ISSN: 2181-3337 | SCIENTISTS.UZ VOLUME 5 ISSUE 11 | NOVEMBER 2026

ANTIMICROBIAL RESISTANCE AND SURVEILLANCE SYSTEMS FOR MONITORING RESISTANCE TO ANTIMICROBIAL DRUGS

Otamuratova Nargiza[1], Abdukhalilova Gulnora[2], Akhmedova Dilshoda[3], Yesbosinova Laura[4], Saftiyarov Rafael[5]

DSc, Senior Lecturer, Department of Epidemiology, Tashkent State Medical University; Senior Researcher, Republican Specialized Scientific-Practical Medical Center for Epidemiology, Microbiology, Infectious and Parasitic Diseases, Tashkent, Uzbekistan.[1]

DSc, Head, Antimicrobial Resistance Center, Republican Specialized Scientific-Practical Medical Center of Epidemiology, Infectious and Parasitic Diseases, Tashkent, Uzbekistan.[2]

PhD, Senior Researcher, Republican Specialized Scientific-Practical Medical Center of Epidemiology, Infectious and Parasitic Diseases, Tashkent, Uzbekistan.[3]

Master's student, Department of Epidemiology, Tashkent State Medical University, Tashkent, Uzbekistan.[4]

Master's student, Department of Epidemiology, Tashkent State Medical University, Tashkent, Uzbekistan.[5]

DOI: 10.67620/sai.511d0001

ABSTRACT

Background: Antimicrobial resistance (AMR) limits treatment options and requires coordinated surveillance. Objective: To synthesize mechanisms of bacterial antibiotic resistance and approaches to AMR surveillance, with relevance to Uzbekistan. Methods: A narrative thematic synthesis was prepared from the 29 scholarly and institutional sources cited in the existing manuscript; no new systematic search or primary data collection was undertaken. Results: The literature describes target modification, antibiotic inactivation, efflux, reduced permeability, horizontal gene transfer, and biofilm-associated tolerance. Surveillance approaches include standardized human clinical reporting through the World Health Organization (WHO) Global Antimicrobial Resistance and Use Surveillance System (GLASS), regional networks, and complementary One Health coordination across human, animal, and environmental sectors. Conclusion: Improved laboratory capacity, data quality, antimicrobial stewardship, infection prevention, and cross-sector collaboration are central priorities for strengthening AMR surveillance and response.

ACCEPTED

23.11.26

Keywords: *antimicrobial resistance; antibiotic resistance; GLASS; One Health; epidemiological surveillance; Uzbekistan.*

CC BY

Introduction

Antimicrobial resistance (AMR) is a major public-health challenge because it can compromise the treatment of bacterial infections, prolong illness, and increase pressure on health systems. Antibiotics transformed the management of infections, yet resistance can emerge through bacterial adaptation and spread under selective pressure. The World Health Organization (WHO) identifies surveillance, infection prevention, awareness, optimized antimicrobial use, and research as interconnected priorities (World Health Organization, 2015).

Bacterial antibiotic resistance is the ability to survive exposure to an antibiotic that would otherwise inhibit growth or kill susceptible organisms. Natural selection and genetic exchange contribute to its emergence, while inappropriate antibiotic use can accelerate the selection of resistant populations (Baquero, 2021; Fedorova et al., 2021; Munita & Arias, 2016). Resistant infections also create clinical and economic challenges through more complex treatment and resource use (Darina et al., 2019; Huemer et al., 2020).

Because resistant organisms and resistance genes move among hospitals, communities, animals, food systems, and the environment, an effective response requires information beyond individual clinical encounters. This review synthesizes established resistance mechanisms, human and multisectoral surveillance systems, and their implications for AMR monitoring priorities in Uzbekistan.

Methods

This article is a narrative literature review based on the 29 scholarly publications and institutional reports already cited in the original manuscript, published between 2009 and 2023. The sources include mechanistic and clinical studies, reviews of environmental and veterinary resistance, and WHO documents on AMR policy and surveillance. Relevant material was grouped into four themes: bacterial resistance mechanisms; clinical and environmental reservoirs; surveillance architectures; and practical implications for national monitoring. Publication years were counted directly from the reference list for a descriptive chart; no bibliometric search was performed.

Findings were synthesized descriptively, with emphasis on concepts supported by the cited sources rather than pooled effect estimates. No original laboratory observations, patient-level data, formal database search, prespecified screening process, or study-quality appraisal were available for this revision. Accordingly, the findings should be read as a thematic overview, not as a systematic review or meta-analysis.

Results

Mechanisms of antibiotic resistance

The reviewed literature identifies several complementary mechanisms. Mutations or acquired genes can alter antibiotic targets; bacterial enzymes, including β-lactamases, can inactivate drug molecules; and lower membrane permeability or active efflux can reduce intracellular antibiotic exposure (Gabibov et al., 2020; Munita & Arias, 2016; Parrino et al., 2020). These mechanisms may coexist, contributing to resistance against multiple drug classes.

Horizontal gene transfer via plasmids and other mobile genetic elements can disseminate resistance determinants between microorganisms (Lerminiaux & Cameron, 2019). Biofilms also complicate treatment because their structure and microbial physiology can limit drug activity and promote survival (Rather et al., 2021). Persistence and genetic resistance are related but distinct phenomena, both relevant to recurrent or difficult-to-treat infection (Eisenreich et al., 2022). Molecular assays designed to detect resistance genes may support more rapid characterization alongside phenotypic susceptibility testing (Mokhov et al., 2023). Table 1 summarizes the principal mechanisms and their implications for surveillance.

ISSN: 2181-3337 | SCIENTISTS.UZ

Table 1

Major antibiotic-resistance mechanisms and implications for surveillance

Mechanism	Mechanistic description	Surveillance relevance
Target modification	Altered antibiotic-binding sites (Munita & Arias, 2016).	Interpret organism–drug susceptibility patterns; investigate the mechanism when indicated.
Enzymatic inactivation	Bacterial enzymes, including β-lactamases, inactivate drugs (Gabibov et al., 2020).	Use susceptibility testing to identify resistance phenotypes; add mechanism-specific tests as appropriate.
Reduced drug accumulation	Efflux pumps and lower cell-envelope permeability reduce intracellular exposure (Parrino et al., 2020).	Recognize that multidrug resistance may have more than one underlying mechanism.
Horizontal gene transfer	Plasmids and other mobile elements spread resistance determinants (Lerminiaux & Cameron, 2019).	Where available, molecular tests complement phenotypic monitoring of resistance.
Biofilm-associated tolerance	Biofilm structure and physiology can reduce antibiotic effectiveness (Rather et al., 2021).	Distinguish biofilm-related treatment tolerance from confirmed heritable resistance.

Note. This table summarizes published evidence rather than original laboratory findings. Surveillance relevance is a practical interpretation of the cited literature.

Clinical consequences and priority settings

Healthcare facilities are important sites for detecting and preventing resistant infections. Antimicrobial exposure, vulnerable patients, and opportunities for transmission make infection prevention and microbiological monitoring essential (Xia et al., 2016). The original manuscript highlights methicillin-resistant Staphylococcus aureus, resistant Gram-negative pathogens, and resistant enterococci as clinically relevant organisms (Denisenko & Alyoshukina, 2020; Miklis et al., 2021). Reliable organism identification and antimicrobial susceptibility testing can support treatment decisions and local stewardship.

Strategies proposed in the literature extend beyond conventional antibiotic development. Research has considered bacteriophages and combinations of photodynamic and antibiotic treatments, although these approaches should not be treated as established substitutes for routine evidence-based care (Popova & Kozhevnikov, 2019; Willis et al., 2022). Reviews also discuss technical approaches to limiting resistance in environmental and treatment settings (Bairán et al., 2020).

Environmental and animal reservoirs

AMR selection and transmission are not confined to clinical medicine. Veterinary antibiotic use and antimicrobial residues in animal waste can affect agricultural soils and crops (Kuppusamy et al., 2018; Tasho & Cho, 2016). Investigations of soil-to-food pathways, plant-associated resistomes, and antibiotic uptake by crops illustrate the environmental dimensions of the problem (Cerqueira et al., 2019; Chen et al., 2019; Pan & Chu, 2017).

Pharmaceutical production waste and contaminated water can introduce antimicrobial compounds into ecosystems, reinforcing the need for environmental risk management (Fick et al., 2009; Prozherina, 2017). Environmental AMR involves complex ecological interactions rather than a simple one-way transfer to humans (Larsson & Flach, 2022). The food-safety perspective likewise supports coordinated

ISSN: 2181-3337 | SCIENTISTS.UZ

measures spanning agriculture, public health, and environmental protection (World Health Organization Regional Office for Europe, 2011).

International surveillance systems and integrated reporting

The WHO Global Antimicrobial Resistance and Use Surveillance System (GLASS) provides a standardized framework for reporting AMR information from human clinical surveillance. Quality-assured laboratory identification, antimicrobial susceptibility testing, data management, and regular analysis are necessary for interpreting resistance trends (World Health Organization, 2023). Regional surveillance, including the Central Asian and Eastern European Surveillance of Antimicrobial Resistance (CAESAR) initiative, further supports comparable information and capacity strengthening (World Health Organization Regional Office for Europe, 2018).

One Health complements clinical surveillance by recognizing interdependence among human health, animal health, and environmental systems. These sectors require coordination and appropriate data-sharing arrangements, but they are not necessarily part of a single GLASS database. Figure 1 illustrates the distinct yet connected pathways from human clinical laboratory results and multisectoral information toward stewardship, infection prevention, and policy responses (World Health Organization, 2023). Table 2 compares these approaches and their interpretive boundaries.

Table 2

Comparison of antimicrobial resistance surveillance approaches

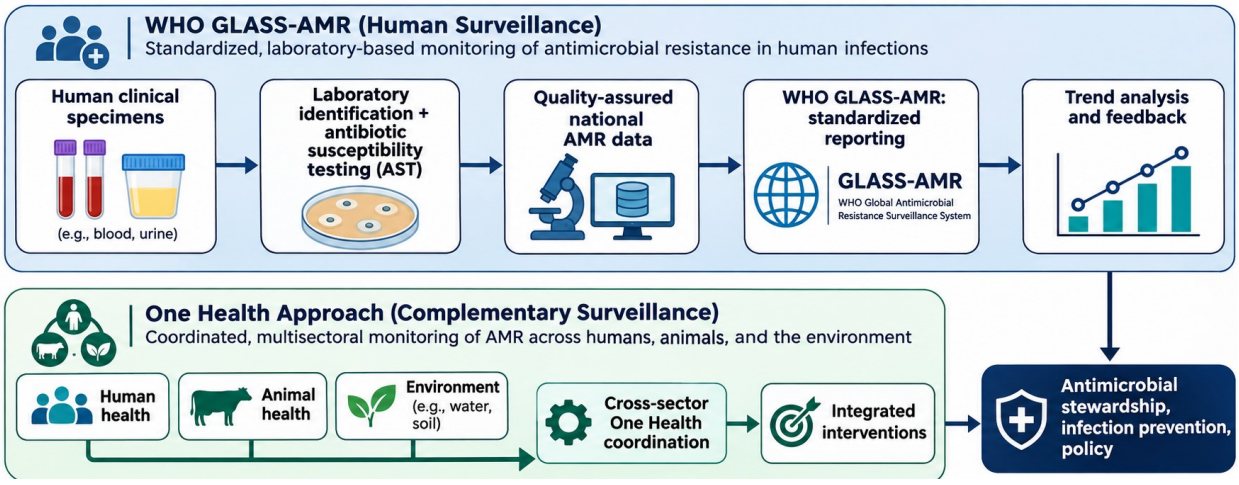
Approach	Principal data and function	Important distinction
WHO GLASS-AMR	Quality-assured human clinical laboratory identification and antimicrobial susceptibility data; standardized reporting (World Health Organization, 2023).	Focuses on human clinical surveillance; it is not a single repository for all One Health data.
CAESAR	Regional reporting and capacity support for clinically relevant AMR in Central Asia and Eastern Europe (World Health Organization Regional Office for Europe, 2018).	Comparisons require attention to participating sites, sampling and data quality.
One Health coordination	Links complementary information from human health, animals, agriculture, and the environment (Larsson & Flach, 2022).	Sector-specific methods and denominators differ; combined interpretation requires coordination.

Note. The comparison describes surveillance functions discussed in the cited literature; it is not a performance evaluation of any country's surveillance system.

ISSN: 2181-3337 | SCIENTISTS.UZ

Figure 1

Integrated antimicrobial resistance surveillance: GLASS-AMR and One Health pathways

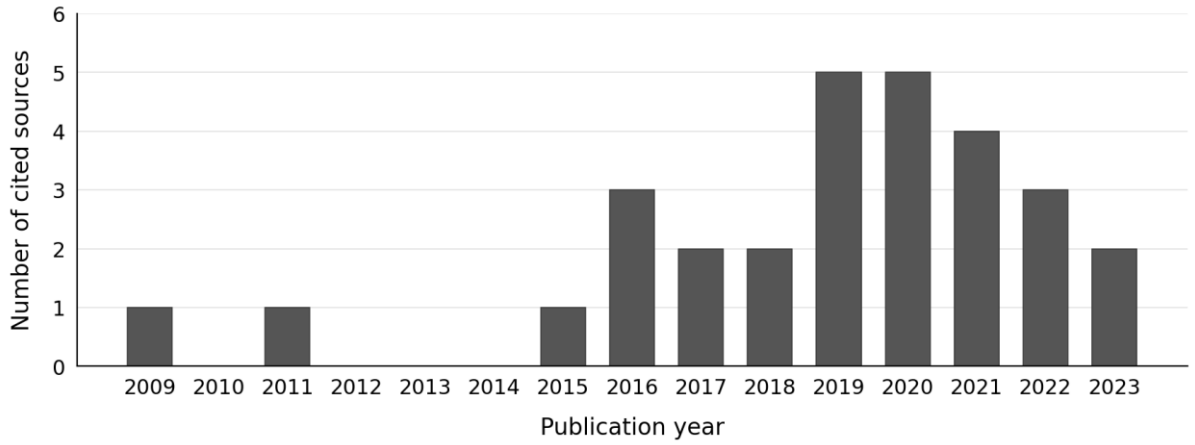


Note. Original illustration created for the manuscript. The human GLASS-AMR surveillance pathway and complementary One Health coordination are conceptually informed by World Health Organization (2023). They do not represent a single shared database.

The reference set spans 2009–2023; its publication-year distribution is shown in Figure 2. These counts describe source metadata, not the global rate of resistance.

Figure 2

Publication-year distribution of sources cited in the narrative review



Note. Counts were derived from publication years in the 29 references of this manuscript, including institutional reports. The figure does not represent AMR prevalence, incidence, or global publication trends.

Discussion

The synthesis indicates that surveillance is most useful when laboratory findings lead to timely action. Standardized testing, consistent organism and antibiotic definitions, internal quality assurance, and complete clinical metadata improve the interpretability of routine AMR data. In turn, feedback to prescribers and infection-control teams can connect observed resistance patterns with antimicrobial stewardship and prevention programs (World Health Organization, 2015, 2023).

The evidence also supports a cross-sector response. Human clinical results alone cannot characterize resistance reservoirs in livestock, crops, soil, and water; however, combining unlike datasets without attention to sampling and comparability can be misleading. A practical One Health model therefore requires sector-specific surveillance linked by governance, common priorities, and coordinated

ISSN: 2181-3337 | SCIENTISTS.UZ

interpretation rather than assuming every sector uses identical reporting methods (Larsson & Flach, 2022; World Health Organization Regional Office for Europe, 2011).

For Uzbekistan, the main priorities identified by this review are to strengthen clinical microbiology and susceptibility-testing capacity, develop dependable reporting from participating facilities, train laboratory and surveillance personnel, and integrate results into prescribing and infection-control decisions. Collaboration among health, veterinary, agricultural, and environmental institutions could provide a foundation for broader One Health monitoring. The regional CAESAR experience offers a relevant surveillance framework, but implementation and national coverage should be assessed with current country-specific data rather than inferred from regional reports (World Health Organization Regional Office for Europe, 2018).

This review has limitations. Its source set was inherited from an existing manuscript rather than obtained through a reproducible search, and no formal risk-of-bias assessment was possible. The cited publications also differ in design, setting, and date. Consequently, the thematic findings describe established concepts and program models but do not provide new prevalence estimates, evaluate Uzbekistan's present surveillance performance, or establish the comparative effectiveness of particular interventions.

Conclusion

Antimicrobial resistance results from interconnected microbial, clinical, and environmental processes. A coherent surveillance response combines quality-assured susceptibility testing and standardized human reporting with appropriately coordinated One Health activities. For Uzbekistan, strengthening laboratory networks, reliable data analysis, antimicrobial stewardship, infection prevention, and intersectoral governance offers a defensible direction for future AMR monitoring. Prospective assessment of national coverage and data quality will be needed to measure progress.

REFERENCES

1. Bairán, G., Rebollar-Pérez, G., Chávez-Bravo, E., & Torres, E. (2020). Treatment processes for microbial resistance mitigation: The technological contribution to tackle the problem of antibiotic resistance. *International Journal of Environmental Research and Public Health, 17*(23), Article 8866. https://doi.org/10.3390/ijerph17238866
2. Baquero, F. (2021). Threats of antibiotic resistance: An obliged reappraisal. *International Microbiology, 24*(4), 499–506. https://doi.org/10.1007/s10123-021-00184-y
3. Cerqueira, F., Matamoros, V., Bayona, J. M., Berendonk, T. U., Elsinga, G., Hornstra, L. M., & Piña, B. (2019). Antibiotic resistance gene distribution in agricultural fields and crops: A soil-to-food analysis. *Environmental Research, 177*, Article 108608. https://doi.org/10.1016/j.envres.2019.108608
4. Chen, Q.-L., Cui, H.-L., Su, J.-Q., Peñuelas, J., & Zhu, Y.-G. (2019). Antibiotic resistomes in plant microbiomes. *Trends in Plant Science, 24*(6), 530–541. https://doi.org/10.1016/j.tplants.2019.02.010
5. Darina, M. G., Svetlichnaya, Y. S., Tatarkin, V. V., Movchan, K. N., Morozov, Y. M., Chernov, K. E., Artyushin, B. S., Romanenko, N. S., Yakovenko, T. V., & Iskhakov, R. B. (2019). Monitoring of antibiotic resistance as a tool to improve the quality of medical care. *Clinical Microbiology and Antimicrobial Chemotherapy, 21*(S1), 24.
6. Denisenko, V. V., & Alyoshukina, A. V. (2020). Mass spectrometric study of antibiotic resistance of Staphylococcus aureus and Pseudomonas aeruginosa using the MALDIquant package. *Problems of Medical Mycology, 22*(3), 69.
7. Eisenreich, W., Rudel, T., Heesemann, J., & Goebel, W. (2022). Link between antibiotic persistence and antibiotic resistance in bacterial pathogens. *Frontiers in Cellular and Infection Microbiology, 12*, Article 900848. https://doi.org/10.3389/fcimb.2022.900848

ISSN: 2181-3337 | SCIENTISTS.UZ

8. Fedorova, O. S., Fedosenko, S. V., Fedotova, M. M., & Chigrina, V. P. (2021). Antibacterial therapy and attitude to the problem of antibiotic resistance in medical practice. *Preventive Medicine, 24*(10), 106–118. https://doi.org/10.17116/profmed202124101106
9. Fick, J., Söderström, H., Lindberg, R. H., Phan, C., Tysklind, M., & Larsson, D. G. J. (2009). Contamination of surface, ground, and drinking water from pharmaceutical production. *Environmental Toxicology and Chemistry, 28*(12), 2522–2527. https://doi.org/10.1897/09-073.1
10. Gabibov, A. G., Dontsova, O. A., & Egorov, A. M. (2020). Overcoming antibiotic resistance in microorganisms: Molecular mechanisms. *Biochemistry (Moscow), 85*(11), 1289–1291. https://doi.org/10.1134/S0006297920110012
11. Huemer, M., Mairpady Shambat, S., Brugger, S. D., & Zinkernagel, A. S. (2020). Antibiotic resistance and persistence—Implications for human health and treatment perspectives. *EMBO Reports, 21*(12), Article e51034. https://doi.org/10.15252/embr.202051034
12. Kuppusamy, S., Kakarla, D., Venkateswarlu, K., Megharaj, M., Yoon, Y.-E., & Lee, Y. B. (2018). Veterinary antibiotics (VAs) contamination as a global agro-ecological issue: A critical view. *Agriculture, Ecosystems & Environment, 257*, 47–59. https://doi.org/10.1016/j.agee.2018.01.026
13. Larsson, D. G. J., & Flach, C.-F. (2022). Antibiotic resistance in the environment. *Nature Reviews Microbiology, 20*(5), 257–269. https://doi.org/10.1038/s41579-021-00649-x
14. Lerminiaux, N. A., & Cameron, A. D. S. (2019). Horizontal transfer of antibiotic resistance genes in clinical environments. *Canadian Journal of Microbiology, 65*(1), 34–44. https://doi.org/10.1139/cjm-2018-0275
15. Miklis, N. I., Burak, I. I., & Izopolskaya, Z. G. (2021). Microflora of patients in a multidisciplinary hospital and its antibiotic resistance. *Health and Environment*, (31), 190–197.
16. Mokhov, A. S., Klimova, A. D., Azarov, D. V., & Goncharov, A. E. (2023). Panel of primers for evaluation of antibiotic resistance genes with real-time detection of results. *Russian Journal of Personalized Medicine, 3*(1), 72–79. https://doi.org/10.18705/2782-3806-2023-3-1-72-79
17. Munita, J. M., & Arias, C. A. (2016). Mechanisms of antibiotic resistance. *Microbiology Spectrum, 4*(2). https://doi.org/10.1128/microbiolspec.VMBF-0016-2015
18. Pan, M., & Chu, L. M. (2017). Fate of antibiotics in soil and their uptake by edible crops. *Science of the Total Environment, 599–600*, 500–512. https://doi.org/10.1016/j.scitotenv.2017.04.214
19. Parrino, B., Carbone, D., Cirrincione, G., Diana, P., & Cascioferro, S. (2020). Inhibitors of antibiotic resistance mechanisms: Clinical applications and future perspectives. *Future Medicinal Chemistry, 12*(5), 357–359. https://doi.org/10.4155/fmc-2019-0326
20. Popova, A. K., & Kozhevnikov, M. A. (2019). The use of bacteriophages as an alternative method of antibacterial therapy against the background of the antibiotic resistance crisis. *A Young Scientist*, (30 (268)), 34–36.
21. Prozherina, Y. (2017). Pharmaceutical waste as a new environmental problem. *Remedium: Journal on the Russian Market of Medicines and Medical Equipment*, (11), 14–19. https://doi.org/10.21518/1561-5936-2017-11-14-19
22. Rather, M. A., Gupta, K., & Mandal, M. (2021). Microbial biofilm: Formation, architecture, antibiotic resistance, and control strategies. *Brazilian Journal of Microbiology, 52*(4), 1701–1718. https://doi.org/10.1007/s42770-021-00624-x
23. Tasho, R. P., & Cho, J. Y. (2016). Veterinary antibiotics in animal waste, its distribution in soil and uptake by plants: A review. *Science of the Total Environment, 563–564*, 366–376. https://doi.org/10.1016/j.scitotenv.2016.04.140

ISSN: 2181-3337 | SCIENTISTS.UZ

24. Willis, J. A., Cheburkanov, V., Chen, S., Soares, J. M., Kassab, G., Blanco, K. C., Bagnato, V. S., de Figueiredo, P., & Yakovlev, V. V. (2022). Breaking down antibiotic resistance in methicillin-resistant Staphylococcus aureus: Combining antimicrobial photodynamic and antibiotic treatments. *Proceedings of the National Academy of Sciences of the United States of America, 119*(36), Article e2208378119. https://doi.org/10.1073/pnas.2208378119
25. World Health Organization. (2015). *Global action plan on antimicrobial resistance.* https://www.who.int/publications-detail-redirect/9789241509763/
26. World Health Organization. (2023). *GLASS manual for antimicrobial resistance surveillance in common bacteria causing human infection.* https://www.who.int/publications/i/item/9789240076600
27. World Health Organization Regional Office for Europe. (2011). *Tackling antibiotic resistance from a food safety perspective in Europe.*
28. World Health Organization Regional Office for Europe. (2018). *Central Asian and Eastern European surveillance of antimicrobial resistance: Annual report 2017.* https://iris.who.int/bitstream/handle/10665/342131/9789289052993-eng.pdf
29. Xia, J., Gao, J., & Tang, W. (2016). Nosocomial infection and its molecular mechanisms of antibiotic resistance. *BioScience Trends, 10*(1), 14–21. https://doi.org/10.5582/bst.2016.01020

ISSN: 2181-3337 | SCIENTISTS.UZ