

Review article

Escherichia coli as a sentinel organism for One Health antimicrobial resistance surveillance: integrating phenotypic, genomic, environmental, and proteomic evidence

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Abstract

Antimicrobial resistance (AMR) surveillance increasingly requires systems that integrate human, animal, food-chain, and environmental data. *Escherichia coli* (*E. coli*) is a valuable sentinel organism for this purpose because it is ubiquitous across One Health compartments, easy to isolate and phenotypically test, clinically relevant as both a commensal and an extraintestinal pathogen, and genetically equipped to acquire and disseminate mobile genetic determinants of AMR. This narrative review revises and updates the scientific rationale for using *E. coli* as an indicator organism in integrated AMR surveillance, with emphasis on current publications and institutional guidance. The evidence supports *E. coli* as a practical cross-sector indicator, but interpretation requires caution: clonal overlap between sectors is often limited, whereas plasmids, resistance genes, and mobile genetic elements (MGEs) may circulate across ecological boundaries. A robust One Health surveillance system should therefore combine standardized sampling, harmonized antimicrobial susceptibility testing, whole-genome sequencing (WGS), selected long-read sequencing for plasmid reconstruction, environmental and wastewater surveillance, metagenomics, and, for selected questions, proteomic approaches that assess the expression and function of resistance mechanisms. The review proposes a pragmatic framework for surveillance design, interpretation, and action. *E. coli* should not be treated as a universal proxy for all AMR hazards, but as a high-value sentinel when data are generated and interpreted through explicit epidemiological objectives, comparable methods, and sector-specific metadata. Finally, this review briefly summarizes the challenges confronting AMR surveillance and recommends key actions to overcome them.

Keywords: Antimicrobial resistance, *Escherichia coli*, Genomic surveillance, One Health, Proteomics, Resistome, Wastewater surveillance

Introduction

Antimicrobial resistance (AMR) remains a major threat to human and animal health, food security, and the sustainability of healthcare systems. Global burden estimates have reported the responsibility of AMR bacteria for millions of deaths annually, and recent surveillance reports continue to document elevated levels of resistance in clinically important Gram-negative pathogens [1, 2, 3]. These trends have accelerated the adoption of One Health surveillance, which recognizes that antimicrobial use, microbial ecology, and resistance transmission are interconnected across humans, animals, food production, and the environment [4, 5]. Within this framework, *Escherichia coli* (*E. coli*) occupies a special position. It is a common intestinal commensal in humans and animals, a frequent cause of gastrointestinal and urinary tract infection, and extraintestinal and systemic infections. *E. coli* harbors plasmids and other mobile genetic elements (MGEs) carrying genes such as *bla*CTX-M, *bla*CMY, *bla*NDM, *bla*KPC, *mcr*-1, and plasmid-mediated quinolone resistance determinants [6, 7, 8]. The same biological versatility that makes *E. coli* an important pathogen also makes it an informative sentinel organism

for AMR surveillance. It means *E. coli* is an efficient indicator bacterium that could be monitored to track resistance trends across clinical, agricultural, and environmental settings [9]. International programs already exploit this property.

The World Health Organization (WHO) Tricycle Protocol, a standardized One Health surveillance framework, is designed to monitor the prevalence of Extended-Spectrum Beta-Lactamase (ESBL)-producing *E. coli* across human, animal (especially poultry), and environmental sectors [10]. Also, the European Union (EU) surveillance frameworks increasingly include *E. coli* or its resistance determinants as interpretable targets. The EU monitors commensal *E. coli* at slaughterhouses and in retail food, alongside zoonotic organisms, wastewater, and the environment. It provides an early warning system for the public [10]. However, the value of *E. coli* depends on methods of sampling, typing, and interpretation. A positive finding in wastewater, poultry, surface water, or clinical isolates does not automatically prove direct transmission between sectors.

Recent comparative genomics suggest that identical clones are not always shared across compartments,

whereas antimicrobial resistance genes (ARGs) and plasmid lineages may move between bacterial populations more readily than the bacterial chromosome itself [11].

The objective of this review is to provide a scientifically coherent and updated overview of *E. coli* as a sentinel organism for AMR in a One Health framework. The manuscript emphasizes practical surveillance design, molecular interpretation, and the complementary role of omics technologies, including proteomics, while identifying limitations that should be explicitly addressed before data are translated into policy or risk-management actions.

Why *E. coli* is a practical sentinel for One Health AMR surveillance

A sentinel organism should be repeatedly detectable, epidemiologically interpretable, technically feasible to test, and capable of reflecting clinically or ecologically meaningful resistance. *E. coli* fulfills many of these criteria. It is abundant in fecal material from humans and animals, can be recovered from food and water matrices, and is compatible with low-cost culture-based methods [12, 13]. It also has long-established laboratory protocols for identification, antimicrobial susceptibility testing, and molecular characterization [14]. The organism is

particularly useful because it links colonization, infection, and environmental contamination.

Commensal *E. coli* can be recovered from healthy humans and animals to estimate community or farm-level AMR pressure, while pathogenic lineages of extraintestinal *E. coli* provide clinically actionable information on resistant infections [15]. In environmental contexts, *E. coli* is a fecal indicator, so it can be used to connect wastewater, surface water, agricultural runoff, and human exposure. However, its abundance alone should not be equated with the risk of infection [16, 17, 18].

Genomic plasticity further strengthens the sentinel role of *E. coli*. It frequently acquires and exchanges plasmids, integrons, and transposons, providing a window into the dissemination of MGEs for AMR. Yet this is also one of the main interpretive challenges. Surveillance can detect a shared resistance gene across sectors. Still, the epidemiological meaning differs depending on whether the gene is carried by the same clone, the same plasmid lineage, unrelated plasmids, or different bacterial hosts [19, 20]. The principal surveillance strengths and caveats associated with the use of *E. coli* as a model organism in One Health AMR surveillance are summarized in Table 1.

Table 1: Sentinel attributes of *E. coli* for One Health AMR surveillance.

Attribute	Surveillance value	Main caveat	Ref.
Cross-sector ubiquity	Enables multisectoral coverage using a single sentinel organism	Environmental variability introduces bias in representativeness and complicates source attribution	[21]
Clinical relevance	Resistance data are directly translatable into clinical and public-health implications.	Commensal isolates do not necessarily reflect the lineages causing invasive disease	[15]
Laboratory feasibility	Cost-effective and scalable techniques implementable across resource settings	Lack of uniform protocols compromises inter-laboratory comparability	[22]
Genomic interpretability	WGS provides information on AST, phylogroup, virulence markers, ARGs, SNPs, and plasmid-associated determinants	Short-read WGS alone cannot fully resolve plasmids or demonstrate horizontal transfer	[23]
Programmatic precedent	Supported by international frameworks facilitating coordinated adoption	Absence of shared standards limits integration and comparability across programs	[10]
Mobile resistome signal	Enables early detection of circulating mobile resistance determinants	Presence of a gene does not predict phenotype or dissemination risk	[24]

AST = antimicrobial susceptibility testing; WGS = whole-genome sequencing; ARG = antimicrobial resistance gene; SNP = single-nucleotide polymorphism.

One Health surveillance compartments

Human sector

Surveillance of AMR *E. coli* in the human sector can be divided into clinical surveillance and carriage surveillance. Clinical isolates, especially from the bloodstream, urinary tract, and extraintestinal infections, provide information on disease burden, therapeutic failure risk, and the emergence of high-risk lineages. The global extraintestinal pathogenic *E. coli* population includes successful lineages such as ST131 and related multidrug-resistant (MDR) clones, which can combine virulence, fluoroquinolone resistance, ESBL genes, and, increasingly, carbapenemase

determinants [25]. Clinical surveillance alone is insufficient for One Health inference because it addresses only individuals admitted within healthcare settings and those delivered for specimen collection [26]. For community carriage studies, screening selected risk groups and wastewater-based approaches can help fill this gap by detecting resistant *E. coli* or ARGs before they lead to severe clinical infections [27]. WHO Global Antimicrobial Resistance and Use Surveillance System (GLASS) and other international systems strengthen comparability by aligning specimen types, pathogen-antibiotic combinations, and reporting methods, but

representativeness remains highly dependent on laboratory access, diagnostic practices, and data quality [28].

Animals, food-producing systems, and the food chain

Food-producing animals are relevant to *E. coli* AMR surveillance for two reasons. First, commensal *E. coli* in livestock and poultry can reflect antimicrobial selection pressure in animal production. Second, resistant *E. coli* and resistant MGEs may move through slaughter, retail meat, manure, soil, water, and direct contact pathways. European surveillance has therefore included indicator commensal *E. coli* from animals and food, in addition to zoonotic pathogens, with particular attention to ESBL-, *AmpC*-, and carbapenemase-producing isolates [29]. The animal-food pathway should not be oversimplified. Antimicrobial use in food animals has been an important driver of selection pressure, and reductions in unnecessary use are a major component of AMR control [30]. Nevertheless, genomic evidence often shows complex population structures rather than a single linear pathway from animals to humans. In some settings, human and livestock *E. coli* populations are distinct, while related plasmids or ARGs may still be detected across compartments. Surveillance should therefore integrate data on animal species, production type, age class, antimicrobial use, sample type, season, geography, and food chain stage.

Environment, wastewater, and water systems

The environment is not merely a passive recipient of resistant bacteria. Wastewater, surface waters, sediments, irrigation waters, manure-amended soils, and hospital effluents can act as dynamic reservoirs, conduits, and transmission routes for AMR bacteria and ARGs, via horizontal gene transfer (HGT) [31, 32]. The United Nations Environment Program (UNEP) has emphasized environmental action as part of the One Health AMR response, particularly around pharmaceuticals, chemicals, agriculture, healthcare, sanitation, and wastewater. *E. coli* is attractive in this compartment because it is already used as a fecal indicator and can be cultured from wastewater and many water matrices. However, environmental AMR surveillance requires careful interpretation. It remains unclear whether the increased abundance of ARGs in sewage and sewage-impacted environments is due to on-site selection pressure from residual antibiotics or simply to fecal contamination by resistant bacteria. The only exception is environments polluted by very high levels of antibiotics from manufacturing, where selection is evident [33]. It is worth noting that the detection of *E. coli* or ARGs in water does not necessarily indicate human health risks, and ARG abundance is not directly proportional to health risk.

Wastewater and environmental surveillance can complement clinical and animal surveillance by providing pooled, community-level information, particularly where clinical microbiology coverage is incomplete. However, recovered results and data are greatly affected by sampling strategy, hydrology, rainfall, wastewater inputs, catchment characteristics, and laboratory methods. Consequently, recent methodological guidance recommends standardized target selection, quality control, composite sampling where feasible, longitudinal designs, and clear policy use-cases before wastewater AMR data are operationalized [34]. Figure 1 summarizes the integration of *E. coli* in different sectors of the One Health paradigm, confirming its potential as a sentinel pathogen for AMR surveillance.

Molecular epidemiology: clones, plasmids, and resistance determinants

A crucial aspect of AMR surveillance is detecting the emergence and spread of high-risk clones. In traditional laboratory surveillance, there are sometimes inconsistencies in the antibiotic panels tested. These inconsistencies lead to the exclusion of samples from the analysis of resistance profile dynamics, hamper cluster detection, and hinder the early detection of novel high-risk clones.

High-risk clones have the propensity to disseminate rapidly, and genomics can improve the detection of their emergence and spread. WGS of bacterial pathogens can identify distinct clonal lineages (strains) on phylogenetic trees, known AMR mechanisms (genes or mutations), and the vehicles for acquired ARGs, which enables enhanced detection and characterization of high-risk clones. Integration of WGS into laboratory-based AMR surveillance can substantially improve the detection of high-risk clones by providing a high-resolution picture of genetic lineages (strains), AMR mechanisms (genes/mutations), and vehicles (MGEs) [35]. Elucidation of resistance mechanisms and their context can be critical for effective infection control. For example, upregulation of efflux pumps and loss of porin function by mutation are vertically transmitted, whereas acquired carbapenemases carried on transmissible plasmids or integrative conjugative elements have the potential for horizontal dissemination between strains and species, thereby necessitating enhanced infection control measures [36].

Escherichia coli surveillance must distinguish among three related but distinct signals: resistant bacterial lineages, MGEs, and individual resistance genes. These three signals differ profoundly in epidemiological resolution. Clone-level evidence requires tight SNP distances (often <10–20 SNPs, lineage-dependent) and conserved accessory genome structure, supporting recent cross-sector transmission. When isolates are genomically distant but share the same ARGs, the signal reflects

independent acquisition or parallel selection rather than movement of bacterial populations. Shared plasmid backbones, especially IncF, IncI, IncX, or IncHI2, with broad host ranges indicate horizontal transfer of MGEs

that follow ecological rather than host-specific pathways. ARG-level detection alone is the least specific, as identical genes may be embedded in distinct plasmids, integrons, or chromosomal contexts with different mobility.

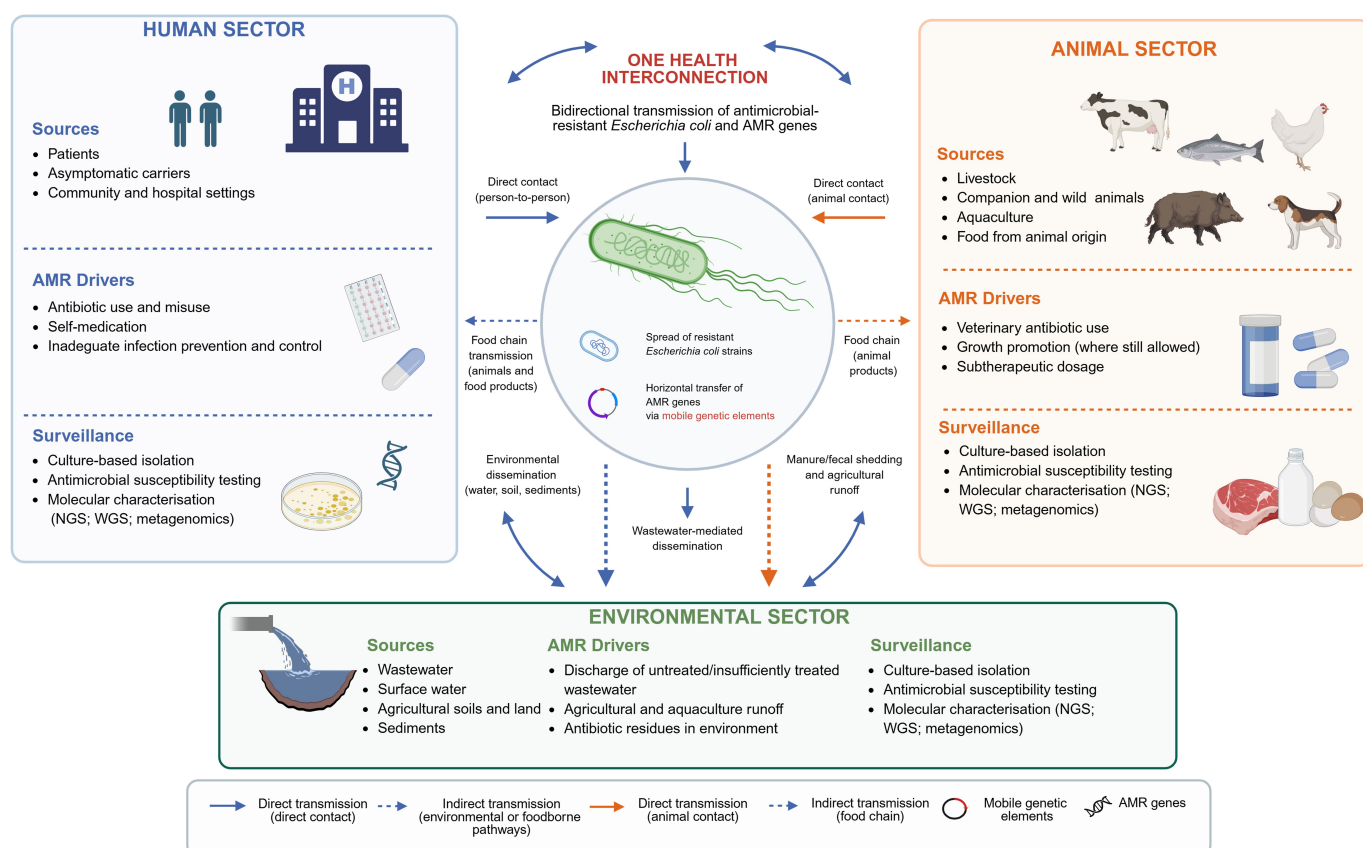


Figure 1: Summary of the integration of *E. coli* in different sectors of the One Health paradigm.

Metagenomic ARG detection adds a population-level resistome signal but cannot resolve host assignment or viability. Correctly distinguishing these layers is essential to avoid false inferences about intersectoral transmission and to prioritize interventions according to the underlying mechanism (clonal spread, plasmid dissemination, or resistome pressure) [19, 37]. Lineage-based spread is important for high-risk clones, including extraintestinal pathogenic lineages associated with MDR and healthcare or community dissemination [38]. Plasmid-mediated spread is equally important because a resistance determinant can move between unrelated *E. coli* lineages or even between different *Enterobacteriales* species. Gene-based detection is a useful tool for screening, but it is the least specific epidemiological signal unless contextualized by the host bacterium, plasmid background, and phenotype [39].

ESBL-producing *E. coli* remains the central indicator for many One Health systems. The WHO Tricycle Protocol intentionally focuses on ESBL-producing *E. coli* in humans, the food chain, and the environment because it is clinically relevant, technically feasible, and comparable

across sectors. Several studies have implemented Tricycle-inspired design and have illustrated both the feasibility and interpretive complexity of this approach. For example, in Madagascar, genomic analysis of ESBL-producing *E. coli* from pregnant women, chickens, and surface water has been conducted. Results showed sector-specific population structures and evidence of intersectoral circulation of strains and plasmids [10]. Another study conducted in Bangladesh used a Tricycle-based protocol, in which environmental samples were collected from hospital wastewater, livestock effluents, aquaculture ponds, and river water. The study recorded the widespread occurrence of third-generation cephalosporin-resistant *E. coli* and clinically important carbapenemase genes at environmental interfaces [21]. In the United Kingdom, One Health genomic surveillance identified distinct *E. coli* lineages and MGEs in isolates from humans and livestock, with limited overlap in MGEs despite some shared resistance genes [19]. Another six-country European analysis of *E. coli* isolated from different One Health compartments revealed few probable vertical transmission events, with detection of conserved plasmid

lineages carrying extended-spectrum cephalosporin resistance determinants [20].

In 2024, an Australian study analyzed thousands of *E. coli* genomes from humans, livestock, companion animals, wildlife, food, and the environment. Results proposed parameters for cross-source genomic surveillance and highlighted the need to use context-specific relatedness thresholds rather than outbreak thresholds alone [21]. In recent years, recorded resistance to colistin, the last group of antibiotics, the polymyxins, confirms why sentinel surveillance must be alerted to emerging mobile mechanisms. Briefly, polymyxin resistance has been associated with chromosomal mutations but has never been reported via HGT. During routine surveillance in China, there was a marked increase in colistin resistance among commensal *E. coli* from food animals. The authors reported the emergence of the first plasmid-mediated polymyxin resistance mechanism, the *mcr-1* gene. The plasmid carrying *mcr-1* was mobilized to an *E. coli* recipient by conjugation. Further investigations revealed *mcr-1* carriage in *E. coli* isolates collected from raw meat, animals, and inpatients with infection. The evidence showed that resistance to a last-line antimicrobial could disseminate through mobile elements across One Health compartments [40]. Current surveillance should therefore prioritize not only common ESBL and *AmpC* determinants, but also carbapenemases, *mcr* genes, plasmid-mediated quinolone resistance, aminoglycoside-modifying enzymes, class 1 integrons, and co-selection markers when appropriate to the local epidemiology and antimicrobial-use context.

Collective data interpretation could be aided by data sharing via interactive web tools such as Microreact (www.microreact.org) and Pathogenwatch (www.pathogen.watch) to leverage the expertise from both Centre for Genomic Pathogen Surveillance (CGPS) and Antimicrobial Resistance Surveillance Reference Laboratory (ARSRL) [41, 35].

Genomics, metagenomics, and data integration

Phenotypic AST remains essential because treatment decisions and surveillance indicators are ultimately expressed as resistant, intermediate, or susceptible phenotypes. However, WGS provides resolution that phenotypic testing cannot, including sequence type, phylogroup, virulence markers, chromosomal mutations, acquired ARGs, SNP-relatedness, and plasmid replicon content. Genomic surveillance also enables retrospective analyses when new mechanisms emerge [42]. Genotype-to-phenotype interpretation requires curated databases, clear quality thresholds, and version-controlled pipelines. Tools such as ResFinder and PointFinder support standardized identification of acquired resistance genes and chromosomal point mutations, but prediction accuracy depends on the organism, drug class, gene

expression, promoter context, gene copy number, porin loss, and efflux regulation [43, 44]. For carbapenemase, ESBL, *AmpC* and *mcr* surveillance, short-read WGS is highly informative, but complete plasmid reconstruction often requires long-read sequencing or hybrid assembly. Metagenomics can broaden surveillance beyond cultured isolates by profiling ARGs and microbial communities directly from wastewater, feces, or environmental matrices. This is useful when a population-level resistome signal is needed or when culture is impractical. Its limitations are equally important: metagenomics may not reliably assign ARGs to host bacteria, discriminate viable from non-viable organisms, or prove expression and transmissibility. For *E. coli* surveillance, metagenomics is best used as a complementary layer alongside culture-based isolation and WGS of representative isolates [42, 45]. Despite progress in AMR surveillance in many countries, particularly in developed ones, the majority of these programs are sector-specific systems that operate separately across the human, animal, and environmental sectors. Integrating these systems through standardized methods can provide a more comprehensive understanding of AMR across all sectors. Unfortunately, data integration remains the weakest component of One Health AMR surveillance and mitigation strategies, posing a major obstacle to the effective elimination of AMR. For proper interpretation, a minimum set of metadata is required, including date, location, host or matrix, sampling frame, laboratory method, AST standard, antimicrobial panel, isolate selection criteria, sequencing platform, assembly quality, bioinformatics pipeline, and database versions [46]. In addition, data are required for environmental samples, such as factors and processes associated with hydrology, ecology, and climate change, catchment, and management data, which are particularly important [47]. For example, without harmonized metadata, a genome sequence may be difficult to interpret (Table 2).

Proteomics and functional AMR surveillance

Genomics identifies the potential for resistance, whereas proteomics can help assess whether resistance mechanisms are expressed and functionally relevant [53]. This distinction is important because the presence of a resistance gene does not always translate into a resistant phenotype, and phenotypic resistance may result from combinations of enzymes, porin changes, efflux systems, and regulatory effects that are not fully captured by gene presence alone. Currently, the proteomic approach has been widely adopted in most laboratories, established as a fundamental tool for unraveling the complex molecular mechanisms that drive AMR and for capturing the biological effectors of resistance. Besides, proteomics is important for assessing the differential expression of bacterial proteins under stress conditions, as well as for

Table 2: Core minimum dataset for integrated *E. coli* AMR surveillance.

Domain	Minimum metadata	Purpose	Ref.
Human clinical isolates	Specimen type, syndrome, date, facility, location, patient age group, inpatient/outpatient status, AST panel, and clinical breakpoint standard	Estimate disease burden, monitor therapeutic risk, and detect high-risk resistant lineages	[48]
Human carriage or community sampling	Population sampled, sampling frame, date, location, recent antimicrobial exposure, healthcare contact, travel history, or occupational exposure, where ethically and legally collectible	Capture colonization and community reservoirs that are not visible in clinical specimens alone	[49]
Animals and the food chain	Species, production type, farm or slaughter/retail stage, age class, sample type, antimicrobial-use or consumption indicators, season, and geography.	Interpret selection pressure and transmission opportunities across production systems	[50]
Environment and wastewater	Type of matrix, geographic location, sample volume, sampling method, and key environmental conditions (rainfall, flow, temperature), plus wastewater treatment stage	To understand how diluted the sample is, how long bacteria or genes may persist, and how different sources may mix or contribute to exposure pathways	[48]
Laboratory and sequencing	Culture media, selective conditions, number of colonies selected, AST standard, QC strain results, sequence platform, genome quality, and pipeline/database versions	Ensure comparability, reproducibility, and auditability	[51]
Integration and governance	Common identifiers, data-sharing permissions, privacy safeguards, FAIR data structure, reporting thresholds, and predefined action triggers	Convert surveillance outputs into transparent public-health and veterinary action	[52]

FAIR = findable, accessible, interoperable, and reusable; AST, = antimicrobial susceptibility testing; QC = quality control

identifying and quantifying changes occurring during and after protein synthesis [54]. Finally, proteomics uncovers novel therapeutic targets.

Among many proteomic techniques, mass spectrometry (MS)-based proteomics and Matrix-assisted laser desorption/ionization-time-of-flight (MALDI-TOF) provide a direct window into the active molecular machinery of pathogens [55]. Untargeted and targeted Liquid Chromatography-Tandem Mass Spectrometry (LC-MS/MS) approaches have been used to detect beta-lactamases, aminoglycoside-modifying enzymes, porins, and other resistance-associated proteins in *E. coli* and *Klebsiella pneumoniae* (*K. pneumoniae*). Proteogenomic workflows can integrate WGS-derived protein databases with mass spectrometry to improve interpretation of resistant phenotypes [56]. Targeted LC-MS/MS has also been developed for direct or rapid detection of multiple beta-lactam, aminoglycoside, and fluoroquinolone resistance mechanisms in blood cultures containing *E. coli* or *K. pneumoniae* complex [57].

Proteomic studies also provide mechanistic insight into stress responses and adaptive pathways (Figure 2). For example, quantitative proteomics of tetracycline-exposed resistant *E. coli* has shown alterations in metabolic and peptidoglycan-related processes [58]. MALDI-TOF mass spectrometry combined with machine learning is being investigated for AMR prediction from routine diagnostic spectra. However, performance, portability, and external validation remain barriers to its use in routine surveillance [59]. These findings confirm the essentiality of integrating proteomics with other omics disciplines, including

genomics, transcriptomics, and metabolomics, to achieve a comprehensive understanding of AMR. This multi-layered approach enables a more holistic, system-level understanding of resistance, allowing researchers to uncover complex regulatory networks and metabolic interdependencies that remain obscured when each omic layer is studied separately [60].

For One Health surveillance, proteomics should currently be considered an adjunct rather than a replacement for AST and WGS. The most fundamental roles of proteomic analysis are validating expression of key resistance mechanisms in selected isolates, resolving genotype-phenotype discordance, characterizing high-risk clones or plasmid-bearing isolates, and supporting research into environmental stress, persistence, and co-selection. Despite the benefits of incorporating proteomics as a diagnostic and surveillance tool in AMR surveillance systems, there are limitations that hinder large-scale deployment. These limitations are represented by the high cost of instruments, the standardization of methodologies across sectors, matrix effects, and the need for expertise [53]. Besides, proteomics is not yet ready for large-scale routine AMR surveillance in most settings. Its current value lies mainly in selected isolates, genotype-phenotype discordance, and targeted detection of resistance-associated proteins, while future applications may include biomarker discovery and functional AMR surveillance. Table 3 summarizes the diagnostic methodology utilized for the identification of *E. coli* AMR surveillance.

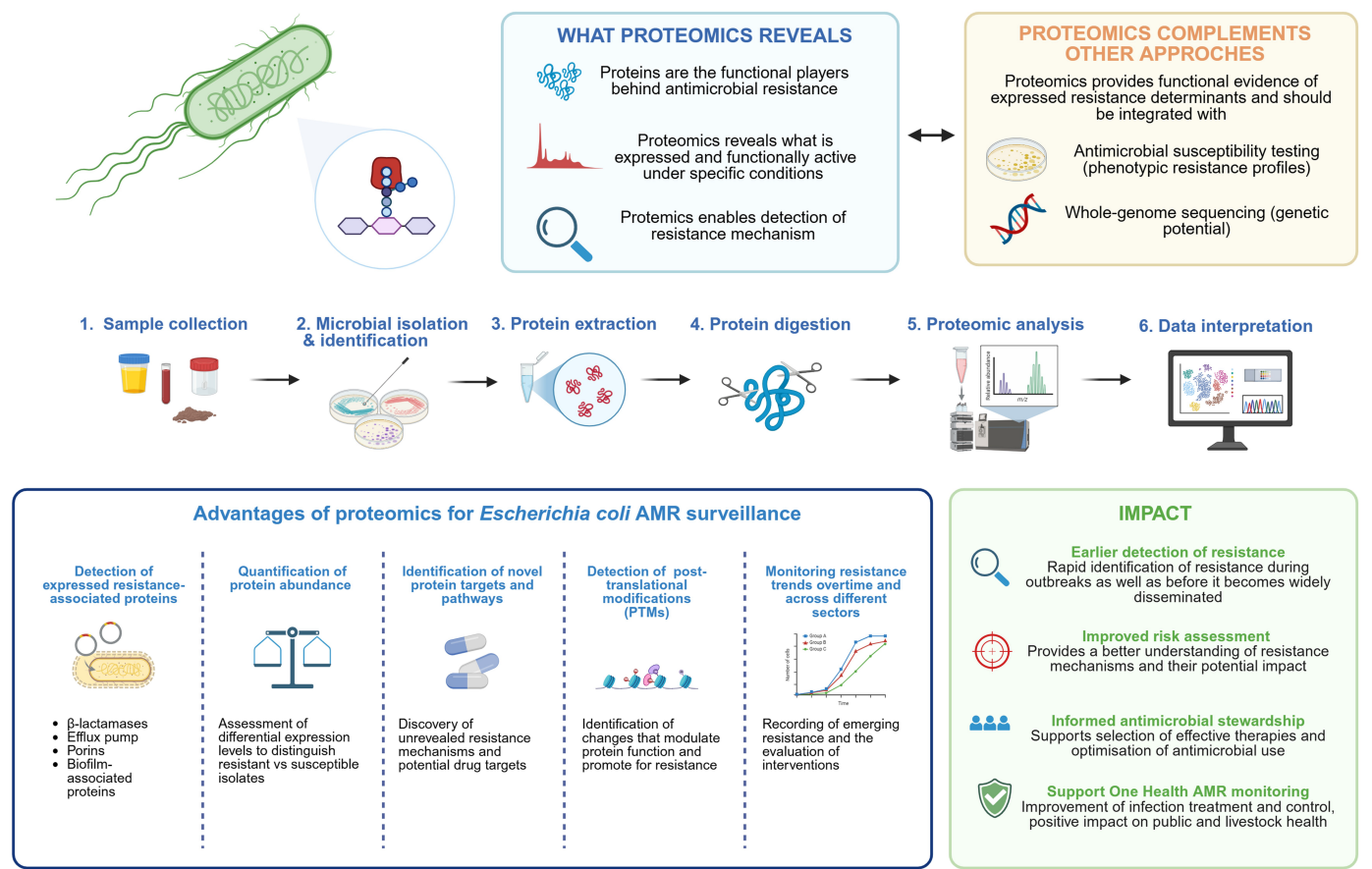


Figure 2: Proteomic approach for identification of AMR *E. coli* in different biological samples.

Table 3: Technology toolbox for *E. coli* AMR surveillance.

Method	Best use	Key limitations	Recommended role	Ref
Phenotypic AST	Determination of resistant phenotype and clinical/veterinary interpretation	Comparability depends on the breakpoint standard, drug panel, and isolate selection criteria	Core method across all sectors	[48]
Selective culture and confirmatory testing	Detection of ESBL, <i>AmpC</i> , carbapenemase or other target phenotypes in specific matrices	Selective media may overestimate prevalence compared with unbiased isolation	Core method when target mechanisms are predefined	[48]
Short-read WGS	Identification of lineage, ARGs, mutations, virulence markers, and SNP relatedness	Incomplete plasmid reconstruction and limited inference on gene expression	Core method for representative isolates and high-risk findings	[49]
Long-read or hybrid sequencing	Resolution of plasmids, structural variants, and linkage between ARGs and MGEs	Higher cost and lower throughput for routine surveillance	Targeted use for plasmids, carbapenemases, <i>mcr</i> genes, and unresolved clusters	[49]
Shotgun metagenomics	Resistome and community profiling directly from wastewater or environmental samples	Limited ability to assign ARGs to viable <i>E. coli</i> or specific hosts	Complementary population-level surveillance layer	[49]
Targeted qPCR/ddPCR	High-sensitivity quantification of selected ARGs or markers	Narrow scope and limited host assignment	Useful for trend monitoring and sentinel targets	[49]
LC-MS/MS proteomics	Detection of expressed proteins, enzymes, and genotype-phenotype discordance	Requires specialized instrumentation and standardization	Adjunct for selected isolates and functional validation	[49]
MALDI-TOF + machine learning	Potential rapid AMR prediction from routine diagnostic spectra	External validation and reproducibility remain unresolved	Research or pilot implementation only	[49]

ARGs = antimicrobial resistance gene; MGEs = mobile genetic elements; ESBL = extended-spectrum beta-lactamase; qPCR = quantitative polymerase chain reaction; ddPCR = droplet digital polymerase chain reaction; LC-MS/M = liquid chromatography mass spectrometry; MALDI-TOF = matrix-assisted laser desorption/ionization – time of flight

Implementation challenges and foresight perspectives for a pragmatic surveillance framework

Since its development, AMR governance has relied on a high degree of organizational capacity to support practical efforts in disease prevention, rational antibiotic use, and AMR eradication, while accounting for the interconnections among humans, animals, and the environment [61]. The main barrier to meaningful One Health surveillance is not a lack of technology but a lack of comparable and interpretable data. Developing an effective AMR-combating strategy must follow a One Health approach that integrates human, animal, and environmental ecosystems and should include establishing a comprehensive tracking system such as the National Antimicrobial Resistance Monitoring System (NARMS), developing tailored action plans, and updating guidelines and regulations. NARMS was established to ensure that the use of antimicrobials in food-producing animals does not undermine the efficacy of the same drugs to treat foodborne infections in humans [62].

The implementation of practical, concise measures is primarily based on reliable epidemiological data on Antimicrobial Use (AMU) and AMR prevalence in targeted areas [63]. Consequently, proper surveillance is a key step for successful strategies, identifying the presence and prevalence of the resistant pathogens to specific antibiotics and highlighting areas requiring urgent action [62]. It could be achieved through strategic steps, including improving access to microbiological diagnostics for pathogen identification and susceptibility testing against potential antimicrobial therapeutics [64].

AMR data availability and quality vary widely between countries and clinical settings. The WHO 2023 report noted that funding resources for implementing multisectoral plans are identified in only 11% of countries. This underscores persistent challenges to AMR control strategies [65]. Low- and middle-income countries (LMICs) face limitations that undermine AMR control strategies. Key limitations include limited availability of routine microbiological diagnostics, scarce surveillance data, restricted access to on-site microbiology laboratories outside large public hospitals, and the predominance of infection management and antibiotic prescribing in primary care settings [63, 64].

In addition to financial and capacity constraints, AMR control strategies face a range of other obstacles that facilitate the emergence and spread of this phenomenon. These factors include the movement and migratory behavior of wildlife and international travel and trade [66]. The environmental dimensions of AMR remain insufficiently addressed, with persistent evidence and policy gaps despite recognition of the environment's

critical role in the development, transmission, and spread of resistance.

Investigating AMR in wildlife faces several difficulties, including small sample sizes, limited spatial or temporal representation, variation in isolation and resistance detection methods, and heterogeneity in reported data [67, 68]. Also, insects such as flies and cockroaches were found to transmit AMR bacteria between ecosystems [69]. Unfortunately, current AMR surveillance systems still primarily focus on clinical and agricultural settings, neglecting environmental dimensions that can serve as valuable sentinels of AMR surveillance and control [70, 71].

In a trial to overcome these challenges, we briefly recommend some key actions that align with the WHO Global Action Plan on Antimicrobial Resistance (GAP-AMR) [72], and advised to be active in place within 2-3 years, and being controlled frequently by national governmental authorities:

1. Immediate actions to raise public awareness about the increasing risk of AMR and its drawbacks by utilizing social communication channels;
2. Fund scouting for improving laboratory capacity;
3. Integrating environmental interventions into the national AMR surveillance and response.
4. Investment in developing new diagnostics, and identification of new antimicrobials/alternative therapies such as “extracts of medicinal herbs”;
5. Improving personnel professionalism via training;
6. Standardization of isolation protocols within each sector;
7. Encourage initiatives and donations for low-income countries;
8. Instant implementation of strict hygiene and infection prevention measures in healthcare settings, livestock farms, slaughterhouses, and food-producing companies to limit the development and spread of AMR infections and MDR bacteria.
9. Prohibit the use of unprescribed antibiotics;
10. Encourage collaboration with medical and pharmaceutical professional bodies;
11. Frequent assessment and update of National Action Plans; encourage research and community collaboration;
12. Cooperation is needed in developing regulations, policies, and surveillance systems for AMR in the environment.
13. Global data sharing and harmonization, with transparency, of antimicrobial-use or antimicrobial-consumption data.

We can conclude that AMR is an open-ended, multi-level challenge, and that a holistic, coordinated, multisectoral approach is required to combat this serious and urgent threat. Efficient AMR surveillance requires constant ongoing governance actions.

Conclusions

Escherichia coli is widely regarded as a premier sentinel organism for One Health AMR surveillance because it is clinically important, ecologically widespread, technically accessible, and genetically informative. Its greatest value lies not in providing a simple model for mapping transmission between sectors, but in serving as a universal indicator of HGT and an epidemiological bridge across humans, animals, food systems, and the environment. The evidence reviewed here supports a balanced interpretation. Resistant *E. coli* clones can spread across populations, but many One Health signals are mediated by plasmids, MGEs, and resistance genes rather than direct clonal transmission. Surveillance should therefore avoid simplistic source-attribution claims unless supported by dense sampling, high-resolution genomics, plasmid context, and epidemiological metadata.

A robust *E. coli* surveillance system should combine standardized sampling protocols, phenotypic AST, WGS, selective long-read sequencing, environmental and wastewater surveillance, and carefully targeted proteomic or metagenomic methods. In this review, we integrate methodological layers into a coherent and practical interpretative framework designed to support operational One Health surveillance. This integrative perspective is novel, moving beyond traditional descriptive reviews and proposing a unified, cross-sector logic for interpreting AMR signals generated through phenotypic, genomic, environmental, and proteomic approaches.

Finally, we outline minimum metadata requirements and sector-specific design principles that enable comparable and actionable AMR data generation across the human, animal, food, and environmental sectors. By articulating these operational principles, the review provides an innovative blueprint for transforming *E. coli* surveillance from a fragmented set of methods into a structured, decision-oriented One Health system. When designed around explicit questions and linked to predefined interventions, *E. coli* surveillance can move from descriptive monitoring to actionable AMR prevention in a One Health framework.

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