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Corresponding author(s): Xiaokui Guo, Jürg Utzinger, Junxia Song, Yongzhang Zhu

Last updated by author(s): Dec 25, 2025

Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our Editorial Policies and the Editorial Policy Checklist.

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a	Confirmed
☐	☒ The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒ A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒ The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☐	☒ A description of all covariates tested
☐	☒ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒ A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☐	☒ For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☒	☐ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☐	☒ Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated

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	No software or computer code was used for data collection. All data were manually extracted from publicly available databases and policy documents.
Data analysis	Data analysis was performed using R (version 4.3.2), Python (version 3.11.14), Stata (version 18), SPSS (version 26.0), Microsoft Excel (version 16.78), and Joinpoint Regression Program (version 5.4.0). In R, key packages included tidyverse, dplyr, forecast, and lcmm. Python was used for sensitivity analyses and subgroup comparisons. Difference-in-differences analyses were conducted in Stata 18. Delphi-based descriptive statistics were computed in SPSS 26.0, and indicator weighting was implemented in Microsoft Excel. Joinpoint regression analyses were conducted using the Joinpoint Regression Program (version 5.4.0).

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.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

All data used in this study are publicly available. Governance indicators were extracted from AMR NAPs and related policy documents, the Tracking AMR Country Self-Assessment Survey (TrACSS, https://amrcountryprogress.org/), UNICEF immunization data (https://data.unicef.org/resources/dataset/immunization/), the Global AMR R&D Hub (https://dashboard.globalamrhub.org/), and the WHO GLASS database (https://worldhealthorg.shinyapps.io/glass-dashboard/). NAPs were obtained from the FAO AMR-LEX database (https://amr-lex.fao.org/main/profile/en), the WHO library of AMR NAPs (https://www.who.int/teams/surveillance-prevention-control-AMR/national-action-plan-monitoring-evaluation/library-of-national-action-plans), the AMR NAP Translation Project (https://sites.google.com/view/amrnaptranslations/introduction), and manual retrieval from national government sources. AMR prevalence, AMU (human, animal, and agricultural), and AMR-related mortality were obtained from publicly accessible datasets including Browne et al.47, Mulchandani et al.48, FAOSTAT (https://www.fao.org/faostat/en/#data/RP), the GBD AMR study (https://vizhub.healthdata.org/microbe/), and WHO Global TB Reports (https://www.who.int/teams/global-programme-on-tuberculosis-and-lung-health/tb-reports/). Detailed data sources are provided in the Supplementary pp 20–55, 111). The analysis-ready datasets required to reproduce all analyses and figures, including governance indicators, outcome variables, imputed values using numeric country identifiers, and datasets used for sensitivity and robustness analyses, are available in a public GitHub repository at: https://github.com/SkylarZeng/global_amr_governance_2017-2022.

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 was conducted at the country level and did not involve individual-level human participants. Sex and gender variables were therefore not applicable to this analysis.
Reporting on race, ethnicity, or other socially relevant groupings	This study does not include analyses or reporting related to race, ethnicity, or other socially relevant groupings. Countries are stratified based on national income groupings and regional classifications used for descriptive purposes rather than individual social characteristics.
Population characteristics	This study did not involve individual-level human participants. The study evaluates AMR governance across 193 countries and territories, using an indicator-based framework derived from national AMR policy documents, the WHO TrACSS survey, and international surveillance and administrative datasets. The analytical unit is the country, and outcomes include antimicrobial use, AMR prevalence, and AMR-related disease burden measured at national or regional levels over time.
Recruitment	No recruitment of human participants was conducted in this study.
Ethics oversight	Ethics approval was not required for this study, as it does not involve human participants, identifiable personal data, or biological samples.

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

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☐ Life sciences ☒ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Behavioural & social sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	This study is a longitudinal, quantitative observational analysis of national AMR governance and outcomes. It integrates an indicator-based governance framework with country-level panel data to evaluate temporal trends in AMR governance and its associations with antimicrobial use, AMR prevalence, and AMR-related disease burden.
Research sample	The unit of analysis in this study was countries and territories, with the country-year as the analytical unit. The study included 193 entities (190 United Nations Member States together with the Cook Islands, the State of Palestine, and Bermuda) for which relevant antimicrobial resistance (AMR) governance indicators and outcome data were available. No individual-level human participants were involved; therefore, demographic characteristics such as age or sex are not applicable. The study used existing, publicly available, aggregated country-level datasets and national policy documents. Governance indicators were derived from national AMR action plans and related policy documents, the Tracking AMR Country Self-Assessment Survey (TrACSS; https://amrcountryprogress.org/), UNICEF datasets (https://data.unicef.org/), the Global AMR R&D Hub (https://

	dashboard.globalamrhub.org/), and the WHO GLASS database (https://worldhealthorg.shinyapps.io/glass-dashboard/). Outcome data were obtained from the Global Burden of Disease AMR study (https://vizhub.healthdata.org/microbe/), FAOSTAT (https://www.fao.org/faostat/en/#data/RP), published global antimicrobial use estimates, and WHO Global TB Reports (https://www.who.int/teams/global-programme-on-tuberculosis-and-lung-health/tb-reports/). The study sample was determined by the availability of these data sources and was chosen to enable a comprehensive, longitudinal assessment of AMR governance and AMR-related outcomes across global regions and income settings.
Sampling strategy	All eligible countries and territories with available AMR policy documents and corresponding governance and outcome data were included. No probabilistic sampling was conducted; instead, a comprehensive census approach was used to maximise global coverage and comparability across countries and over time.
Data collection	No primary data were collected from human participants. All data were obtained from existing, publicly available databases and national AMR policy documents. Governance data were collected through systematic identification, review, and coding of national action plans and related policy or legal documents. Four researchers independently reviewed and rated governance indicators using standardized coding protocols informed by Cochrane Systematic Review standards, with discrepancies resolved through group discussion or third-party arbitration. Outcome data were compiled from established international surveillance and modelling datasets. No participant interaction, experimental manipulation, or blinding procedures were applicable given the use of secondary, aggregated country-level data.
Timing	Data were collected retrospectively from publicly available sources covering the study period from 2017 to 2022.
Data exclusions	No countries were excluded from the analyses beyond those lacking the required data for the relevant indicators, in accordance with predefined inclusion criteria.
Non-participation	This study did not involve recruitment of human participants; therefore, non-participation was not applicable.
Randomization	This study did not involve experimental manipulation or allocation of participants to groups. Randomization was therefore not applicable.

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	*Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.*
Novel plant genotypes	*Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.*
Authentication	*Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosiacism, off-target gene editing) were examined.*