follows historical trends, with moderate economic development and emissions, and partial progress towards sustainability, but lacking radical behavioral shifts or large advances in green technology.

SSP3-7.0 links a fragmented world scenario (SSP3) with a high-emission trajectory (RCP7.0), portraying a future of regional disputes, prioritizing national security over global environmental concerns, leading to high emissions and scant international cooperation on climate change, potentially resulting in notable global warming and adaptation challenges.

SSP5-8.5 combines a fossil-fuel intensive development pathway (SSP5) with the highest greenhouse gas concentration trajectory (RCP8.5), imagining a future driven by rapid economic growth reliant on fossil fuels, resulting in high energy consumption and emissions—a scenario that could lead to severe climate change impacts due to extremely high global temperatures.

To explore different future outcomes, we developed four socioeconomic scenarios, each incorporating two intervention strategies aimed at addressing AMR. The first strategy envisions a 50% reduction in AMC, reflecting the potential impact of antimicrobial stewardship initiatives[85]. The second strategy focuses on sustainable development, outlining a future in which, by 2050, there is universal access to WASH services, comprehensive immunization coverage[86] and health investments that support sustainable development (at least 5% of GDP). These goals also aim to prevent catastrophic household health expenditure by limiting out-of-pocket costs to less than 20% of total health expenditures[87]. Furthermore, we broke down sustainable development efforts into four specific interventions to assess their individual effects. Extended Data Fig. 4 illustrates the evolving trends of the variables used in our forecasting model.

Ethics and inclusion statement

This study used publicly available datasets, with no further primary data collection involving human or animal subjects. The AMR profiles and associated variables analyzed in this study were derived from the globally recognized and accessible databases, including ResistanceMap, CAESAR, EARS-Net, CARSS, GLASS, ESAC-Net, GRAM and others. These data sources reflect the efforts of international research communities and institutions with diverse representation and inclusivity, whose contributions we acknowledge with gratitude.

The authorship reflects substantial contributions to funding acquisition, data analysis interpretation, manuscript preparation and critical revisions. We have a research team comprising authors from Mainland China, Australia, the United Kingdom, China Hong Kong SAR and the United States.

Reporting summary

Further information on research design is available in the Nature Portfolio Reporting Summary linked to this article.

Data availability

The datasets analyzed during the current study are all publicly available. The AMR data derived primarily from ResistanceMap (https://resistancemap.onehealthtrust.org/AntibioticResistance.php), supplemented by EARS-Net, https://www.ecdc.europa.eu/en/antimicrobial-resistance/surveillance-and-disease-data) and CARSS (https://www.carss.cn/). AMC data were sourced from GRAM (https://www.tropicalmedicine.ox.ac.uk/gram/research/visualisation-app-antibiotic-usage-and-consumption), GLASS (https://www.who.int/initiatives/glass), ESAC-Net (https://www.ecdc.europa.eu/en/antimicrobial-consumption/surveillance-and-disease-data/database) and ANIMUSE (https://amu.woah.org/amu-system-portal/home). Historical environmental data were obtained from ERA5 (https://cds.climate.copernicus.eu/datasets), the Atmospheric Composition Analysis Group (https://sites.wustl.edu/acag/datasets/surface-pm2-5/) and FAOSTAT (https://www.fao.org/faostat/en/#data/ET). Scenario-forecast data were acquired from CMIP6 (https://cds.climate.copernicus.eu/datasets) and the SSP public database (https://tntcat.iiasa.ac.at/SspDb/). Socioeconomic data were sourced from the Databank (https://databank.worldbank.org/) and International Transparency (https://us.transparency.org/). The final data were obtained through a combination of manual recording and direct export from various established databases. The materials and datasets that support the findings of this study are available at https://github.com/Li-weibin/AMR-in-climate-change. Source data are provided with this paper.

Code availability

Codes to reproduce the statistical analysis are made available at https://github.com/Li-weibin/AMR-in-climate-change.

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Author contributions

L.Y., W.L. and T.H. designed the study and analysis. W.L., T.H., C.L., H.W., X.Y., R.W., H.X., X.L., S.Q., S.C., H.C.H., C.H., L.S., G.T., G.L., K.L.E. and L.Y. made substantial contributions to acquisition of funding, data materials, interpretation of data and results. W.L., T.H. and L.Y. verified and analyzed the data. W.L. and L.Y. drafted the article. C.L., L.Y., K.L.E., X.G. and C.H. revised the data critically for important intellectual content. L.Y. supervised this research work. W.L., T.H. and L.Y. were responsible for the decision to submit the manuscript, and all authors contributed to final approval of the paper.

Competing interests

The authors declare no competing interests.

Additional information

Extended data is available for this paper at https://doi.org/10.1038/s41591-025-03629-3.

Supplementary information The online version contains supplementary material available at https://doi.org/10.1038/s41591-025-03629-3.

Correspondence and requests for materials should be addressed to Lianping Yang.

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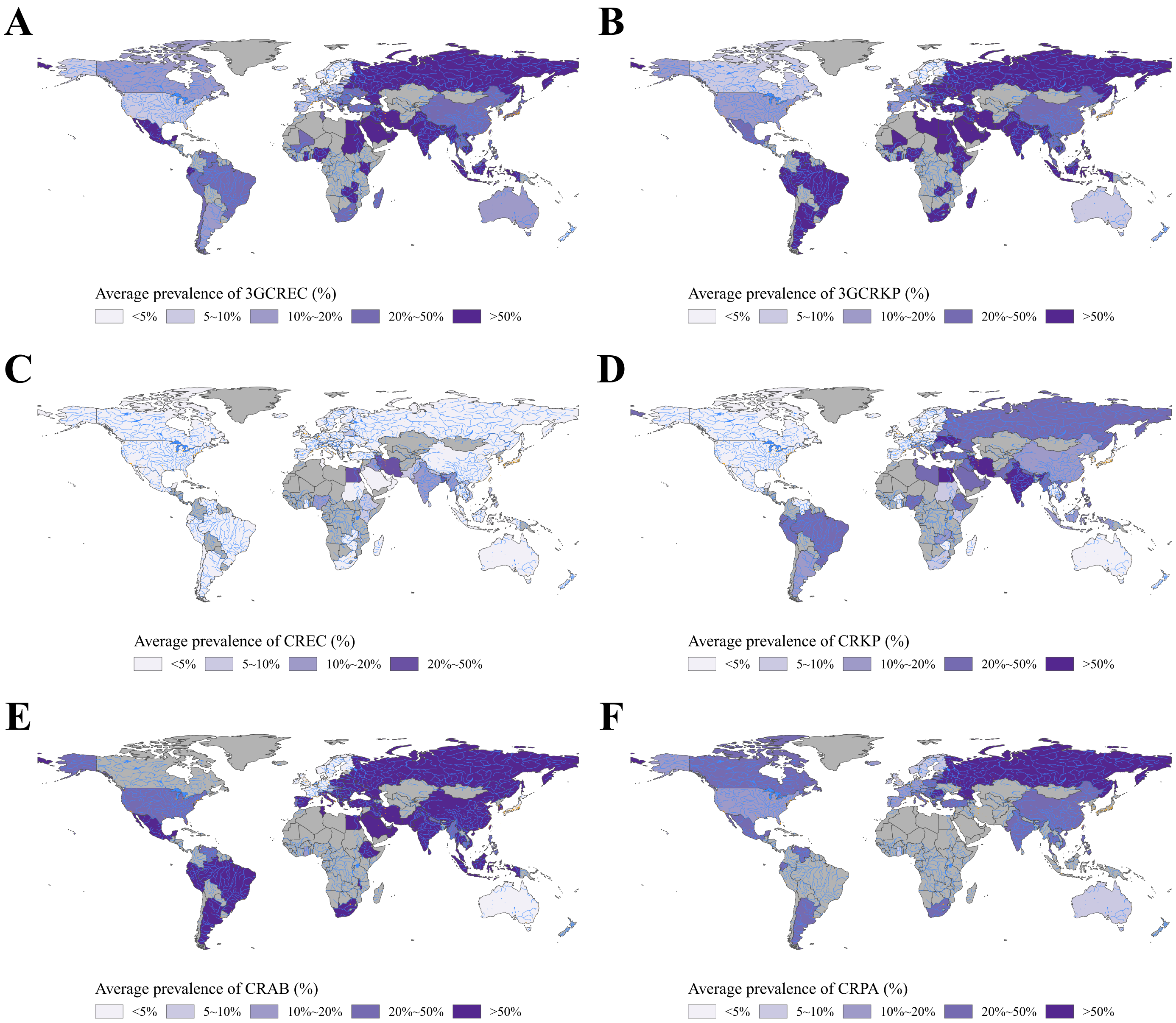
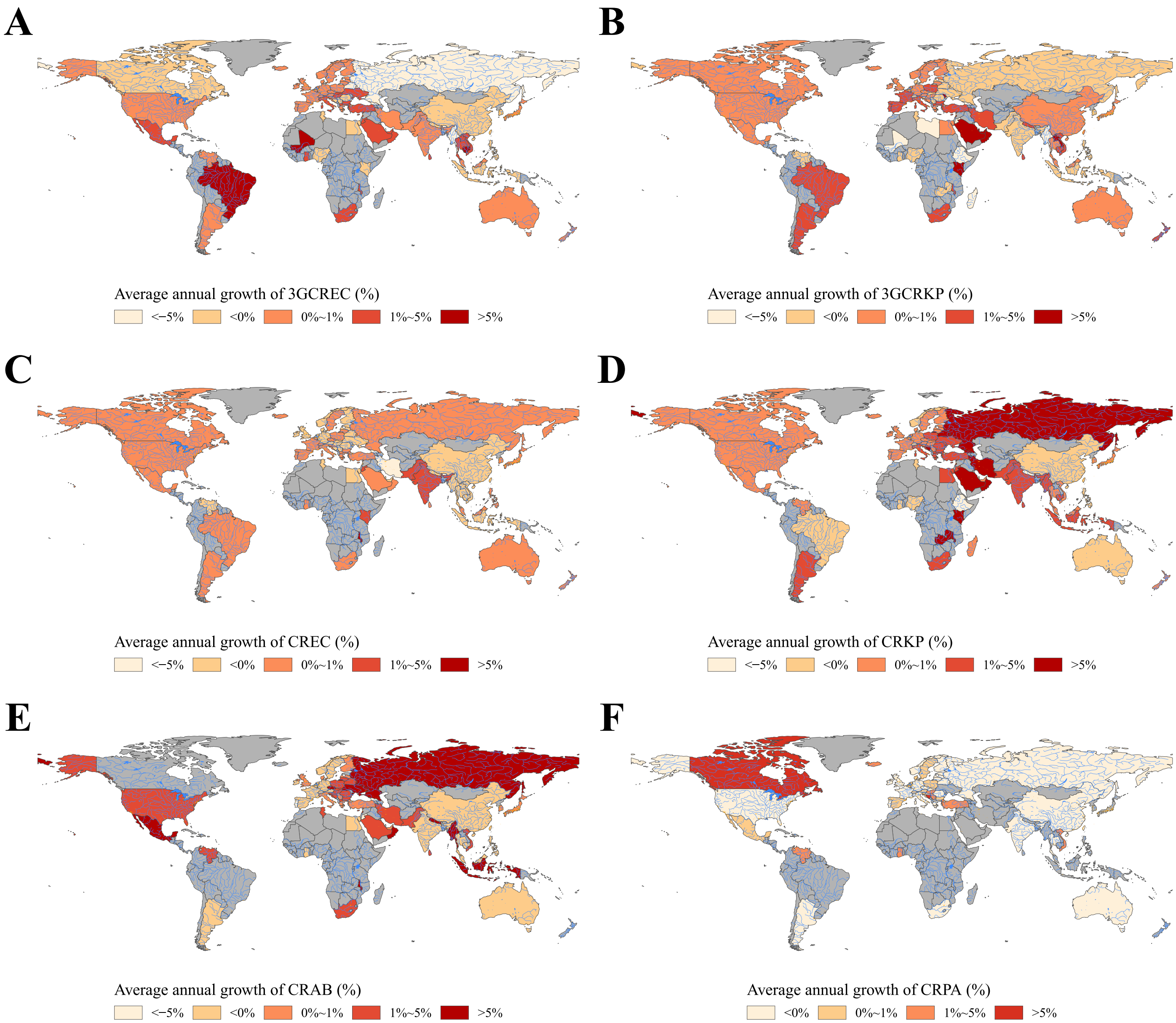
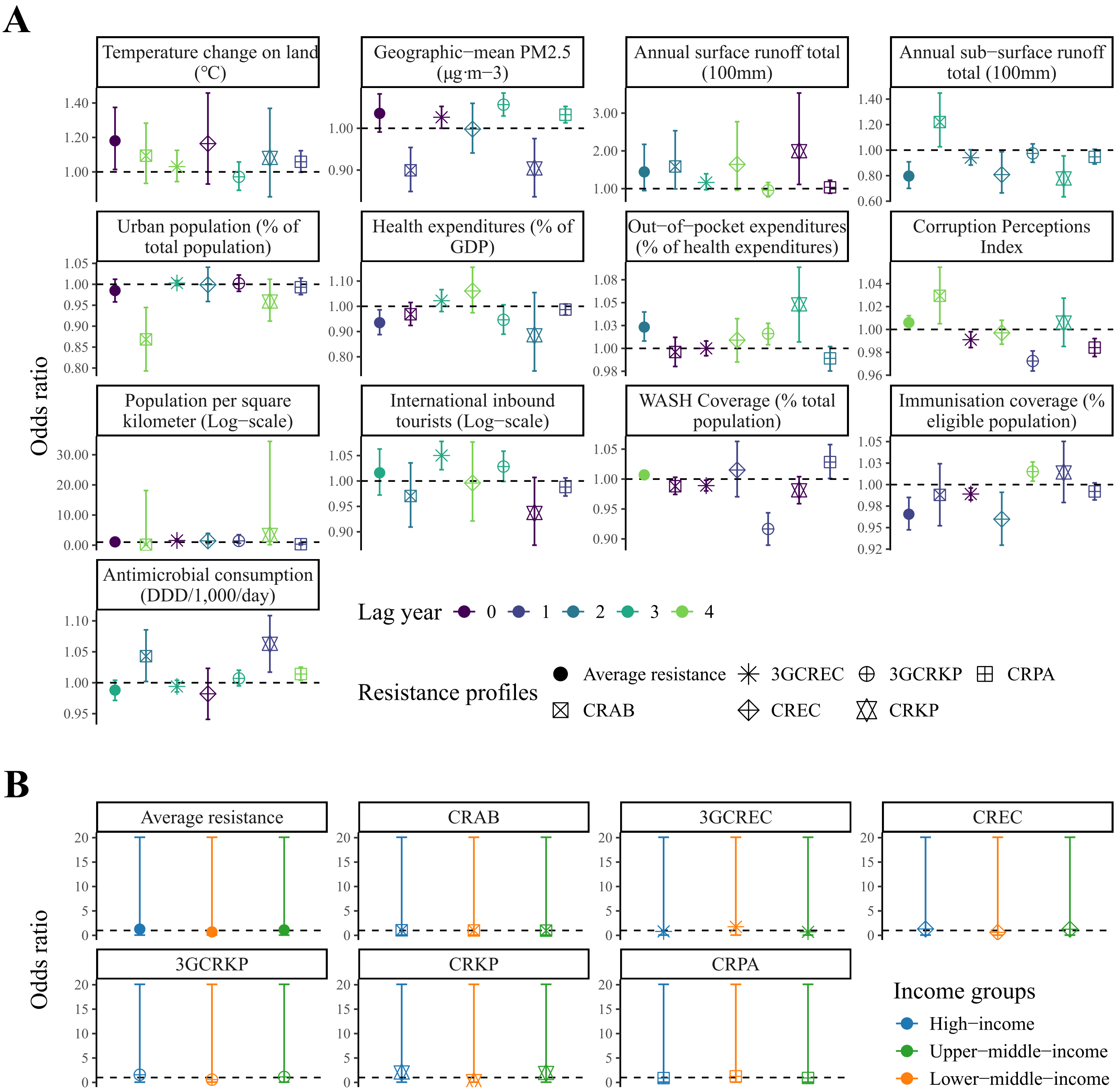


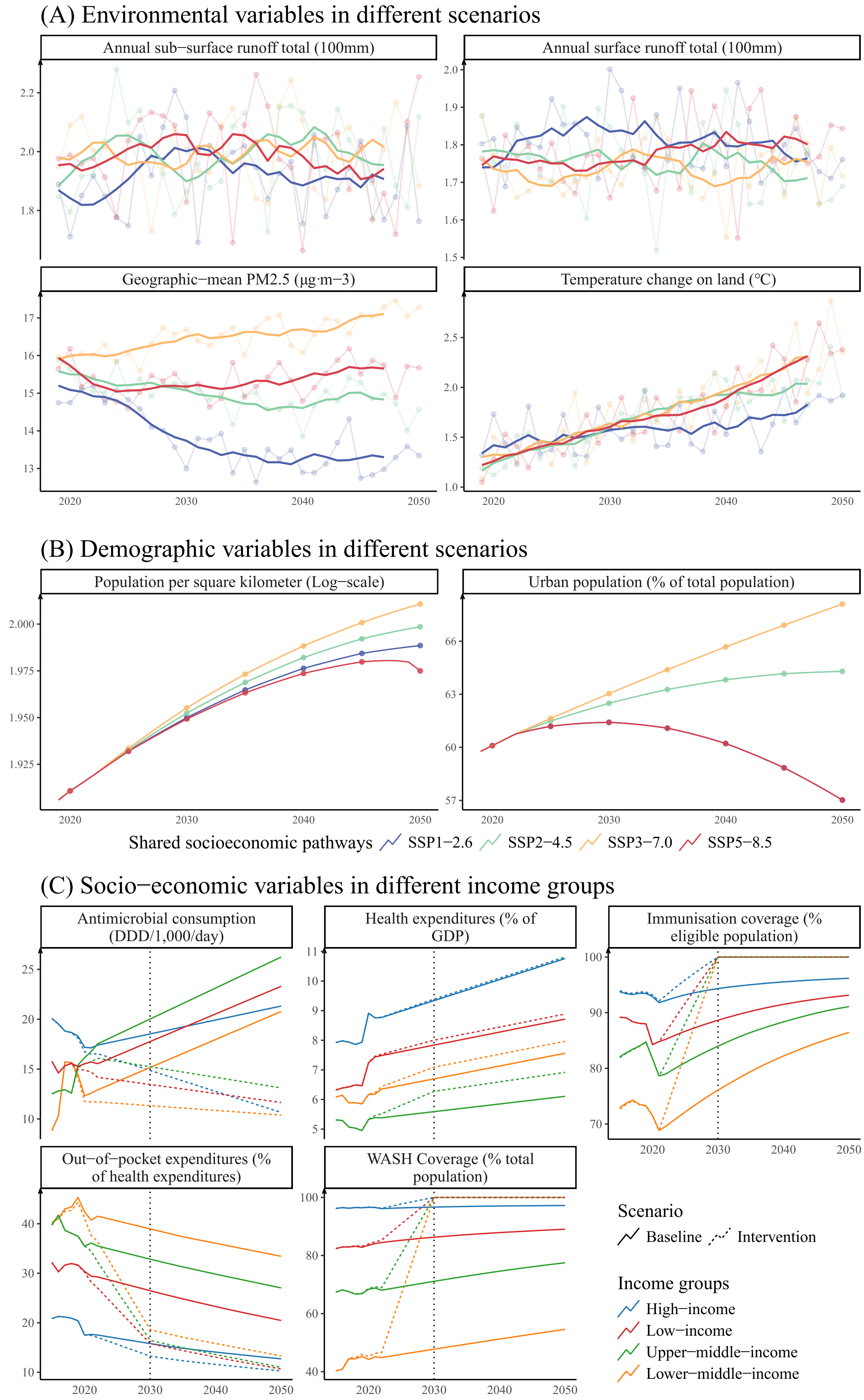
Extended Data Fig. 1 | Global distribution of antimicrobial resistance of different profiles. (**a**) Third-generation cephalosporin-resistant *Escherichia coli*. (**b**) Third-generation cephalosporin-resistant *Klebsiella pneumoniae*. (**c**) Carbapenem-resistant *Escherichia coli*. (**d**) Carbapenem-resistant *Klebsiella pneumoniae*. (**e**) Carbapenem-resistant *Acinetobacter baumannii*. (**f**) Carbapenem-resistant *Pseudomonas aeruginosa*.



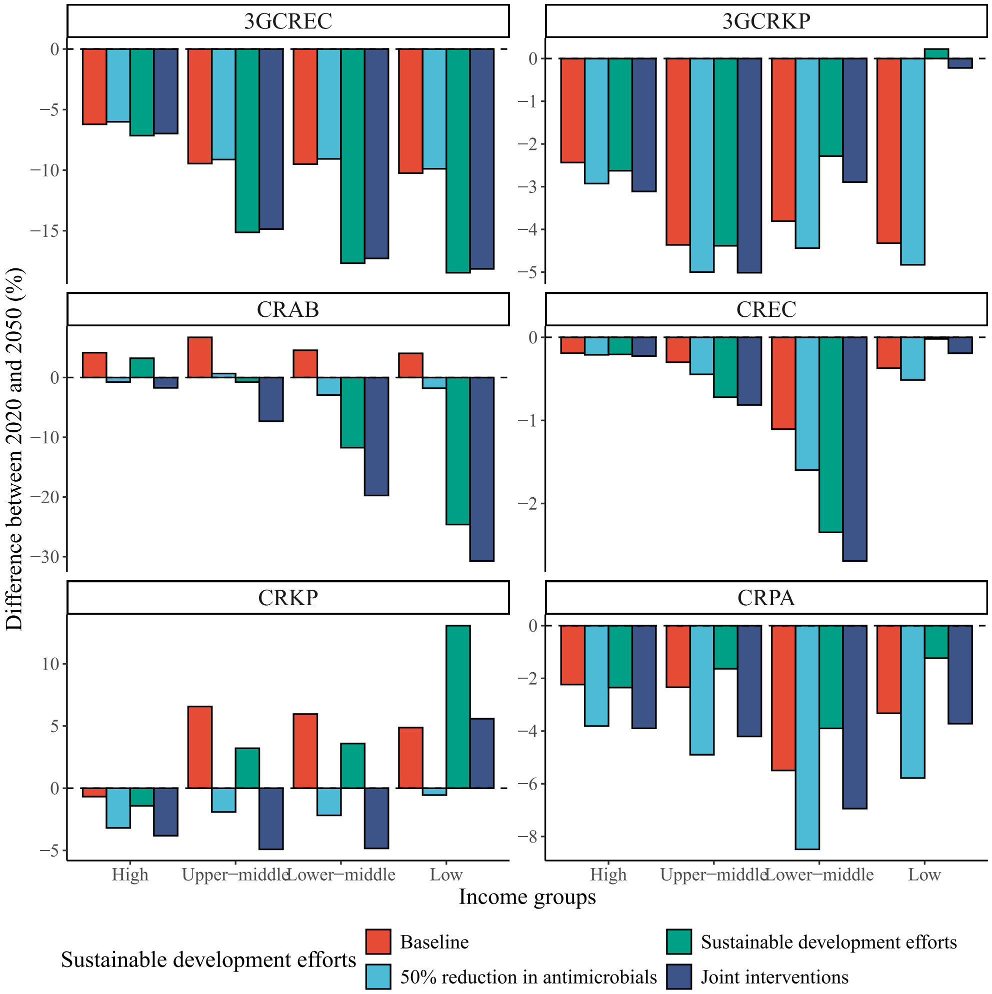
Extended Data Fig. 2 | Changes of antimicrobial resistance of different profiles. (**a**) Third-generation cephalosporin-resistant *Escherichia coli*. (**b**) Third-generation cephalosporin-resistant *Klebsiella pneumoniae*. (**c**) Carbapenem-resistant *Escherichia coli*. (**d**) Carbapenem-resistant *Klebsiella pneumoniae*. (**e**) Carbapenem-resistant *Acinetobacter baumannii*. (**f**) Carbapenem-resistant *Pseudomonas aeruginosa*.



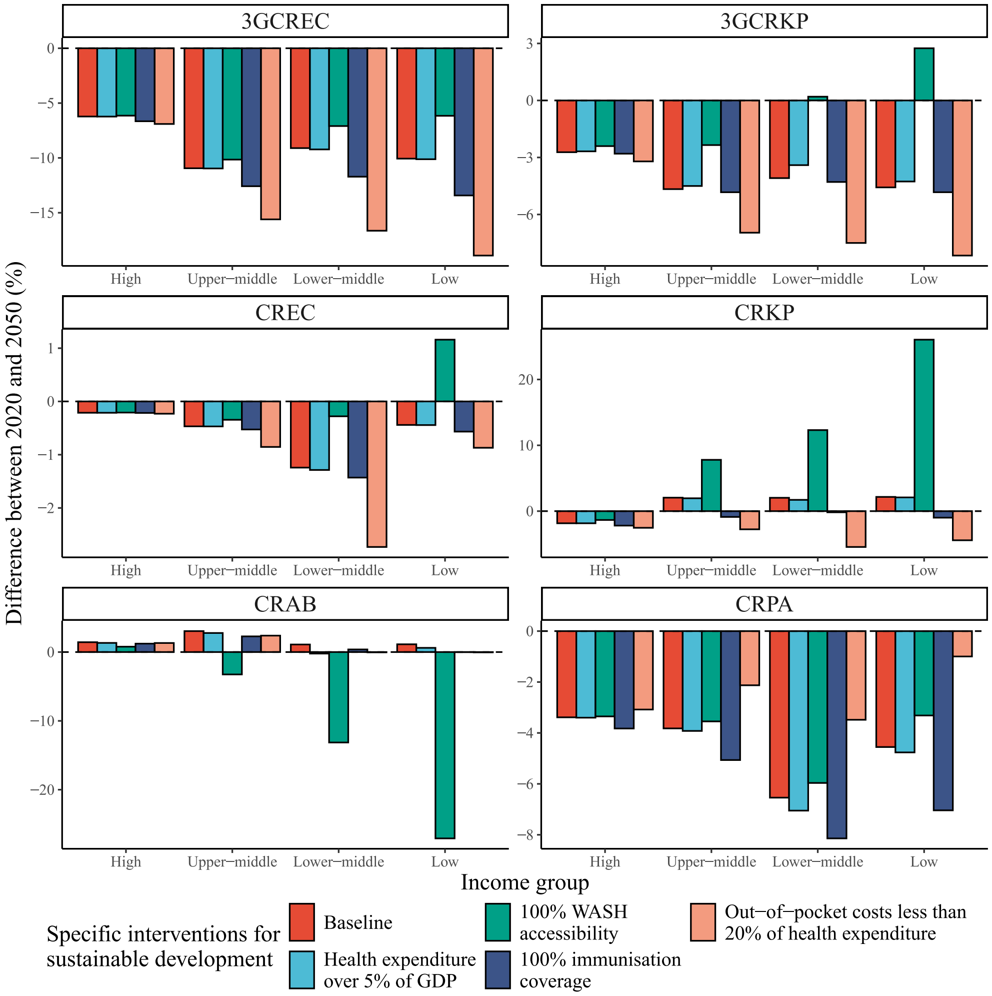
Extended Data Fig. 3 | Subgroup analysis based on the European Antimicrobial Resistance Surveillance Network (EARS-Net). Spatial-temporal mixed effects models with structured random effects were independently fitted for each AMR profile. Results are presented as adjusted odds ratios (points) with 95% confidence intervals (error bars). EARS-Net contributed 2,891 observations covering six AMR profiles, accounting for 64.2% of our total data. We selected EARS-Net data for this analysis to minimize the impact of surveillance network heterogeneity. The optimal lag year for each predictor was determined by selecting the model with the minimum Deviance Information Criterion (DIC) value. Panel (**A**) shows the effects of quantitative variables, including environmental and socioeconomic factors. Panel (**B**) displays the influence of income groups, demonstrating no statistically significant effect of income classification on antimicrobial resistance patterns after adjusting for potential confounding factors. WASH = Water, Sanitation, and Hygiene. 3GCREC = third-generation cephalosporin-resistant *Escherichia coli*. 3GCRKP = third-generation cephalosporin-resistant *Klebsiella pneumoniae*. CREC = carbapenem-resistant *Escherichia coli*. CRKP = carbapenem-resistant *Klebsiella pneumoniae*. CRAB = carbapenem-resistant *Acinetobacter baumannii*. CRPA = carbapenem-resistant *Pseudomonas aeruginosa*.



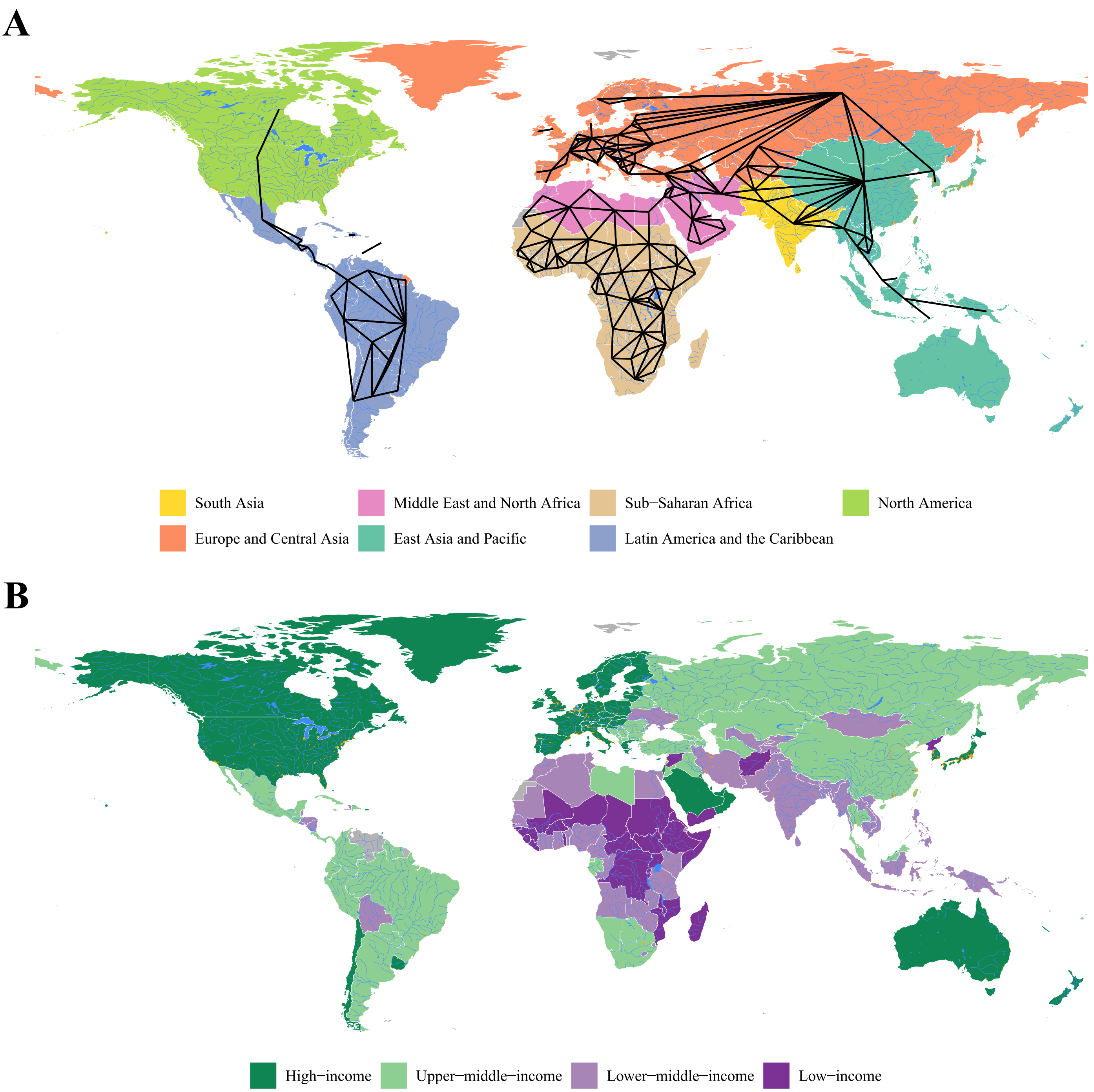
Extended Data Fig. 4 | Changing trends of the variables used in forecast modelling. Panel (a) shows the trend of environmental variables in different scenarios, with the smooth solid line representing the seven-year moving average, and panel (b) shows the demographic variables, while panel (c) shows the socioeconomic variables. The vertical dashed line in panel (c) represents the year of 2030. WASH = Water, Sanitation, and Hygiene.



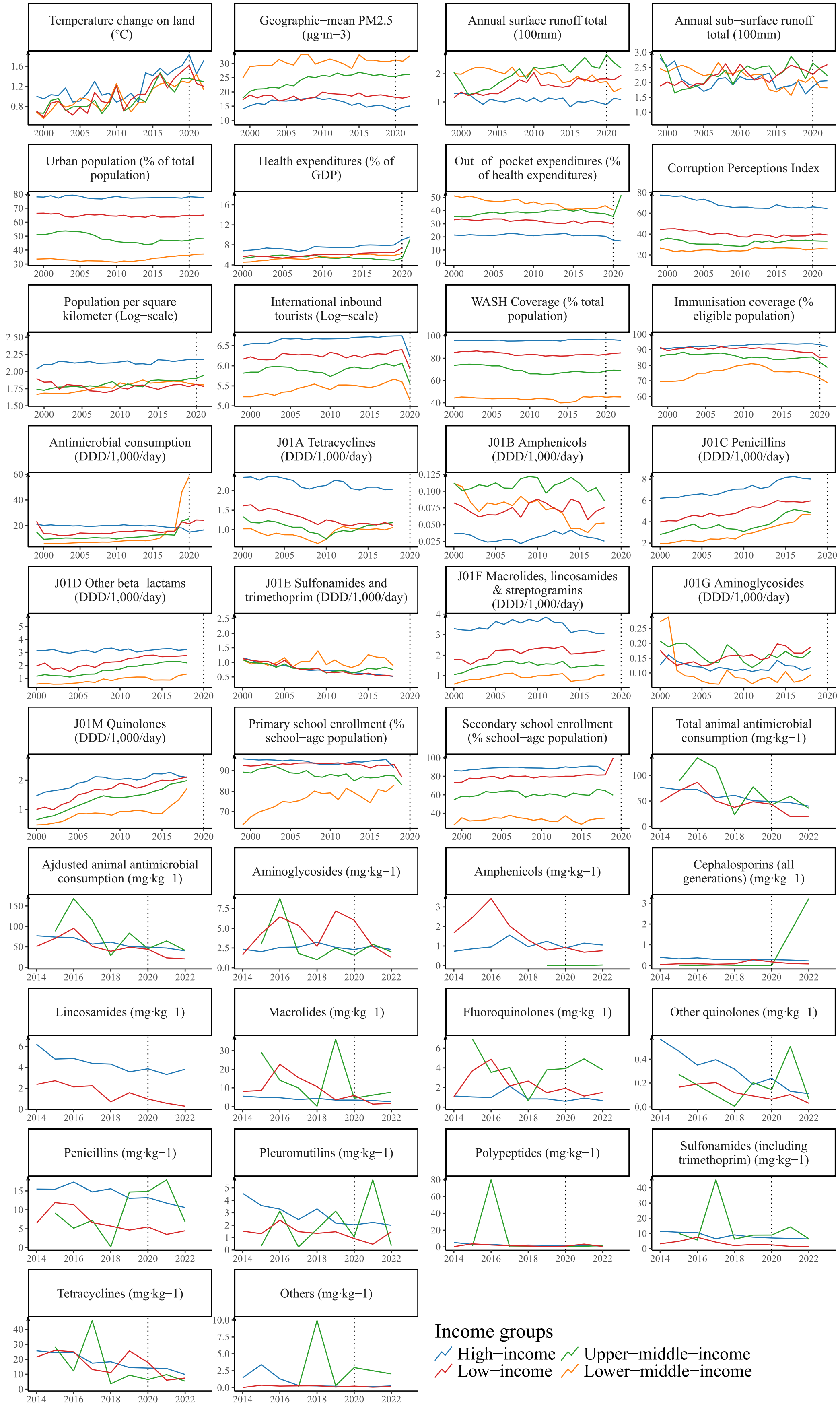
Extended Data Fig. 5 | The impact of specific sustainable development efforts on different resistant profiles. 3GCREC = third-generation cephalosporin-resistant *Escherichia coli*. 3GCRKP = third-generation cephalosporin-resistant *Klebsiella pneumoniae*. CREC = carbapenem-resistant *Escherichia coli*. CRKP = carbapenem-resistant *Klebsiella pneumoniae*. CRAB = carbapenem-resistant *Acinetobacter baumannii*. CRPA = carbapenem-resistant *Pseudomonas aeruginosa*.



Extended Data Fig. 6 | The impact of individual intervention measures on different resistant profiles. 3GCREC = third-generation cephalosporin-resistant *Escherichia coli*. 3GCRKP = third-generation cephalosporin-resistant *Klebsiella pneumoniae*. CREC = carbapenem-resistant *Escherichia coli*. CRKP = carbapenem-resistant *Klebsiella pneumoniae*. CRAB = carbapenem-resistant *Acinetobacter baumannii*. CRPA = carbapenem-resistant *Pseudomonas aeruginosa*.

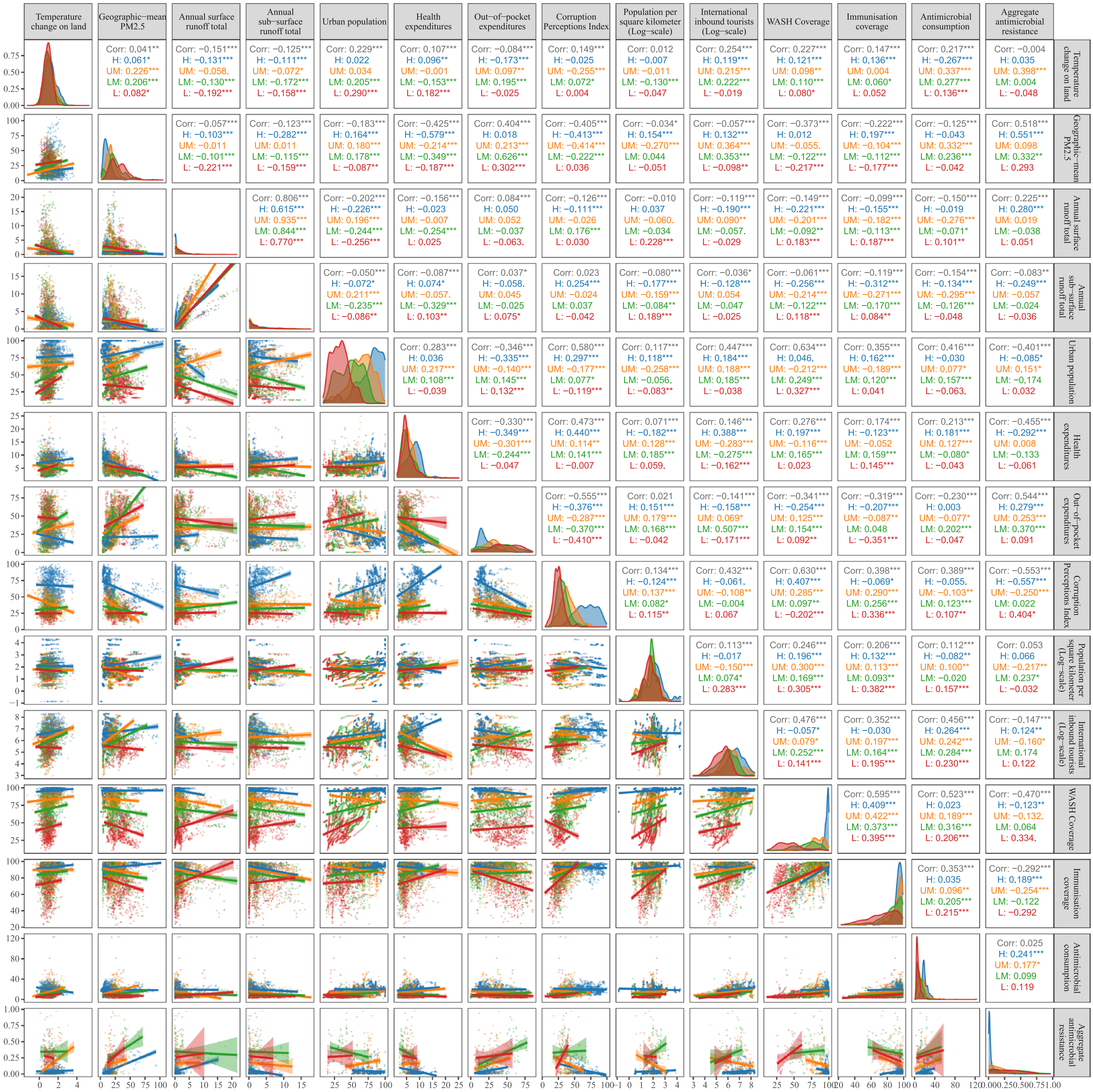


Extended Data Fig. 7 | Classification of regions and income groups. (**a**) Regions. The black grid represents the adjacency matrix composed of countries with shared borders. (**b**) Income groups.

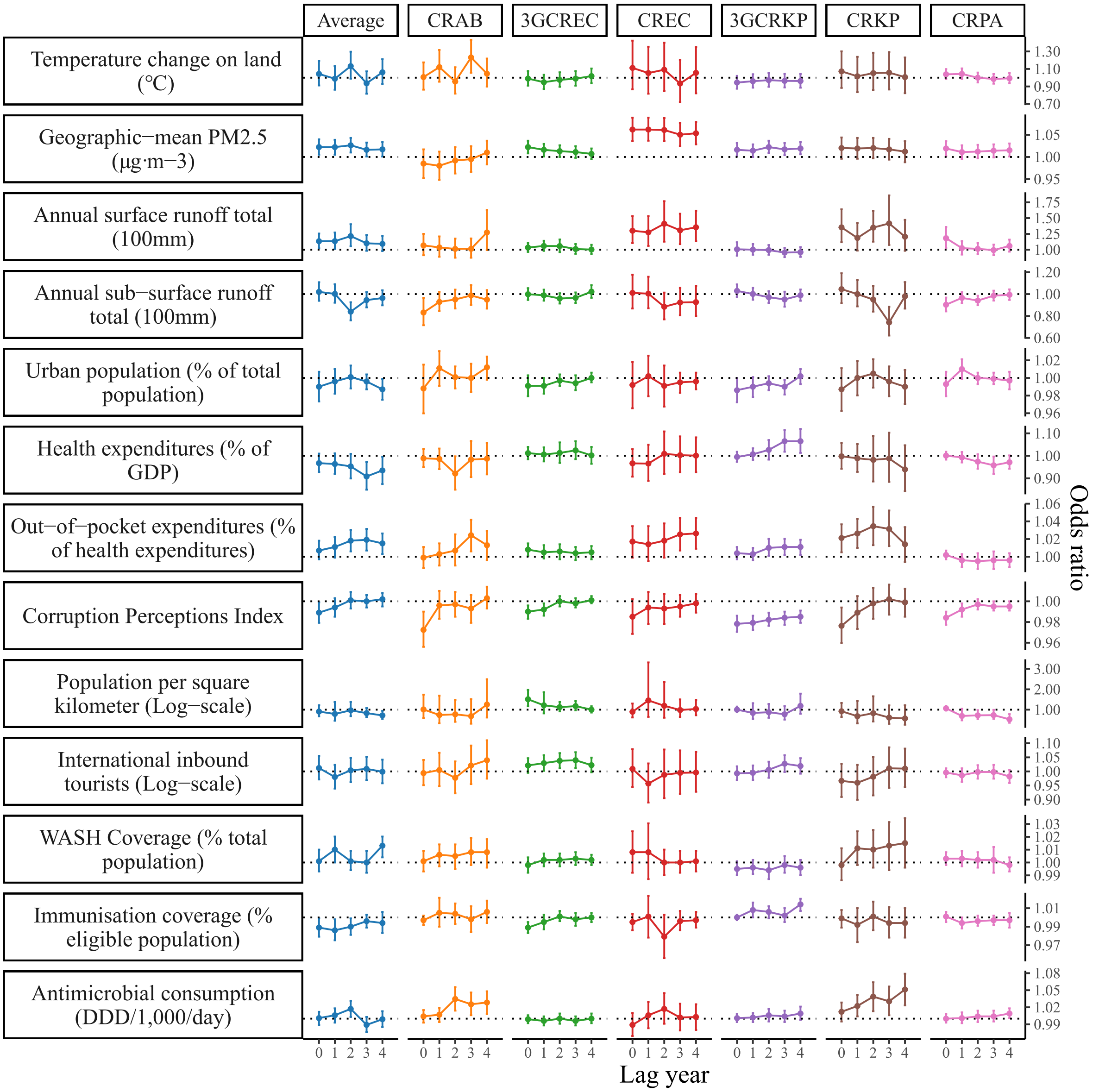


Extended Data Fig. 8 | Changing trends of the independent variables used for statistical modelling in the countries with different income over the period from 1999 to 2022. The vertical dashed line represents the year 2020. WASH = Water, Sanitation, and Hygiene.

https://doi.org/10.1038/s41591-025-03629-3



Extended Data Fig. 9 | Correlations between average antimicrobial resistance and independent variables. This comprehensive visualization presents pairwise relationships between variables through a scatterplot matrix. The lower triangular section displays bivariate relationships, showing observed values (scatter points) overlaid with linear regression fits and corresponding confidence intervals, stratified by national income groups. The upper triangular section presents Pearson correlation coefficients with significance levels indicated by asterisks (*$p < 0.05$, **$p < 0.01$, ***$p < 0.001$). The diagonal elements contain variable distribution stratified by different income groups. Different colours indicate data from different income groups, in which blue, orange, green, red represent high-income, upper-middle, lower-middle and lower-income economies, respectively. WASH = Water, Sanitation, and Hygiene.



Extended Data Fig. 10 | Estimates of variables with different lag period in the models. We incorporated the lagged values of each variable with a maximum of 4 years into the models for analysis. The optimal lag period is in the model which has the smallest Deviance Information Criterion (DIC). The analysis included 975 independent biological observations for average AMR, with specific profiles comprising 945 (3GCREC), 805 (3GCRKP), 870 (CREC), 774 (CRKP), 510 (CRAB), and 598 (CRPA) observations, respectively. Results are presented as adjusted odds ratios (points) with 95% confidence intervals (error bars). WASH = Water, Sanitation, and Hygiene. 3GCREC = third-generation cephalosporin-resistant *Escherichia coli*. 3GCRKP = third-generation cephalosporin-resistant *Klebsiella pneumoniae*. CREC = carbapenem-resistant *Escherichia coli*. CRKP = carbapenem-resistant *Klebsiella pneumoniae*. CRAB = carbapenem-resistant *Acinetobacter baumannii*. CRPA = carbapenem-resistant *Pseudomonas aeruginosa*.

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Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	We used R (4.4.1) software. All analyses were conducted in R 4.4.1 (R Foundation for Statistical Computing) with the 'INLA' package. Given the spatiotemporal nature of the dependent variable, 'year' and 'country' were incorporated as structured random effects in the model (Equation 3), with 'year' modelled using a random walk (RW1) process and 'country' modelled using a Besag-York-Mollié (BYM) approach based on a spatial adjacency matrix W. Code availability Statement Codes to reproduce the statistical analysis are made available at https://github.com/Li-weibin/AMR-in-climate-change.
Data analysis	We used R (4.4.1) software to calculate aggregate value of each variable for each country and year, as well as statistical analysis.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio guidelines for submitting code & software for further information.

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The datasets analysed during the current study are all publicly available.
The Antimicrobial resistance data primarily derived from ResistanceMap (https://resistancemap.onehealthtrust.org/AntibioticResistance.php), supplemented by the European Antimicrobial Resistance Surveillance Network (EARS-Net, https://www.ecdc.europa.eu/en/antimicrobial-resistance/surveillance-and-disease-data), and the China Antimicrobial Resistance Surveillance System (CARSS, https://www.carss.cn/).
Antimicrobial consumption data were sourced from the Global Research on Antimicrobial Resistance project (GRAM, https://www.tropicalmedicine.ox.ac.uk/gram/research/visualisation-app-antibiotic-usage-and-consumption), the Global Antimicrobial Resistance and Use Surveillance System (GLASS, https://www.who.int/initiatives/glass), the European Surveillance of Antimicrobial Consumption Network (ESAC-Net, https://www.ecdc.europa.eu/en/antimicrobial-consumption/surveillance-and-disease-data/database), and ANImal antiMicrobial USE Global Database (ANIMUSE, https://amu.woah.org/amu-system-portal/home).
Historical environmental data were obtained from the European Centre for Medium-Range Weather Forecasts Reanalysis v5 (ERA5, https://cds.climate.copernicus.eu/datasets), the Atmospheric Composition Analysis Group (https://sites.wustl.edu/acag/datasets/surface-pm2-5/), and Agriculture Organization Statistics (FAOSTAT, https://www.fao.org/faostat/en/#data/ET). Scenario-forecast data were acquired from the Coupled Model Intercomparison Project Phase 6 (CMIP6, https://cds.climate.copernicus.eu/datasets) and Shared Socioeconomic Pathways Public Database (https://tntcat.iiasa.ac.at/SspDb/).
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The final data were obtained through a combination of manual recording and direct export from various established databases. The materials and datasets that support the findings of this study are available at https://github.com/Li-weibin/AMR-in-climate-change.

Research involving human participants, their data, or biological material

Policy information about studies with human participants or human data. See also policy information about sex, gender (identity/presentation), and sexual orientation and race, ethnicity and racism.

Reporting on sex and gender	This study does not include analyses or reporting related to sex and gender, as it relies on aggregated national and annual-level data that do not necessitate gender-specific analysis.
Reporting on race, ethnicity, or other socially relevant groupings	This study categorizes countries based on income groups (high, middle, and low) according to World Bank Country and Lending Groups. It does not include analyses or reporting related to race, ethnicity, or other socially relevant groupings.
Population characteristics	We established a dataset of 4,502 AMR observations covering 101 countries from 1999 to 2022, alongside a range of associated climate and socioeconomic variables. It was observed that nearly all economic development indicators, including urban population, population density, international tourists, health expenditures, out-of-pocket expenditures, Corruption Perceptions Index, WASH coverage, immunisation coverage and vaccination coverage, demonstrate a distinct gradient distribution. Environmental factors such as PM2.5 decrease as income levels rise. Antimicrobial consumption is found to be lowest in high-income countries, with the greatest usage in middle and low-income countries.
Recruitment	There was no recruitment of participants, as this study does not involve human subjects.
Ethics oversight	Since this study does not involve human participants, no ethics approval or oversight was required.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

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Ecological, evolutionary & environmental sciences study design

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Study description	This longitudinal observational study analyzes the association between the prevalence of antimicrobial resistance and various socioeconomic and environmental variables. A mixed linear model is used for multivariate analysis, with country and year as random intercept variables. The study also predicts the future global AMR development based on the model.
Research sample	The research sample consists of 975 country-year data units, aggregated from 4,502 AMR phenotype observations collected across

Research sample	101 countries between 1999 and 2022. To ensure data consistency and comprehensiveness, when data overlaps occurred between different AMR monitoring networks, the more comprehensive dataset from the monitoring network with the most complete records was used as the primary source. These country-year units also include aggregated national-level data on socioeconomic factors (such as urban population, population density, international tourists, health expenditures, out-of-pocket expenditures, Corruption Perceptions Index, WASH coverage, immunisation coverage and vaccination coverage), and environmental variables (such as air pollution and climate data). All datasets were linked using the country-year field. And the sample was chosen to represent global trends in AMR.
Sampling strategy	The sampling procedure involved selecting countries with available and complete longitudinal data on AMR prevalence, socioeconomic variables, and environmental factors. No formal sample-size calculation was performed, as this study utilized all available data from global surveillance networks and international databases to ensure comprehensive coverage. The sample size is considered sufficient due to the extensive geographic and temporal coverage, allowing for robust analysis of AMR trends and their association with socioeconomic and environmental factors.
Data collection	The data were sourced from publicly available global databases and surveillance networks. The researcher was not blinded to the experimental condition or the study hypothesis.
Timing and spatial scale	The data collection period spans from 1999 to 2022. Data on AMR prevalence, and socioeconomic variables, depending on the reporting schedules of the surveillance networks and international databases used. Climate data were derived from high-resolution spatiotemporal datasets and averaged to align with the country-year format, which is the fundamental unit of record in the database.
Data exclusions	Only those country-year units with complete data on AMR prevalence, socioeconomic variables, and environmental factors were included in the final analysis. Observations with missing data for any of these key variables were excluded.
Reproducibility	Data collection and verification were independently conducted by five researchers to ensure accuracy and consistency across the datasets. The data processing and statistical analysis were implemented using R (version 4.4.1), with all steps thoroughly documented to enable full reproducibility. The core code used for data processing and model implementation is publicly available at https://github.com/Li-weibin/AMR-in-climate-change, providing transparency and allowing other researchers to replicate the analysis.
Randomization	No randomization was applied, as the study is observational and uses national-level data from international databases.
Blinding	Blinding was not applicable, as the study is based on publicly available country-level data without individual or experimental interventions.

Did the study involve field work? ☐ Yes ☒ No

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study	
☒	☐	Antibodies
☒	☐	Eukaryotic cell lines
☒	☐	Palaeontology and archaeology
☒	☐	Animals and other organisms
☒	☐	Clinical data
☒	☐	Dual use research of concern
☒	☐	Plants

Methods

n/a	Involved in the study	
☒	☐	ChIP-seq
☒	☐	Flow cytometry
☒	☐	MRI-based neuroimaging

Plants

Seed stocks	This study does not involve novel plant genotypes.
Novel plant genotypes	This study does not involve the use of seed stocks.
Authentication	There are no cell lines, biological samples, or other materials requiring authentication used in this study.