



Wastewater-Based Surveillance for Antimicrobial Resistance in Low- and Middle-Income Countries: A Narrative Review

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Abstract

Hospital-based antimicrobial resistance (AMR) surveillance misses information from asymptomatic individuals and the community at large. Wastewater-based (WBS) surveillance is a viable alternative. This review aimed to identify current WBS surveillance practices in Low- and Middle-Income Countries, outline areas of convergence and divergence, and identify gaps for future work. A literature search was carried out on Google Scholar using the queries “wastewater-based surveillance” OR “wastewater-based epidemiology” AND “antimicrobial resistance” OR “antibiotic resistance genes” AND “low- and middle-income countries”. We reduced the initial 957 papers to 31 articles after excluding reviews, meta-analyses, letters, conference abstracts, and commentaries. We assessed the 31 articles for methodology and findings. We found surveillance methods to be either culture-dependent or culture-independent. Culture—dependent methods required isolating and characterizing pathogens. Culture-independent methods included quantitative polymerase chain reaction (qPCR), high-throughput qPCR, metagenomic sequencing, Oxford Nanopore-based whole-genome sequencing, and measuring pharmaceutical residues and chemical markers. The studies agreed that AMR findings in wastewater properly reflected AMR patterns in the population. Disagreements remained over the best wastewater sampling method, the impact of tourism, and the effect of seasonal changes on local antimicrobial resistance profiles. The review shows a need for more longitudinal studies, as well as studies that link clinical AMR data and antibiotic use in a given environment to corresponding environmental data. It also provides an evidence base and research agenda for scaling WBS in resource-limited settings. Wastewater-based surveillance for AMR is a viable, cost-efficient option for monitoring AMR in resource-poor settings. Therefore, it should be integrated into the national antimicrobial resistance surveillance system. The government should also prioritise investment in portable sequencing platforms and rapid analytical methods to strengthen timely detection of emerging AMR threats.

Keywords: *Antimicrobial Resistance, Wastewater-Based Surveillance, Low- and Middle-Income Countries*

Introduction and Background

The transmission of infectious diseases demonstrates a close interconnection among humans, animals, and the environment. Consequently, effective control measures must account for

environmental factors. The One Health concept captures this perspective, emphasizing that human health is intrinsically linked to animal health and the shared environment. Among the issues One Health addresses is antimicrobial resistance (AMR). Antimicrobial-resistant organisms can rapidly disseminate through communities, the food supply, healthcare settings, soil, and water, thereby complicating the prevention and control of certain infections in both animals and humans.

Antimicrobial resistance (AMR) is a global public health problem (WHO, 2024). However, low- and middle-income countries (LMICs) bear the greater burden of morbidity and mortality due to AMR and are likely to continue to do so for some time (Murray et al., 2022; WHO, 2024). Challenges that drive AMR in LMICs include: high burden of infectious diseases, limited laboratory diagnostic capacity, inadequate surveillance systems, and inappropriate use of antibiotics in both humans and animals (Laxminarayan et al., 2013; O'Neill, 2016; Sriram et al., 2021). To track AMR, surveillance is necessary.

AMR surveillance is an important public health measure. It makes the early detection of changes in AMR incidence and prevalence possible and informs the early institution of appropriate interventions. Currently, the majority of AMR surveillance programs in LMICs are hospital-based. Individuals who show signs and symptoms of infectious diseases are the targets. The limitations of hospital-based surveillance include missing out on resistance in the community and environmental reservoirs (Ashley et al., 2018; Tacconelli et al., 2018). To mitigate the limitations of hospital-based AMR surveillance systems in LMICs, various alternative approaches have been explored, including Wastewater-based Surveillance (WBS) (Choi et al., 2018; Rusiñol et al., 2020; Medema et al., 2020; Sims & Kasprzyk-Hordern, 2020). The objectives of this review were to (1) identify the current WBS surveillance practices in LMICs, (2) outline areas of convergence and divergence, and (3) identify gaps in the literature.

Design and Methodology

Literature search

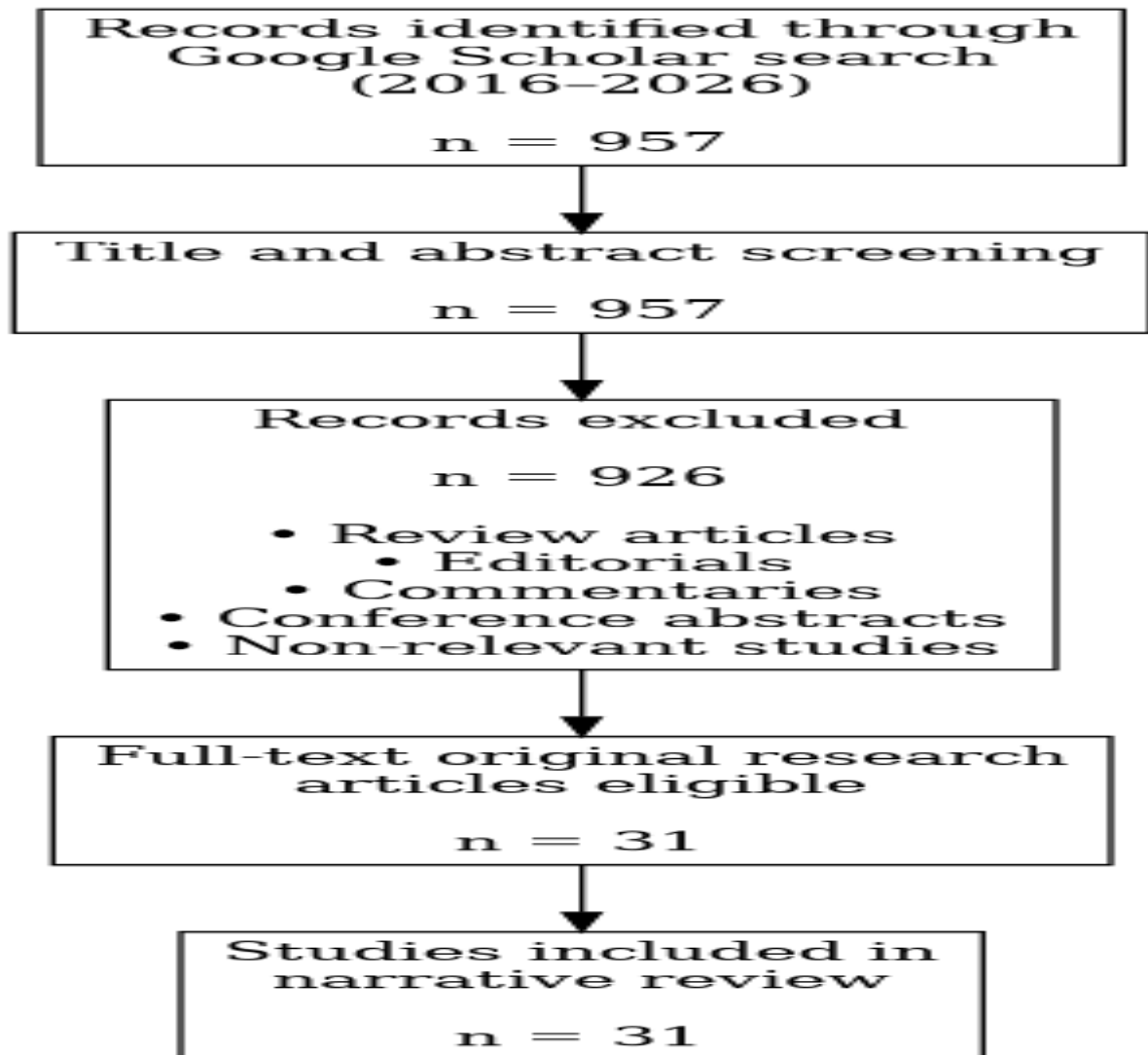
The queries “wastewater-based surveillance” OR “wastewater-based epidemiology” AND “antimicrobial resistance” OR “antibiotic resistance genes” AND “low- and middle-income countries” were used to conduct a Google Scholar search. The search returned 957 papers.

Inclusion and Exclusion Criteria

All 957 papers underwent title and abstract screening for original research articles, excluding reviews, meta-analyses, letters, conference abstracts, and commentaries. A final list of 31 articles was arrived at for this review.

Data Extraction and Analysis

The 31 articles reviewed for this paper were assessed for their methodology, laboratory work, and findings. Where appropriate, articles were compared for convergent and/or divergent findings, as well as gaps in the literature that future studies could address.



Results and Discussions

Surveillance methods used

The studies utilized various types of wastewater samples, such as household wastewater, fecal sludge from on-site sanitation systems, open drain samples, urban river water, hospital wastewater, and various types of waste from abattoirs and slaughterhouses (Muhammad et al., 2026; Capone et al., 2025; Heljanko et al., 2024; Stange et al., 2025; Yapi et al., 2025; Cheung et al., 2025; Gomi et al., 2024).

The methods used were either culture-dependent or culture-independent. Culture-dependent methods followed standard pathogen isolation and characterization procedures (Stange et al., 2025; Santosaningsih et al., 2023; Njoga et al., 2025; Rodríguez Guevara et al., 2025; Garba et al., 2026; Boum et al., 2026; Evoung Chandja et al., 2026; Alam et al., 2026). Culture-independent methods included quantitative polymerase chain reaction (qPCR), high-throughput qPCR, metagenomic sequencing, Oxford Nanopore-based Whole Genome Sequencing and measuring pharmaceutical residues and chemical markers (Cheung et al., 2025; Smith et al., 2024; Gomi et al., 2024; Secker et al., 2026; Freitas et al., 2026; Radwan et al., 2026; Kumari et al., 2025; Mtetwa et al., 2024; Deedat et al., 2025; Pimenta et al., 2025).

Areas of convergence

- i. Wastewater Antimicrobial Resistance (AMR) status as an indicator of population AMR profile

Several studies came to the same conclusion: that the status of wastewater and related environmental samples can serve as an indicator of population health with respect to AMR and infection trends (Muhammad et al., 2026; Ousmane et al., 2023; Smith et al., 2024; Capone et al., 2025; Jamtsho et al., 2026; Islam et al., 2024; Hassard et al., 2022). Household water in Nigeria, community wastewater in Niger, and Bangladesh showed antibiotic resistance genes and pathogen patterns that were comparable with community exposures (Muhammad et al., 2026; Ousmane et al., 2023; Saha et al., 2026). Studies from South Africa and India showed that resistome patterns in influent water correlated well with the urban-rural distribution of antibiotic use (Smith et al., 2024; Secker et al., 2026). These findings support the conclusion that WBS status is a cost-effective, non-invasive marker of infection trends and antibiotic use in the community.

- ii. Hospital and abattoir WBS as a reflection of AMR in human and animal health

Studies from Uganda, Nepal, Burkina Faso, Cameroon, Gabon, Egypt and Bangladesh reported high levels of ESBL, AmpC- β -lactamase and carbapenemase genes among *E. coli*, *Klebsiella* spp and other *Enterobacteriaceae* in hospital wastewater, often exceeding levels found in municipal wastewater (Stange et al., 2025; Thakali et al., 2021; Garba et al., 2026; Boum et al., 2026; Evoung Chandja et al., 2026; Radwan et al., 2026; Alam et al., 2026). Research in South African abattoirs also showed that the level of AMR markers in abattoir wastewater corresponded to the levels of antibiotic use in animal production settings (Heljanko et al., 2024; Santosaningsih et al., 2023). Thus, prioritizing surveillance of hospital and abattoir wastewater would provide a reflection of AMR in human and animal health settings.

iii. Pervasiveness of multidrug-resistant pathogens

The majority of studies found that multidrug-resistant (MDR) bacteria, such as extended-spectrum beta-lactamase (ESBL) producing bacteria, were found in wastewater, hospital effluents, and corresponding environmental samples (Stange et al., 2025; Cheung et al., 2025; Gomi et al., 2024; Njoga et al., 2025; Rodríguez Guevara et al., 2025; Garba et al., 2026; Boum et al., 2026; Evoung Chandja et al., 2026; Radwan et al., 2026; Alam et al., 2026). These studies found high levels of *E. coli*, *Klebsiella* spp, *Campylobacter*, *Enterobacter cloacae* complex, and other *Enterobacteriaceae* species in hospital wastewater that were resistant to various antibiotics. In addition, ESBL, AmpC- β -lactamase, and carbapenemase genes were frequently found in these bacteria (Garba et al., 2026; Evoung Chandja et al., 2026; Alam et al., 2026). Multidrug-resistant profiles of environmental isolates from rivers, hospital effluents, and municipal wastewater from Panama and South Africa showed both environmental and clinical origins of multidrug-resistant pathogens (Rodríguez Guevara et al., 2025; Smith et al., 2024).

Areas of divergence

A. Sampling method efficiency

There were mixed results in terms of the efficiency of the sampling methods used for detecting microorganisms and/or genetic determinants in wastewater. For example, the use of passive sampling methods such as activated carbon-based sampling devices and Moore Swabs was efficient for the detection of Antibiotic Resistance Genes (ARGs) at very low concentrations (Holzer et al., 2025; Yapi et al., 2025). In contrast, grab sampling at various sewer nodes and at sewer pumping stations using well-designed sampling protocols yielded high sensitivities for detecting *Salmonella typhi* in environmental samples as well as for estimating the number of typhoid cases in the community (Oktaria et al., 2025). Thus, the efficiency of the various sampling methods appears to be pathogen-specific.

B. Impact of tourism on local resistomes

A study conducted in Guadeloupe showed that international tourism did not have a significant impact on local AMR profiles (Pimenta et al., 2025). However, a study conducted in several cities in Brazil showed that tourism-related human mobility influenced the ARG and virulence gene composition found in the urban wastewater, thus influencing the local resistome pattern (Freitas et al., 2026).

C. Seasonal dynamics

Studies investigating seasonal changes in wastewater samples have produced different results. Studies conducted in Uganda and Mozambique showed some seasonal changes in the load of pathogens and ARGs, which were partly linked to hydrological changes due to rainfall (Stange et al., 2025; Capone et al., 2025). Metagenomic analyses conducted over several sampling campaigns in Brazil also revealed temporal changes in resistomes (Freitas et al., 2026). In contrast, studies conducted in South Africa and Bangladesh showed relatively stable resistomes over periods of sampling (Smith et al., 2024; Saha et al., 2026).

Identified research gaps

i. Paucity of longitudinal data

Most of the studies carried out were cross-sectional or short-term (Muhammad et al., 2026; Ousmane et al., 2023; Cheung et al., 2025; Gomi et al., 2024; Saha et al., 2026; Radwan et al., 2026). Only a few long-term WBS studies have been conducted. These were carried out in Mozambique, Indonesia, and Brazil (Capone et al., 2025; Murni et al., 2024; Freitas et al., 2026). Long-term wastewater-based surveillance studies are urgently needed to understand AMR dynamics and to assess the impact of interventions in LMICs.

ii. Lack of linked metadata

There is a need for studies using WBS for AMR detection and resistome characterization to include information on associated clinical AMR data. So far, only a few hospital-based studies have information on associated clinical microbiology data from the pharmacy and/or from patient samples and have linked this to information on the corresponding hospital effluent resistomes (Deedat et al., 2025; Garba et al., 2026).

Conclusion

This review identified wastewater-based surveillance for AMR as a viable, cost-efficient option for monitoring AMR in resource-poor settings, providing surveillance data and serving as an early warning system for emerging resistance before it leads to treatment failure in clinical settings. However, to maximize public health impact, more longitudinal studies are needed, as well as studies that provide clinically linked metadata. This paper provides an LMIC-focused synthesis of methodological approaches, convergent and divergent findings, and critical evidence gaps in wastewater-based AMR surveillance. This provides an evidence base and research agenda for scaling WBS in resource-limited settings.

Recommendations

1. Wastewater-based surveillance (WBS) should be formally integrated into the Nigerian national antimicrobial resistance surveillance system, with national public health laboratories and reference centres designated as coordinating hubs for metagenomic analysis and data interpretation. Such integration would enable environmental surveillance data to be included in public health decision-making.
2. The government, through the Ministry of Health, should prioritise investment in portable sequencing platforms and rapid analytical methods, e.g., Nanopore-based whole-genome sequencing. This will strengthen the timely detection of emerging AMR threats.

References

- Alam, M. S., Hossain, H., Das, S., Rahman, A., Brishty, K. A., & Rahman, M. M. (2026). Biofilm properties and multidrug resistance profile of *Klebsiella pneumoniae*, *Escherichia coli*, and *Staphylococcus aureus* isolated from hospital wastewater in Bangladesh. *Journal of Water and Health*, 24(5), 651–665. <https://doi.org/10.2166/wh.2026.075>
- Ashley, E. A., Recht, J., & Verma, S. (2018). Harnessing data to improve antimicrobial use and resistance surveillance in low- and middle-income countries. *BMJ Global Health*, 3(6), e000914. <https://doi.org/10.1093/jac/dky487>
- Boum, Y., Goufack, R., Ezzo, L., & Gonsu, H. (2026). Multidrug-resistant bacteria in hospital effluents: Evidence from a tertiary hospital in Cameroon and implications for One Health antimicrobial resistance control. *Health Sciences and Disease*, 27(Suppl 1), 92–99. <https://doi.org/10.5281/zenodo.18314940>
- Capone, D., Chiluvane, M., Cumbane, V., Dalton, J., Holcomb, D., Kowalsky, E., Lai, A., Mataveia, E., Monteiro, V., Rao, G., Viegas, E., & Brown, J. (2025). Environmental pathogen surveillance in cities without universal conventional wastewater infrastructure. <https://doi.org/10.1371/journal.pgph.0004994>
- Cheung, S., Zhou, N. A., Ruhanya, V., Jesser, K. J., Nezomba, I., Musvibe, J., Manyisa, B.,

- Nyandoro, G., Chibukira, P., Mukaratirwa, A., Muserere, S. T., Masunda, K., Ong, A., & Meschke, J. S. (2025). Characterization of enteric pathogens in Harare, Zimbabwe using environmental surveillance and metagenomics. *Journal of Water and Health*, 23(4), 477–492. <https://doi.org/10.2166/wh.2025.333>
- Choi, P. M., Tschärke, B. J., Donner, E., O'Brien, J. W., Grant, S. C., Kaserzon, S., et al. (2018). Wastewater-based epidemiology biomarkers: Past, present and future. *TrAC Trends in Analytical Chemistry*, 105, 453–469. <https://doi.org/10.1016/j.trac.2018.06.004>
- Deedat, F. Z., Faya, A. M., Gumbi, B. P., Johnston, D. M. G., Karpoormath, R., & Essack, S. Y. (2025). The association between antibiotic use in hospitals and residual antibiotic concentrations in hospital effluents: A pilot study. *JAC-Antimicrobial Resistance*, 7(3), dlaf070. <https://doi.org/10.1093/jacamr/dlaf070>
- Evoung Chandja, W. B., Dikoumba, A.-C., Mbehang Nguema, P. P., Onanga, R., Falque, G., Mouanga-Ndzime, Y., Godreuil, S., & Ngoubangoye, B. (2026). Antibiotic resistance and phylogenetic diversity of *Escherichia coli* isolated from hospital wastewater in Gabon. *Microorganisms*, 14(5), Article 987. <https://doi.org/10.3390/microorganisms14050987>
- Freitas, J. F., Oliveira, T. T., & Agnez-Lima, L. F. (2026). Longitudinal wastewater metagenomics reveals distinct environmental and anthropogenic associations with resistance, virulence, and viral communities. *Environmental Pollution*, 397, Article 127943. <https://doi.org/10.1016/j.envpol.2026.127943>
- Garba, Z., Natama, H. M., Sylla, A., Lompo, P., Kouamé-Sina, M. S., Bonkougou, I. J. O., Kakou-Ngazoa, S., Tinto, H., Barro, N., Kantele, A., & Haukka, K. (2026). Detection of ESB, AmpC- β -lactamase and carbapenemase-encoding genes among *Escherichia coli* and *Klebsiella* spp. from clinical samples and hospital wastewater in Burkina Faso. *Journal of Water and Health*, 24(4), 592–606. <https://doi.org/10.2166/wh.2026.222>
- Gomi, R., Matsumura, Y., Yamamoto, M., Tanaka, M., Komakech, A. J., Matsuda, T., & Harada, H. (2024). Genomic surveillance of antimicrobial-resistant *Escherichia coli* in fecal sludge and sewage in Uganda. *Water Research*, 248, Article 120830. <https://doi.org/10.1016/j.watres.2023.120830>
- Hassard, F., Smith, T. R., Boehm, A. B., Nolan, S., O'Mara, O., Di Cesare, M., & Graham, D.

- (2022). Wastewater surveillance for rapid identification of infectious diseases in prisons. *The Lancet Microbe*, 3(8), e556–e557. [https://doi.org/10.1016/S2666-5247\(22\)00154-9](https://doi.org/10.1016/S2666-5247(22)00154-9)
- Heljanko, V., Karama, M., Kymäläinen, A., Kurittu, P., Johansson, V., Tiwari, A., Nyirenda, M., Malahlela, M., & Heikinheimo, A. (2024). Wastewater and environmental sampling holds potential for antimicrobial resistance surveillance in food-producing animals - a pilot study in South African abattoirs. *Frontiers in Veterinary Science*, 11, Article 1444957. <https://doi.org/10.3389/fvets.2024.1444957>
- Holzer, C., Ho, J., Tiehm, A., & Stange, C. (2025). Wastewater monitoring - passive sampling for the detection of SARS-CoV-2 and antibiotic resistance genes in wastewater. *Science of the Total Environment*, 959, Article 178244. <https://doi.org/10.1016/j.scitotenv.2024.178244>
- Islam, M. A., Kumar, R., Sharma, P., Zhang, S., Bhattacharya, P., & Tiwari, A. (2024). Wastewater-based surveillance of mpox (monkeypox): An early surveillance tool for detecting hotspots. *Current Pollution Reports*, 10, 312–325. <https://doi.org/10.1007/s40726-024-00299-6>
- Jamtsho, N., Thomson, T. N., Lane, C. R., Mercoulia, K., Rimal, G., Howden, B. P., & Rai, A. (2026). *Escherichia coli* in water samples at Bhutan's National Food Testing Laboratory: Baseline findings and scoping for antimicrobial resistance surveillance. *Journal of Water and Health*, 24(6), 905–912. <https://doi.org/10.2166/wh.2026.052>
- Kumari, L. S., Siriwardhana, D. M., Liyanapathirana, V., Jinadasa, R., & Wijesinghe, P. (2025). Rapid whole-genome sequencing for AMR surveillance in low- and middle-income countries: Oxford Nanopore Technology reveals multidrug-resistant *Enterobacter cloacae* complex from dairy farms in Sri Lanka. *BMC Veterinary Research*, 21, Article 351. <https://doi.org/10.1186/s12917-025-04800-1>
- Laxminarayan, R., Duse, A., Wattal, C., Zaidi, A. K. M., Wertheim, H. F. L., Sumpradit, N., et al. (2013). Antibiotic resistance—the need for global solutions. *The Lancet Infectious Diseases*, 13(12), 1057–1098. [https://doi.org/10.1016/S1473-3099\(13\)70318-9](https://doi.org/10.1016/S1473-3099(13)70318-9)
- Medema, G., Been, F., Heijnen, L., & Petterson, S. (2020). Implementation of environmental surveillance for SARS-CoV-2 virus to support public health decisions: Opportunities and challenges. *Current Opinion in Environmental Science & Health*, 17, 49–71. <https://doi.org/10.1016/j.coesh.2020.09.006>

- Mtetwa, H. N., Amoah, I. D., Kumari, S., Bux, F., & Reddy, P. (2024). Optimisation of analytical methods for tuberculosis drug detection in wastewater: A multinational study. *Heliyon*, 10(9), Article e30720. <https://doi.org/10.1016/j.heliyon.2024.e30720>
- Muhammad, Z., Adamu, M. T., Garba, L., Umar, T. A., Adamu, S. S., Yusuf, I., & Aworh, M. K. (2026). Household wastewater as a sentinel for community-level antimicrobial resistance: A cross-sectional study in Gombe, Nigeria. *Scientific Reports*, 16, Article 4535. <https://doi.org/10.1038/s41598-025-29778-6>
- Murni, I. K., Oktaria, V., McCarthy, D. T., Supriyati, E., Nuryastuti, T., Handley, A., Donato, C. M., Wiratama, B. S., Dinari, R., Laksono, I. S., Thobari, J. A., & Bines, J. E. (2024). Wastewater-based epidemiology surveillance as an early warning system for SARS-CoV-2 in Indonesia. *PLOS ONE*, 19(7), Article e0307364. <https://doi.org/10.1371/journal.pone.0307364>
- Murray, C. J. L., Ikuta, K. S., Sharara, F., Swetschinski, L., Robles Aguilar, G., Gray, A., et al. (2022). Global burden of bacterial antimicrobial resistance in 2019: A systematic analysis. *The Lancet*, 399(10325), 629–655. [https://doi.org/10.1016/S0140-6736\(21\)02653-2](https://doi.org/10.1016/S0140-6736(21)02653-2)
- Njoga, E. O., Mshelbwala, P. P., Ogugua, A. J., Enemuo-Edo, E. C., Onwumere-Idolor, O. S., Ogunniran, T. M., Bernard, S. N., Ugwunwarua, J. C., Anidobe, E. C., Okoli, C. E., Godwin, E., Enem, S. I., & Oguttu, J. W. (2025). *Campylobacter* colonisation of poultry slaughtered at Nigerian slaughterhouses: Prevalence, antimicrobial resistance, and risk of zoonotic transmission. *Tropical Medicine and Infectious Disease*, 10(9), Article 265. <https://doi.org/10.3390/tropicalmed10090265>
- Oktaria, V., Murni, I. K., Handley, A., Donato, C. M., Nuryastuti, T., Supriyati, E., McCarthy, D. T., Watts, E., Dinari, R., Sari, H. M., Thobari, J. A., Laksono, I. S., & Bines, J. E. (2025). Environmental surveillance for *Salmonella Typhi* to detect the typhoid burden in Yogyakarta, Indonesia. *International Journal of Hygiene and Environmental Health*, 266, Article 114572. <https://doi.org/10.1016/j.ijheh.2025.114572>

- O'Neill, J. (2016). Tackling drug-resistant infections globally: Final report and recommendations. *Archives of Pharmacy Practice*, 7(3). <https://doi.org/10.4103/2045-080x.186181>
- Ousmane, S., Kollo, I. A., Jambou, R., Boubacar, R., Arzika, A. M., Maliki, R., Amza, A., Liu, Z., Lebas, E., Colby, E., Zhong, L., Chen, C., Hinterwirth, A., Doan, T., Lietman, T. M., & O'Brien, K. S. (2023). Wastewater-based surveillance of antimicrobial resistance in Niger: An exploratory study. *The American Journal of Tropical Medicine and Hygiene*, 109(4), 725–729. <https://doi.org/10.4269/ajtmh.23-0204>
- Pimenta, M., Alexa, M., Mabandza, D. B., Dulaurent, S., Huynh, B.-T., Gaschet, M., Opatowski, L., Breurec, S., Ploy, M.-C., & Dagot, C. (2025). Wastewater-based AMR surveillance associated with tourism on a Caribbean island (Guadeloupe). *Journal of Global Antimicrobial Resistance*, 43, 27–34. <https://doi.org/10.1016/j.jgar.2025.03.010>
- Radwan, H. M., El Menofy, N. G., Tharwat, E. K., Mysara, M., & Radwan, S. M. R. (2026). Metagenomic profiling of microbial communities and the resistome within Egyptian hospital wastewater and tap water. *Scientific Reports*, 16, Article 13894. <https://doi.org/10.1038/s41598-026-49481-4>
- Rodríguez Guevara, G. A., Michelangelli, E., Medina-Sánchez, J. R., Mejía-Meléndez, F., Espino, C. I., Moreno P., J. E., Martínez Torres, A. O., & Querol-Audí, J. (2025). Determination of phylogroups, pathotypes and antibiotic resistance profiles of *E. coli* isolates from freshwater and wastewater in the City of Panama. *Pathogens*, 14(7), Article 617. <https://doi.org/10.3390/pathogens14070617>
- Rusiñol, M., Medema, G., & Blaak, H. (2020). The potential of wastewater-based epidemiology to track antimicrobial resistance. *Current Opinion in Environmental Science & Health*, 17, 43–48. <https://doi.org/10.1038/s44221-023-00093-6>
- Saha, A., Hasan, R., Ami, J. Q., Hasan, M. M., Amin, N., Haque, R., Rahman, M., Jahan, F., Hasan, R., Liu, P., Moe, C. L., Hossain, M. E., & Rahman, M. Z. (2026). Genetic diversity and occurrence of antibiotic resistance genes from community wastewater in Dhaka and Cox's Bazar, Bangladesh. *One Health*, 22, Article 101301. <https://doi.org/10.1016/j.onehlt.2025.101301>
- Santosaningih, D., Fadriyana, A. P., David, N. I., & Ratridewi, I. (2023). Prevalence and

- abundance of beta-lactam resistance genes in hospital wastewater and Enterobacterales wastewater isolates. *Tropical Medicine and Infectious Disease*, 8(4), Article 193. <https://doi.org/10.3390/tropicalmed8040193>
- Secker, B., Nayak, A., Husain, A. A., Arora, S., Nag, A., Shrivastava, S. K., Singer, A. C., Gomes, R. L., Acheampong, E., Chidambaram, S. B., Bhatnagar, T., Vetrivel, U., Kashyap, R. S., Atterbury, R. J., Blanchard, A. M., & Monaghan, T. M. (2026). Metagenomic insights into the urban–rural variation of antimicrobial resistance and pathogen reservoirs in untreated wastewater from central India. *Frontiers in Microbiology*, 16, Article 1722229. <https://doi.org/10.3389/fmicb.2025.1722229>
- Sims, N., & Kasprzyk-Hordern, B. (2020). Future perspectives of wastewater-based epidemiology: Monitoring infectious disease spread and resistance to the community level. *Environment International*, 139, 105689. <https://doi.org/10.1016/j.envint.2020.105689>
- Smith, A. M., Ramudzulu, M., Munk, P., Avot, B. J. P., Esterhuyse, K. C. M., van Blerk, N., Kwenda, S., & Sekwadi, P. (2024). Metagenomics analysis of sewage for surveillance of antimicrobial resistance in South Africa. *PLOS ONE*, 19(8), Article e0309409. <https://doi.org/10.1371/journal.pone.0309409>
- Stange, C., Kalyetsi, R., Owokuhaisa, J., Ntaro, M., Leon, A., Hunter, P. R., Tiehm, A., & Mulogo, E. M. (2025). Monitoring of antimicrobial resistance in hospital, municipal, and treated wastewater in Mbarara, Uganda. *Journal of Global Antimicrobial Resistance*, 45, 100–106. <https://doi.org/10.1016/j.jgar.2025.09.002>
- Sriram, A., Kalanxhi, E., Kapoor, G., Craig, J., Balasubramanian, R., Brar, S., Criscuolo, N., Hamilton, A., Klein, E., Tseng, K., Van Boeckel, T., & Laxminarayan, R. (2021). *State of the world's antibiotics 2021: A global analysis of antimicrobial resistance and its drivers*. Center for Disease Dynamics, Economics & Policy. https://cddep.org/wp-content/uploads/2021/02/SOWA_01_02_2021_Low-Res.pdf
- Tacconelli, E., Sifakis, F., Harbarth, S., Schrijver, R., van Mourik, M., Voss, A., et al. (2018). Surveillance for control of antimicrobial resistance. *The Lancet Infectious Diseases*, 18(3), e99–e106. [https://doi.org/10.1016/S1473-3099\(17\)30485-1](https://doi.org/10.1016/S1473-3099(17)30485-1)
- Thakali, O., Malla, B., Tandukar, S., Sthapit, N., Raya, S., Furukawa, T., Sei, K., Sherchand, J.

- B., & Haramoto, E. (2021). Release of antibiotic-resistance genes from hospitals and a wastewater treatment plant in the Kathmandu Valley, Nepal. *Water*, 13(19), Article 2733. <https://doi.org/10.3390/w13192733>
- World Health Organization. (2024). *Global Antimicrobial Resistance and Use Surveillance System (GLASS) Report 2024*. World Health Organization. <https://www.who.int/data/gho/data/themes/topics/topic-details/GHO/global-antimicrobial-resistance-surveillance-system-glass>
- Yapi, E. A. M., Mossoun, A. M., Zan-Bi, T. T., Dindé, A. O., Gossé, L. G., Vakou, S. N., Gnaly, G., Yao, E. K., Coulibaly, J. K., Sidibé, M., Tiomé, D. K., Zobo, A. A., Danho, T., Yapi, C. B., Yapi, R., Bibby, K., Gheri, B. M., Burgess, T., Amuguni, H., Nutter, F., Saila-Ngita, D., Gass, J., Konan, D. A. O., & Lantagne, D. (2025). Expanding access to wastewater surveillance beyond sewer networks: Effectiveness of active and passive sampling of waste effluent streams in Côte d'Ivoire. *PLOS Water*, 4(6), Article e0000290. <https://doi.org/10.1371/journal.pwat.0000290>