

Plasmid-Mediated Colistin Resistance mcr Gene Dynamics in Poultry-to-Human Transmission Chains in Lagos State: A Narrative Review

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ABSTRACT

Poultry production is an important reservoir of colistin-resistant bacteria with potential implications for human exposure through food, occupational contact, and the environment. In Nigeria, mobile colistin resistance (*mcr*) genes and colistin-resistant *Enterobacterales* have been detected in poultry and abattoir settings, indicating that resistant organisms can circulate across production and processing chains. This is particularly relevant to Lagos State, where poultry farming, meat handling, and dense human contact create conditions that may support the movement of resistant bacteria between animals, environments, and people. This review examined the dynamics of plasmid-mediated colistin resistance in poultry-to-human transmission chains in Lagos State. It focuses on the occurrence of *mcr* genes in poultry, the role of plasmids in resistance spread, and the pathways through which resistant organisms may move from farms to slaughterhouses, markets, households, and surrounding environments. The review also considered the public-health importance of antimicrobial use practices, environmental contamination, and food-chain exposure in sustaining these transmission routes. The evidence explored in this review suggests that plasmid-mediated colistin resistance should be treated as a One Health concern rather than an isolated animal-health issue. Strengthened genomic surveillance, improved antibiotic stewardship, better slaughterhouse hygiene, and coordinated policy enforcement are needed to reduce the risk of dissemination across the poultry-human-environment interface in Lagos State.

Keywords: Colistin resistance; *mcr* genes; Poultry; One Health; Lagos State.

Introduction

The epidemiology of colistin resistance increasingly demonstrates that food-producing animals, particularly poultry, represent an important reservoir of resistant *Escherichia coli* with potential relevance to human exposure. Evidence from the food chain indicates that colistin-resistant *E. coli* occurs across poultry, meat, and other food-producing

compartments, with higher resistance prevalence reported in poultry and pigs and in developing countries. In Nigeria, Anyanwu et al. [1] identified colistin-resistant *Enterobacterales* in chicken faecal and cloacal samples collected from farms in Southeast Nigeria, while more recent evidence from commercial day-old chicks in southeastern Nigeria found phenotypic colistin-resistant *E. coli*, suggesting that resistant organisms may already be present at an early stage of poultry production [1, 2]. These findings are epidemiologically important because resistant bacteria present within poultry can subsequently reach slaughter and processing environments, food products, farm workers, and surrounding environments, creating multiple opportunities for dissemination along the poultry-to-human transmission chain [3]. In Lagos State, this concern is reinforced by evidence that 86.4% of surveyed poultry farms reported using antibiotic cocktails that included colistin, ciprofloxacin, chloramphenicol, and gentamicin, with no farms observing withdrawal before sale of products, indicating strong selection pressure for antimicrobial resistance in the poultry production system [4].

The emergence of mobile colistin-resistance genes, particularly *mcr*-1, has transformed colistin resistance from an essentially chromosomal phenomenon into a readily transmissible threat [5].

20 May 2026: Received

09 June 2026: Revised

02 July 2026: Accepted

01 August 2026: Available Online

Citation: Ayoade Babatunde Olanrewaju, Temitope Olamide Akinmoye, Oguzie Blessing Chinyere, Nathan Rimamsanati Yohanna, Moses Adondua Abah and Micheal Oladosu Abimbola (2026). Plasmid-Mediated Colistin Resistance mcr Gene Dynamics in Poultry-to-Human Transmission Chains in Lagos State: A Narrative Review. *Acta Pharma Reports*.
DOI: <https://doi.org/10.51470/APR.2026.05.01.129>

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Unlike chromosomal mutations, which are commonly transmitted vertically within bacterial lineages, *mcr* genes are frequently carried on plasmids capable of horizontal gene transfer between bacterial cells and, in some circumstances, across bacterial species [6]. The encoded MCR enzymes modify lipid A in the outer membrane lipopolysaccharide of Gram-negative bacteria by adding a phosphoethanolamine moiety, reducing the negative charge targeted by colistin and consequently impairing its antibacterial activity [7]. The public-health significance of this mechanism is further increased by the capacity of *mcr*-carrying plasmids to coexist with determinants conferring resistance to other critically important antibiotics, including carbapenems, fluoroquinolones, tigecycline, extended-spectrum cephalosporins, and fosfomycin [8]. Poultry production is especially relevant to this problem because birds may acquire and maintain colistin-resistant *Escherichia coli* within their intestinal microbiota while appearing clinically healthy [9]. Resistant organisms may move through poultry-to-human transmission chains involving direct contact with birds, contaminated feed and water, manure, farm workers, equipment, work clothing, slaughtering activities, and the handling or consumption of contaminated meat, eggs, and related products [7]. Food-chain exposure is therefore not restricted to infected animals; it may also occur through contamination of production, processing, marketing, preparation, and household environments [10]. The potential movement of *mcr* genes through these connected pathways illustrates why colistin resistance should be examined within a One Health framework rather than as an isolated clinical or veterinary problem [11].

Evidence from Nigeria reinforces the need for such investigation. In poultry birds sampled in Ekpoma, Edo State, colistin resistance was detected in *E. coli* isolates, while a proportion of the resistant isolates carried *mcr*-1 [9].

Although these findings cannot be directly extrapolated to Lagos State, they demonstrate that poultry can serve as a reservoir of mobile colistin resistance in Nigeria. Lagos State is consequently a relevant setting for examining poultry-to-human transmission chains because the proposed focus connects animal production, food-chain exposure, environmental dissemination, and human-health risk within a single epidemiological framework. Such transmission may contribute to colonisation or infection with organisms for which therapeutic choices are increasingly restricted [12]. Accordingly, this review aims to explore the available evidence from the supplied literature on colistin use in poultry, the occurrence and mobility of *mcr* genes, the routes linking poultry with human exposure, and the implications of these processes for investigating plasmid-mediated colistin resistance in Lagos State.

Overview of Colistin Resistance in Poultry-Associated Production Systems

Colistin is a polymyxin antimicrobial that has historically been used in veterinary medicine, particularly in food-producing animals, while also retaining an important therapeutic role against infections caused by multidrug-resistant Gram-negative bacteria in human medicine [13]. Its extensive use in animal production has created concern because antimicrobial exposure can select resistant bacterial populations that may subsequently circulate within animals, food products, humans and the surrounding environment [3]. In developing countries, these concerns are intensified by variable antimicrobial stewardship, limited surveillance and the continued availability of antimicrobials for food-animal production [14]. Nigeria is particularly relevant to this problem because food animals and their production environments have been identified as important reservoirs of antimicrobial-resistant bacteria and antimicrobial residues entering the human food chain [15].

Table 1: Scope of the literature reviewed across poultry-associated colistin resistance

Domain	Evidence considered in the review
Poultry production	Farm-level poultry isolates, faecal and cloacal samples, poultry-associated <i>Enterobacterales</i> and resistant bacteria
Processing and marketing	Slaughterhouses, abattoirs, meat-processing facilities, carcasses and handling environments
Human exposure	Farmers, poultry handlers, slaughterhouse personnel, veterinarians, meat sellers and consumers potentially exposed to resistant organisms
Environment	Farm waste, litter, water, wastewater and contaminated production or processing environments
Antimicrobial use	Colistin exposure, antimicrobial practices and selection pressure within food-animal production
Molecular epidemiology	<i>mcr</i> variants, plasmid-mediated resistance, bacterial hosts and genetic diversity of resistant isolates

Source: Founou et al.¹⁴

Table 1 demonstrates the interconnected domains considered in the review, extending from poultry production and antimicrobial exposure to processing environments, human exposure, environmental contamination and the molecular characteristics of resistance. This broader scope is important because colistin resistance can move across these compartments rather than remaining restricted to the animal reservoir [14].

Poultry production represents an important component of this interface because chickens can harbour resistant *Enterobacterales* within intestinal and cloacal populations, allowing antimicrobial resistance to persist within production systems and potentially move beyond the farm [16].

The importance of poultry-associated resistance is supported by evidence from different regions showing that resistant bacteria may occur in poultry faeces, litter, carcasses, meat and production environments, thereby creating several points at which resistance can be maintained or disseminated along the food chain [1].

A worldwide systematic review and meta-analysis similarly found that colistin-resistant *Escherichia coli* was particularly prevalent in samples originating from poultry and pigs, with higher resistance estimates reported in developing countries [17]. These findings indicate that colistin resistance should not be considered solely as a clinical problem because food-animal production can provide an important ecological setting for its selection and dissemination.

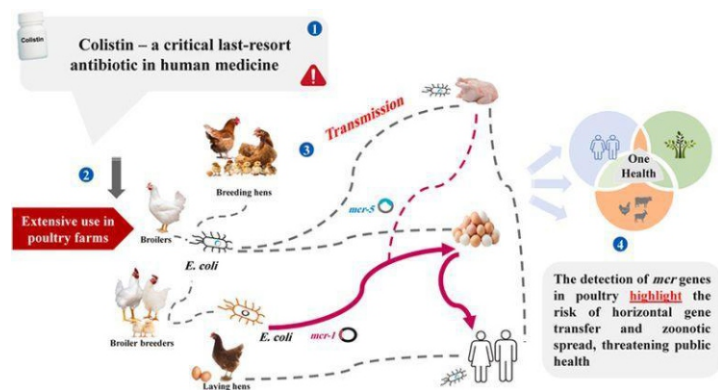


Figure 1. Potential poultry-to-human transmission pathway of colistin-resistant bacteria
Source: Akkari et al. [4]

Figure 1 illustrates the interconnected pathways through which colistin-resistant bacteria may move from poultry production into processing, environmental and human compartments. The pathway is conceptual and represents potential transmission interfaces rather than proof of direct transmission in every setting.

The emergence of colistin-resistant organisms in poultry is also relevant because antimicrobial exposure can exert selective pressure on bacterial populations even when resistance is not initially associated with a clinically important pathogen [3]. Resistant organisms selected within poultry may subsequently be introduced into slaughtering and processing environments through faecal contamination, animal handling and contact with contaminated equipment or water [16]. Such environments can therefore connect farm-level resistance with occupational and food-associated human exposure, particularly where hygiene, waste management and antimicrobial-resistance surveillance are insufficient [15]. The broader food-chain literature supports this farm-to-fork perspective, demonstrating that resistant *E. coli* can occur at multiple stages between food-producing animals and retail food products [17].

The potential movement of resistance beyond poultry farms is further illustrated by Nigerian Lagos State evidence from abattoir and food-animal environments. A study of human, beef cattle, and abattoir environments in Nigeria showed that these interconnected settings can share antimicrobial-resistant bacteria, supporting the relevance of livestock-to-environment transmission [18]. In addition, a Lagos State study reported widespread antibiotic use in poultry farms, with 86.4% of farms using antibiotic cocktails that included colistin, indicating strong selection pressure for resistance in the production chain [4]. This is consistent with the wider One Health concept that antimicrobial resistance may circulate between animals, humans, and environmental compartments rather than remaining confined to a single reservoir [3]. Nigerian evidence has likewise shown that antimicrobial residues and resistant bacteria occur in food-animal production systems and associated environments, reinforcing the need to consider animal production and environmental contamination together when assessing resistance risks [15]. As additional confirmation, Omoruyi et al. (2023) detected plasmid-borne *mcr-1* among bacteria recovered from water, wastewater, utensils, and handlers in abattoir environments in Benin City, showing that food-processing settings can also serve as routes of exposure to colistin-resistant organisms [19].

Within this context, poultry-associated colistin resistance is particularly important because resistance occurring in an animal reservoir may become relevant to humans through several interconnected pathways, including direct animal contact, occupational exposure, slaughter and processing, contaminated food, wastewater and environmental dissemination [1]. The increasing detection of colistin-resistant *E. coli* throughout the food chain therefore provides a rationale for investigating poultry not only as a source of resistant bacteria but also as part of a broader transmission network linking production systems with human and environmental compartments [17]. Understanding these connections provides the necessary foundation for examining the transferable genetic mechanisms responsible for colistin resistance and, subsequently, the dynamics of *mcr* genes within poultry-to-human transmission chains.

mcr Genes and the Molecular Basis of Colistin Resistance

Colistin is an important last-line antimicrobial for infections caused by multidrug-resistant Gram-negative bacteria, particularly organisms for which therapeutic alternatives may be limited [20, 21]. The epidemiology of colistin resistance changed substantially following the identification of *mcr-1*, because resistance that had previously been associated mainly with chromosomal mutations could also be mediated by a transferable plasmid-borne determinant [5, 22]. The *mcr-1* gene encodes a phosphoethanolamine transferase that modifies lipid A, a major component of the outer membrane lipopolysaccharide of Gram-negative bacteria, thereby reducing the negative surface charge that facilitates binding of the cationic colistin molecule [23, 24]. At the molecular level, MCR-1 catalyzes the transfer of phosphoethanolamine from phosphatidylethanolamine to lipid A, producing a modified lipid A structure with reduced affinity for colistin [25]. This modification interferes with the electrostatic interaction between colistin and the bacterial outer membrane, thereby reducing membrane disruption and allowing resistant organisms to survive exposure to the drug [24]. Structural studies further indicate that MCR-1 contains a membrane-associated region and a periplasmic catalytic domain, with zinc-dependent catalytic activity contributing to phosphoethanolamine transfer [23]. The functional importance of the catalytic region is supported by experimental studies showing that alteration of key residues involved in phosphoethanolamine transfer can restore colistin susceptibility [23, 24].

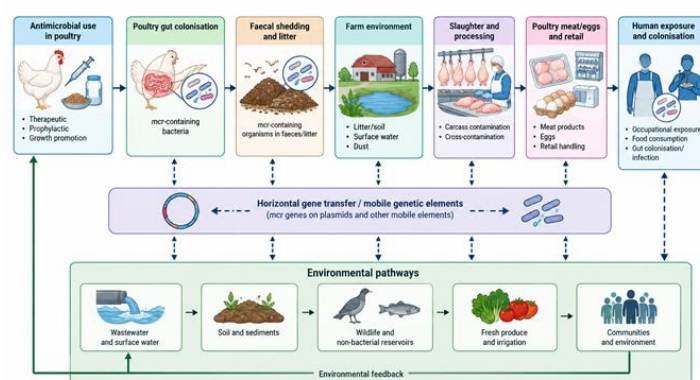


Figure 2. Potential pathways of *mcr*-mediated colistin resistance dissemination from poultry production to humans
Source: Anyanwu et al. [1]

As illustrated in Figure 2, antimicrobial exposure in poultry production can create selection pressure favouring the persistence of resistant bacteria, which may colonize the poultry intestinal tract and subsequently be shed through faeces and litter. Resistant organisms can then move through farm environments and enter slaughter and processing settings, where carcass contamination and cross-contamination may create opportunities for their presence in poultry meat, eggs and retail products. Environmental release through wastewater, contaminated water, soil, litter and other farm-associated materials provides additional pathways through which mcr-carrying organisms may circulate beyond the production unit. These interfaces can result in occupational exposure among poultry workers and handlers or consumer exposure through contaminated food, creating potential opportunities for human colonization or infection and subsequent dissemination of mcr-positive organisms. The central role of horizontal gene transfer in Figure 2 reflects the ability of mcr genes carried on plasmids and other mobile genetic elements to move between bacterial populations, while the environmental pathway illustrates how animal production, environmental compartments and human communities may become interconnected within a One Health framework [1, 7, 17]. However, this pathway should be interpreted as a potential epidemiological route rather than

evidence of direct poultry-to-human transmission, because available studies more consistently demonstrate reservoirs, resistance determinants and exposure opportunities than direct transmission between specific poultry and human isolates [1]. Environmental and processing settings may nevertheless contribute to this pathway because resistant organisms can be released through animal waste and contaminated water or surfaces, creating additional interfaces between animal production and human populations [19].

Plasmid-Mediated Dissemination and Diversity of mcr Genes

The epidemiological importance of mcr-1 derives not only from the resistance phenotype itself but from its capacity to occur on mobile genetic elements that facilitate movement between bacterial populations [5, 22]. The original description of mcr-1 demonstrated its occurrence in both animal and human isolates and established its plasmid-mediated nature, providing an important mechanistic explanation for the rapid international dissemination subsequently observed [5]. mcr-1 has subsequently been identified in diverse Enterobacterales, including *Escherichia coli*, *Klebsiella pneumoniae* and *Salmonella* species, demonstrating that dissemination is not restricted to a single bacterial lineage [22].

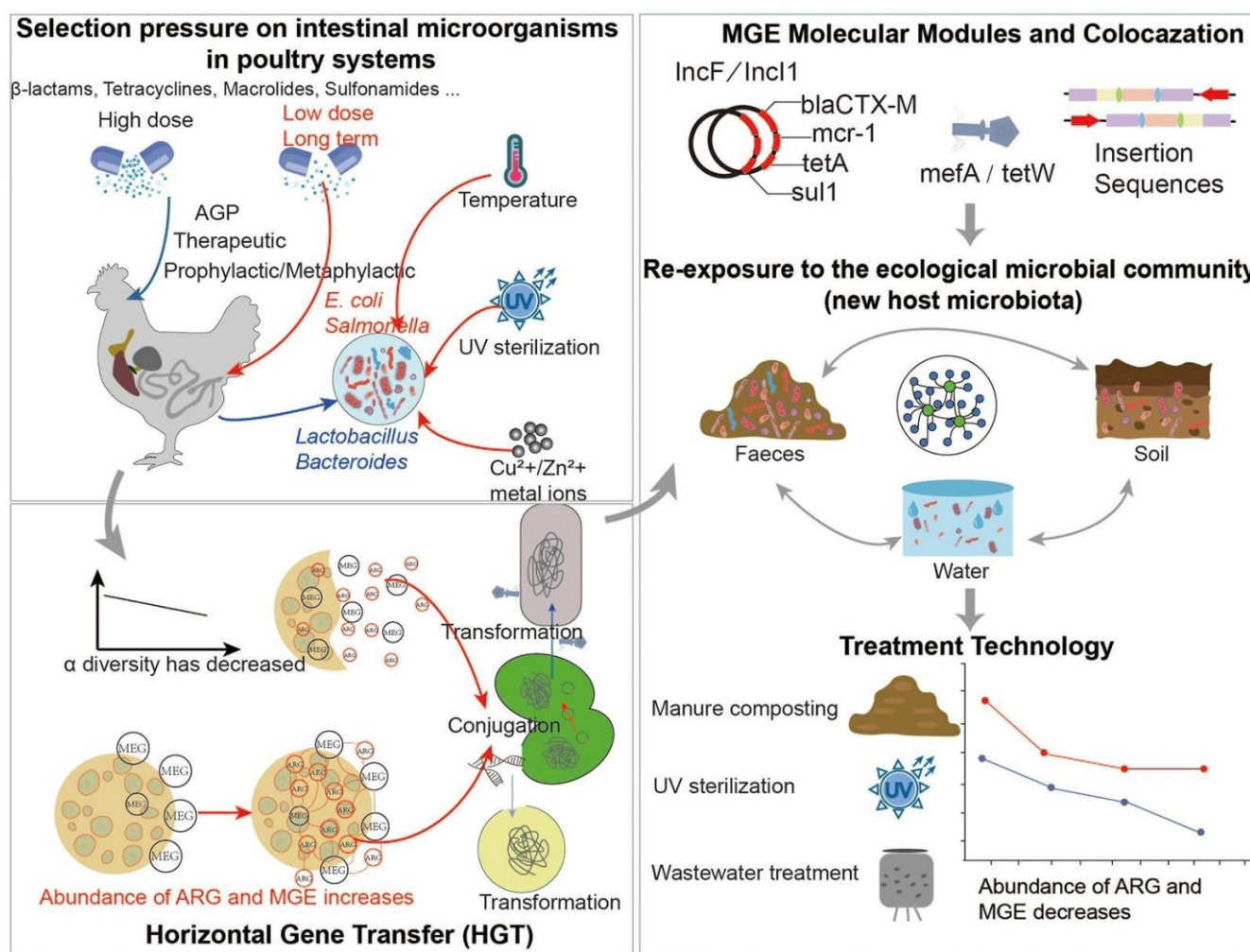


Figure 3. Plasmid-mediated dissemination of mcr genes across bacterial hosts and transmission interfaces
Source: Li et al. [24]

Figure 3 summarizes the relationship between *mcr* carriage on mobile genetic elements, its occurrence among different Enterobacterales hosts, horizontal movement between bacterial populations, and its potential dissemination through poultry-associated and environmental interfaces. The co-resistance component reflects the occurrence of *mcr* alongside other antimicrobial-resistance determinants described in poultry-associated isolates.

The diversity of mobile colistin-resistance determinants has expanded considerably since the discovery of *mcr*-1, with *mcr*-2, *mcr*-3, *mcr*-4, *mcr*-5, *mcr*-6, *mcr*-7, *mcr*-8, *mcr*-9 and *mcr*-10 subsequently identified [25, 26]. These variants do not represent simple copies of *mcr*-1, because their nucleotide and protein sequences differ substantially, indicating considerable evolutionary diversification among phosphoethanolamine-transferase resistance determinants [25]. The *mcr*-3 family, for example, contains numerous recognised variants, whereas *mcr*-6 and *mcr*-7 have historically shown much more limited variant diversity [25, 27]. The later identification of *mcr*-9 and *mcr*-10 further demonstrated that transferable or potentially mobilisable phosphoethanolamine-transferase mechanisms extend beyond the earlier *mcr*-1 to *mcr*-8 groups [26, 28]. The genetic context in which these determinants occur is particularly important because *mcr* genes have been detected on several plasmid backbones, including IncI2, IncX4 and IncHI2, as well as other plasmid types [29]. Such plasmid association provides a mechanism through which resistance determinants can move horizontally between bacterial strains and, under appropriate conditions, across bacterial species [5, 22]. The significance of this mobility is illustrated by Nigerian poultry research, where *mcr*-positive *E. coli* isolates demonstrated substantial genetic diversity, while conjugative transfer of *mcr*-1.1 to other organisms has also been reported in Nigerian livestock-associated isolates [1]. The epidemiological threat is further complicated by the occurrence of *mcr* genes alongside other antimicrobial-resistance determinants [3, 15]. Studies of poultry-associated *mcr*-positive organisms have identified additional resistance genes affecting β -lactams, aminoglycosides, quinolones and other antimicrobial classes,

creating multidrug-resistant backgrounds in which selection by one antimicrobial may indirectly maintain organisms carrying several resistance determinants [1]. This co-resistance is particularly relevant where antimicrobial use involves multiple drug classes, because selection pressure may favour persistence of plasmids or bacterial populations carrying linked resistance determinants even when colistin itself is not being administered [3, 16].

Antimicrobial Selection and Persistence of *mcr*-Mediated Resistance

Evidence from experimental poultry research provides direct support for the role of antimicrobial selection in maintaining *mcr*-mediated resistance. In broiler chicks carrying *mcr*-1-positive *Salmonella*, administration of colistin increased the level and persistence of *mcr*-1 within the intestinal microbiota, suggesting that antimicrobial exposure can favour the expansion or maintenance of resistant populations [30]. Nigerian poultry studies likewise indicate that frequent antimicrobial use, including preparations containing colistin, represents an important concern for the selection and dissemination of resistant organisms within poultry production systems [1, 31].

Nigerian Poultry Evidence and Epidemiological Significance

Nigerian evidence therefore provides an important connection between the molecular properties of *mcr* and the epidemiology of poultry-associated resistance. Anyanwu et al. [1] detected *mcr*-1 in 23 of 48 colistin-resistant Enterobacterales recovered from 785 chicken samples and identified the novel *mcr*-1.22 allele in two *E. coli* isolates, demonstrating both circulation and genetic diversification of mobile colistin resistance in poultry [1]. These findings support the interpretation that poultry systems can provide an ecological setting in which antimicrobial selection, bacterial colonization and mobile resistance determinants interact, although the detection of *mcr* in poultry alone does not establish direct transmission to humans [1].

Table 2: Major *mcr* variants and their epidemiological significance

Variant / characteristic	Main significance
<i>mcr</i> -1	Most extensively reported plasmid-mediated colistin-resistance determinant and the first widely recognised mobile <i>mcr</i> mechanism [24]
<i>mcr</i> -2	Additional mobile colistin-resistance determinant demonstrating that transferable resistance extends beyond <i>mcr</i> -1 [12]
<i>mcr</i> -3	Major member of the expanding <i>mcr</i> family with numerous variants and broad geographical distribution [12]
<i>mcr</i> -4 to <i>mcr</i> -10	Demonstrate continued diversification of mobile phosphoethanolamine-transferase resistance mechanisms [12, 24]
Plasmid association	Provides an important basis for horizontal movement of resistance determinants among bacterial populations [30]
Co-resistance	Co-occurrence with other antimicrobial-resistance genes can contribute to multidrug-resistant bacterial populations and facilitate persistence under antimicrobial selection [1, 14]

Source: Elbediwi et al. [12]

The information summarized in Table 2 demonstrates why the epidemiological significance of *mcr* extends beyond the presence of a single resistance gene, because the combination of enzymatic resistance, plasmid mobility, genetic diversity and co-resistance can create multiple opportunities for persistence and dissemination [26, 29]. In poultry systems, these mechanisms can interact with antimicrobial exposure and production practices to maintain resistant bacterial populations, thereby creating potential opportunities for dissemination through animals, products, handlers and contaminated environments [1, 16].

Future Directions

Future research in Lagos State should move beyond routine detection of colistin resistance and prioritise genomic epidemiology to clarify how *mcr* genes, resistance plasmids, and bacterial clones circulate across poultry, environmental, and human reservoirs. The review by Anyanwu et al. [1] shows that *mcr* genes occur within diverse plasmid backbones and mobile genetic elements [7], while the first description of plasmid-mediated *mcr*-1 established that colistin resistance can disseminate through horizontal transfer rather than through chromosomal mutation alone [5, 7].

This is particularly relevant in Nigeria, where poultry-associated colistin-resistant Enterobacterales have already been documented and a novel *mcr*-1.22 variant has been reported in chicken isolates, indicating ongoing local genetic diversification [1]. For Lagos State, future work should therefore combine whole-genome sequencing, plasmid replicon typing, and resistome analysis with systematic sampling from farms, slaughterhouses, and poultry-associated environments so that clonal spread, plasmid movement, and cross-sector transmission can be distinguished more accurately [19, 28, 32].

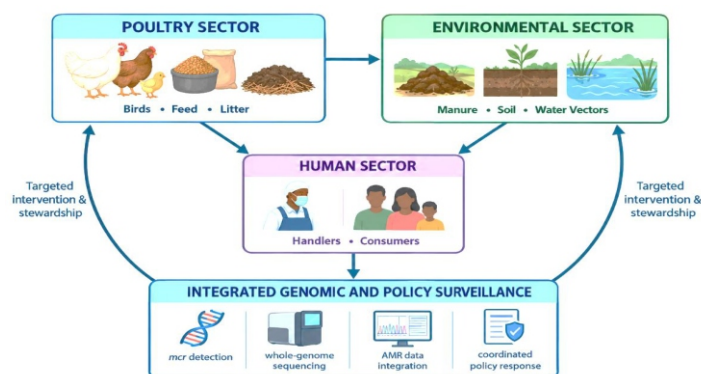


Figure 4. Future one health framework for monitoring *mcr* transmission
Source: Anyanwu et al. [1]

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Conclusion

Plasmid-mediated colistin resistance in poultry is best understood as a One Health challenge rather than a problem confined to animal production alone. Evidence from Nigeria shows that colistin-resistant Enterobacterales and *mcr*-positive *Escherichia coli* are already present in poultry, while abattoir environments provide additional opportunities for contamination and human exposure. Broader evidence further shows that *mcr* genes are carried on mobile genetic elements and may co-occur with resistance determinants to other critically important antimicrobials, thereby increasing the public-health significance of their spread.

For Lagos State, the key implication is that poultry, human, and environmental reservoirs should be investigated and monitored together rather than in isolation.

An effective response will require tighter antibiotic regulation, improved slaughterhouse hygiene, integrated One Health surveillance, and practical policy implementation supported by laboratory capacity and routine compliance monitoring. The evidence synthesized from Lagos State and other parts of Nigeria highlights the need to investigate and monitor poultry, human, and environmental reservoirs within an integrated one health framework. Further genomic and epidemiological studies across Nigeria will be important for clarifying transmission pathways and identifying opportunities for intervention. Ultimately, controlling *mcr*-mediated resistance will depend not only on detecting resistant organisms, but also on coordinated prevention across the poultry production, processing, and consumption chain.

Authors' Contributions

The authors of this research have significantly contributed to the study's conception, data collection, and manuscript development. All authors were involved in writing the manuscript or critically reviewing it for its intellectual value. They have reviewed and approved the final version for submission and publication and accepted full responsibility for the content and integrity of the work.

Acknowledgement

We thank all the researchers who contributed to the success of this research project.

Conflict of Interest

The authors declared that there are no conflicts of interest.

Funding

No funding was received for this research work.

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