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Causal effects of extreme climate hazards on antimicrobial resistance across One Health reservoirs: protocol for a scoping review and evidence gap map

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ABSTRACT

Introduction Extreme climate events are increasing in frequency and intensity, with potential consequences for antimicrobial resistance (AMR) across One Health reservoirs. However, the evidence base remains fragmented, and the capacity of existing studies to support causal inference has not been systematically assessed. This scoping review aims to map evidence linking extreme climate hazards to AMR outcomes across human, animal and environmental reservoirs; assess causal inference potential of identified studies and identify critical evidence gaps.

Methods and analysis 10 bibliographic databases are being searched for studies published from January 2000 to August 2026, with final updates and supplementary searches planned for November 2026. Searches began in December 2025; screening of records retrieved to date is complete, but data extraction and causal inference assessment have not started. Two reviewers (CH and TPN), with SL adjudicating disagreements, will independently extract data and assess studies of six extreme climate hazard categories across human, animal and environmental reservoirs. An eight-criterion causal inference potential framework will provide criterion profiles and descriptive scores from 0 to 16; its unvalidated weighting and classification thresholds will be examined in sensitivity analyses. Inter-rater agreement will be reported before consensus. A 6×8 evidence gap map will summarise study coverage, with separate sub-reservoir and outcome domain displays for antimicrobial use, phenotypic resistance and genotypic resistance. Harvest plots and narrative synthesis will preserve these distinctions. The review is expected to be completed in February 2027.

Ethics and dissemination This scoping review will analyse existing published data; therefore, ethical approval is not required. The completed review will be submitted for publication in a peer-reviewed open access journal. The evidence gap map, harvest plots and underlying dataset will be made publicly available through an open data repository. Findings will be disseminated through scientific conferences and briefing materials for relevant international initiatives.

STRENGTHS AND LIMITATIONS OF THIS STUDY

⇒ Searches cover 10 bibliographic databases without language restrictions and include supplementary terminology and citation searches.
⇒ Two reviewers will independently extract data and assess causal inference potential, with agreement measured before consensus.
⇒ Evidence maps will retain linked study identifiers and separate sub-reservoirs and antimicrobial use, phenotypic resistance and genotypic resistance outcomes.
⇒ The unvalidated causal inference scoring framework will be accompanied by criterion profiles and sensitivity analyses of thresholds, weighting and applicability.
⇒ Heterogeneous exposure definitions, incomplete reporting and literature outside the searched sources may limit the completeness and comparability of the evidence map.

INTRODUCTION

Antimicrobial resistance (AMR) and climate change are increasingly recognised as interconnected threats to global health,[1] yet the nature of their interaction remains poorly characterised. Bacterial AMR was associated with an estimated 4.95 million deaths in 2019,[2] while extreme climate events, including heat waves, floods, droughts and severe storms, have increased in frequency and intensity across most regions and are projected to intensify further under continued warming.[3]

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The question of whether extreme climate events accelerate AMR has gained increasing attention but remains largely unresolved.

Mechanistic plausibility exists across laboratory, infrastructural and behavioural pathways: Experimental studies demonstrate that elevated temperatures can enhance horizontal gene transfer of resistance plasmids and accelerate bacterial replication[4–6]; systems-level evidence suggests that flooding can overwhelm wastewater treatment and sanitation infrastructure, potentially redistributing resistant organisms and resistance genes across environmental compartments[7 8] and observational data suggest that droughts may concentrate pathogens in diminishing water sources and alter antimicrobial use practices in water-stressed agricultural systems, though these relationships remain poorly quantified.[1] But plausibility is not causation, and the evidence base linking specific climate hazards to measurable changes in resistance outcomes, including antimicrobial use, phenotypic resistance and resistance gene abundance, has not, to our knowledge, been systematically evaluated through a causal inference lens.

Van Bavel and colleagues recently mapped the broad intersections between climate change and AMR, identifying over 500 articles that discuss these topics in relation to one another.[1] This work revealed that the literature is growing rapidly and spans multiple disciplines. However, their scoping review treated 'climate change' as an undifferentiated exposure category, encompassing gradual warming trends, seasonal variation, land use change and acute extreme events within a single frame. This conflation obscures a critical methodological distinction. Gradual trends operate through slow-moving selection pressures and adaptive responses that are difficult to isolate from co-evolving social and economic changes; extreme events, by contrast, are discrete in time and space, and the occurrence of such hazards is largely exogenous to short-term AMR trajectories, while acknowledging that their health impacts may be modified by baseline infrastructure and prior antimicrobial use patterns. This characteristic makes extreme events amenable to quasi-experimental contrasts, before versus after and affected versus unaffected, which gradual trends do not readily support.[9]

This distinction matters because the policy questions are different. Asking whether 'climate change' affects AMR invites answers about long-term trajectories and shared root causes. Asking whether a specific flood, heat wave or drought caused a measurable increase in resistance carriage or antimicrobial consumption invites answers about preparedness, response and adaptation. The second question is more immediately actionable, but it demands a different kind of evidence: studies with temporal or spatial contrasts that can support counterfactual reasoning, not merely studies that observe co-occurrence.[10–12]

The existing evidence base has not been examined through this lens. We do not know how many studies have measured AMR outcomes before and after documented extreme events, how many have compared affected and unaffected areas or how many have employed designs capable of addressing confounding and exposure misclassification. We do not know whether the apparent concentration of research on certain hazard–reservoir combinations, such as floods and environmental antibiotic resistance gene abundance in surface water, reflects genuine causal signal, data availability or investigator convenience. And we do not know where the critical gaps lie: which hazard types, which One Health reservoirs and which transmission pathways remain essentially unstudied. These uncertainties persist in part because existing studies are scattered across disciplines, use inconsistent hazard definitions and exposure windows and rarely align outcome measurement temporally with the exposure event. Without answers to these questions, we cannot reliably prioritise surveillance, preparedness or adaptation investments in climate-vulnerable settings.

This protocol describes a systematic scoping review designed to address these questions.[13] We will systematically identify studies linking extreme climate hazards, including heat waves, floods, droughts, tropical cyclones, wildfires and compound events, to AMR outcomes across human, animal and environmental reservoirs. Our aims are three-fold: to map the distribution of existing evidence across hazard types and One Health reservoirs; to characterise the causal inference potential of included studies and to identify critical gaps that should guide future research and integrated One Health surveillance efforts in climate-vulnerable settings.

METHODS AND ANALYSIS

Study design and registration

The completed scoping review will be reported according to the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) extension for Scoping Reviews (PRISMA-ScR),[14] and this protocol is informed by the PRISMA-P statement.[15] The PRISMA-ScR checklist is provided in online online supplemental appendix 5. The protocol was registered on the Open Science Framework (OSF) on 7 April 2026 (doi: 10.17605/OSF.IO/27Y3H). Amendments introduced during peer review will be recorded as a dated OSF update, with their rationale and the review stage at which they were introduced.

The review methodology additionally incorporates guidance for evidence gap maps from the Campbell Collaboration and the International Initiative for Impact Evaluation (3ie),[13 16] which will be used as the primary synthesis method.

Project status and timeline

As of 16 October 2026, screening of records retrieved to date is complete; data extraction and causal inference potential scoring have not started. Initial searches began in December 2025. MEDLINE and Scopus were updated on 13 August 2026, Web of Science on 16 August 2026 and CNKI and Wanfang were searched on 20 August 2026

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Table 1 Eligibility criteria summary (Population, Exposure, Comparator and Outcome framework)

Domain	Inclusion	Exclusion
Population/ Reservoir	Human (clinical; community; occupational and other exposed groups); Animal (livestock and poultry; aquaculture; wildlife, companion animals and vectors); Environment (water and wastewater; soil, sediment, air and food). Eight reservoir categories; sub-reservoirs in online supplemental table S20	Populations with no link to extreme climate event; pure laboratory models
Exposure	Heat wave; flood; drought; storm; wildfire; compound events, meeting threshold, catalogue, meteorological or author-defined criteria	Gradual trends only; seasonal variation; exposure not linkable to outcome
Comparator	Pre-post; affected versus unaffected; intensity gradient; concurrent control; none (flagged)	None
Outcome	AMU (DDD, prescriptions); Phenotypic (MIC, S/I/R, prevalence); Genotypic (ARGs, resistome)	Antibiotic concentrations without resistance; antiviral/antifungal only
Study design	RCT; quasi-experimental; cohort; case-control; cross-sectional; ecological; modelling with empirical data	Reviews; editorials; protocols; purely theoretical
Other	January 2000 onwards; all languages; peer-reviewed, dissertations, reports, preprints	Before 2000; news articles

AMU, antimicrobial use; ARGs, antibiotic resistance genes; DDD, defined daily doses; MIC, minimum inhibitory concentration; RCT, randomised controlled trial; S/I/R, susceptible/intermediate/resistant.

(online supplemental table S19). Searches cover publications from January 2000 to the source-specific search date. Final database updates, terminology sensitivity searches and documented citation searching are planned for November 2026, extending coverage to the final search date; newly retrieved records will undergo screening. Completion of the review is expected in February 2027. The revised assessment and stratification rules will be fixed before data extraction begins.

Eligibility criteria

The eligibility criteria are structured according to the Population, Exposure, Comparator and Outcome (PECO) framework adapted for One Health scope and summarised in table 1.

We will include studies examining AMR outcomes in any of the three One Health sectors, which are divided into eight reservoir categories that form the columns of the evidence gap map and, within these, into sub-reservoirs (table 1; online supplemental table S20). The human sector comprises clinical populations (hospitalised patients, outpatients and clinical laboratory isolates), community populations (general population surveys, household and carriage studies) and occupational and other exposed groups, such as disaster response workers, agricultural workers in affected areas and displaced populations. The animal sector comprises livestock and poultry (cattle, swine and poultry), aquaculture (finfish, shellfish and crustaceans) and wildlife, companion animals and arthropod vectors. The environment sector comprises water and wastewater (surface water including rivers, lakes and floodwater; groundwater and drinking water; wastewater and sewage) and soil, sediment, air and food (soil and sediment; agricultural matrices such as manure; air and dust including wildfire smoke particulates and food products sampled in the context of climate events). Linked records preserve each sampled sub-reservoir, outcome domain and distinct contrast; mixed or inseparable samples are recorded as such rather than divided artificially.

Eligible exposures are extreme climate hazards defined according to established meteorological, climatological or disaster-epidemiological criteria. We will include six hazard categories: (i) heat extremes, (ii) precipitation extremes and flooding, (iii) drought, (iv) tropical cyclones and severe storms, (v) wildfire and smoke events and (vi) compound or cascading events involving multiple concurrent or sequential hazards. To be eligible, an exposure must satisfy at least one of four operational criteria (table 1): threshold-based definition requiring exceedance of a specified percentile threshold (eg, temperature exceeding the local 90th percentile for three or more consecutive days) or standardised index value (eg, standardised precipitation index ≤−1.5 for drought); event catalogue inclusion requiring documentation in established disaster databases such as EM-DAT, DesInventar or NOAA Storm Events; meteorological classification requiring satisfaction of established thresholds such as Saffir-Simpson Category 1 or higher for tropical cyclones or author-defined extremes requiring explicit definition and justification with clear temporal and spatial boundaries. Studies examining only gradual climate trends, seasonal variation without extreme threshold exceedance or average climate conditions without reference to specific extreme events will be excluded.

No comparator is required for inclusion, as descriptive studies characterising resistance patterns following extreme events remain informative for gap mapping. However, study design characteristics related to

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comparators, including temporal contrasts (pre-event vs post-event), spatial contrasts (affected vs unaffected areas), intensity gradients and concurrent control groups, will inform the causal inference potential assessment described below.

Eligible outcomes are grouped into three distinct domains: antimicrobial use (defined daily doses, prescription counts, sales data and treatment incidence), phenotypic resistance (minimum inhibitory concentrations, disk diffusion zone diameters, categorical classifications, resistance prevalence and multiple antibiotic resistance indices) and genotypic resistance (resistance gene presence, abundance or diversity, resistance-associated mobile genetic elements and resistome profiles). Antimicrobial use is an upstream indicator and will not be interpreted as a direct measure of resistance. Studies must report at least one eligible outcome; descriptive studies and results without an assessable direction remain eligible. Microbial community composition alone, without an eligible resistance or use outcome, does not meet the outcome criterion.

Eligible designs include randomised trials, quasi-experimental studies, cohort, case-control, cross-sectional and ecological studies, post-event surveys and modelling studies with empirical data. Design labels alone will not determine causal inference potential; the assessment will consider the features of each reported contrast. Narrative reviews, editorials, protocols without results and laboratory studies without field sampling will be excluded. Studies published from 1 January 2000 to the final search date in any language will be eligible; the start date defines the review scope and may omit earlier evidence.

Information sources and search strategy

We searched eight international databases (MEDLINE via PubMed, Embase via Ovid, Web of Science Core Collection, Scopus, CAB Abstracts and Global Health via Ovid, GreenFILE and the Cochrane Library) and two Chinese databases (CNKI and Wanfang). The international databases were initially searched in December 2025, with source-specific updates through August 2026. Searches cover publications from January 2000 without language restriction and will be updated in November 2026 to the date of the final search. Exact search dates are in online supplemental appendix 6 (online supplemental table S19). Supplementary sources include backward and forward citation searching, World Health Organization's Institutional Repository for Information Sharing (WHO IRIS), the Food and Agriculture Organization of the United Nations (FAO) and national public health agency repositories, medRxiv, bioRxiv and ProQuest dissertations.

The team developed the search iteratively using scoping searches and domain expertise, with MetaScreener assisting candidate term identification. Block 1 captures extreme climate hazards; Block 2 captures resistance phenotypes, resistant organisms, antimicrobial use and environmental/genomic vocabulary, including resistance genes, resistomes, integrons, mobile genetic elements and named resistance determinants. The final strategy combines Block 1 AND Block 2. The drafted One Health reservoir block (Block 3) was not applied, so retrieval is not conditional on conventional reservoir labels. Draft database strategies are provided in online supplemental appendix 1, and the executed MEDLINE strategy in online supplemental table S21. An information specialist will review the final update and supplementary strategies before they are run.

Search methods are reported according to PRISMA-S.[17] International database records were imported into Covidence (Veritas Health Innovation, Melbourne, Australia), which automatically identifies duplicates within and across imports using title, year, volume and author information. CH and TPN will check suspected residual duplicates manually during supplementary screening and extraction. Duplicate citations to the same report will be removed, whereas distinct reports from the same study will be retained and linked to a common study identifier. CNKI and Wanfang records were screened on their platforms; potentially eligible reports will be checked against the Covidence library using bibliographic details and DOI where available. Import, duplicate removal and source-provenance records will be retained for the PRISMA flow diagram.

To assess retrieval beyond conventional AMR vocabulary, we will run a terminology sensitivity search in MEDLINE, Web of Science and Scopus, combining the hazard block with susceptibility-testing terms, additional resistance gene terms and broad metagenomic or microbial community terms linked to environmental or animal matrices (online supplemental table S22). The expanded search will be exported in full and de-duplicated against the retained main search library. Identical eligibility rules will apply. Backward and forward citation searching of all included studies will be repeated with a separate search log because the earlier reference list checks did not record yield separately. For each route, we will report raw records, duplicates, newly screened records and newly included unique studies, retaining all source tags and identifying studies found only by supplementary routes. Source attribution and overlap rules are specified in online supplemental table S22.

Study selection

CH and TPN independently assess every record at title/abstract and full-text stages; SL adjudicates disagreements unresolved by discussion. MetaScreener 2.0 assists in record organisation and screening, but all eligibility decisions are independently checked by both human reviewers. No record is excluded solely on an automated decision. At full text, reviewers confirm that an operational exposure criterion and an eligible outcome are present and that the exposure and outcome are linked in time or geography. They assign hazard and reservoir categories and record standardised exclusion reasons. The same independent human screening applies to records

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Table 2 Data extraction domains

Domain	Key fields
Study characteristics	First author; year; journal; country; design; funding; conflicts of interest
Exposure	Hazard category; operational definition type; event dates; severity; geographic extent; data source
Reservoir	Sector; reservoir category; sub-reservoir; specific population or matrix; sample size; sampling method; interface study (Y/N)
Outcome	Domain (AMU/phenotypic/genotypic); measure; organisms; antimicrobials; method; timing
Comparator and design	Comparator type; pre-event baseline (Y/N); number of time points; confounding approach
Results	Direction (increase/decrease/no change/mixed/indeterminate); measure; estimate; CI; denominator/normalisation; sampling time; dose-response
Causal inference	Eight criteria scores (0–2); total score; classification (see table 3)
Quality	Tool applied; domain ratings; overall rating

AMU, antimicrobial use.

retrieved through the final updates and supplementary searches.

Data extraction

CH and TPN will independently extract data using a structured form in MetaScreener (table 2; online supplemental appendix 2), with SL adjudicating unresolved discrepancies. The form will be piloted on 10 diverse studies before full extraction. Distinct hazard, sub-reservoir and outcome–domain combinations will form linked records under a common study identifier; reports of the same study will be linked rather than counted separately. Each record will identify the sampled population or matrix, outcome measure, organism, antimicrobial, denominator or normalisation and sampling time. Multi-sector studies will be flagged as interface studies only when measurements across sectors are linked analytically. Record allocation and overlapping population rules are specified in online supplemental table S20.

Causal inference potential assessment

The causal inference potential framework is an exploratory mapping tool for describing design features relevant to causal interpretation (figure 1). It is not a validated risk-of-bias instrument, a measure of effect size or a certification of causality.

The framework covers four domains and eight criteria (table 3). Temporal structure describes baseline measurements and follow-up; counterfactual contrast describes comparison groups and parallel-trend evidence; exposure ascertainment describes hazard definitions and



Figure 1 Causal inference potential assessment and robustness checks. Four domains contain eight criteria, each scored 0–2. The total score of 0–16 defines descriptive High (12–16), Moderate (7–11) and Low (0–6) bands. These unvalidated bands do not establish causality or replace risk-of-bias assessment. Criterion profiles, pre-consensus inter-rater agreement and the sensitivity analyses in online supplemental table S23 accompany the score; criterion-specific rationale and applicability are given in online supplemental table S24.

exposure–outcome alignment and confounding control describes confounder handling and analysis. The original eight criteria and 0–2 scale are retained; scoring guidance is provided in online supplemental appendix 3 (online supplemental tables S15 and S16), with rationale and applicability in online supplemental table S24. Ratings will be specific to the linked contrast when design features or follow-up differ within a study; otherwise, the shared study-level profile will be reused.

The sum of eight scores (0, 1 or 2 each) defines descriptive bands of High (12–16), Moderate (7–11) and Low (0–6) causal inference potential. These labels describe the rubric score, not verified causal validity. Assignment will depend on documented study features, not on the design name alone.

Equal weights provide a transparent starting rule in the absence of empirically established weights for these heterogeneous studies; they do not imply equal causal importance. The thresholds are pragmatic mapping conventions, not empirically calibrated boundaries. A High score corresponds to a mean criterion score of at least 1.5, but can coexist with a missing critical safeguard. Because sums can conceal such weaknesses,[18] criterion profiles and design-appropriate risk-of-bias judgments will accompany every classification. Three months of follow-up is a duration descriptor, not a universal adequacy standard, and parallel trends are not an assumption of every eligible design.

Sensitivity analyses will examine shifted thresholds, a counterfactual/confounding gate, leave-one-criterion-out scores, omission of inapplicable parallel-trend criteria with outcome-specific follow-up assessment and alternative weights emphasising comparison and confounding (online supplemental table S23). Rules will be fixed before scoring. Reclassification will be reported for rated

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Table 3 Causal inference potential assessment framework

Domain	Criteria	Score 0	Score 1	Score 2
Temporal structure	Pre-event baseline	None	Single measurement	Multiple time points
	Post-event follow-up duration	Immediate only	<3 months	≥3 months
Counterfactual contrast	Comparison group	None	Historical/external	Concurrent geographic/ within-population
	Parallel trends	Not assessed	Assumed	Supporting pre-trend evidence
Exposure ascertainment	Exposure definition	Vague	Author-defined criteria	Standardised framework (Expert Team on Climate Change Detection and Indices (ETCCDI), Emergency Events Database (EM-DAT))
	Exposure–outcome alignment	Unclear linkage	Plausible indirect	Direct measurement in affected area/time
Confounding control	Confounder identification	None discussed	Acknowledged not controlled	Systematically identified and controlled
	Analytic approach	Unadjusted	Basic adjustment	Design-appropriate methods with assumptions addressed

Classification: High (12–16), Moderate (7–11), Low (0–6); total=sum of eight criteria (0–16). These are unvalidated descriptive bands. Follow-up duration is not equivalent to adequacy for every outcome. Parallel-trend applicability and evidence are recorded separately; non-applicability is examined in sensitivity analysis (online supplemental tables S23 and S24).

contrasts, unique studies and occupied map cells; these checks assess robustness, not empirical validity. Independent agreement will assess reproducibility, while external validation of the framework remains future work.

CH and TPN will independently score the criteria, retaining both pre-consensus ratings; SL will adjudicate unresolved discrepancies. Calibration will use 10 diverse studies, with pilot and subsequent agreement reported separately. We will report percentage agreement and linear-weighted κ[19] for each criterion and the three-level class, and a two-way random-effects, absolute-agreement, single-rater ICC[20] for total scores, with 95% CIs where estimable. Percentage agreement will accompany κ because imbalanced score distributions can yield low κ despite high agreement.[21] Interval estimation and handling of repeated contrasts, missing ratings and degenerate score distributions are specified in online supplemental table S23.

Quality assessment

Risk of bias will be assessed using design-appropriate tools: Cochrane Effective Practice and Organisation of Care (EPOC) criteria for quasi-experimental studies,[22] the Newcastle-Ottawa Scale for cohort and case-control studies[23] and the Joanna Briggs Institute (JBI) critical appraisal checklist for cross-sectional studies.[24] For ecological studies, we will apply a modified checklist addressing ecological fallacy, confounding and temporal alignment. Tool selection by study design and the modified ecological checklist are provided in online supplemental appendix 4 (online supplemental tables S17 and S18).

CH and TPN will independently assess risk of bias, with SL adjudicating unresolved disagreements. Domain-level judgments will inform interpretation alongside the causal inference profiles and will not be replaced by the summed score. Appraisal will not exclude studies from the evidence map; critical limitations will be flagged in the synthesis.

Data synthesis

Consistent with the objectives of a scoping review, the aim of this synthesis is to map the architecture of evidence linking extreme climate hazards to AMR, characterising distribution across hazards and reservoirs, identifying methodological capacity for causal inference and locating critical gaps, rather than to estimate pooled effect magnitudes. Given the anticipated heterogeneity in exposures, outcomes and study designs, formal meta-analysis is not planned.

The primary display is a 6×8 matrix of six hazards by eight reservoir categories grouped into three sectors (figure 2a). Bubble area represents unique studies contributing to a cell; colour shows the highest descriptive causal inference band present. This colour does not represent the certainty or typical quality of the whole cell, so the full High/Moderate/Low distribution will accompany each cell in the underlying table. Empty cells mean that no eligible studies were identified by this review. Linked multi-sector studies will be flagged. Studies count once per cell and once within each row, column and overall margin, irrespective of the number of linked records. Sub-reservoir and outcome–domain maps (figure 2b)

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Figure 2 Illustrative hierarchical evidence gap map. (a) Six hazards are crossed with eight reservoir categories grouped within human, animal and environment sectors. Bubble area and the embedded number show unique studies in each cell; colour indicates the highest descriptive causal inference band present. A diamond flags a linked multi-sector study; dashed circles indicate no studies in this illustrative example. Margins de-duplicate studies within each row, column and overall total. (b) The flooding×water/wastewater cell is disaggregated by sampled matrix and outcome domain. Antimicrobial use is not plotted as an environmental sample measurement; linked human or animal use data are allocated to the corresponding sector. Blank dash entries indicate no example study. Studies may contribute to multiple cells, but are counted only once within each cell or margin. All values are synthetic illustrations of the planned display, not review findings; the illustration source records are supplied with the figure.

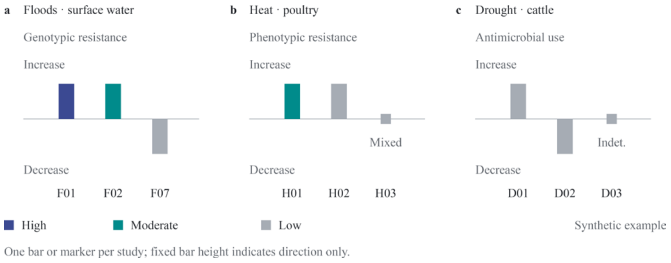


Figure 3 Illustrative harvest plots stratified by hazard, sub-reservoir and outcome domain. Each bar denotes one synthetic example study within the stated combination. Equal-height bars encode reported increase or decrease, with a separate marker for mixed or indeterminate findings; colour consistently retains the descriptive causal inference band. Numerical estimates, denominators and uncertainty will be reported in the accompanying review tables rather than encoded as bar height. Lack of statistical significance will not be interpreted as absence of an effect. All example records are synthetic and do not represent findings of this review.

will be reported separately, with geographic stratification where data permit.

Harvest plots will be used where at least three studies address a common hazard, sub-reservoir and outcome domain (figure 3).[25] Measures, organisms, denominators and sampling times will be kept distinct in the accompanying table. Bars will have equal height and show reported direction, with colour retaining the causal inference band. Exactly null estimates or explicitly unchanged measurements will be coded as no change; mixed or indeterminate findings will be shown separately. Nonsignificance will not be treated as proof of no effect, and counts of positive findings will not be interpreted as a pooled effect or a test of association. The estimate-selection and direction-coding rules are given below online supplemental table S20.

Narrative synthesis will be organised by hazard, sub-reservoir and outcome domain, describing study volume, criterion profiles, risk of bias, estimates and uncertainty, consistency or discordance and evidence gaps. Antimicrobial use, phenotypic resistance and genotypic resistance findings will not be combined into a common effect statement. Cross-cutting themes will address geographic representation, linked One Health interfaces, temporal research patterns and recurring methodological limitations.

The research agenda will identify combinations with little or no eligible evidence, recurrent design limitations and feasible improvements in surveillance, comparison groups, exposure ascertainment and follow-up. Priorities will consider methodological weaknesses and relevance together, without treating a high rubric score as a minimum guarantee of causal validity.

Assessment of evidence certainty

We will provide a structured narrative assessment of confidence within each hazard, sub-reservoir and outcome–domain combination, informed by risk of bias, consistency, directness and precision where available.[26] The causal inference score will not be converted into a GRADE certainty rating.

This assessment will consider estimates and uncertainty alongside design assumptions and mechanistic coherence. Because outcomes and estimands may remain too heterogeneous for a coherent body-of-evidence judgement, no formal modified-GRADE High/Moderate/Low/Very Low rating will be assigned. A summary table will state the evidence, limitations and unresolved uncertainties for each interpretable combination.

DISCUSSION

Anticipated contributions

This scoping review will map studies linking extreme climate hazards to AMR and antimicrobial use across One Health settings. The evidence map will show where

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studies exist and which design features strengthen or limit causal interpretation, while preserving differences in sampled reservoirs and measured outcomes.

The map and its underlying record-level data will help researchers and decision makers distinguish limited study coverage from limitations in the available designs. It will identify where further investigation is needed without treating a high-scoring study or a populated map cell as sufficient evidence for an intervention.

The framework offers a transparent way to describe heterogeneous designs, but its summed score and thresholds require validation before wider use. Criterion-level reporting, independent agreement and sensitivity analyses will make its limitations visible and identify priorities for future evaluation.

Strengths

Several methodological features strengthen this review. The eligibility criteria employ operational definitions for extreme climate exposures that balance standardisation with the heterogeneity inherent in climate health research. The four acceptable pathways for exposure definition (threshold-based, event catalogue, meteorological classification and author-defined with justification) ensure that relevant studies are not excluded due to rigid definitional requirements while maintaining sufficient rigour to distinguish discrete extreme events from gradual climate trends.

The One Health framing ensures comprehensive coverage across human, animal and environmental reservoirs, enabling identification of cross-reservoir patterns that might be missed by reviews restricted to single sectors. This scope is particularly important given the recognised role of environmental and animal reservoirs as sources of resistance determinants affecting human health and the potential for extreme climate events to disrupt the boundaries between these reservoirs through mechanisms such as flooding, infrastructure failure and population displacement.

The synthesis strategy, combining evidence gap mapping with harvest plots and structured narrative synthesis, is well-suited to the review's objectives. Unlike traditional systematic reviews that prioritise pooled effect estimation, our approach acknowledges that the primary value lies in characterising evidence distribution and methodological quality rather than quantifying effect magnitudes that may not be meaningfully comparable across heterogeneous exposures and outcomes.

The protocol was registered before data extraction. The revisions introduced after initial screening will be documented separately from the registered methods, and the revised scoring and stratification rules will be fixed before extraction and assessment. This chronology supports transparency without implying that every revised method preceded the search or screening.

Limitations

Relevant studies may be indexed outside the searched databases or disseminated through difficult-to-search grey literature channels, and the January 2000 start date excludes earlier reports. Broader terminology and documented citation searching may reduce missed retrieval; their incremental yield cannot establish the sensitivity of the search or prove that no eligible studies remain unidentified.

Second, heterogeneity in exposure definitions across studies may complicate classification into hazard categories. Studies may define extreme events using different thresholds, reference periods or spatial scales, and some exposures may span multiple hazard categories. Our operational criteria provide guidance for classification, but borderline cases will require judgement, and we will conduct sensitivity analyses excluding studies with ambiguous exposure definitions.

The causal inference framework is unvalidated and combines criteria whose relevance varies by design, hazard and outcome. Calibration, criterion profiles, agreement statistics and sensitivity analyses will assess reproducibility and robustness, not establish criterion validity. Residual within-category heterogeneity, residual screening error and selective publication may also affect the map. Broad cell colours and direction counts will therefore be interpreted with the underlying risk-of-bias judgements, effect estimates and uncertainty.

Implications for policy and practice

The findings of this review will have several implications for policy and practice, contingent on the evidence patterns identified. If the review identifies hazard–reservoir combinations with substantial high-quality evidence supporting causal relationships, this would strengthen the rationale for integrating antimicrobial stewardship considerations into climate adaptation planning and disaster preparedness frameworks. Specific implications might include enhanced AMR surveillance following extreme weather events, targeted infection prevention measures in disaster-affected populations and climate-informed forecasting of antimicrobial demand.

Conversely, if the review reveals that most evidence is of low causal inference potential, dominated by post-event surveys, ecological correlations and studies lacking pre-event baselines, this would highlight the need for methodological upgrading before causal claims can be confidently advanced. The research agenda will specify minimum methodological standards and identify opportunities to leverage existing climate monitoring and disaster surveillance infrastructure for prospective AMR research.

Regardless of the evidence patterns identified, the review will contribute to ongoing efforts to operationalise the One Health approach to AMR by providing a systematic assessment of climate as a cross-cutting driver affecting human, animal and environmental reservoirs. This perspective complements existing frameworks that emphasise antimicrobial use, infection prevention and access to diagnostics as pillars of AMR response, by

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highlighting environmental and climatic determinants that may modulate resistance dynamics across sectors.

ETHICS AND DISSEMINATION

This scoping review will analyse existing published data from peer-reviewed and grey literature sources; therefore, ethical approval is not required. No primary data collection involving human or animal participants is planned.

The completed review will be submitted for publication in a peer-reviewed journal with scope encompassing climate change, infectious diseases and One Health research. We will target journals that support open access publication and supplementary data sharing to maximise accessibility. The evidence gap map, harvest plots and underlying dataset will be made available as supplementary materials or through an open data repository.

To enhance policy relevance, we will prepare derivative products including an executive summary for policymakers highlighting key findings and research priorities and an interactive online version of the evidence gap map enabling users to explore the evidence base and briefing materials for relevant international initiatives including the WHO Global Action Plan on Antimicrobial Resistance, the Quadripartite One Health Joint Plan of Action and working groups of the Intergovernmental Panel on Climate Change (IPCC) addressing climate change and health.

Findings will be presented at relevant scientific conferences spanning climate science, infectious disease epidemiology and One Health disciplines to reach diverse research communities and stimulate cross-disciplinary collaboration. We will engage with stakeholders in climate adaptation and AMR policy to identify opportunities for translating review findings into practice.

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