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ENVIRONMENTAL SCAN APPENDICES

Appendices: Rapid synthesis of environmental antimicrobial resistance (AMR) knowledge and surveillance in Canada

6 February 2025

Suggested citation: Taing L, Whitelaw H, Wilson MG. Appendices: Rapid synthesis of environmental antimicrobial resistance (AMR) knowledge and surveillance in Canada. Hamilton: McMaster Health Forum, 6 February 2025.

Appendices

- Appendix 1: Methodological details
- Appendix 2: Organizing framework
- Appendix 3: Global jurisdiction scan
- Appendix 4: Global evidence scan
- Appendix 5: Canadian jurisdiction scan of environmental AMR surveillance
- Appendix 6: Canadian scientific evidence data extraction
- Appendix 7: Evidence syntheses data extraction
- Appendix 8: Documents excluded from the review
- References

Appendix 1: Methodological details

Background to the rapid synthesis

This rapid synthesis mobilizes both global and local research evidence about a question submitted to the McMaster Health Forum's Rapid Response program. Whenever possible, the rapid synthesis summarizes evidence drawn from existing evidence syntheses and from single research studies in areas not covered by existing evidence syntheses and/or if existing evidence syntheses are old or the science is moving fast. A systematic review is a summary of studies addressing a clearly formulated question that uses systematic and explicit methods to identify, select and appraise research studies, and to synthesize data from the included studies. The rapid synthesis does not contain recommendations, which would have required the authors to make judgments based on their personal values and preferences.

The Forum produces timely and demand-driven contextualized evidence syntheses such as this one that address pressing health and social system issues faced by decision-makers (see our website for more details and examples - www.mcmasterforum.org/find-domestic-evidence/contextualized-es). This includes evidence syntheses produced within:

- days (e.g., rapid evidence profiles or living evidence profiles)
- weeks (e.g., rapid syntheses that at a minimum include a policy analysis of the best-available evidence which can be requested in a 10-, 30-, 60- or 90-business-day timeframe)
- months (e.g., full evidence syntheses or living evidence syntheses with updates and enhancements over time)

This rapid synthesis involved six steps:

1) submission of a question from a policymaker or stakeholder (in this case, Public Health Agency of Canada (PHAC)
2) identifying, selecting, appraising and synthesizing relevant research evidence about the question
3) conducting and synthesizing a jurisdictional scan of experiences about the question from other countries and Canadian provinces and territories
4) conducting key informant interviews
5) drafting the rapid synthesis in such a way as to present concisely and in accessible language the research evidence
6) finalizing the rapid synthesis based on the input of at least two merit reviewers.

Identification, selection, quality appraisal and synthesis of evidence

The evidence review took place between 15 October to 15 December 2024 and had three parts: global jurisdiction scan (Appendix 5), global evidence scan (Appendix 4), and Canadian jurisdiction scan (Appendix 5) and scientific evidence data extraction (Appendices 6 and 7). Each part focused on surveillance of AMR-associated microorganisms, agents and

pollutants in the natural environment, covering sources like water (sewage, effluent, wastewater, runoff), air (aerosols, bioaerosols), soil (sediment, sludge, manure, biosolids), and wildlife (wild animals and plants).

Canadian and global jurisdiction scans

For primary research in the Canadian jurisdiction scan, we documented the dimension of the organizing framework (Appendix 2) with which it aligns, jurisdiction studied, methods used, a description of the sample and intervention, declarative title and key findings. We then used this extracted information to develop a synthesis of the key findings from the included syntheses and primary studies. During this process we include published, pre-print and grey literature. All of the information provided in the appendix tables was taken into account by the authors in describing the findings in the rapid synthesis. We excluded documents that did not directly address the research questions and the relevant organizing framework. Some excluded Canadian scientific literature articles are captured in Appendix 7, along with European Council-related projects and documents that could not be reviewed due to time constraints.

For each rapid synthesis, we worked with the requestors to collectively decide on what countries (and/or states or provinces) to examine based on the question posed. The main goal of the jurisdiction scans was to understand the current state of environmental AMR surveillance in Canada, and key knowledge and surveillance gaps as compared to global progress and evidence. Given that the topic of environmental AMR is nascent and there are no standard working definitions or approaches that comprehensively cover its complexity, jurisdictional experiences, grey literature, and databases were identified via Google Advanced Searches per Canadian province and territory. The top three pages of results for public records of environmental AMR surveillance and relevant databases on water, soil, air, and wildlife monitoring were reviewed. A snowball method was applied to identify additional experts, documents, and databases, and included materials referred by subject matter experts if they met the synthesis' criteria. Where information was not available in English, we attempted to use site-specific translation functions or Google Translate. Table A-1 summarizes the search string structure, key terms searched, and inclusion and exclusion criteria. Additionally, we manually searched websites of research-intensive Canadian universities, focusing on the U15 group and other institutions with notable AMR experts (Table A-2) to identify relevant Pan-Canadian or regional projects and databases on environmental AMR data.

For other countries, a comparative analysis on environmental AMR approaches in other G7 countries (United States (US), United Kingdom (UK), France, Germany, Italy, and Japan) was conducted by reviewing each country's latest National Action Plan (NAP). These were sourced from the World Health Organization (WHO) library. English NAPs were reviewed if available; the Italian NAP was reviewed using Google Translate. Hand-searches were conducted for France, the UK and US due to their progress on environmental AMR surveillance and, in the case of the US, its shared border with Canada across maritime, freshwater, and land resources.

For global guidance, WHO and United Nations Environment Programme's (UNEP) websites were searched for guidelines (defined as providing recommendations or normative statements derived from an explicit process). The global review of One Health and integrated AMR surveillance guidance also involved interviewing two WHO officials on October 22, 2024, to understand the Quadripartite approach and country-specific progress for planning and implementing environmental surveillance systems at a national level.

Table A-1: Search string structure and key terms for the Canadian jurisdiction scan

Search string structure	[environmental pollutant] AND Surveillance or Monitoring AND antimicrobial resistance OR antibiotic resistance AND [Geographic region: Canada, Province or Territory]
Pollutant key term	• Sewage OR effluent OR runoff OR waste • Soil OR Sludge OR biosolids OR manure OR Sediment • Bioaerosols OR air OR emissions • Wildlife
Inclusion	English and French websites with relevant content from 2019 to present
Exclusion	Pre-2019 webpages and content

Table A-2: Research universities

AL	University of Alberta University of Calgary	ON	University of Toronto University of Ottawa McMaster University University of Western Ontario	Queen's University University of Waterloo University of Guelph
BC	University of British Columbia			
MB	Winnipeg			
NB	University of New Brunswick	QC	McGill University Universite de Montreal	Universite Laval
NL	Memorial University			
NS	Dalhousie University	SK	University of Saskatchewan	
PEI	University of Prince Edward Island	YT	Yukon University	

Global evidence scan

A systematic search was carried out PubMed and Web of Science on 23 October 2024 for: 1) single studies (when no guidelines or evidence syntheses are identified), 2) evidence syntheses, and 3) modelling papers. Table A-3 summarizes the key terms searched, and inclusion and exclusion criteria for English or French publications from 2019-2024, of which no filtering processes were applied for geographic location. A Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) diagram outlines included studies (Figure A-1).

For each evidence synthesis identified from the Global Evidence Scan (Appendix 7), we recorded several details: we documented the dimension of the organizing framework it aligns with (see Appendix 2), key findings, whether it is a living review, methodological quality (using the Assessing the Methodological Quality of Systematic Reviews (AMSTAR) tool), the last year literature was searched, availability of a GRADE profile, and equity considerations (using PROGRESS PLUS). Two reviewers independently assess the quality of highly relevant evidence syntheses using the AMSTAR tool, resolving any disagreements with a third reviewer. AMSTAR scores range from 0 to 11, with: high-quality being scores of 8–11; medium-quality having scores of 4–7, and low-quality having scores below 4. AMSTAR was designed to evaluate clinical intervention reviews, so some criteria may not fully apply to reviews on health-system arrangements, implementation strategies, or qualitative studies. Even so, AMSTAR remains the best available general tool for assessing methodological quality. Some qualitative evidence syntheses address other types of questions, such as involving citizens or experts, researcher competency, and reflexivity—criteria not covered by AMSTAR. If some AMSTAR criteria are deemed irrelevant, scores are adjusted (e.g., 8/8 is comparable to 11/11). A high score indicates high confidence in the findings; a low score suggests its findings require closer scrutiny for limitations.

Limitations

- The jurisdiction scans relied only on data, information, and documents that were publicly accessible. Government data, however, is often not publicly available or shared between departments or agencies, which likely limited the review.
- An initial focus on environmental surveillance approaches for AMR yielded limited results due to a lack of available government data and information. The scope was consequently expanded to include hand searches of research-intensive universities in Canada and integrated or One Health surveillance approaches that incorporate environmental considerations, both in Canada and globally.
- This is a deeply complex and broadly framed topic with a lack of standardised language and approaches across sectors and jurisdictions, which complicated the design of the scoping methods and limited our ability to apply a structural approach across different types of environmental pollutants and institutions.
- Focus: There was significantly more found on water and wild animals over soil, air and wild plant AMR risks. This might have resulted in a potential overrepresentation of health risks. Google Translate was used, when necessary, to translate documents into English, which can limit critical analysis.

Table A-3: Search string structure and key terms for the Canadian jurisdiction scan

Pollutant terms	Ecosystem* OR habitat* OR "environmental pollution" OR wastewater* OR runoff OR soil OR sediment OR *aerosol OR wildlife*
Env. surv. terms	"Environmental surveillance" OR "environmental monitoring" OR "environmental sampling"
AMR key terms	"Anti*bacterial resistance" OR "anti*biotic resistance" OR "anti*microbial resistance" OR "resistant gene"
Search strings	In PubMed, we searched for evidence syntheses using: • ("monitor*"[TIAB] OR "sampl*"[TIAB] OR "surveil*"[TIAB]) AND ((("Anti-Bacterial Agents"[Mesh]) AND resistance[TIAB]) OR ("Anti*bacterial resistance"[TIAB] OR "antibiotic resistance"[TIAB] OR "anti*microbial resistance"[TIAB] OR "resistant gene"[TIAB:~3])) AND (bioaerosol*[TIAB] OR "Ecosystem"[Mesh] OR ecosystem*[TIAB] OR "Environmental Pollution"[Mesh] OR habitat*[TIAB] OR pollut*[TIAB] OR runoff[TIAB] OR run-off[TIAB] OR "Soil"[Mesh] OR soil[TIAB] OR "Wastewater"[Mesh] OR wastewater*[TIAB] OR wildlife*[TIAB]) AND (review[PT] OR "comparative study"[PT] OR effect[TIAB] OR occurrence[TIAB] OR projection[TIAB] OR collect[TIAB] OR collection[TIAB] OR level[TIAB] OR risk[TIAB]) NOT (Editorial[PT] OR Letter[PT] OR News[PT] OR comment[PT]) • ("Ecological Parameter Monitoring"[Majr] OR "Environmental Monitoring"[Majr] OR "Wastewater-Based Epidemiological Monitoring"[Majr]) AND ((("Anti-Bacterial Agents"[Mesh]) AND resistance[TIAB]) OR ("Anti*bacterial resistance"[TIAB] OR "antibiotic resistance"[TIAB] OR "anti*microbial resistance"[TIAB] OR "resistant gene"[TIAB:~3])) AND (bioaerosol*[TIAB] OR "Ecosystem"[Mesh] OR ecosystem*[TIAB] OR "Environmental Pollution"[Mesh] OR habitat*[TIAB] OR pollut*[TIAB] OR runoff[TIAB] OR run-off[TIAB] OR "Soil"[Mesh] OR soil[TIAB] OR "Wastewater"[Mesh] OR wastewater*[TIAB] OR wildlife*[TIAB]) AND (review[PT] OR "comparative study"[PT] OR effect[TIAB] OR occurrence[TIAB] OR projection[TIAB] OR collect[TIAB] OR collection[TIAB] OR level[TIAB] OR risk[TIAB]) • ("résistance aux antibiotiques"[TIAB] OR "résistance aux antimicrobiens"[TIAB] OR "Résistance virale aux médicaments"[TIAB] OR "gène de résistance"[TIAB]) AND (bioaerosol*[TIAB] OR "Animaux sauvages"[TIAB] OR "Eaux usées"[TIAB] OR Écosystème[TIAB] OR Environnement[TIAB] OR habitat[TIAB] OR "Pollution de l'eau"[TIAB] OR "Pollution de l'environnement"[TIAB] OR Sol[TIAB]) • ("Surveillance des paramètres écologiques"[TIAB] OR "Surveillance de l'environnement"[TIAB] OR "Surveillance épidémiologique fondée sur les eaux usées"[TIAB]) In Web of Science, we searched for evidence syntheses using: • (monitor* OR sampl* OR surveil*) (Topic) AND ("anti*bacteria* resist*" OR "antibiotic* resist*" OR "anti*microbial* resist*" OR "gene* resist*" OR "resistant gene*") (Topic) AND (bioaerosol* OR ecosystem* OR environment* OR habitat* OR pollut* OR runoff OR run-off OR soil OR wastewater* OR wildlife*) (Topic) (Topic) and 2024 or 2023 or 2022 or 2021 or 2020 or 2019 (Publication Years) and Article or Review Article or Other or Data Set or Preprint (Document Types) and Web of Science Core Collection or BIOSIS Previews or Preprint Citation Index (Database) and English (Languages) and CANADA or USA or GERMANY or FRANCE or ENGLAND or ITALY or JAPAN (Countries/Regions) • ("résistance aux antibiotiques" OR "résistance aux antimicrobiens" OR "Résistance des champignons aux medicaments" OR "Résistance virale aux médicaments" OR "gène de résistance") (Topic) and 2024 or 2023 or 2022 or 2021 or 2020 or 2019 (Publication Years) and Article or Review Article or Other or Early Access (Document Types) and Web of Science Core Collection or BIOSIS Previews (Database) and English or French (Languages) and CANADA or FRANCE or USA or ENGLAND or ITALY (Countries/Regions)
Inclusion	English and French content from 2019 to 2024 that included environmental samples taken from the natural environment and research from G7 and other high-income countries.
Exclusion	Studies in built environments that had no natural environment monitoring method (for example, anthropogenic indoor or built environments, including farms); were lab-based studies or focused on diagnostic method; and focused on climate change factors.

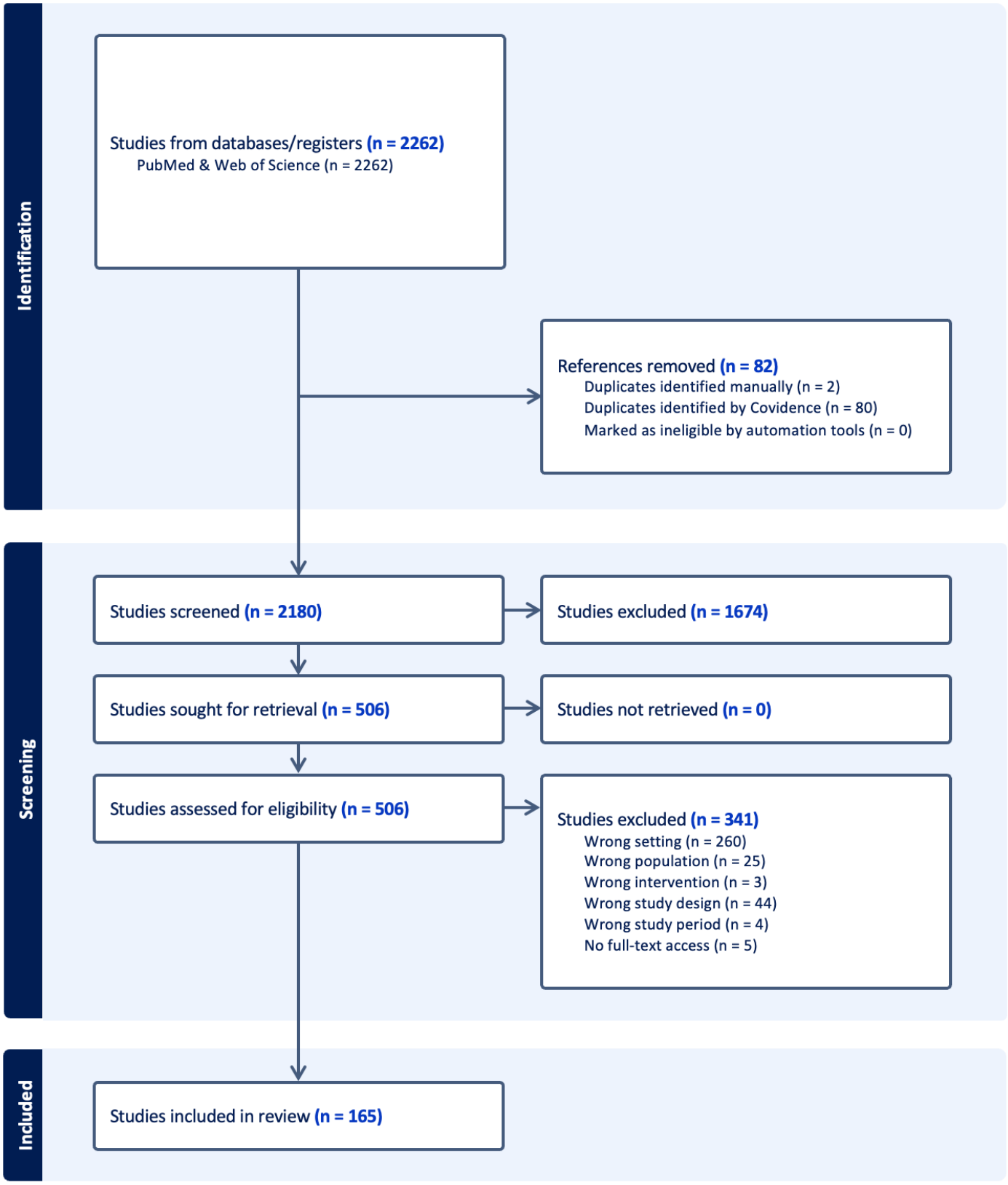

Figure A-1: PRISMA diagram

Appendix 2: Organizing framework

The organizing framework (Table A-4) outlines how information was extracted and is structured for the global evidence scan (Appendix 4), Canadian jurisdiction scan (Appendix 5), Canadian scientific evidence (Appendix 6).

This detailed framework was not an effective tool for the Global jurisdiction review's high-level policy documents, so that section follows a descriptive narrative format with a summative table outlining the reviewed jurisdiction, whether there was an explicit environmental AMR definition, the surveillance program name, and what was monitored in Appendix 3.

Table A-4: AMR pollution source type and one health origin domain and origin type

Organizing framework	

• Environmental AMR definition
  ○ Environmental dimensions
  ○ One Health / Integrated surveillance approach
• Environmental AMR surveillance
  ○ Ongoing monitoring of environmental AMR
  ○ Surveillance program name
  ○ Responsible agency or department
• Type of environmental AMR surveillance
  ○ Occurrence / Prevalence
  ○ Selection
  ○ Dissemination
  ○ Transmission
• Environmental samples
  ○ Water
  ○ Soil
  ○ Air
  ○ Wildlife
• Comparative study
  ○ Water/Soil/Air: Natural vs built environment sites
  ○ Wildlife: Wild vs domestic populations
  ○ All: Different environmental media
	• Type of pollution sources (See Table A-5)
	• Pollution source one health domain (See Table A-5)
	• Pollution source origin type (examples: wastewater treatment works, pharmaceutical industry, farm)
	• Type of AMR microorganism, AMR determinants or antimicrobial agents monitored
	  ○ Microorganism
	  ○ Resistant microorganism
	  ○ ESBL-producing *E. coli*
	  ○ Class 1 integron
	  ○ Antimicrobial-resistant genes (ARGs)
	  ○ Antimicrobial: Antibiotic
	  ○ Antimicrobial: Antiviral
	  ○ Antimicrobial: Antifungal
	  ○ Antimicrobial: Antiparasitic
	  ○ Mobile genetic elements (MGEs)
	  ○ Microplastics
	  ○ Pesticide
	  ○ Other
	• Sampling site (examples: discharge points, rivers)
	• Sampling frequency

Table A-5: AMR pollution source type and one health origin domain and origin type

Pollution source	One Health Origin domain		Origin type
Water, sanitation and hygiene-related: • Sewage, wastewater or effluent • Run-off • Animal waste • Solid waste or compost **Soil-related:** • Soil • Sludge, biosolids or manure • Sediment **Air-related:** • Bioaerosol • Particulate matter **Wildlife (not excreta)** • Wild animal • Wild plant	**Human**	Human population	Hospital, Airport, Wastewater treatment, Landfills
	Animal	Food-producing and companion animals	Run-off and leaching, processing waste stream
	Plant	Food-producing crops	Run-off and leaching, processing waste stream
	Environment	Natural resources (water, soil and air) and wildlife	• Point pollution / Hotspots: Discharge sites in receiving waters; between farms • Non-point pollution

Appendix 3: Global jurisdiction scan

Key informant discussions with WHO revealed a lack of globally agreed upon AMR targets or protocols for environmental surveillance. Considering this, the global jurisdictional scan explores how environmental AMR risks are addressed within a One Health framework, the current Quadripartite integrated surveillance recommendations, and the related national action plans and surveillance activities of G7 countries. Finally, it highlights surveillance and monitoring activities in non-G7 countries identified from the global evidence scan that may be of interest to PHAC.

One Health definition and AMR environmental dimensions

Taking a holistic One Health approach is universally recognized as the most effective way to address the diverse and complex threats posed by AMR. The One Health High-Level Expert Panel (OHHLEP) definition of One Health (see Box A-1) was developed through consensus to provide a clear framework addressing interconnected human, animal and ecosystem health risks. While OOHLEP did not provide a definition of environmental or ecosystem health, the environment is characterized as "shared" or "wider" and interdependent with the health of humans, animals (both wild and domestic) and plants (Adisasmito et al., 2022, pp. 1, 2). This characterization is similar to UNEP's framing of the environmental dimensions of AMR.

Box A-1: One Health definition from the interdisciplinary One Health High-Level Expert Panel (OHHLEP)

"One Health is an integrated, unifying approach that aims to sustainably balance and optimize the health of people, animals, and ecosystems. It recognizes the health of humans, domestic and wild animals, plants, and the wider environment (including ecosystems) are closely linked and interdependent.

The approach mobilizes multiple sectors, disciplines, and communities at varying levels of society to work together to foster well-being and tackle threats to health and ecosystems, while addressing the collective need for healthy food, water, energy, and air, taking action on climate change and contributing to sustainable development" (Adisasmito et al., 2022, p. 2).

After joining the Quadripartite in 2022, UNEP (2022) published a summary for policymakers on AMR's environmental dimensions. While a definition of environmental AMR is not provided, the document recognizes the environmental media water, soil, and air as "vehicles" for spreading, disseminating and transmitting AMR. Wildlife is also noted as spreading resistant microbes and important to include in One Health approaches, but it is not described as an environmental vector in UNEP's framing, which focused on prevention, control and treatment of major anthropogenic pollution sources. The five main pollution sources responsible for widespread environmental releases or biological and chemical AMR pollutants and antimicrobial agents originate from: poor sanitation, sewage, and waste effluent; pharmaceutical manufacturing effluent and waste; health care facilities effluent and waste; crop production antimicrobial and manure use, and animal production effluent and waste.

UNEP (2022) recommended governments undertake the following when addressing AMR's environmental dimensions:
(1) enhance environmental governance and regulatory action by including Ministries of Environment and environmental agencies in AMR NAPs and binding policy instruments;
(2) identify priority AMR pollutants and target at their origins through prevention and control measures;
(3) improve reporting and surveillance by monitoring antimicrobial pollution impacts on biodiversity and integrating into ongoing environmental monitoring data of water, solid waste and airborne particulate matter with extant AMR surveillance and pollutants data; and
(4) prioritize funding for action, innovation and capacity development.

One Health or integrated surveillance approach

One Health surveillance of AMR is often called integrated surveillance because it combines monitoring efforts across multiple sectors. To date, integrated national-level AMR surveillance at a national seems limited, with a recent scoping

review (Delpy et al., 2024) indicating that only 6 out of 14 high-income countries reporting some level of structural and operational integration of at least two One Health dimensions:

- Structural: the UK reported having environmental components, and
- Operational:
  - Environmental media: Only Switzerland was found to be actively monitoring wastewater at a national level; no other environmental components highlighted.
  - Wildlife: Monitored in the G7 country Germany, and in the Scandinavian countries of Denmark, Norway, and Sweden.

The Quadripartite is trying to address limited environmental monitoring through tools such as the WHO Tricycle Protocol.

WHO Tricycle Protocol (2021)

The WHO (2021) Tricycle Protocol presently is the only integrated AMR surveillance tool from the Quadripartite that has a human, food and environmental risk lens. It establishes a simple, harmonized approach to track the spread and resistance patterns of Extended Spectrum Beta-Lactamase producing *E. coli* (ESBL-Ec) as an indicator organism to reduce cost and complexity of integrated monitoring. ESBL-Ec was selected by WHO (2021: 2) as a "relevant and representative proxy for the magnitude and trends of the global AMR problem" given its prevalence in humans, animals and environmental sources, and substantial disease burden. The first three of eight Tricycle work packages address AMR dissemination, transmission and development amongst humans, within the food chain (mainly animal) and in impacted environments. For environmental samples, it is recommended to:

- align sampling with institutions monitoring drinking water quality (WHO, 2021, pp. 17, 25).
- detect and quantify ESBL-Ec in sources of hotspots, and wastewater receiving bodies. Hotspots were described as human communal wastewater, and wastewater polluted with animal fecal waste (WHO, 2021, pp. 3, 31).
- sample sites with different source types for concentrations of *E. coli* and ESBL-Ec.

Described both as a "powerful" tool for One Health AMR dissemination monitoring (Milenkov et al., 2024, p. 1), the WHO Tricycle Protocol mostly has had uptake from low- and middle-income countries with limited cross-sectoral surveillance capacity (Ruppé, 2023). Limited uptake by high-income countries may partly be due to the Tricycle's original design, which prioritized a single indicator to simplify and lower the cost of integrated surveillance for low- and middle-income countries (LMICs) with limited resources and capacity (IACG, 2018). For countries with advanced surveillance systems, the Tricycle might be viewed as covering "basic minimum qualities" in environmental settings (Hart et al., 2023, p. 4). However, recommendations like sampling wet markets may not be suitable for high-income countries. Four European countries have contributed to the protocol's design (Ruppé, 2023), and French and Dutch experts are continuing to partner in the Tricycle's pilot extension funded by the Joint Programming Initiative on Antimicrobial Resistance (JPIAMR), of which Canada is a member.

Box A-2: WHO antibiotic manufacturing pollution regulatory guidance (2024)

While regulating industrial pollution is not included in the scope, the recently published WHO (2024) guidance on the neglected issue of managing wastewater and solid waste from antibiotic manufacturing sites can help inform the development of indicators and identify surveillance partners across the production chain of a major environmental AMR pollutant.

- To date, manufacturing pollution is largely unregulated, and their environmental emissions are generally not monitored or addressed in quality assurance standards.
- Indicators: Includes guidance for determining human health-based and aquatic ecotoxicological targets in binding policy or market instruments to reduce AMR risk in liquid effluent, solid waste and zero liquid discharges of antibiotic products intended for humans, animals or plants.
- Potential surveillance partners: Outlines stakeholders across the entire production chain - from active pharmaceutical ingredient manufacturing to packaging and including regulatory bodies (national or regional) and industrial, waste and wastewater actors.

G7 countries National Action Plans

Table A-6 provides an overview of the current AMR NAPs of the six other G7 countries with regards to each country's one health and environmental surveillance approaches.

Table A-6. Overview of current AMR NAPs of 6 G7 countries (Bundesministerium für Gesundheit, 2023; Government of Japan, 2023; HM Government, 2024; Ministere des Solidarites et de la sante, 2022; Ministero della Salute, 2022; US Federal Task Force on Combating Antibiotic-Resistant Bacteria, 2020).

	France	Italy	US	UK	Germany	Japan
Year range	2022-2025	2022-2025	2020-2025	2024-2029	2023-2030	2023-2027
AMR focus	Antibiotic	Antibiotic	Antibiotic, antifungal	Antibiotic, antifungal	Antibiotic	Antimicrobial
One health definition		Human health outcomes through multi-sector controls		Multi-disciplinary health collaboration		Also integrate aquaculture, livestock, and food hygiene
Tricycle surveillance					One Health approach example	Research commitment
Env. AMR: Water	Water, groundwater	Water	Water	Water	Water	Water
Soil				Crops, land	Soil	Soil
Air						
Wildlife: Animals		Linked to food safety, zoonotic disease risk		Linked to animals (food, companion)		Associated with environment
Plants						
Env. AMR priorities	Strong production and use focus, from responsible manufacturing to supply chain monitoring and community dispensation, mitigating clinical waste risk	Waste-related microbial population focus (e.g. wastewater, sewage, livestock or aquaculture waste); zoonotic disease risk; food residues	Science-driven approach, from advanced molecular testing of ABR pathogens to deeper understanding of ABR one health transmission	Focused on waste minimisation and effective waste management to mitigate AMR and AMR-driving chemicals env. dissemination	Env. release, including factors like biofilms and soil AMR impact post-wastewater and slurry discharge	One health surveillance and research of AMR organisms and residual antimicrobials in aquatic and terrestrial environments, and wild animals
Env. AMR surveillance	Measures 36-38: Limiting environmental pollution when producing (36) and when using (37) antibiotics; and controlling liquid (effluent) or solid waste production (especially infectious waste) from care activities (38)	Establishing monitoring of: antibiotics, ABROs, and ARGs in env.; antimicrobial producers with significant discharge; and zoonoses prevention: main zoonotic microorganisms and ARGs in food supply chain, and protecting biodiversity	Developing env. component of National AMR Monitoring System (NARMS); Veterinary Laboratory Investigation and Response Network (Vet-LIRN) to ID ABR isolates from food and animals in existing CDC and FDA banks	Developing env. components of UK-wide Pathogen Surveillance in Agriculture, Food and Environment (PATH-SAFE) Programme focused on agri-food tracking of foodborne human pathogens and AMR from farm to fork	Undertaking "phased approach" integrating human, vet, agriculture, env. monitoring, drawing from resistance monitoring in fed/regional government vet. sector, and *SARS-CoV-2* wastewater monitoring	Establishing a One Health system linking data from multiple ongoing programs, including the Japan Nosocomial Infections Surveillance (JANIS) and Japanese Veterinary Antimicrobial Resistance Monitoring System (JVARM)

Table key:	Data was found and recorded	No data was captured

One health commitment and surveillance:

- While each NAP approached AMR from a One Health perspective with human, animal and environmental dimensions, the predominant focus was on human and animal health. The US also noted a plant focus, and UK, Germany and Japan noted food safety as an important dimension in their One Health approach.

- Three countries (UK, Italy, Japan) provided a one health definition. The UK definition followed conventional framing of one health across the health of people, animals and the environment. The Japanese definition expanded that their one health approach by including integration across livestock, aquaculture and food hygiene industries as well; and the Italian definition only had a public health outcome focus, which could be achieved through controls such as zoonotic and food safety measures.
- Water is addressed as an environmental concern in all other G7 countries.
- Only two countries (Germany, Japan) mentioned the WHO Tricycle Protocol, the globally recommended surveillance protocol for designing integrated AMR surveillance. Japan noted its commitment to conduct research on ESBL-producing E. coli, while Germany has commenced monitoring of agricultural livestock (poultry, pigs and cattle).
- Soil was noted in three countries (UK, Germany, Japan). Notably, the remaining countries' (France, Italy, US) each are expected to publish new NAPs in 2026.
- Wild animals seen as a risk in three countries, with each associating it with a different one health dimension. UK and Japan only note wild animals in relation to overall animal health concerns (UK) or in relation to the environment (Japan). Italy is the only one that expands on wild animal risks in terms of zoonotic disease, focused especially on food safety.
- None of the six other G7 countries noted airborne or wild plant AMR risks.

Environment in a one health context definition and environmental components:

- No G7 country had an explicit environment definition, though UK distinguished "natural" or "wider" vs. built environment which was consistent with all countries' framing.
- All countries expressed environmental AMR priorities in terms of prevention and control, mainly to mitigate antimicrobial exposure and contamination in the natural environment.
- None indicated having a systematically collected and representative environmental AMR data monitoring system. Each seems to be at different stages of establishing surveillance measures focused on AMR risk in the natural environment, with the general intention being developing a One Health or integrated surveillance system by developing environmental components of ongoing AMR monitoring programmes (US, UK, Germany, Japan).

Phased environmental surveillance approach: A common method in this "phased approach" (as labelled by Germany) is to focus on media-specific research and pilot and scale thereafter as initial steps of a longer-term goal of linking molecular data across all One Health domains. For example, in the UK, they have piloted river catchment AMR surveillance and increased storm overflow monitoring in England; conducted ABR testing in Scottish bathing waters; and established an AMR-driving pharmaceutical monitoring programme in Northern Ireland. In the US, they are focusing on surface water and presently piloting monitoring program at a watershed level while integrating AMR considerations in a national scale survey.

Greater attention for One Health implementation support and with regards to environmental concerns align with findings of a recently published review of G7 progress between 2017 to 2023 based on the Quadripartite Tracking Antimicrobial Resistance Country Self-Assessment Survey (TrACSS) data (Sabbatucci et al., 2024). Comparing Canada to other G7 countries, Canada reported less multi-sector capacity and One Health coordination than all other 6G countries. Moreover, Canada and Germany data indicate their lagging behind other G7 countries as approved action plans lack financial support and budget (Sabbatucci et al., 2024). Most G7 countries also reported limited progress with implementation:

- While all G7 countries have some legislation or regulation in place to prevent environmental contamination through discharge of antimicrobials, compounds and their metabolites, only three (France, US, Italy) reported having established regular water quality monitoring of resistant bacteria, ARGs, antimicrobial compounds, metabolites or residues.
- In 2023, only France reported having a national assessment of AMR compound residues and pathogens in the environment. The UK published their risk assessment and prioritization tool of water, soil and air-related pathogenic ARB in October 2024 (Environment Agency, 2024a).

The next sections delve deeper into the progress that France, the UK and the US have made with regards to defining the environmental dimension in a One Health approach and establishing a corollary surveillance program.

France

Environmental surveillance focus: antibiotics and water (surface, ground and sea) and wildlife

This section mostly covers peer-reviewed publications from officials working at ANSES, Agence nationale de sécurité sanitaire / Agency for Food, Environmental and Occupational Health & Safety).

ANSES AMR program has a strong animal and human health focus. In 2020, the French government commissioned a multidisciplinary expert appraisal group to identify ABR environmental contamination and antibiotics that select or favor ABR persistence in French aquatic environments (surface water, groundwater and coastal water) and terrestrial environment (soils and plants) (Haenni et al., 2022). Wildlife was noted as under the umbrella of environmental health, but the literature reviewed focused on animals, not plants. While the resulting report reviews the limited available evidence on AMR selection and ARG transmission, their main findings highlighted how anthropogenic activities have contaminated the environment, and that resistant genes persist longer in the environmental that resistant bacteria. The report was later expanded upon by Haenni et al. (2022) with further publication of Predicted No-Effect Concentrations for Resistance (PNEC-R) or Persistence (PNEC-P) threshold data.

Environmental surveillance approach: France does not have a national scale environmental surveillance program implemented for different environmental media yet. The global evidence scan identified three ANSES-associated articles focused on AMR indicator identification in the shared marine environment of the English Channel and North Sea that is contaminated by receiving rivers, man-made offshore structures and maritime shipping. The *sul1* and *intI1* genes were found suitable to AMR indicators for a marine environment given its prevalence and abundance in seawater (Bourdonnais et al., 2022), phyto- and zooplankton (Bourdonnais et al., 2024a), and wild flatfish (Bourdonnais et al., 2024b).

Besides seawater-associated matrices, Collineau et al. (2024) indicated that surface water and groundwater are monitored for antibiotics at a national scale, though surveillance targeting such as downstream of wastewater treatment plants or farm environments are yet to be established (Collineau et al., 2023). No publicly available information on AMR-related water monitoring programs or databases were found for this review.

For countries with similar attributes as France, Haenni et al. (2022) and Collineau et al. (2024) recommended**:**

- Harmonizing hotspot sampling, methods and indicators for environmental surveillance programs by:
  - Identifying a list of common indicators that will allow spatial and temporal comparison between studies and across the environment. For example, Tricycle ESBL-producing E. coli approach.
  - Defining a list of priority antibiotics that are widely used and are environmentally persistent.
- Identifying environmental conditions facilitating persistence and dissemination
- Determine PNEC-R or PNEC-P thresholds for highly prescribed antibiotics
- Monitoring resistance patterns of pathogenic species ubiquitous in the environment and humans.
- Monitoring spatial and temporal dissemination in distinct receiving environments to evaluate variability over time (e.g., contaminant concentrations) and geographic diversity.

Cross-sectoral collaboration: While France has reported establishing an ABR surveillance system covering the human, animal, food and environmental sectors, a recent assessment indicates that cross-sectoral collaboration is highly fragmented and environmental concerns continue to be overlooked (Collineau et al., 2024). On the former, cross-sectoral data sharing and joint data analyses furthermore continues to be constrained by interoperability issues and limited resources. Collineau et al. (2024) shared recommendations following an analysis of France's One Health AMR surveillance approach that included establishing an operational body for national coordination facilitating cross-sectoral collaboration and creating a national cross-sectoral working group to define common indicators and integrate data

analysis. In recognition of the country's need for greater capacity, Collineau et al. (2024) noted the following initiatives have been established:

- PROMISE, a national network is being set up to improve structured One Health surveillance, including the set-up of a One Health oriented common surveillance data warehouse. The AMR-Env working group brings together 17 research units and four environmentally focused networks to standardize sampling and analysis of environmental ABR in six indicators**:** *E. coli* ESBL (culture method); *E. coli* 16S RNA (qPCR, fecal contamination); *intI* (qPCR, global resistance indicator); *aacA4* (qPCR, human contamination marker) and *aadA/aadB* (qPCR, animal contamination marker).
- The online ABRomics platform for national One Health AMR surveillance data sharing.

Key definitions: For environmental monitoring, the expert working group focused on identifying potential hotspots. Characterized a **hotspot** for AMR development and potential transmission route as environmental conditions that are "favorable to the transfer of antibiotic resistance genes to pathogenic bacterial species" (Haenni et al., 2022, p. 5). This follows the WHO (2021) hotspot focus on environmental AMR sources; for example, Haenni et al (2022) viewed wastewater effluent, organic waste products and fish farm effluents as hotspots.

UK

Environmental surveillance focus: antibiotics & antifungals in environmental water, soils, air & wild animals

This section covers materials primarily found during a hand search of the UK Environment Agency's website.

The UK has been a leader in global AMR stewardship, particularly in One Health surveillance that integrates human, animal, and environmental dimensions. This proactive approach stems from the UK's early recognition of the environment's role in public health. A key initiative is the Pathogen Surveillance in Agriculture, Food and Environment (PATH-SAFE) programme, which is addressing gaps in environmental AMR monitoring, including what and how to monitor microorganisms, genes, and antimicrobials. They focus on antibiotics and antifungals.

Environmental surveillance approach: While the UK does not have a national scale environmental surveillance program implemented for different environmental media yet, the Environment Agency has instrumentally documented the research and rationale underpinning their holistic environmental AMR surveillance approach in various technical reports and peer-reviewed publications on:

- river catchment pilot and bathing water surveillance review (Environment Agency, 2024b, 2023a; Robins et al., 2024),
- biosolid (Martin and Hart, 2023) and airborne risk and monitoring reviews (Environment Agency, 2023b, 2022a, 2020),
- their wildlife strategy and biomonitoring (Environment Agency, 2023c, 2023d),
- biological monitoring methods (Environment Agency, 2024c, 2023e, 2022b),
- reflections from the environmental policymaking perspective (Hart et al., 2023; Singer et al., 2016), and
- an environmental AMR risk assessment and prioritization (Environment Agency, 2024a, 2024d) using a source-pathway-receptor approach in a preliminary qualitative risk modelling framework that evaluates risk according to human exposure to resistant environmental pathogens.

The above-mentioned reviews include assessments of existing environmental monitoring networks in the UK that can potentially be leveraged to rapidly deploy an early warning system (Environment Agency, 2023b), and for potential cost sharing in sampling and other operational factors such as site access (Hart et al., 2023).

A primary focus of the Environment Agency (2024a: 8) is on risk pathways, hence the development of a risk assessment tool to assess "exposure routes to be considered and their relative significance for human health." In recognition that there are "uncertainties" of environmental AMR exposure on human health impact, the Environment Agency (2024a: 8) developed its risk assessment tool that reflects a flexible, transparent and user-friendly approach that allows for adaptation for different microorganisms, scenarios, uncertainty and new knowledge:

- **Flexibility**: Can be used for various microorganisms or exposure scenarios.

- **Transparent**: Qualitative risk estimation process is presented, with uncertainties addressed in framework outcomes.
- **User-friendly**: Allowing easy integration of new knowledge in the nascent field so decision-making is based on best available evidence.

Key definitions: The UK's Environment Agency (2024a) provided more distinction for environmental AMR terms than other G7 countries:

- The **environment** is described as "natural," denoting a framing of a surrounding environment that would not be subjected to AMR administration.
- Additionally, they clarify that direct **environmental exposure** refers to resistant pathogens presenting risk to human health via ingestion, inhalation, and skin contact at point of environmental exposure, and Environment Agency (2024a, pp. 13, 17) explicitly defined the three main environmental components of concern:
- **Water**: "surface waters including both fresh (e.g., rivers and lakes) and marine or coastal (seawaters and estuaries), and groundwater", and excludes any water outside the natural environment, such as domestic or municipal water that would be subject to physical of chemical treatment.
- **Soils**: "natural/unmanaged soils, agricultural/rural soils, and garden/urban soils focusing on surface soils as these would be the typical point of human exposure," which would include river sediment and beach sands.
- **Air**: "outdoor air" or "ambient air," including water vapor and dust particles.

Indicator development:

- Need to indicate who and what should be protected (human, animal or ecosystem health) (Environment Agency, 2024b, 2024a).
- **Wildlife**: The Environment Agency (2023d) importantly noted that indicator selection should be based on abundance and wide distribution in country; and presence across impacted and non-impacted environments, allowing for anthropogenic spillover comparison. They selected fish/bivalves, waterfowl, and otters for aquatic (freshwater and coastal/marine) species, and rodents and earthworms for terrestrial systems. They did not recommend wild plant monitoring due to perceived lack of direct exposure and hence public health risk.

US

Environmental surveillance focus: resistant bacteria and surface water

This section covers materials found during a hand search of US government websites (EPA, NARMS) on AMR surveillance and its pilot surface water monitoring program.

Cross-sectoral collaboration: The National Antimicrobial Resistance Monitoring System (NARMS) has monitored enteric bacteria in human and food-animal systems since the mid-1990s (Franklin et al., 2024). NARMS began piloting its multi-agency preliminary surface water sampling scheme in 2021 to monitor environmental bacteria as part of a One Health approach (See Table A-7). Surface water was selected as the initial environmental media due to watersheds being a hotspot of various human and animal waste inputs; similar to Haenni (2022), hotspots are understood as "areas with significant AMR hazards" (Franklin et al., 2024, p. 4).

Environmental surveillance approach: The US does not have a national scale environmental surveillance program implemented for different environmental media yet. Franklin et al (2024) detailed the development of the national Surface Water AMR Monitoring program (SWAM) at the watershed level in an interagency publication co-authored by counterparts from the Environmental Protection Agency (EPA), Centers for Disease Control (CDC), US Department of Agriculture (USDA), and Food and Drug Administration (FDA). They report the rationale underpinning SWAM and their phased development and national monitoring implementation approach (Table A-8).

Table A-7: US federal agencies and partners for NARMS environmental bacteria component

Component	Agency & Link	Partner	Source	Bacteria
Env. Bacteria	CDC, FDA, USDA & EPA	• Division of Foodborne, Waterborne, and Environmental Diseases (DFWED) • Center for Veterinary Medicine (CVM) Center for Food Safety and Applied Nutrition (CFSAN) • Agricultural Research Service (ARS) • Office of Research and Development (ORD) Office of Water (OW)	Pilot watershed scale studies: 2022-2024	Salmonella, Escherichia coli, Enterococcus, Metagenome

Table A-8: SWAM goal, and development and implementation approach (Franklin et al., 2024)

SWAM goals	• Assess public health risks associated with AMR pathogens in surface water • Provide spatial and temporal relationship of resistant strains in a watershed • Assess how anthropogenic drivers and intervention strategies impact AMR transmission within human, animal and env. systems.
SWAM development process	1. Defined objectives and questions 2. Developed study and sampling design 3. Selected AMR indicators 4. Established analytical methods 5. Developed data management, analytics, and metadata plans
SWAM national monitoring implementation approach	1. Method development evaluation and in-lab validation 2. Field validation of methods in a single watershed pilot 3. Probabilistic national study 4. Finalized national monitoring program 5. Additional focused studies to address specific research needs and monitoring questions

SWAM was developed by six sub-groups (data end use, sampling design, metadata, field sampling, culture and molecular), with the former focused on alignment with extant NARMS reporting structures. Antibiotic analysis is currently excluded due to cost, human resource, and antibiotic selection constraints. Their development process (see Table A-8) was based on current recommendations for environmental AMR monitoring. For example, Franklin et al. (2024: 4) noted WHO guidance as part of rationale for selecting indicators that facilitate assessment AMR transmission within and among human and animal populations is the ultimate objective; and that ARGs should be selected based on prevalence (clinically relevant, have anthropogenically sensitive genes, common occurrence) and selection factors (abundant, propensity for horizontal transfer, pathogen ARG expression).

Franklin et al (2024) report that the US is currently completing a yearlong watershed-level study to comprehensively examine AMR dynamics through varied sampling strategies and environmental contexts to inform risk assessment and identify critical control points, and a national scale study spanning two years to assess how water quality parameters and spatial variation correlate with AMR. The latter is part of the EPA's National Rivers and Streams Assessment (NRSA) program that monitors water quality and would build on a previous EPA national rivers and streams ARG assessment (Keely et al., 2022). The EPA is also funding national priority grants evaluating AMR in wastewater and sewage sludge treatment. Future directions include:

- Generate library of isolates to facilitate multi-scale comparison and cross-referencing with NARMS library isolates and metagenomes.
- Produce watershed and national scale standard measurement protocols, sampling design parameters, and reporting guidelines.

Appendix 4: Global evidence scan

A total of 165 scientific articles were included on environmental AMR research from 32 jurisdictions (Table A-9). Twelve (7.3%) had a global outlook, while the majority (69.1%, n=114) featured research from 19 European countries. 80% of the regional studies (n=4) also had a European focus (Danube River Basin, North and Baltic Seas or Pan-Europe), and one focused on the Arctic. Scientific evidence from or on three jurisdictions in North America (Canada, Greenland and the US) comprised of 20.6% (n=34) of the articles. Half of the articles (50.3%, n=83) are from G7 countries. Some low- and middle-income countries from Africa and Asia were included as comparative studies.

Table A-9: Jurisdiction breakdown of scientific articles identified from global evidence scan

Jurisdiction	Count	Jurisdiction	Count
Global	**12**	**Europe**	**114**
Regional	**5**	*Austria*	*4*
		Belgium	*4*
Africa	**1**	*Bulgaria*	*1*
Namibia	*1*	*Croatia*	*4*
		France	*11*
Asia	**11**	*Germany*	*11*
China	*2*	*Georgia*	*1*
India	*1*	*Hungary*	*1*
Japan	*4*	*Ireland*	*3*
Singapore	*1*	*Italy*	*17*
South Korea	*1*	*Netherlands*	*3*
Taiwan	*2*	*Norway*	*4*
		Poland	*10*
Australia/Oceania	**6**	*Portugal*	*7*
Australia	*6*	*Romania*	*2*
		Spain	*15*
North America	**34**	*Sweden*	*1*
Canada	*7*	*Switzerland*	*5*
Greenland	*1*	*UK*	*10*
US	*26*		

None of the scientific articles had an explicit definition of environment or environmental AMR in a One Health context definition and 6.7% (n=11) reported associations with a government monitoring program. The majority of research (see Figure 2) had an AMR occurrence (87.3%, n=144) focus, followed by dissemination (29.7%, n=49), selection (15.2%, n=25) and transmission 6.7% (n=11). A third of the articles (33.3%, n=55) focused on multiple aspects of AMR, with occurrence and dissemination being the most common combination (18.8%, n=31). This was followed by occurrence and selection research (7.3%, n=12) or understanding factors facilitating occurrence, selection and dissemination (2.4%, n=4) or occurrence, dissemination and transmission (3.0%, n=5). Occurrence and transmission research had the least number of publications (1.8%, n=3).

With regard to environmental media (see Figure 3), most focused on water (60%, n=99), followed by wildlife (40.0%, n=66). Soil comprised of 20.6% (n=34) of global science articles, and air as an environmental media in 3.0% (n=5). On the latter, four were reviews, and one investigated methicillin-resistant *Staphylococcus aureus* risk at and downwind of poultry farms in Taiwan (Tsai et al., 2024). No included articles focused on wild plants. 29 articles (17.6%) focused on AMR associated with multiple environmental media. Four were reviews: one focused on all environmental sources in a global review on the widespread contamination of carbapenem-resistant bacteria in the

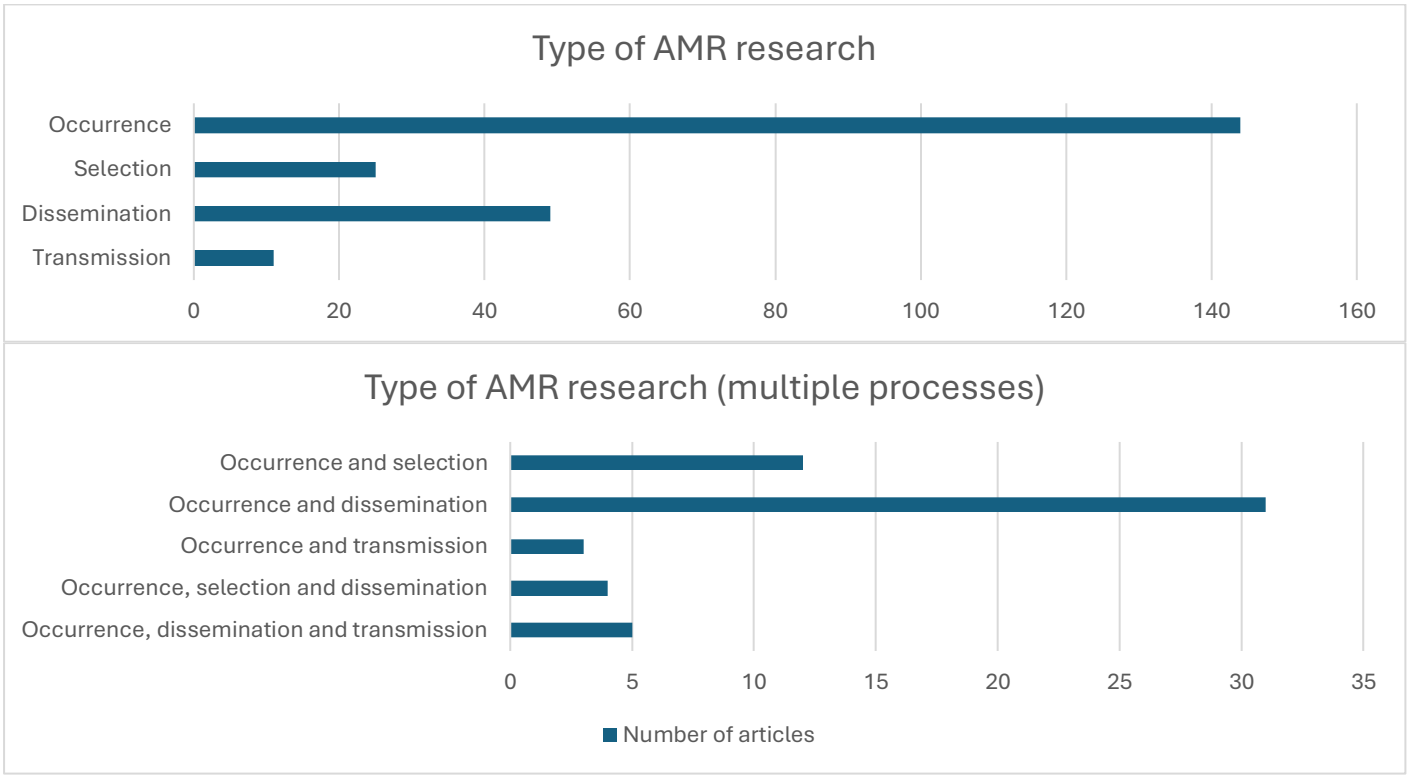

Figure 2: Type of AMR research (top, n=165), including multiple processes (bottom, n=55)

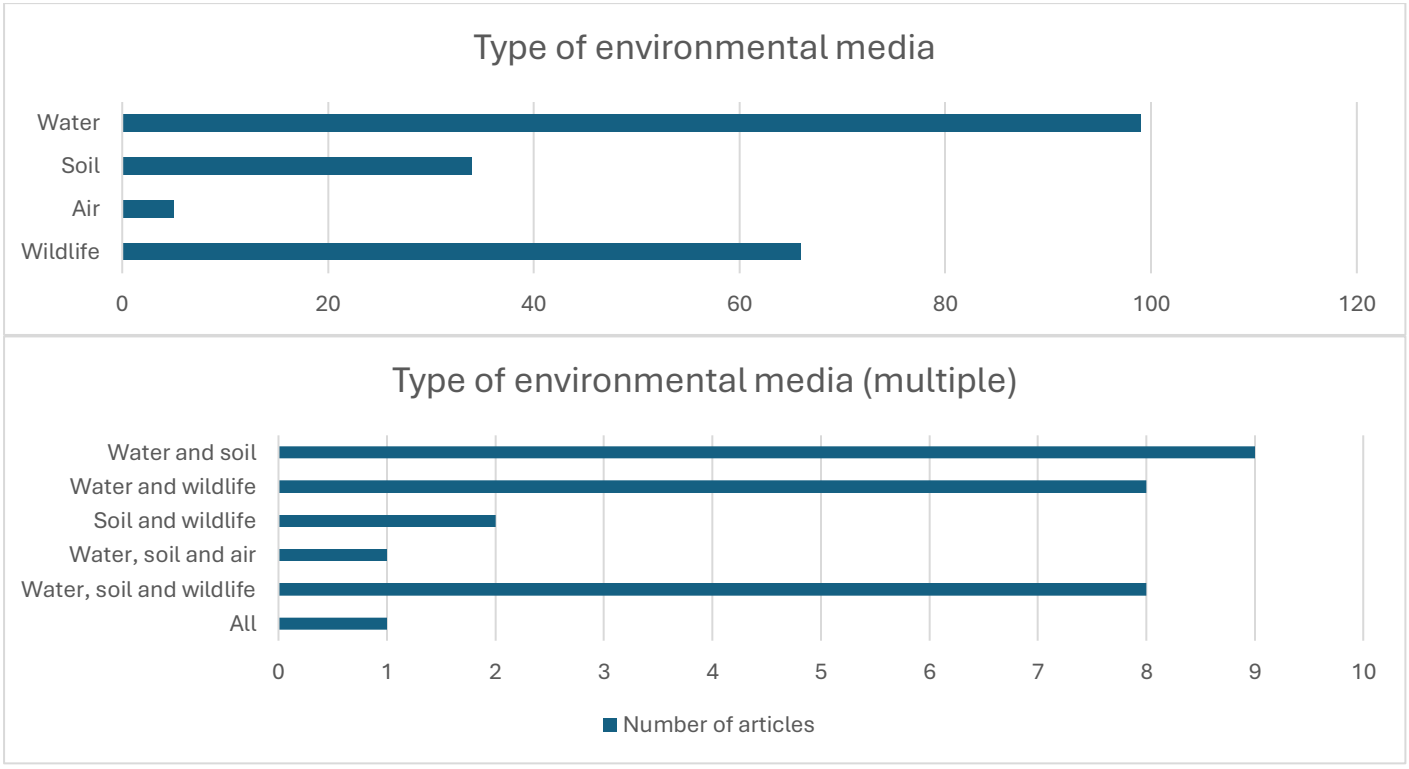

Figure 3: Type of environmental media (top, n=165), including multiple media (bottom, n=29)

environment (Mills and Lee, 2019); Burch et al. (2022) reviewed environmental AMR risk assessment methods for water and wildlife; and Haenni et al. (2022) and Treskova et al. (2022) included water, soil and wildlife in their reviews of

environmental antibiotic resistance evidence in France, Austria, Germany and Switzerland. The remaining 25 articles involved comparing environmental samples of different media. Water was the most sampled in combination with soil (5.5%, n=9), wildlife (4.2%, n=7), or soil and wildlife (3.6%, n=6). Two studies focused on soil and wildlife. The only article that sampled water, soil and air had quantified bio-pollutant risk for workers at e-waste recycling facilities in Switzerland (Agarwal et al., 2024).

Table A-10 summarizes the wildlife articles from G7 countries by country and a wide variety of species (n=34). Half included mammal sampling, with wild boar being sampled nearly in a quarter of studies (23.5%, n=8) from Germany and Italy, followed by deer (11.7%, n=4) from Germany, Italy, and the UK, and raccoons (8.8%, n=3) from Canada and the US. A quarter of the samples were a variety of wild birds (26.5%, n=9) and a third aquatic species (32.3%, n= 11).

Table A-10: G7 wildlife articles from the global evidence scan by country and species (n=34)

Jurisdiction	Author (Year)	Mammals	Birds	Aquatic species
Canada	Vogt 2021	Raccoons		
	Vogt 2022	Raccoons		
France	Bollache 2019			Fish
	Vittecoq 2023	Rodents		
	Vittecoq 2022		Yellow-legged gull chick	
France, UK	Bourdonnais 2024			10 species
	Bourdonnais 2024			Fish
UK	Elsby 2022	Deer (red, roe, sika, fallow)		
	Rodrigues 2021		Wild birds	
	Watson 2024	Seal (harbour, grey)		
Germany	Perez-Etayo 2022	Wild boar		
	Gross 2022	Harbour porpoise, seals (harbour, grey, ring)		Fish
	Günther 2022	Wild boar		
	Plaza-Rodríguez 2020	Wild boar, roe deer	Wild duck	
Germany, Austria, Switzer.	Treskova 2022		Black-headed gull	
Italy	Agnoletti 2019			Bivalve shellfish
	Andriani 2024	Wild boar		
	Carella 2022	Deer (red, roe), red fox, beech marten, Alpine ibex		
	Chiaverini 2022	Wild boar, deer (red, roe, fallow), European badger, red fox, wolf, porcupine, otter, and hedgehog	5 bird species (magpie, jay, goose, sparrow hawk and starling	
	Floris 2024	Chamois, deer, wild boar		
	Fioriti 2021			Zooplankton
	Formenti 2021		15 bird species	
	Marotta 2020	Wild boar		
	Siddi 2024	Wild boar		
Japan	Fukuda 2021		Migratory geese	
US	Drovetski 2022		Wild prairie grouse	
	Fang 2019			Fish, oysters
	Hain 2023			Oysters
	Kim 2024		Geese, sea gull	
	Lagerstrom 2023			Periphyton and fish
	Mills 2022			Periphyton and fish
	Mills 2024			Fish
	Worsley-Tonks 2020	Coyote, Possom, Raccoon		
	Worsley-Tonks 2021	Raccoon		
	Count	**17**	**9**	**11**

On origin of AMR contamination (see Figure 4), non-point pollution in the broader environment was the source for three quarters of articles (74.5%, n=123). Other one health sources – such as from human (37.6%, n=62), animal (17%, n=28), or plant (0.6%, n=1) sources – were noted if researchers specifically investigated and found associations between point

sources such as wastewater treatment facilities or food-agricultural systems. Wild animals, notably, is captured as an environmental source rather than under the animal health dimension.

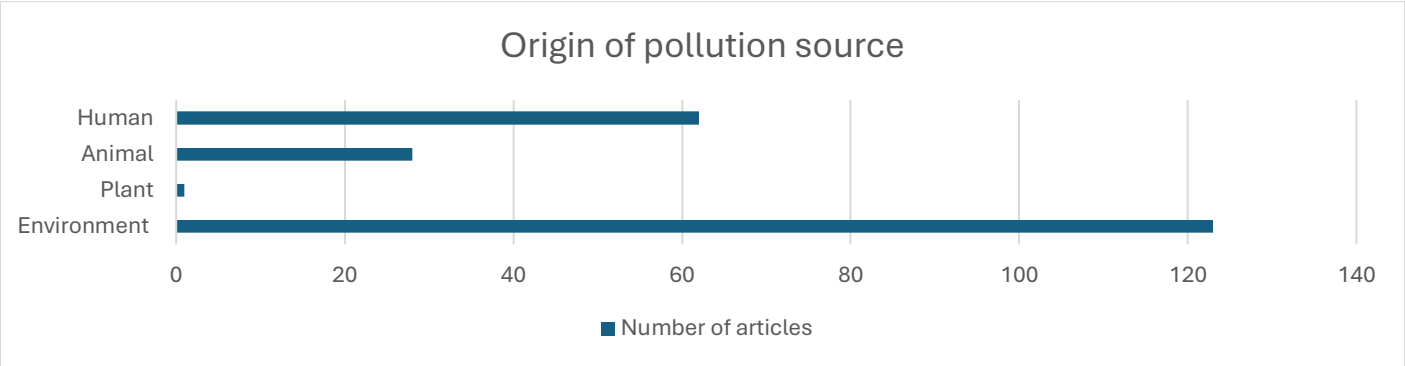

Figure 4: Origin of pollution source by One Health domain (n=165)

Table A-10 summarizes what was monitored. Nearly two thirds (69.7%, n=115) investigated antimicrobial resistant genes (ARGs), followed by over a third monitoring resistant microorganisms (38.8%, n=64) or microorganisms (31.5%, n=52). Of microorganisms, bacteria were the most commonly monitored (60.6%, n=100), with 9.7% (n=16) including ESBL-producing *Escherichia coli*. Of the 16 articles that monitored for ESBL-producing *Escherichia coli* (Table A-11), 75% (n=12) were from Europe, with three articles from Japan, and one from the US. Half focused on wildlife, and half on water-related monitoring,

Table A-10: Type of AMR microorganisms, AMR determinant or antimicrobial agent monitored (n=165)

Type of AMR microorganisms, determinant or agent monitored	Count	% of articles
Microorganism	**52**	**31.5%**
Resistant microorganisms	**64**	**38.8%**
ESBL-producing Escherichia coli	*16*	*9.7%*
Bacteria	**100**	**60.6%**
Fungi	**1**	**0.6%**
Virus	**5**	**3.0%**
Antimicrobial residues	**19**	**11.5%**
Antibiotics	*15*	*9.1%*
Antifungals	*3*	*1.8%*
Antivirals	*1*	*0.6%*
Antimicrobial resistant genes (ARGs)	**115**	**69.7%**
Mobile genetic elements (MGEs)	**34**	**20.6%**
Class 1 integron	*14*	*8.5%*
*Plasmid**s***	*1*	*0.6%*
Hormones and sucralose	**1**	**0.6%**
Pharmaceuticals and personal care products	**2**	**1.2%**
Disinfectants	**1**	**0.6%**
Microplastics	**1**	**0.6%**
Heavy metal	**3**	**1.8%**
Pesticides	**1**	**0.6%**
Metal resistant genes	**4**	**5.5%**
Biocide resistant genes	**1**	**0.6%**

Table A-11: Articles that included ESBL-producing *Escherichia coli* testing **(n=16)**

Jurisdiction	Author (date)	Water	Wildlife
Regional: North & Baltic Seas	Gross et al. (2022)		Marine mammal sentinels, fish

Austria	Skof et al. (2024)	Surface water, biofilm	
France	Bollache et al. (2018)		Freshwater fishes
	Brendecke et al. (2022)		Black-headed gulls
	Günther et al. (2022)		Wild boar
	Herrig et al. (2020)	Surface water	
Germany	Plaza-Rodriguez et al. (2020)		Wild boar, roe deer, wild ducks, geese
Italy	Formenti et al. (2021)		Wild boar
	Azuma et al. (2022)	Surface water, WW	
	Fukuda et al. (2021)		Migratory geese
Japan	Ogura et al. (2020)	Surface water	
Poland	Lenart-Boroń et al. (2020)	Surface water	
	Blanco et al. (2020)	Surface water	
	Garcias et al. (2021)		Hedgehogs
Spain	Pérez-Etayo et al. (2020)	Surface water, WW	
US	Cho et al. (2023)	Surface water, WW	

Only one (0.6%) included fungi, and five (3.0%) included viruses. Among antimicrobial agents largely used in human and agri-food safety, antibiotics also was the most investigated residue (9.1%, n=15), followed by antifungals (1.8%, n=3) and antivirals (0.6%, n=1). A fifth of the articles (20.6%, n=34) investigated mobile genetic elements (MGEs), with Class 1 integron monitored in 8.5% (n=14) studies. Co-occurrence of a wide range of other indicators made up nearly 10% of the rest of included articles (9.1%, n=15), with most focusing on contaminants - ranging from other pharmaceuticals and personal care products (1.2%, n=2), heavy metals (1.8%, n=3) and their resistant genes (5.5%, n=4) and pesticides (0.6%, n=1).

Sampling campaigns for different environmental media was variable, including the frequency and time periods used to collect the range of media (Table A-12). Nearly two thirds of articles (63%, n=104) seemed to have an opportunistic sampling campaign that ranged from sampling once to six or more times over an extended period. 12.7% (n=21) had routine campaigns that ranged from daily to monthly collection over an extended period, as well as seasonal sampling of 2-4 times over a 6–12-month period.

Table A-12: Frequency and time periods for non-regular and regular sampling (n=165)

Sampling frequency and period	Count	%	Sampling frequency and period	Count	%
Once	73	44.2%	**Daily for one month**	1	0.6%
Twice	10	6.1%	**Weekly for 6+ months**	2	1.2%
Thrice	9	5.5%	**Monthly for 5-12 months**	6	3.6%
4 to 5	6	3.6%	**Bimonthly for 12+ months**	3	1.8%
6+	6	3.6%	**Multiple times a month for 9+ months**	2	1.2%
Varied dependent on source	3	1.8%	**Seasonal sampling over 6-12 months**	7	4.2%
Unclear or unstated frequency/period	24	14.5%	**N/A (Review)**	13	7.9%

Appendix 5: Canadian jurisdiction scan of environmental AMR surveillance

Environmental surveillance in Canada: Status of AMR knowledge and monitoring

Public Health Agency of Canada (PHAC) is the custodian for a Pan-Canadian One Health AMR stewardship approach. Table A-13 provides an overview of a National Action Plan (NAP) for AMR developed by PHAC and a Year 1 progress report. While an explicit definition of environment or environmental AMR in a One Health context is not provided, the environment is framed as being "shared" between humans, animals and crops, with environmental components or media outlined as water, soil, wild animals, and wild plants. Environmental surveillance is not as developed as the human, animal or food dimensions, with PHAC's initially focusing on surface water and wastewater. Bioaerosols are not mentioned, and soils and wildlife only noted in terms of AMR environmental risks.

Table A-13. Overview of current Canadian NAP and Year 1 progress (PHAC, 2024, 2023a, 2023b)

Year range	2023-2027			
AMR focus	Antimicrobial			
One health framing	Human – Animal – Environment – Food			
One health definition	"close interplay between humans, animals, crops and their shared environment" (PHAC, 2023b, p. 4)			
Tricycle surveillance	Not discussed			
Env. AMR:	Water	Soil	Wild animals	Wild plants
Env. AMR priorities	• Targeting environment transmission pathways: "identify and mitigate AMR reservoirs and pathways for the transmission of medically-significant drug-resistant organisms through soil, water, flora, and fauna" (PHAC, 2023a, p. 4). • Focus on water quality monitoring, water use management and wastewater treatment, as well as marine sediments; no mention of aerosols.			
Env. AMR surveillance, including potential leverage points	1) Environmental exposure monitoring: Exploring leveraging FoodNet Canada's surface water data collection for AMR and antimicrobial testing to better understand linkages between AMR sources and the environment, such as transmission pathways to humans or animals. 2) Leveraging infrastructure and experience from Pan-Canadian SARS-CoV-2 wastewater surveillance being applied to help with early AMR detection, including current pilot in three Canadian cities. It is important to note that this can potentially be leveraged if effluent is monitored.			

Going forward, PHAC aims to address its environmental AMR research and data gaps, with a "focus on AMR transmission in the environment,: improving "data from the environment" and understanding "transmission pathways between sectors." Following the UNEP's key pollution sources, PHAC is especially interested in strengthening environmental action for:

- **Pharmaceuticals and other chemical manufacturing**: Understand potential environmental impact of Canada's limited active pharmaceutical ingredients (APIs) activities.
- **Terrestrial animal, crop production, and aquaculture**: Investigate environmental exposure across food production, aquaculture and freshwater pathways.
- **Healthcare-associated risks**: Targeted surveillance to understand full environmental impact of health facilities and pharmacies though expanded wastewater surveillance.

PHAC (2024) is enhancing FoodNet Canada's collection of surface water to better understand food- and waterborne environmental exposures, as well as investigating wastewater surveillance's potential for population-level detection of antibiotic residues and AMR/AMU trends. PHAC indicated a need for a rapid synthesis of existing publicly available AMR surveillance information in Canada's environment, and an identification of gaps that will serve as input for:

- Informing the development of PHAC's AMR environmental surveillance strategy.
- An ongoing living evidence synthesis for areas of emerging science where additional evidence/research may be required to inform the PHAC approach.

The next sections describe the **current actions** being undertaken in Canada to monitor the development and spread of AMR in the environment by assessing publicly available national, provincial and territorial datasets for AMR hazard and risk assessments (Table A-14), and relevant research projects identified from hand searches (Table A-15).

Table A-14: Publicly available monitoring systems: AMR and relevant non-AMR surveillance programs by jurisdiction

Jurisdiction	Organising framework	Key features of environmental AMR surveillance or relevant programmes
AMR SURVEILLANCE		
National	• Surveillance program name • Responsible agency or department • Sampling site (examples: discharge points, rivers	• The Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS) is a national collaborative surveillance program that analyzes trends in AMU and AMR for targeted enteric bacteria in humans, animals, and retail meat across Canada with federal, provincial, academic and industrial partners. ○ For example, the Canadian Feedlot Antimicrobial Use (AMU) and Antimicrobial Resistance (AMR) Surveillance Program (CFAAS) is an industry partner that collects from feedlot cattle veterinarians and cattle farms from across Canada to report antimicrobial use in feedlot cattle and the resistance of different bovine respiratory pathogens and enteric bacteria. ○ Data is used to detect differences in AMU and AMR over time and is used to inform evidence-based policies in various settings.
National	• Surveillance program name • Responsible agency or department	• AMRNet is a lab-based surveillance program developed by the Public Health Agency of Canada that integrates a 'One Health Approach' by monitoring both human and animal AMR data from seven provinces/territories. • Priority AMR pathogens include *Acinetobacter* spp., *Escherichia coli*, *Klebsiella pneumonia*, *Neisseria gonorrhoeae*, *Salmonella* spp., *Shigella* spp., *Staphylococcus aureus*, and *Streptococcus pneumoniae*.
National	• Surveillance program name • Responsible agency or department • Type of environmental AMR surveillance ○ Occurrence / Prevalence ○ Transmission • Environmental samples ○ Water • Sampling site (examples: discharge points, rivers)	• FoodNet Canada is a national food safety surveillance system led by the Public Health Agency of Canada that monitors enteric bacteria data from 4 sentinel sites (public health units, public health and private laboratories, farms, retail food outlets, and sources of drinking water) located in Alberta, British Columbia, Ontario, and Quebec. • Data from 2015 to 2022 is publicly available. ○ While bacterial resistance profiles are not assessed, its on-farm manure sampling is integrated with CIPARS. ○ Farm animal pooled manure samples are collected within and around sentinel site boundaries. This indicates some surrounding environment data is collected. • Raw water samples from irrigation, surface and recreational sources are collected within and around sentinel site boundaries.
National	• Surveillance program name • Responsible agency or department	• The Canadian Animal Health Surveillance System (CAHSS), a division of Animal Health Canada, is a network of animal health surveillance data that tracks animal health for commercial and food animal to detect disease patterns. Its data is not included in CIPARS. • Partnered government, university, and industry lead initiatives use AMR data on resistant pathogens and antibiotics use in animals to guide decision-making.
Ontario	• Surveillance program name • Responsible agency or department	• The Ontario Antimicrobial Stewardship Program (ASP) & Antimicrobial Resistance (AMR) Comparison Tool developed by Public Health Ontario brings together data on hospital and community AMU across the province of Ontario.
RELEVANT NON-AMR SURVEILLANCE		
National	Wastewater-based monitoring • Surveillance program name • Responsible agency or department • Environmental samples ○ Water • Sampling frequency	• PHAC's Respiratory Virus Activity Wastewater Monitoring Dashboard monitors wastewater across Canada's provinces and territories for various respiratory viruses (polio, *mpox, SARS-CoV-19, RSV,* and influenza). • Participating wastewater treatment plants across Canada monitor wastewater weekly. Weekly updates for Ontario ended in June 2024 when the province ended its funding. • Statistics Canada coordinates the Canadian Wastewater Survey (CWS) to detect and track the presence of regulated and unregulated substances or organisms in wastewater treatment plant samples. ○ It has two components on licit and illicit drugs in collaboration with Health Canada, informing its Canadian Drug and Substance Watch observatory), and *SARS-CoV-2* with Public Health Agency of Canada. ○ Influent from 17 wastewater treatment plants in 7 cities (Metro Vancouver, Edmonton, Prince Albert, Saskatoon, Toronto, Montreal and Halifax) report either monthly or weekly data on water flow data, water quality test results and events such as significant weather that can impact results.

National	• Surveillance program name • Responsible agency or department • Environmental samples ○ Water Sampling site (examples: discharge points, rivers)	• The National Aquaculture Public Report Data organized by the Department of Fisheries and Oceans collects data from fish industry owners and operators to fulfil the reporting requirement of the Aquaculture Activities Regulations. • Land-based and freshwater data is collected from BC, New Brunswick, Newfoundland and Labrador, Nova Scotia and Quebec, and fish data from the first four provinces. • Fish industry owners and operators submit the use of drugs and pesticides, and the measures taken to mitigate drug-related impacts as part of broader transparency around industry practices, but Department of Fisheries and Oceans do not monitor AMR. Monitored drugs to combat microbial pathogens and combat pests include **antibiotics** (Erythromycin, Florfenicol, Oxytetracycline hydrochloride, Sulfadimethoxine, Ormetoprim, Trimethoprim/Sulfadiazine powder) and **antiparasitics** (Emamectin Benzoate, ivermectin, lufeneron, Praziquantel).

National	Environmental program
	• Surveillance program name
	• Responsible agency or department
	• Environmental samples
	  ○ Water
	  ○ Air
	  ○ Wildlife
		• The National Pollutant Release Inventory organized by the Government of Canada monitors industrial pollutants from the air, water, and land, across all provinces and territories in Canada. It includes a public inventory of pollutant releases, disposals and transfers of over 300 pollutants (nutrients, heavy metals, chemicals) across 7,000 facilities updated on an annual basis.
		• The National Air Pollution Surveillance (NAPS) developed by Environment and Climate Change Canada (ECCC) and the Government of Canada monitors ambient air quality nationally across 286 sites in 203 communities in Canada. Air pollutants and particulate matter are monitored quarterly in 24-hour samples.
		• The Canadian Environmental Sustainability Indicators (CESI) developed by ECCC monitors key environmental indicators for water, air, biodiversity, climate and waste and contaminants.
		  ○ The National Long-term Water Quality Monitoring Data program organized by Environment and Climate Change Canada (ECCC) and the Canada Water Agency measures freshwater quality data across federal and federal-provincial sample sites across Canada. Its data informs CESI.
		• The Community Aquatic Monitoring Program (CAMP) from Fisheries and Oceans Canada is a water, sediment, and wildlife (fish, shrimps, crabs, aquatic plants) health monitoring program for New Brunswick, Nova Scotia, and Prince Edward Island. 36 coastal communities are monitored, with 6 stations monitored monthly.

Alberta	Environmental program
	• Surveillance program name
	• Responsible agency or department
	• Environmental samples
	  ○ Water
	  ○ Wildlife
		• The Water Quality Data Portal developed by the Government of Alberta monitors ambient water quality periodically through 132 water survey stations every 2-3 years across the province of Alberta.
		• The Alberta Biodiversity Monitoring Institute monitors over 2,500 species across 6 different ecosystems in the province of Alberta through status, trend, and targeted survey monitoring programs

British Columbia	Environmental program
	• Surveillance program name
	• Responsible agency or department
	• Environmental samples
	  ○ Water
	  ○ Air
		• The Surface Water Quality Monitoring Sites program organized by the Government of British Columbia, Environmental Monitoring System monitors freshwater quality of lakes, rivers, streams, creeks, and ponds in the province of British Columbia.
		• The Air Quality Health Index organized by the Government of British Columbia monitors the ambient air quality and air particulate matter across British Columbia through 150 air quality monitoring stations (100 continuous, 50 non-continuous).

Manitoba	Environmental program	• No publicly available program or datasets found.
New Brunswick	Environmental program • Surveillance program name • Responsible agency or department • Environmental samples ○ Water	• The Department of Environment and Local Government River Water Quality Data developed by the Government of New Brunswick monitors ambient water quality and data trends through monitoring stations across the province of New Brunswick quarterly. • The New Brunswick Volunteer Lakes Monitoring Program Data developed by the Government of New Brunswick monitors lake ambient water quality and data trends on an annual basis.
Newfoundland & Labrador	Environmental program • Surveillance program name • Responsible agency or department • Environmental samples ○ Water	• The Drinking Water Quality Data program developed by the Government of Newfoundland & Labrador, Department of Environment and Climate Change monitors provincial drinking water quality from public water supplies across the province every 2-3 years.
Nova Scotia	Environmental program • Surveillance program name	• The Nova Scotia Automated Surface Water Quality Monitoring Network organized by the Government of Nova Scotia monitors ambient water quality at water monitoring stations across the province periodically.

	• Responsible agency or department • Environmental samples ○ Water	

Ontario	Environmental program
	• Surveillance program name
	• Responsible agency or department
	• Environmental samples
	  ○ Water
	  ○ Soil
	  ○ Air
	  ○ Wildlife
		• The Drinking Water Surveillance Program organized by the Government of Ontario monitors provincial drinking water from selected municipal drinking water systems for inorganic, organic and radiological parameters.
		• The Air Quality Health Index organized by the Government of Ontario monitors the ambient air quality and air particulate matter across Ontario through various air monitoring stations on an hourly basis.
		• The On-Farm Applied Research and Monitoring (ONFARM) program developed by the Ontario Soil and Crop Improvement Association monitors agricultural soil and groundwater from 23 agricultural sites across Ontario on an annual basis, assessing soil health and groundwater quality.
		• The Ministry of Environment, Conservation and Parks had made available a Fish Contaminants Dataset on toxic chemical contaminants in waterbodies that can accumulate in fish.

Prince Edward Island	Environmental program • Surveillance program name • Responsible agency or department • Environmental samples	• The PEI Department of Environment, Energy and Climate Action has publish dashboards for Water Quality (called the Water Registry) and Air Quality Monitoring data, including particulate matter information. • Water quality includes a watershed report card based on estuary dissolved oxygen, drinking water, surface water quality, nitrates in streams, pesticides in drinking water/streams/stream sediment, suspended sediment monitoring, PFAS sampling, and wastewater treatment outflow. Sampling frequency and sites varies by indicator.

Quebec	Environmental program
	• Surveillance program name
	• Responsible agency or department
	• Environmental samples
	  ○ Water
	  ○ Air
		• The Water Atlas developed by the Government of Quebec, Ministry of the Environment monitors ambient water quality and sources of pollution in the St. Lawrence River, Quebec rivers, and lakes on a daily-weekly (drinking water), annually-biannually (groundwater), monthly-quarterly (surface water), and seasonal or targeted (specific contaminants) basis.
		• The Quebec Air Quality Monitoring Network (QAQSN) developed by the Government of Quebec, Ministry of the Environment monitors ambient air quality and air particulate matter at approximately 100 monitoring sites across the province on both a continual and periodic basis.

Saskatchewan	Environmental program • Surveillance program name • Responsible agency or department • Environmental samples	• The Saskatchewan Environmental Quality Guidelines, developed by the provincial Ministry of Environment, are a set of standardized chemical contaminant thresholds, soil and sediment quality criteria, drinking water protection levels and land use standards for soil, sediment, surface water, groundwater and air that are legally determined by Saskatchewan legislation, permits, and codes, and updated periodically .
Northwest Territories	Environmental program • Surveillance program name • Responsible agency or department • Environmental samples ○ Water	• The NWT-wide Community-based Monitoring Program organized by the Government of Northwest Territories, Department of Environment and Climate Change is a community-based ambient water quality monitoring program that includes 21 communities and over 40 monitoring sites on 24 NWT rivers and lakes.
Nunuvut	Environmental program	• No publicly available program or datasets found.
Yukon	Environmental program • Surveillance program name • Responsible agency or department • Environmental samples ○ Water	• The Yukon Water Data Catalogue organized by the Government of Yukon monitors ambient water quality from water monitoring sites across the territory on a continuous and periodic basis.

Table A-15: Canadian jurisdiction scan of potentially relevant research projects

Project	Organising framework	Key features of environmental AMR surveillance or relevant programmes	Data extracted
Frontiers	• Surveillance program name • Responsible agency or department • Environmental samples ○ Air • Comparative study	**Frontiers:** Professor Caroline Duchaine is presently a Canada Research Chair (2020-2027) on bioaerosols at the Universite Laval and was the Principal Investigator of a Natural Sciences and Engineering Research Council of Canada (NSERC) Discovery Frontiers grant (2020-2024) titled 'Antimicrobial resistance genes (ARG) in bioaerosols in Canadian arctic, rural and urban environments: sources, profiles, transport, and fate.' The multidisciplinary project had several air sampling campaigns in natural and man-made environments, including capturing samples from clouds, atmospheric particles, the Arctic, hospitals, wastewater treatment facilities and farms, and investigating alternative sampling methods such as the use of conifer needles as passive monitors.	George et al. (2022, 2024); Provencher et al. (2024); Rossi et al. (2023, 2024)

ECO²	• Surveillance program name
	• Responsible agency or department
	• Environmental samples
	  ○ Water
	  ○ Soil
	  ○ Air
	  ○ Wildlife
	• Comparative study
		Environmental Change One Health Observatory (ECO²): This Agriculture and Agri-food Canada (AAFC) project monitors the interactions between agricultural activities, environmental health, and human health through collaborations with government agencies, agricultural producers, and non-government organizations. Relevant lines of research include: understanding aero-microbiome synergies in plant and animal pathogen surveillance, including AMR tracking, and metagenomic analysis of agricultural drainage.	None

GDRI	• Surveillance program name
	• Responsible agency or department
	• Type of environmental AMR surveillance
	  ○ Occurrence / Prevalence
	  ○ Selection
	  ○ Dissemination
	  ○ Transmission
	• Environmental samples
	  ○ Water
	  ○ Soil
	  ○ Air
	  ○ Wildlife
	• Comparative study
		Genomics Research and Development Initiative (GDRI): The multi-agency research team's first AMR project from 2016-2022 applied a cross-sectoral genomics-based approach to understand how food production contributes to the human AMR impact, but did not have a strong environmental focus.
		• The second AMR project funded from 2022-2027 will examine natural and wastewater systems, fisheries and health care to identify intervention targets through One Health mapping of the development and distribution of AMR in health care settings, animals, plants, wastewater and the environment.
		• It is unclear which environmental media found in nature will be of focus.
		• Key deliverables include:
		  ○ **Hotspot Identification**: Identifying priority environmental hotspots and key drivers for mitigation.
		  ○ **Dissemination vectors identification**: Identifying how AMR spreads in natural and human-impacted terrestrial and aquatic ecosystems.
		  ○ **Transfer Pathway mapping**: Using molecular epidemiology to link resistant bacteria in human-agri-food systems and the environment.
			Subirats et al. (2023); Zaheer et al. (2019); Zaidi et al. (2022, 2023)

GSA	• Responsible agency or department • Environmental samples ○ Wildlife	**Gwich'in Settlement Area (GSA):** A range of wildlife research and monitoring projects in Northwest Territories of Dall's sheep, muskrat, beaver, muskox, caribou, moose, and small mammals including hares.	None

INSPIRE	• Surveillance program name
	• Responsible agency or department
	• Type of AMR surveillance
	  ○ Occurrence / Prevalence
	  ○ Dissemination
	• Environmental samples
	  ○ Water
	• Type of AMR microorganism, AMR determinants or antimicrobial agents monitored
	  ○ Microorganism
	  ○ Resistant microorganism
	• Sampling site (examples: discharge points, rivers)
		Integrated Network for the Surveillance of Pathogens: Increasing Resilience and capacity (INSPIRE): Aims to develop a rapid and flexible pandemic early warning system that improves the resilience of Canada's biomanufacturing sector and health supply chains while driving technology innovation.
		• The Canadian Hub for Health Intelligence & Innovation in Infectious Diseases (HI³ Hub) is leading the multi-institute team of 43 experts from Canadian and US universities and public and private sectors, including experts from the Universities of Windsor, Guelph, Waterloo and York and Unity Health Toronto.
		• Building from previous SARS-CoV-2 surveillance efforts, this iteration of the project will coordinate with health system data and supply networks to expand and integrate extant saliva-based pathogen and wastewater surveillance capabilities at strategic airports and land border crossings.
		Wastewater surveillance objectives include developing and applying high throughput metagenomic sequencing to detect existing, new and emerging pathogens and AMR, including a retrospective analysis of historical wastewater data to monitor pathogen evolution.
			None

NCCS	• Surveillance program name • Responsible agency or department	**Nunavut Climate Change Secretariat (NCCS):** Research project on 'Foodborne and Waterborne Disease Mitigation: Community-based Surveillance for Environmental Health' led by Prof Sherilee Harper in collaboration with Department of Health and Nunavut Research Institute.	None

	• Environmental samples ○ Water		

Appendix 6: Canadian scientific evidence data extraction

Jurisdiction	Organising framework	Key features of environmental AMR surveillance or relevant programmes

AB	• Comparative study
	  ○ Different sources
	• Type of environmental AMR surveillance
	  ○ Occurrence / Prevalence
	  ○ Dissemination
	• Environmental samples
	  ○ Water
	• Type of pollution sources (See Table A-5)
	• Pollution source one health domain (See Table A-5)
	• Pollution source origin type (examples: wastewater treatment works, pharmaceutical industry, farm)
	• Type of AMR microorganism, AMR determinants or antimicrobial agents monitored
	  ○ Resistant microorganism
	• Sampling site (examples: discharge points, rivers)
		Whole genome sequencing differentiates presumptive Extended Spectrum Beta-Lactamase Producing *Escheria coli* along segments of the One Health continuum (Adator et al., 2020)
		• Assessed presumptive ESBL-EC across One Health continuum of beef production system from cattle feces (n=40), feedlot catch basins (n=42), surrounding streams (n=21), a beef processing plant (n=4), municipal sewage (n=30), and clinical patients (n=25).
		• Findings:
		  ○ Human and cattle AMU differences likely explain prevalence and specificity of ARG sources in presumptive ESBL-EC.
		  ○ Comparative genomics showed distinct phylogenic clusters for human and cattle isolates, which suggests human ESBL-EC infections in the region likely are not from beef production sources.
		• Methods: Cattle feces and catch basin water collected from four feedlots, and surrounding stream surface water for one feedlot. Sewage samples collected upstream of Calgary treatment plant and downstream of a major feedlot region in Medicine Hat.

ON	• Comparative study
	  ○ Different areas
	• Environmental AMR surveillance
	• Surveillance program name
	• Responsible agency or department
	• Type of environmental AMR surveillance
	  ○ Occurrence / Prevalence
	• Environmental samples
	  ○ Water
	• Type of pollution sources (See Table A-5)
	• Pollution source origin type (examples: wastewater treatment works, pharmaceutical industry, farm)
	• Sampling site (examples: discharge points, rivers)
	• Sampling frequency
		Microbial water quality at contrasting recreational areas in a mixed-use watershed in eastern Canada (Butler et al., 2021)
		• PHAC FoodNet and the Ontario Ministry of the Environment, Conservation and Parks explored the sources and factors influencing contamination in river and recreational waters.
		• Findings:
		  ○ Beach water samples had lower pathogen levels than river samples, with *E. coli* concentrations serving as reliable indicators of contamination and health risks.
		  ○ Pathogen subtyping indicated a limited range of sources, with sampling site characteristics influencing pathogen prevalence and types.
		  ○ Pathogen profiles suggested that wild bird management could help reduce public health risks at beach sites.
		  ○ Enhanced surveillance of recreational waters can complement water quality monitoring and improve understanding of human illness risks.
		• Methods:
		  ○ This analysis investigated compared prevalence and human enteric pathogen and fecal indicator organism associations from five sites along the Grand River Watershed (6,800 km²) in Ontario between 2011 and 2013.
		  ○ River samples were collected twice a month at two reference sites upstream of drinking water intake and downstream of WWTP discharge point; and recreational waters from two sandy beach on river tributary and one site on main river.

PHAC data	• Comparative study
	  ○ Different sources
	• Type of environmental AMR surveillance
	  ○ Transmission
	• Environmental samples
	  ○ Water
	• Type of AMR microorganism, AMR determinants or antimicrobial agents monitored
	  ○ Microorganism
		A comparative exposure assessment of foodborne, animal contact and waterborne transmission routes of *Salmonella* in Canada (Christidis et al., 2020)
		• PHAC FoodNet salmonella exposure comparing 15 transmission routes based on 2005-2015 data and food, animal contact and water exposure assessment models.
		• Limitations include drinking water model based on Ontario data and concentration and prevalence contamination for meat models based on Ontario and BC sentinel sites, which might not serve as good Pan-Canadian proxies.
		• Findings:
		  ○ Chicken meat exposure was highest, with other foodborne and waterborne transmission routes being 3 log lower.

		○ Two waterborne exposure routes were considered: drinking water and recreational water, and both were found to have roughly similar exposure.
QC	• Comparative study ○ Water/Soil/Air: Natural vs built environment sites • Type of environmental AMR surveillance ○ Occurrence / Prevalence ○ Dissemination • Environmental samples ○ Air • Type of pollution sources (See Table A-5) • Pollution source origin type (examples: wastewater treatment works, pharmaceutical industry, farm) • Type of AMR microorganism, AMR determinants or antimicrobial agents monitored ○ Antimicrobial-resistant genes (ARGs) ○ Mobile genetic elements (MGEs) • Sampling site (examples: discharge points, rivers)	Conifer Needle Phyllosphere as a Potential Passive Monitor of Bioaerosolised Antibiotic Resistance Genes (George et al., 2022) • Frontiers associated proof-of-concept assessment of conifer needles as passive bioaerosol samplers. • Findings: ○ Number and quantity of ARGs was significantly lower in forest sites compared to farm and village: 26 ARGs or MGEs detected in needles near farms, 24 near village, and 13 from forest site. ○ Most common ARGs were tetracyclines and sulfonamides found close to agricultural activities. ○ Limited results but indicate potential for conifers as passive monitors for large-scale ARG surveillance over long distances from point sources. • Methods: Needles collected from trees adjacent to pig farms (n=12, 3-50m), villages (n=5, 3-9km away from farms), and protected forest as a control site (n=3, 80km north) in Quebec. Used multiple conifer species with *Picea* sp. being most common, and 4 *Abies balsema* and 1 *Pinus strobus*.
QC, Wales	• Comparative study ○ Different sources • Type of environmental AMR surveillance ○ Occurrence / Prevalence ○ Dissemination • Environmental samples ○ Water ○ Air • Type of pollution sources (See Table A-5) • Pollution source origin type (examples: wastewater treatment works, pharmaceutical industry, farm) • Type of AMR microorganism, AMR determinants or antimicrobial agents monitored ○ Antimicrobial-resistant genes (ARGs) • Sampling site (examples: discharge points, rivers)	Needles in haystack: monitoring the potential escape of bioaerosolised antibacterial resistance genes from wastewater treatment plants with air and phyllosphere sampling (George et al., 2024) • Frontiers-associated comparative study of WWTP ARG bioaerosol dispersal using conifer needles as passive bioaerosol monitors. • Findings: ○ ARG diversity significant lower in conifer phyllosphere samples than wastewater samples. ○ While distinct but limited ARG profile trend observed across dispersal gradient, findings were incongruous with wastewater samples so links to WWTP not evident. • Methods: Compared WWTP WW and air samples with conifer needles from surrounding trees in Quebec (~150m radius, and upwind control site 10.5km away) and Bangor, Wales (across ~16km transect – upwind, near city centre, distant sites, and control site 65km away).
AB, BC, ON	• Comparative study ○ Different sources • Environmental AMR surveillance • Surveillance program name • Responsible agency or department • Type of environmental AMR surveillance ○ Transmission • Environmental samples ○ Water • Type of AMR microorganism, AMR determinants or antimicrobial agents monitored ○ Microorganism • Sampling site (examples: discharge points, rivers)	Attributing *salmonellosis* cases to foodborne, animal contact and waterborne routes using the microbial subtyping approach and exposure weights (Hurst et al., 2023) • PHAC FoodNet study attributing cases of salmonella to retail meats, food animal manure contact and surface water sources in three FoodNet sentinel sites in Ontario, BC and Alberta. • Findings: ○ 3.0% of cases attributed to water exposure, including recreational water, irrigation ditches, and general environmental impacted by wildlife and agricultural run-off. ○ Overall, Hurst et al. (2023) characterised this as “very low” compared to retail meat risks, and a similar result to other Canadian data sources (2.1-8% ranges) and an EU study (0.5%). • Methods: Water samples collected from Grand and Thames River watershed (ON), Fraser River watershed – recreational and irrigation ditches (BC), and Bow River watershed irrigation ditches (AB).
ON	• Comparative study ○ Different areas ○ Different types of same media	Antimicrobial resistance of *Salmonella* and generic *Escherichia coli* isolated from surface water samples used for recreation and a source of drinking water in southwestern Ontario, Canada (Kadykalo et al., 2020)

	• Environmental AMR surveillance
	• Surveillance program name
	• Responsible agency or department
	• Type of environmental AMR surveillance
	  ○ Occurrence / Prevalence
	• Environmental samples
	  ○ Water
	• Type of pollution sources (See Table A-5)
	• Pollution source origin type (examples: wastewater treatment works, pharmaceutical industry, farm)
	• Type of AMR microorganism, AMR determinants or antimicrobial agents monitored
	  ○ Microorganism
	  ○ Resistant microorganism
	• Sampling site (examples: discharge points, rivers)
	• Sampling frequency
		• PHAC FoodNet and Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS) investigated AMR patterns in watershed to describe composition, trends and potential AMR risks.
		• Findings:
		  ○ Found 16% of *Salmonella* and 22% of *E. coli* isolates resistant to at least one antimicrobial, including five isolates resistant to Category 1 antimicrobials of very high importance for serious bacterial infections.
		• Greatest proportion of resistant *E. coli* isolates found in river upstream of drinking water intake likely impacted by range of agricultural activities, and greatest proportion of resistant *Salmonella* isolates found upstream at a recreational water site.
		• Methods:
		  ○ Bi-weekly samples from Grand River (upstream, including from drinking water intake, and downstream WWTP and tributaries with agricultural land-use, rural communities and WWTP. Three recreational sites also sampled in summer (2011-2013).
		  ○ Tested for the presence and antimicrobial susceptibility of *Salmonella* spp. (2005–2013) and generic *Escherichia coli* (2012–2013).

AB, MB, QC, India	• Comparative study
	  ○ Different areas
	  ○ Different sites (natural vs built)
	• Type of environmental AMR surveillance
	  ○ Occurrence / Prevalence
	  ○ Selection
	• Environmental samples
	  ○ Water
	• Type of pollution sources (See Table A-5)
	• Pollution source origin type (examples: wastewater treatment works, pharmaceutical industry, farm)
	• Type of AMR microorganism, AMR determinants or antimicrobial agents monitored
	  ○ Microorganisms
	• Sampling site (examples: discharge points, rivers)
		Anthropogenic activities and geographic locations regulate microbial diversity, community assembly and species sorting in Canadian and Indian freshwater lakes (Obieze et al., 2022)
		• Sampling of six impacted freshwater lakes in Canada and India to examine selective factors such bacterial diversity, assembly mechanisms and co-occurrence patterns.
		• Findings:
		  ○ Freshwater bacterial community changes linked to anthropogenic activities, affecting especially species distribution.
		  ○ Homogenous selection increased with higher concentrations of nutrients and reduced stochasticity.
		  ○ Co-occurrence complexity increased in more impacted lakes, with species sorting being affected by both competition and the anthropogenic activity.
		• Method: Duplicate water samples collected one summer from 8 points of 6 impacted lakes in Canada (AB, MB, QC) and India (Kashmir) impacted by copper mines, agricultures, oil sands, urban-industrial activities, houseboats, and human sewage.

NU	• Comparative study
	  ○ Different habitats
	  ○ Different sources
	• Type of environmental AMR surveillance
	  ○ Occurrence / Prevalence
	  ○ Dissemination
	• Environmental samples
	  ○ Water
	  ○ Air
	• Type of pollution sources (See Table A-5)
	• Pollution source origin type (examples: wastewater treatment works, pharmaceutical industry, farm)
	• Type of AMR microorganism, AMR determinants or antimicrobial agents monitored
	  ○ Antimicrobial-resistant genes (ARGs)
	• Sampling site (examples: discharge points, rivers)
		Microbial antibiotic resistance genes across an anthropogenic gradient in a Canadian High Arctic watershed (Provencher et al., 2024)
		• Frontiers-associated assessment of ARG presence and distribution across three different anthropogenically impacted habitats in an Arctic watershed, from high- to low-impact.
		• Findings:
		  ○ 984 ARGs (grouped into 17 resistance genes belonging to 9 ARG families) detected across all samples and habitats.
		  ○ High-impact site had significantly more families than low-impact ones. Likely contamination from 20th century wastewater effluent.
		  ○ Microbial mats contained greatest relative abundance of ARGs, whereas only only one aerosol sample had ARGs, which also had the lowest ARG diversity.
		  ○ ARGs mostly associated with bacterial genome; also observed ARG present in mimivirus, which might be first scientific observation.
		• Methods:
		  ○ 63 samples collected in July 2018, August 2019 and August 2021 from three study sites on Cornwallis Island in Canadian Arctic Archipelago: Lake Meretta near airport that had significant anthropogenic activity (including a closed military base) that discharged wastewater into local watershed, thereby

		reducing the lake's water quality; Resolute lake connected to impacted lake by 1 km stream and is popular for fishing, and Char lake unconnected to impacted lake. ○ Aerosols collected in duplicate over the course of 1 hour; water samples in triplicate at multiple depths (Meretta: 2 and 6m, Resolute: 2, 10 and 15 m, and Char: 2, 7, and 15m); microbial mats in triplicate from wetlands around Meretta Lake and near Arctic Ocean.
France	• Comparative study ○ Resistome origin • Type of environmental AMR surveillance ○ Occurrence / Prevalence ○ Dissemination • Environmental samples ○ Air • Type of AMR microorganism, AMR determinants or antimicrobial agents monitored ○ Antimicrobial-resistant genes (ARGs) • Sampling site (examples: discharge points, rivers) •	Quantification of antibiotic resistance genes (ARGs) in clouds at a mountain site (puy de Dôme, central France) (Rossi et al., 2023) • Please note: Although conducted in France, this study is included in Canadian research because half of its co-authors—including the lead author and a Canada Research Chair on bioaerosols—are affiliated with Université Laval, the study was partially funded by the Natural Sciences and Engineering Research Council of Canada, and the study focuses on ARG atmospheric transport, a major knowledge gap in Canada and globally. • Frontiers-associated assessment of clouds: ARG presence and abundance, as well as long distance dissemination by atmospheric transport in French mountain site. • Findings: ○ High atmospheric routes can disseminate ARGs at large scale: 29 ARG subtypes found from seven main ABR families found, including one MGE. ○ Air masses over marine area (Atlantic Ocean) had more quinolone resistant genes and continental clouds had higher sulfonamide, tetracycline, glycopeptide, beta-lactamase and macrolide resistant genes. ○ Cloud resistome can be a mosaic of long-distance and local ABR. ○ Attributed veterinary use as main ARG contributor in free atmosphere. • Methods: 12 clouds with different geographic origins collected between September 2019 and October 2021 at a meteorological station.
France	• Comparative study ○ Resistome origin • Type of environmental AMR surveillance ○ Occurrence / Prevalence ○ Dissemination • Environmental samples ○ Air • Type of AMR microorganism, AMR determinants or antimicrobial agents monitored ○ Antimicrobial-resistant genes (ARGs) • Sampling site (examples: discharge points, rivers) •	Temporal variations of antimicrobial resistance genes in aerosols: A one-year monitoring at the puy de Dôme summit (Central France) (Rossi et al., 2024) • Please note: Although conducted in France, this study is included in Canadian research because half of its co-authors—including the lead author and a Canada Research Chair on bioaerosols—are affiliated with Université Laval, the study was partially funded by the Natural Sciences and Engineering Research Council of Canada, and the study focuses on ARG atmospheric transport, a major knowledge gap in Canada and globally. • Frontiers-associated cloud assessment: ARG presence and long-distance dissemination by atmospheric transport in French mountain site. • Findings: ○ 33 ARG subtypes that had had seasonal fluctuations in abundance and diversity. ○ The majority of ARGs detected were from the quinolone resistance family, with *qepA* accounting for over 95% of the ARGs found. The high presence of Sphingomonas bacteria suggests that much of the airborne ARGs came from natural sources. ○ ARGs likely originate from natural sources such as surface ecosystems (water, sediment, soils) and hotspots (wastewater). • Methods: Sampled between July 2016-2017 in a mountain site that is >80% cropland/vegetation and <20% forest and urban area.
NS, NT, QC	• Comparative study ○ Different species • Type of environmental AMR surveillance ○ Occurrence / Prevalence • Environmental samples ○ Wildlife • Type of AMR microorganism, AMR determinants or antimicrobial agents monitored	Occurrence and antimicrobial resistance of *Salmonella* species and potentially pathogenic *Escherichia coli* in free-living seals of Canadian Atlantic and eastern Arctic waters (Saab et al., 2023) • Investigated the occurrence and AMR potential of *Salmonella* spp., *Escheria coli*, and *Listeria monocytogenes* in grey and ringed seals. • Findings: ○ Seals may act as a sentinel species for monitoring as reservoirs or vectors for resistant and virulent *Salmonella* and *E. coli* species. ○ Grey seals: *E. coli* detected in 77%, pathogenic *E. coli* in 29%.

	○ Microorganism ○ Resistant microorganism ○ Antimicrobial-resistant genes (ARGs) • Sampling site (examples: discharge points, rivers) • Sampling frequency •	○ Ringed seals: 9% of sample from Frobisher Bay (n=4/45) had *E. coli*, but no virulent or AMR detected in isolates. 16% of Eclipse Sound had *E. Coli* (n=8/50) and 10% had pathogenic *E. Coli* detected. ○ *Salmonella* Typhimurium detected in 16% of ringed seals (n=8/50) from Eclipse Sound, with all isolates resistant to tetracycline, ampicillin, sulfisoxazole and streptomycin. One seal had *E. coli* isolates resistant to beta-lactams. ○ No Listeria monocytogenes detected. • Method: Faecal samples harvested from 44 grey seals (*Halichoerus grypus*) in the Gulf of St. Lawrence (NS and QC) in January/February 2017/2018 and from 95 ringed seals (*Pusa hispida*) in Baffin Island, Nunavut (spring 2017/2018 and fall 2018).
Meta-analysis: ON and UK	• Comparative study ○ Different sources ○ Different countries • Type of environmental AMR surveillance ○ Occurrence / Prevalence ○ Selection ○ Dissemination • Environmental samples ○ Water	Exploring the mobilome and resistome of *Enterococcus faecium* in a One Health context across two continents (Sanderson et al., 2022) • Investigation of *Enterococcus faecium* resistance determinants, virulence factors and mobile genetic elements (MGEs), providing a workflow for MGE-centric Enterococcus AMR surveillance that can potentially be adapted for other pathogens. • Findings: ○ 1,273 genomes from two different locations (UK and Ontario, Canada) from a range of different habitats associated with agriculture, clinical settings and natural environment. ○ Did not find that E. faecium lineages, ARGs and MGEs were constrained by geography, but there was a strong association between habitats and ARGs and MGEs – especially from clinical and municipal wastewater sources. • Method: Analysed genome isolates collected from five sources (clinical, agricultural, municipal wastewater, agricultural wastewater, and surface water sources from two previous studies Zaheer (2020) and Gouliouris et al.
Meta-analysis: Global	• Comparative study ○ Different sources • Type of environmental AMR surveillance ○ Occurrence / Prevalence ○ Selection	Metagenome meta-analysis reveals an increase in the abundance of some multidrug efflux pumps and mobile genetic elements in chemically polluted environments (Subirats et al., 2023) • GDRI-associated meta-analysis of metagenomes in public domain that compared whether pollution in terrestrial and aquatic environments influenced ARG and MGE abundance and composition, focusing on IS26 and class 1 integrons (intI1). • Findings: ○ Polluted environments had greater relative abundance of ARGs, IS26 and intI1 than unpolluted environments. ○ Various forms of chemical pollution can promote the growth of bacterial populations equipped with efflux pump systems, which confer resistance to multiple classes of medically important antibiotics.
ON	• Comparative study ○ Different sources • Type of environmental AMR surveillance ○ Occurrence / Prevalence ○ Dissemination ○ Transmission • Environmental samples ○ Soil (farm, manure) ○ Wildlife • Type of AMR microorganism, AMR determinants or antimicrobial agents monitored ○ Microorganism ○ Resistant microorganism ○ Antimicrobial-resistant genes (ARGs) • Sampling site (examples: discharge points, rivers)	Using whole-genome sequence data to examine the epidemiology of *Salmonella, Escherichia coli* and associated antimicrobial resistance in raccoons (*Procyon lotor*), swine manure pits, and soil samples on swine farms in southern Ontario, Canada (Vogt et al., 2021) • Examined whole genome sequence data of *Salmonella* and *Escheria coli* isolates from raccoons and farm environmental sources (soil and manure pits) to assess for potential transmission. • Findings: ○ 159 *Salmonella* and 96 resistant *E. coli* isolates found. ○ Similar or identical Salmonella isolates and resistant genes found between racoons, soil and wine manure pits. ○ Soil-raccoon transmission may occur frequently, while swine manure-raccoon transmission is uncommon. • Methods: Collected from five swine farms (2011-2013) with environmental samples collected only from the swine farms. Soil collected from within 2m radius of animal traps, and swine manure pits sampled from two different depths at three different locations around pit.

ON	• Comparative study
	  ○ Different sources
	• Type of environmental AMR surveillance
	  ○ Transmission
	• Environmental samples
	  ○ Water
	  ○ Wildlife
	• Type of AMR microorganism, AMR determinants or antimicrobial agents monitored
	  ○ Microorganism
	  ○ Resistant microorganism
	  ○ Antimicrobial-resistant genes (ARGs)
	• Sampling site (examples: discharge points, rivers)
		Rural Raccoons (*Procyon lotor*) Not Likely to Be a Major Driver of Antimicrobial Resistant Human *Salmonella* Cases in Southern Ontario, Canada: A One Health Epidemiological Assessment Using Whole-Genome Sequence Data (Vogt et al., 2022)
		• PHAC FoodNet-associated whole-genome sequence data assessment from select human, raccoon, livestock and environmental sources to demonstrate possible Salmonella transmission and ARGs between different sources in a watershed.
		• Findings:
		  ○ 608 isolates identified, including blaCMY−2 found in humans, livestock and environmental sources but not raccoons.
		  ○ Raccoons unlikely to be a major AMR contributor to humans in rural Ontario: most resistant genes were identified in livestock or human isolates than raccoon, and human isolates were more similar to livestock and environmental source isolates than raccoons.
		  ○ Possible poultry-associated Salmonella detected in raccoons.
		• Methods: 608 isolates collected from: humans (n = 58), raccoons (n = 92), livestock (n = 329), and river or beach water samples (n = 129); see Kadykalo et al. (2020) for water sample method.

NL	• Comparative study
	  ○ Different sources
	  ○ Different areas
	• Type of environmental AMR surveillance
	  ○ Occurrence / Prevalence
	  ○ Dissemination
	• Environmental samples
	  ○ Sediment
	• Type of AMR microorganism, AMR determinants or antimicrobial agents monitored
	  ○ Microorganism
	  ○ Resistant microorganism
	  ○ Antimicrobial-resistant genes (ARGs)
	  ○ Mobile genetic elements (MGEs)
	• Sampling site (examples: discharge points, rivers)
		Anthropogenic contamination sources drive differences in antimicrobial-resistant *Escherichia coli* in three urban lakes (Wight et al., 2024)
		• Assessed sediment of three lakes (Bowring Park duck pond, Mundy Pond, Quidi Vidi Lake) in three separate watersheds (with no known underground cross-connections) that typically are ice-free over winter over a 15-month time series to determine antimicrobial susceptibilities and genetic determinants of resistance for antimicrobial-resistant E. coli.
		• Findings:
		  ○ Despite being close in proximity, found each site had different *E. coli* populations with distinct antimicrobial and multidrug resistance patterns, indicating different non-point sources of anthropogenic contamination, ranging from agriculture, livestock, land runoff, and sanitary sewers.
		  ○ Environmental persistence, site transmission (via wild birds) and mobile genetic element transfer likely contributed to these patterns.
		  ○ ESBL phenotype detected.

AB	• Comparative study
	  ○ Different sources
	• Type of environmental AMR surveillance
	  ○ Occurrence / Prevalence
	  ○ Dissemination
	• Environmental samples
	  ○ Water
	  ○ Soil
	• Type of pollution sources (See Table 5)
	• Pollution source one health domain (See Table A-5)
	• Pollution source origin type (examples: wastewater treatment works, pharmaceutical industry, farm)
	• Type of AMR microorganism, AMR determinants or antimicrobial agents monitored
	  ○ Microorganism
	  ○ Antimicrobial-resistant genes (ARGs)
	• Sampling site (examples: discharge points, rivers)
		Comparative diversity of microbiomes and Resistomes in beef feedlots, downstream environments and urban sewage influent (Zaheer et al., 2019)
		• GDRI-associated comparative analysis of microbiomes and resistomes of environments between animal production and urban systems.
		• Findings:
		  ○ Proteobacteria most abundant in catch basin water (64%), soil (60%) and sewage influent (83%).
		  ○ Sewage influent had highest AMR diversity, and metal and biocide resistance, and had drug classes associated with human use.
		  ○ Fecal samples had highest ARG abundance, and soil samples' small resistome was unique and did not overlap with that of the fecal samples or catch basin.
		  ○ Overall, greater divergence of microbiome and resitome nature as feedlot distance increases.
		• Method: Metagenomic data from composite cattle feces (n=12) from four penned lots, water samples from catch basins (n=13), soil from nearby field (n=4), and urban sewage influent of two municipalities (n=6).

AB	• Comparative study ○ Different sources	Genomic Characterization of *Enterococcus hirae* From Beef Cattle Feedlots and Associated Environmental Continuum (Zaidi et al., 2022)

	• Type of environmental AMR surveillance
	  ○ Occurrence / Prevalence
	  ○ Dissemination
	• Environmental samples
	  ○ Water
	• Type of pollution sources (See Table A-5)
	• Pollution source origin type (examples: wastewater treatment works, pharmaceutical industry, farm)
	• Type of AMR microorganism, AMR determinants or antimicrobial agents monitored
	  ○ Microorganism
	  ○ Antimicrobial-resistant genes (ARGs)
	• Sampling site (examples: discharge points, rivers)
		• GDRI-associated genomic analysis of bacterium comparing beef production system (feedlot feces, manure and catch basin) of four feedlots in Southern Alberta from March 2014 – March 2016, two wastewater treatment plants in catch basins, and natural water (upstream and downstream), and human clinical samples.
		• Findings:
		  ○ The majority of isolates (4,601) were from beef production systems, including bovine feces (89.5%), catch-basin water (66.5%), and natural water near feedlots (32%). A small number were from urban wastewater (0.2%).
		  ○ Natural water source isolates showed prevalence of tetracycline, macrolides, nitrofurantoin, tigecycline, and quinupristin/dalfopristin resistance.
		  ○ The phenotypic resistance profiles of 1,319 *E. hirae* isolates showed AMU linkages: isolates associated with beef cattle production present in feedlot feces, manure, the catch basin, and nearby natural surface water. Urban wastewater, in contrast, had isolates more commonly associated with drugs treating human infections.

AB, BC, ON, QC	• Comparative study
	  ○ Different sources
	• Type of environmental AMR surveillance
	  ○ Occurrence / Prevalence
	  ○ Dissemination
	• Environmental samples
	  ○ Water
	  ○ Wildlife
	• Type of pollution sources (See Table A-5)
	• Pollution source origin type (examples: wastewater treatment works, pharmaceutical industry, farm)
	• Type of AMR microorganism, AMR determinants or antimicrobial agents monitored
	  ○ Microorganism
	  ○ Antimicrobial-resistant genes (ARGs)
	  ○ Mobile genetic elements (MGEs)
	• Sampling site (examples: discharge points, rivers)
		Comparative Genomic Analysis of *Enterococci* across Sectors of the One Health Continuum (Zaidi et al., 2023)
		• GDRI-associated genomic analysis comparing virulome, resistome, and mobilome of 246 E. faecium and 376 E. faecalis isolates from livestock (swine, beef cattle, poultry, dairy cattle), human clinical samples, domestic animals, municipal wastewater, and environmental sources
		• Findings:
		  ○ Despite differences in AMU across continuum, tetracycline (tetL, tetM) and macrolide (ermB) resistant genes were common ARGs prevalent across and found in association with mobile genetic elements (MGE) and other ARGs conferring resistance for aminoglycosides, aminoglycosides, and aminoglycosides.
		  ○ Core genome analysis identified two primary clades: Clade A associated with humans and municipal wastewater had more virulent genes and ARGs, especially against category I antimicrobials; and Clade B originated from other sources. Thus, despite AMU differences across the continuum, tetracycline and macrolide resistance genes persist across all sectors.
		• Methods: Data from AB, ON, QC and BC, with municipal wastewater and natural water sources from AB (March 2014 – April 2016) and river water and wild animals from Ontario (2004). The wild animal species is not specified.

AB, US, China, Germany	• Comparative study
	  ○ Different sites (natural vs built)
	  ○ Different countries
	• Type of environmental AMR surveillance
	  ○ Dissemination
	• Environmental samples
	  ○ Air
	• Type of AMR microorganism, AMR determinants or antimicrobial agents monitored
	  ○ Microorganism
	  ○ Antimicrobial-resistant genes (ARGs)
	  ○ Mobile genetic elements (MGEs)
	• Sampling site (examples: discharge points, rivers)
	• Sampling frequency
		Air pollution could drive global dissemination of antibiotic resistance genes (Zhu et al., 2021)
		• Comparative study of snow as a mechanism for atmospheric transport of ARGs in major Chinese cities, three North American (Washington, New Jersey, Edmonton) and a German city (Munich).
		• Findings: Snowfall effectively spread ARGs from point sources over Earth's surface.
		• Methods: ARG and MGE analysis of 44 fresh snow samples from 48 sampling sites from major Chinese cities, Munich, Washington, New Jersey, and Edmonton. In total, 5 replicate samples were taken per sampling site during snowfall events.

Appendix 7: Evidence syntheses data extraction

Dimension of organizing framework	Declarative title and key findings	Living status	Quality (AMSTAR)	Last year literature searched	GRADE profile availability	Equity considerations

• Type of environmental AMR surveillance
  ○ Occurrence/Prevalence
  ○ Dissemination
• Environmental samples
  ○ Water
  ○ Soil
  ○ Air
  ○ Wildlife
• Type of AMR microorganism, AMR determinants or antimicrobial agents monitored
  ○ Antimicrobial-resistant genes (ARGs)
	Carbapenemase-producing genes, a leading cause of antibiotic-resistant infections, are found in water, soil, animal, and food reservoirs globally (Mills and Lee, 2019)
	• The review identifies global environmental reservoirs of carbapenemase-producing genes, which are the cause of a large majority of antibiotic resistance infections, and potential routes of human transmission
	• The review identified carbapenemase-producing genes in water, soil, animals, and food across the globe
		No	2/9	2019	No	No

• Type of environmental AMR surveillance
  ○ Occurrence/Prevalence
• Environmental samples
  ○ Water
• Type of AMR microorganism, AMR determinants or antimicrobial agents monitored
  ○ Microorganism
  ○ Resistant microorganism
  ○ Antimicrobial-resistant genes (ARGs)
	Operationalizing wastewater environmental sampling is key to developing a systematic One Health disease surveillance approach for detecting human health risks (Hill et al., 2024)
	• Case studies are highlighted discussing the current global approach to tackle antibiotic resistance with a focus on wastewater testing
	• Avenues to operationalize wastewater environmental sampling using a One Health surveillance system including identifying key environmental conditions and regions are identified in implementing a systematic approach to surveillance
		No	1/9	2024	No	No

• Type of environmental AMR surveillance
  ○ Occurrence/Prevalence
  ○ Dissemination
• Environmental samples
  ○ Water
• Type of AMR microorganism, AMR determinants or antimicrobial agents monitored
  ○ Microorganism
  ○ Resistant microorganism
	Environmental contamination in a high-income country (France) by antibiotics, antibiotic-resistant bacteria, and antibiotic resistance genes: Status and possible causes (Haenni et al., 2022)
	• The review identifies the mechanisms leading to the emergence and persistence of antimicrobial resistance in France
	• Effluents of wastewater treatment plants are a main source of contamination
	• Fluoroquinolones and trimethoprim were found to be high risk resistant antibiotic molecules in the country
		No	2/9	2016	No	No

• Type of environmental AMR surveillance
  ○ Occurrence/Prevalence
  ○ Dissemination
• Environmental samples
  ○ Water
• Type of AMR microorganism, AMR determinants or antimicrobial agents monitored
  ○ Microorganism
  ○ Resistant microorganism
	Waterborne organisms of public health concern are present in bathing waters across Europe, including a widespread occurrence of antimicrobial resistant bacteria (Farrell et al., 2021)
	• The review investigated the potential exposure of waterborne organisms of public health concern (bacterial, viral, and protozoan contaminants) in bathing waters across Europe
	• Of the synthesized investigations, 58% of the waterborne organisms present in bathing waters were found to be bacterial, 36% viral, and 17% were protozoan contaminants
	• Antimicrobial resistant bacteria had a 47% detection rate, highlighting their widespread presence in public bathing waters
		No	5/9	2020	No	No

• Type of environmental AMR surveillance ○ Occurrence/Prevalence • Environmental samples	Standardizing culture methods for key antibiotic-resistant bacteria (*Acinetobacter*, *Aeromonas*, and *Pseudomonas*) found in wastewater and	No	3/9	2020	No	No

○ Water • Type of AMR microorganism, AMR determinants or antimicrobial agents monitored ○ Resistant microorganism	environmental waters is important for study consistency and understanding antibiotic resistant targets (Milligan et al., 2023) • The review identified key antibiotic-resistant bacteria (*Acinetobacter, Aeromonas*, and *Pseudomonas*) for their persistence and ability to engage in horizontal gene transfer with other environmental bacteria in wastewater and environmental waters • Standardizing methodologies for culturing these bacteria are beneficial for consistency and accuracy of antibiotic-resistant targets for cross-study comparison					
• Type of environmental AMR surveillance ○ Occurrence/Prevalence • Environmental samples ○ Water • Type of AMR microorganism, AMR determinants or antimicrobial agents monitored ○ Resistant microorganism	Recent research on human pathogens and antimicrobial resistance detection in human wastewater and sludge increased after the emergence of COVID-19 and primarily explores detection through respiratory and vector-borne pathways (Corrin et al., 2024) • The review identified characteristics of research conducted on human pathogens and antimicrobial resistance detection in human wastewater and sludge • The review found that recent research is primarily focussed on respiratory and vector-borne pathways of transmission, with a high increase of research published after the emergence of COVID-19	No	5/9	2023	No	No
• Type of environmental AMR surveillance ○ Occurrence/Prevalence ○ Dissemination • Environmental samples ○ Water ○ Soil/Sediment ○ Wildlife • Type of AMR microorganism, AMR determinants or antimicrobial agents monitored ○ Microorganism ○ Resistant microorganism	Research on and occurrence of antimicrobial resistant bacteria in Germany, Austria, and Switzerland is present across many environmental sources using a variety of methodologies (Treskova et al., 2022) • The review synthesized the current research on environmental antimicrobial resistance in Germany, Austria, and Switzerland • Antimicrobial resistant bacteria were studied and identified in water sources, wastewater, animal husbandry environments, wildlife, and sediment/soil using a wide variety of sampling sources and methodologies	No	4/9	2021	No	No
• Type of environmental AMR surveillance ○ Occurrence/Prevalence ○ Dissemination • Environmental samples ○ Wildlife • Type of AMR microorganism, AMR determinants or antimicrobial agents monitored ○ Microorganism ○ Resistant microorganism ○ Antimicrobial-resistant genes (ARGs)	Honeybee (*Apis mellifera* L.) colonies have been used in detection of both external environmental AMR and ARG and in symbiotic bacteria colonizing the bee gut, suggesting honey bees potential role as a monitor of ecosystem health (Resci and Cilia, 2023) • The review investigated the role of honeybee (*Apis mellifera* L.) colonies as a biological monitor of antimicrobial resistance pathogenic bacteria (AMR) and antimicrobial resistance genes (ARG) • AMR and ARG have been detected in environmental bacteria present on the external body of the honeybees as well as in symbiotic bacteria colonizing the bee gut • The review highlights the potential use of honeybees as a monitor of ecosystem health	No	4/9	2023	No	No
• Type of environmental AMR surveillance ○ Occurrence/Prevalence ○ Dissemination • Environmental samples ○ Air • Type of AMR microorganism, AMR determinants or antimicrobial agents monitored	Aerosols play a role in antimicrobial resistance spread, with fecal bacterial signatures identified in urban ambient air across the globe (Ginn et al., 2022) • The review investigated the current evidence of enteric pathogens and ARGs that have been measured in aerosol samples in high-risk urban settings	No	6/9	2020	No	No

○ Microorganism ○ Resistant microorganism ○ Antimicrobial-resistant genes (ARGs)	• The review found that human fecal signatures are found in urban ambient air globally, and that research suggests aerosols play a role in antimicrobial resistance spread					
• Type of environmental AMR surveillance ○ Occurrence/Prevalence ○ Dissemination • Environmental samples ○ Wildlife • Type of AMR microorganism, AMR determinants or antimicrobial agents monitored ○ Microorganism ○ Resistant microorganism	The use of testudines as sentinel species for antimicrobial resistance monitoring identified anthropogenic pressures for resistance development in sea turtles and the larger marine environment (Drane et al., 2021) • The review assessed the use of testudines (turtles) as sentinel species for monitoring antimicrobial resistance dissemination in marine environments • Higher incidence of resistant bacteria was identified in sea turtles in proximity to wastewater treatment facilities and at turtle rehabilitation centres, highlighting the anthropogenic pressures of antimicrobial resistance development in sea turtles	No	4/10	2020	No	No
• Type of environmental AMR surveillance ○ Occurrence/Prevalence ○ Dissemination • Environmental samples ○ Wildlife • Type of AMR microorganism, AMR determinants or antimicrobial agents monitored ○ Microorganism ○ Resistant microorganism	Antimicrobial resistant bacteria, including Gram-postive, Gram-negative, and multi-drug-resistant bacteria, have been identified in bat species, highlighting a major concern for AMR transmission to humans and the environment (Devnath et al., 2023) • The review investigated the presence of AMR in bats and the association to AMR persistence at the human-animal level • Both Gram-positive and Gram-negative resistance bacteria and multi-drug-resistant bacteria (Methicillin Resistant *Staphylococcus aureus* (MRSA), ESBL producing, and Colistin resistant Enterobacterales) were identified in bat species across studies • The researchers highlight these findings as a major concern for AMR transmission in humans and the environment	No	4/9	2022	No	No
• Type of environmental AMR surveillance ○ Occurrence/Prevalence ○ Dissemination • Environmental samples ○ Air • Type of AMR microorganism, AMR determinants or antimicrobial agents monitored ○ Resistant microorganism ○ Antimicrobial-resistant genes (ARGs)	Bioaerosol studies focussed on AMB and AMG monitoring use a variety of sampling methods, and are primarily based in outdoor environments, with limited research on bioaerosol monitoring in indoor environments (Lee and Yoo, 2022) • The review identified recent findings of bioaerosol studies focussed on monitoring antimicrobial resistance in bioaerosols • Bioaerosol studies utilize a variety of sampling methods with no standard method for ARGs yet to be established • ARGs in outdoor environments have been detected in studies of wastewater treatment plants, composting plants, public parks, and farm areas • There is limited research on ARGs in indoor environments	No	1/9	2022	No	No
• Type of environmental AMR surveillance ○ Occurrence/Prevalence • Environmental samples ○ Air • Type of AMR microorganism, AMR determinants or antimicrobial agents monitored ○ Antimicrobial-resistant genes (ARGs)	ARGs in air samples across various settings suggest a higher presence and consistency of ARGs in urban settings and a comparable exposure risk to drinking water (Kormos et al., 2022) • The review identified the current evidence of bacterial ARGs in air samples across various settings • Urban settings are associated with a higher presence of ARGs compared to rural settings, with greater consistency in type and concentration of ARGs in urban settings • Several included studies suggest comparable ARG exposure through the air as in drinking water • A variety of sampling techniques and methodologies makes cross-study comparison difficult	No	3/9	2021	No	No

• Type of environmental AMR surveillance
  ○ Occurrence/Prevalence
  ○ Dissemination
• Environmental samples
  ○ Water
  ○ Soil/sediment
  ○ Air
  ○ Wildlife
• Type of AMR microorganism, AMR determinants or antimicrobial agents monitored
  ○ Microorganism
  ○ Resistant microorganism
  ○ Antimicrobial-resistant genes (ARGs)
	Trends in environmental AMR research identify a higher percentage of targeted methodology use over non-targeted methodology use, with the need for both method types necessary for the long-term understanding and surveillance of environmental AMR (Burch et al., 2022)
	• The review investigated recent methodological trends in environmental antimicrobial resistance research
	• The majority of research studies used targeted methods (>80%) and 33% used non-targeted methods, with the use of method type varying depending on environmental matrix studied
	• Targeted and non-targeted research are both necessary for the continued understanding of known threats and long-term frequency of threats for environmental antimicrobial resistance
		No	2/9	2020	No	No

Appendix 8: Documents excluded from the review

Document type	Hyperlinked title
European Council-related projects/documents	
EC Resolution	Official Journal of the European Union (2024), Council recommendation on stepping up EU actions to combat antimicrobial resistance in a One Health approach, Brussels: European Council.
EC-JRC Directive	European Commission Joint Research Council (EC-JRC) presently reviewing methods for new articles 17 and 22 in the EC urban wastewater treatment directive that include AMR and multi-pathogen WES.
EU Briefing	European Parliament (2022), The EU's zero pollution ambition: Moving towards a non-toxic environment, Brussels: European Parliamentary Research Service.
Website	Joint Programming Initiative on Antimicrobial Resistance (JPIAMR) studies: https://www.jpiamr.eu/projects/#/
Website	Global Sewage surveillance project and COMPARE project
Canadian experiments in labs or controlled environment	
Article	Contribution of Manure-Spreading Operations to Bioaerosols and Antibiotic Resistance Genes' Emission
Article	Descriptive analyses of bacterial communities in marine sediment microcosms spiked with fish wastes, emamectin benzoate, and oxytetracycline
Canadian research in built environments / domesticated populations	
Article	Bioaerosols Play a Major Role in the Nasopharyngeal Microbiota Content in Agricultural Environment
Article	Effect of Odor-Treatment Biofilter on Bioaerosols from an Indoor Wastewater Treatment Plant
Article	Examining the impact of agricultural drainage ditch management on in-stream bacterial communities involved in nitrogen cycling insights from the Environmental Change One Health Observatory (ECO_2)
Article	Dynamics of integron structures across a wastewater network – Implications to resistance gene transfer (Jurisdiction – Spain)
Article	Multiplexed Amplicon Sequencing Reveals High Sequence Diversity of Antibiotic Resistance Genes in Québec Sewers
Article	Antibiotic resistance gene sequencing is necessary to reveal the complex dynamics of immigration from sewers to activated sludge
Article	One Health, One Hive: A scoping review of honeybees, climate change, pollutants, and antimicrobial resistance

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