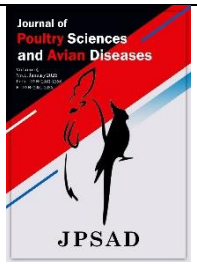
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Escherichia fergusonii in poultry: A scoping review of occurrence, antimicrobial resistance, pathogenic potential, and One Health relevance

Mohammad Barari[1], Seyed Mostafa Peighambari[1*]

[1] Department of Avian Health and Diseases, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran

*** Corresponding author email address**: mpeigham@ut.ac.ir

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A B S T R A C T

Escherichia fergusonii is a close relative of *Escherichia coli* that is increasingly detected in poultry, yet its veterinary and public-health significance remains poorly defined. This scoping review mapped evidence concerning its occurrence, identification, pathogenicity, antimicrobial resistance, genomic characteristics, ecological functions, and One Health relevance in poultry. PubMed and Scopus were searched from inception to 20 July 2026. Two reviewers independently screened records and extracted data, with disagreements resolved by consensus. Of 89 records identified, 31 duplicates were removed, 58 unique records were screened, 40 full texts were assessed, and 34 studies were included. *Escherichia fergusonii* was reported in healthy broilers and layers, ducks, diseased ostriches, retail chicken meat, manure, eggshells, and other poultry-associated sources. Species-specific PCR and whole-genome sequencing indicated that conventional biochemical systems may underestimate occurrence. Most isolates were recovered from apparently healthy birds. In contrast, clinical and experimental evidence supported strain-dependent pathogenicity, including fibrino-necrotic typhlitis in ostriches and mortality following experimental challenge with a broiler-derived strain. Antimicrobial resistance was the most consistent concern. Poultry-associated isolates carried *mcr-1*, *blaNDM-5*, *tet(X4)*, extended-spectrum β-lactamase genes, plasmid-mediated quinolone-resistance determinants, integrons, insertion sequences, and diverse conjugative plasmids. Viable, resistant, and enterotoxin-positive isolates were also recovered from retail chicken meat. Ecological studies suggested roles in nutrient competition, environmental persistence, and cecal ammonia production. The evidence identifies *E. fergusonii* as an underrecognized poultry-associated organism with limited but credible pathogenic potential and a documented capacity to harbor and transfer clinically important mobile antimicrobial-resistance elements. Standardized molecular surveillance, plasmid-resolved genomics, representative farm-to-food sampling, and natural-route pathogenicity studies are needed to define its veterinary and One Health importance.

Keywords: *Antimicrobial Resistance, Escherichia fergusonii, One Health, Pathogenicity, Poultry*

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1 Introduction

Escherichia fergusonii was formally described in 1985 as a distinct species within the genus *Escherichia* after characterization of isolates recovered primarily from human clinical specimens (Farmer et al., 1985). It is closely related to *Escherichia coli* and shares many phenotypic and ecological characteristics with other *Enterobacterales*. Since its original description, *E. fergusonii* has been recovered from human infections, domestic animals, wildlife, food products, and environmental sources. Reported human infections have included bacteremia, urinary tract infection, wound infection, and gastrointestinal disease, whereas animal-associated isolates have been recovered from both clinically affected and apparently healthy hosts (Gaastra et al., 2014). Nevertheless, its epidemiology and biological significance remain incompletely defined, and the species is generally regarded as an underrecognized opportunistic pathogen rather than a well-established cause of disease.

Poultry represents an increasingly important component of the reported host range of *E. fergusonii*. The organism has been recovered from the intestinal contents and feces of healthy broilers and laying hens, indicating that asymptomatic colonization can occur within commercial production systems. It has also been associated with severe fibrino-necrotic typhlitis and systemic involvement in ostriches (Herráez et al., 2005). Experimental characterization of the broiler-derived strain ECD-227 subsequently demonstrated multidrug resistance, systemic dissemination, and mortality in challenged chicks, providing evidence that at least some strains possess clinically relevant pathogenic potential (Forgetta et al., 2012). However, frequent detection in healthy poultry indicates that isolation alone does not establish causation and suggests that pathogenicity may depend on strain-specific virulence characteristics, host susceptibility, and environmental or management-related factors.

The true prevalence of *E. fergusonii* in poultry may be underestimated due to limitations in routine species identification. Its biochemical similarity to *E. coli* can lead to inaccurate or inconsistent identification with conventional phenotypic systems. In a Canadian broiler study, species-specific duplex polymerase chain reaction identified substantially more *E. fergusonii* isolates than the API 20E system when both methods were applied to the same presumptive colonies (Simmons et al., 2014). More recent investigations have increasingly used validated species-specific PCR, matrix-assisted laser desorption/ionization time-of-flight mass spectrometry, and whole-genome sequencing to improve taxonomic resolution. These methodological differences are important because occurrence estimates based on biochemical identification, molecular confirmation, selective culture, and microbiome sequencing do not represent equivalent levels of evidence.

In addition to its uncertain pathogenic role, poultry-associated *E. fergusonii* has attracted increasing attention as a reservoir of antimicrobial resistance and mobile genetic elements. High frequencies of resistance to β-lactams, tetracyclines, aminoglycosides, sulfonamides, and quinolones have been reported among broiler isolates (Simmons et al., 2016). Poultry-associated strains have also carried resistance determinants of major clinical concern, including *mcr-1*, *blaNDM-5*, *tet(X4)*, extended-spectrum β-lactamase genes, and plasmid-mediated quinolone-resistance genes. Several of these determinants were located on conjugative IncI2, IncX1, IncX4, IncHI2, and other plasmid backbones capable of transfer to *E. coli* recipients (Lin et al., 2022; Shi et al., 2025; Tang et al., 2022). These findings support the possibility that *E. fergusonii* participates in antimicrobial-resistance exchange within poultry-associated bacterial communities. Comparable concerns are well established among avian *E. coli*, in which pathogenic and commensal populations may carry diverse virulence-associated and antimicrobial-resistance determinants, including plasmid-mediated quinolone-resistance mechanisms in APEC from commercial poultry (Rezatofighi et al., 2021; Tahmasbi Ghasabsaraei et al., 2025).

Virulence-associated mobile elements provide an additional connection between poultry and public health. Heat-labile enterotoxin-producing *E. fergusonii* has been isolated from healthy commercial chickens, and *eltAB*-bearing IncF plasmids were transferred experimentally to *E. coli* (Oh et al., 2012). Related enterotoxin-positive strains were subsequently detected in broiler flocks and in retail chicken meat, indicating that potentially virulent lineages or their plasmids may persist throughout the poultry production chain (Kakita, Kudeken, et al., 2023; Kakita et al., 2024). Moreover, comparative genomic analysis identified a poultry-farm isolate carrying an *elt1*-bearing plasmid closely related to the enterotoxin-associated element detected in a human diarrheal isolate (Okuno et al., 2023). Although these findings do not demonstrate direct poultry-to-human transmission, they highlight plausible food-chain and horizontal gene-transfer pathways that warrant consideration within a One Health framework.

Despite the expanding literature, poultry-related evidence remains dispersed across occurrence surveys, diagnostic studies, clinical reports, experimental infection models, antimicrobial-resistance investigations, plasmid analyses, comparative genomic studies, food-safety research, and intestinal-ecology experiments. Differences in poultry populations, sampling units, culture methods, identification approaches, and outcome definitions further complicate interpretation. Accordingly, the aim of this scoping review was to systematically map and synthesize the available evidence on the occurrence, identification, pathogenicity, antimicrobial resistance, genomic characteristics, ecological roles, food-safety implications, and One Health significance of *E. fergusonii* associated with poultry.

2 Materials and Methods

2.1 Review design and reporting framework

This scoping review was conducted to map and synthesize the available evidence on the occurrence, identification, pathogenicity, antimicrobial resistance, genomic characteristics, ecological relevance, and One Health implications of *E. fergusonii* associated with poultry. A scoping review design was selected because the literature comprised heterogeneous study types, including surveillance studies, cross-sectional studies, case reports, experimental infection studies, diagnostic method studies, genomic analyses, microbiome studies, and in vitro ecological investigations. The review was developed in accordance with the methodological guidance of the Joanna Briggs Institute and reported in accordance with the Preferred Reporting Items for Systematic Reviews and Meta-Analyses extension for Scoping Reviews (PRISMA-ScR) (Peters et al., 2021; Tricco et al., 2018). The review protocol was not prospectively registered.

2.2 Information sources and search strategy

PubMed and Scopus were systematically searched from database inception, with the final database searches conducted on 20 July 2026. The search was limited to PubMed and Scopus because access to additional subscription-based veterinary and agricultural databases was not available through the authors' institution. Screening, eligibility assessment, and data extraction were subsequently completed during July 2026. The search strategy was intentionally broad because *E. fergusonii* is infrequently reported and poultry-related information may not be explicitly stated in article titles or abstracts. Search terms included the complete species name, abbreviated forms, and the term "*fergusonii*," with syntax adapted for each database. No restrictions were applied according to publication year, language, study design, poultry species, or full-text availability. The complete search strategies for PubMed and Scopus are provided in Supplementary Table S1. All retrieved references were imported into Rayyan for duplicate removal and eligibility screening (Ouzzani et al., 2016).

2.3 Eligibility criteria

Original studies were eligible when they reported extractable data on *E. fergusonii* originating from poultry, poultry products, or poultry-associated environments. Eligible poultry populations included chickens, ducks, turkeys, geese, quails, ostriches, and other domesticated avian species. Poultry-associated sources included feces, cloacal swabs, intestinal contents, tissues, carcasses, retail meat, eggs, eggshells, manure, litter, feed, water, and samples collected from farms, slaughterhouses, processing facilities, diagnostic laboratories, or retail settings. Studies were considered eligible when they addressed occurrence or prevalence, intestinal carriage, clinical disease, pathological lesions, experimental pathogenicity, species identification, antimicrobial susceptibility, multidrug resistance, resistance genes, virulence-associated determinants, plasmids and other mobile genetic elements, whole-genome sequencing, phylogenetic relationships, food safety, One Health relevance, intestinal ecology, or poultry-production effects. Studies involving human, mammalian, environmental, or non-poultry food isolates were only included when they provided a direct poultry-related comparison, such as a shared genomic lineage, plasmid, virulence element, resistance determinant, or other finding relevant to poultry-associated transmission. Studies were excluded if they contained no poultry-related evidence, investigated species other than *E. fergusonii*, reported the organism exclusively in non-poultry populations without a direct poultry comparison, did not present original data, or failed to provide species-specific results that could be reliably extracted. Reviews, editorials, commentaries, conference abstracts without sufficient data, and duplicate publications were excluded from the primary synthesis.

2.4 Study selection

Two reviewers independently screened the titles and abstracts of all unique records using the predefined

eligibility criteria. Articles were retained for full-text assessment when eligibility could not be confidently determined from the title and abstract alone. The same reviewers independently evaluated the full texts of potentially eligible studies. Disagreements during either screening stage were resolved through discussion and consensus. All reports selected for full-text assessment were successfully retrieved, and the principal reason for exclusion was recorded for each ineligible full-text article. The study-selection process, including the numbers of records identified, screened, assessed for eligibility, excluded at each stage, and ultimately included, was documented using a PRISMA-ScR flow diagram. Reasons for exclusion of individual reports at the full-text stage were recorded and are provided in Supplementary Table S2.

2.5 Data extraction

A standardized extraction workbook was developed before full-text data collection. Two reviewers independently extracted data from each included study, and discrepancies were resolved through discussion and consensus. Extracted study-level information included authorship, publication year, country, journal, study design, poultry species, production category, health status, sampling setting and period, sample source, total samples, positive samples, isolate numbers, and bacterial identification method. Additional variables included antimicrobial susceptibility methods and interpretive criteria, resistance frequencies and minimum inhibitory concentrations, multidrug-resistance definitions, resistance and virulence genes, plasmid replicons and structures, integrons, insertion sequences, transposons, sequence types, phylogenetic relationships, transferability findings, genome accessions, clinical signs, mortality, pathological lesions, tissue distribution, challenge design, and findings relevant to food safety, intestinal ecology, microbiome composition, and poultry production. Poultry-specific results were separately extracted whenever possible, pooled mixed-host findings were explicitly identified, and overlapping populations were flagged to prevent double counting.

Because *E. fergusonii* may be misidentified as *E. coli* by conventional phenotypic methods, confidence in species identification was classified into high, moderate, low, microbiome-inference, and unclear categories according to the identification method used. Whole-genome sequencing, validated species-specific PCR, or equivalent molecular confirmation was considered high confidence; MALDI-TOF mass spectrometry or sequence-supported identification was considered moderate confidence; biochemical or automated phenotypic identification alone was considered low confidence; microbiome-only taxonomic assignments were classified as microbiome inference; and insufficiently described methods were categorized as unclear.

2.6 Data synthesis

The extracted evidence was descriptively and thematically synthesized. Studies were grouped according to occurrence and epidemiological distribution, diagnostic methods, clinical significance and pathogenicity, virulence-associated determinants, antimicrobial-resistance phenotypes, resistance genes and mobile genetic elements, genomic diversity, poultry-meat contamination, food-safety and One Health relevance, and intestinal ecology or production-related effects. Studies were classified as core when they provided extractable poultry-derived data directly informing a primary review domain. In contrast, mechanistic, microbiome, and cross-source comparative studies were classified as contextual, qualitatively synthesized, and excluded from poultry occurrence estimates. Study-specific counts, percentages, resistance rates, and molecular findings were summarized where appropriate. A meta-analysis was not performed due to substantial heterogeneity across poultry species, sampling units, health status, sample sources, culture conditions, identification methods, antimicrobial panels, interpretive standards, and outcome definitions. Findings based on individual birds, pooled flock samples, selectively recovered resistant or virulence-associated isolates, retail products, isolate-confirmation proportions, and microbiome relative abundance were not directly considered comparable and were therefore separately summarized. A formal risk-of-bias assessment was not undertaken because the aim was to map the breadth and characteristics of the evidence rather than estimate a pooled effect; however, methodological limitations and the reliability of identification were considered throughout the synthesis.

3 Results

3.1 Review Findings

The database searches identified 89 records, including 51 from PubMed and 38 from Scopus. After removal of 31 duplicate records, 58 unique records underwent title and abstract screening. Eighteen records were excluded for not

meeting the eligibility criteria, leaving 40 reports for full-text assessment. The full text of every potentially eligible report was successfully retrieved. Six reports were excluded after full-text evaluation: four because the population or sample source was ineligible, one because it had no direct poultry connection, and one because it did not provide sufficient species-specific data for reliable extraction. Consequently, 34 studies were included in the scoping review. The study selection process is shown in Figure 1, and the excluded full-text reports and their reasons for exclusion are detailed in Supplementary Table S2.

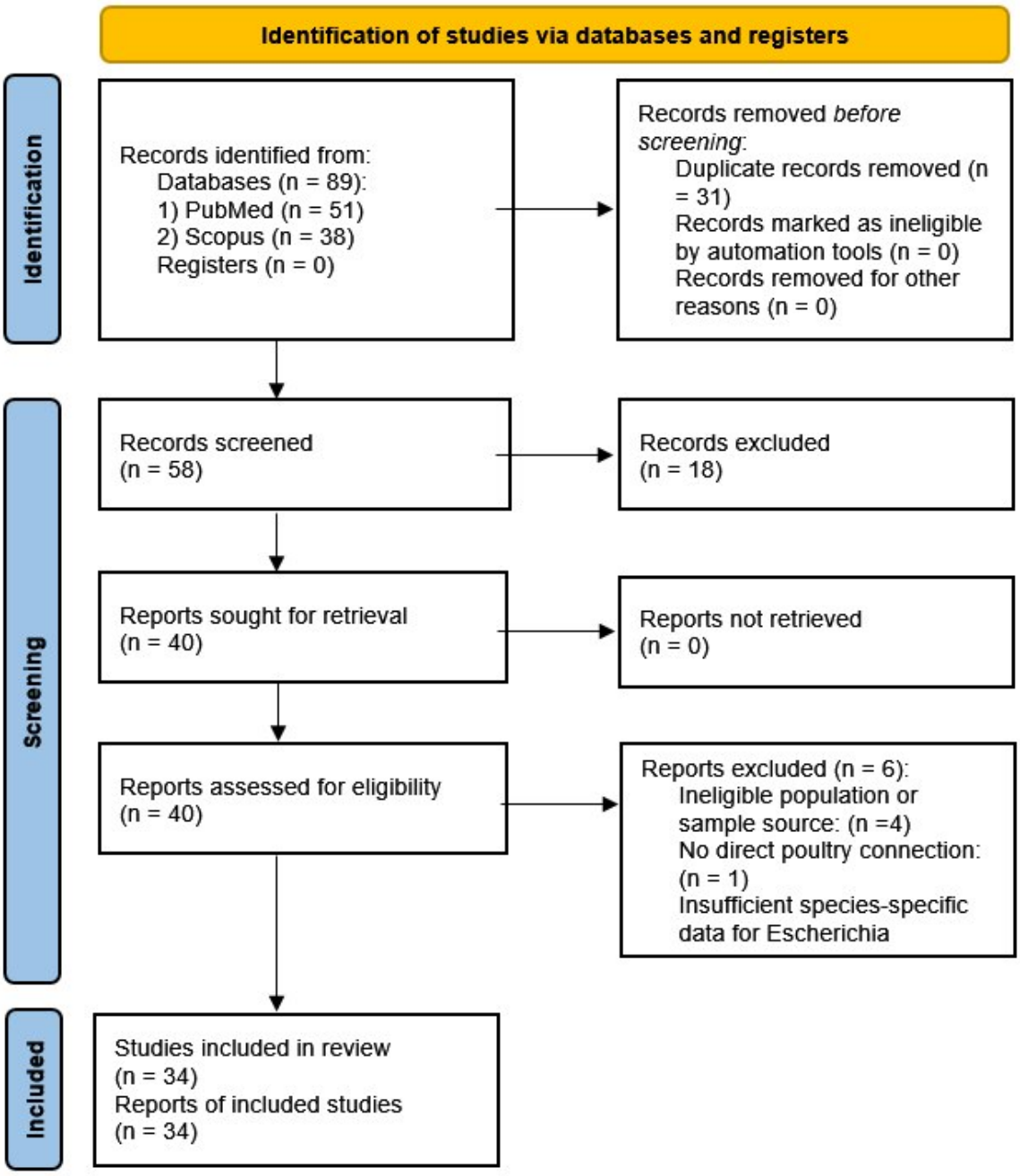


Figure 1. PRISMA-ScR flow diagram showing database identification, duplicate removal, title and abstract screening, full-text eligibility assessment, reasons for exclusion, and final inclusion of 34 studies examining *Escherichia fergusonii* in poultry and poultry-associated sources.

3.2 *Characteristics of the included studies*

The 34 included studies were published between 1994 and 2026, with a marked increase in research activity after 2020. Twenty-eight studies were classified as core poultry studies. In contrast, six were classified as contextual studies comprising two mechanistic in vitro investigations (Ha et al., 1995; Ha et al., 1994), two microbiome studies (Khongthong et al., 2024; Poudel et al., 2025), one cross-source comparative genomic study (Okuno et al., 2023), and one global genomic analysis containing avian isolates (Wang et al., 2025). Contextual studies informed ecological or comparative interpretation but were not included in poultry occurrence estimates.

The literature represented 16 national or multinational settings. Studies from Asia predominated, particularly China (n=9) and Japan (n=4). Four studies originated from Brazil, and Canada and the United States each contributed three. Additional investigations were conducted in South Korea, India, Bangladesh, Iran, Thailand, Algeria, Spain, and the Netherlands, as well as one pan-European study and one global comparative analysis. Chickens were the principal poultry population; broilers dominated, while evidence involving layers, ducks, ostriches, retail poultry products, and poultry environments was more limited. Study scale ranged from single-isolate genomic reports and individual clinical cases to nationwide surveys involving several hundred samples.

The reliability of species identification varied considerably. Twenty-four studies used whole-genome sequencing, validated species-specific PCR, or another molecular confirmation method and were classified as high confidence. Five relied primarily on biochemical or automated phenotypic systems and were classified as low confidence; one used sequence-supported or mass spectrometry-based identification and was considered moderate confidence; two inferred the organism from microbiome sequencing; and the method was unclear in two early in vitro investigations. The general characteristics of the included studies are summarized in Table 1, and their temporal and geographical distribution is illustrated in Figure 2. Overlapping study populations and reused isolates are documented in Supplementary Table S3.

Table 1. General characteristics of the 34 studies included in the scoping review of *Escherichia fergusonii* in poultry, arranged chronologically by publication year.

Study	Country/region	Design	Poultry population and sample source	Identification method	Confidence	Principal evidence domain
(Ha et al., 1994)†	United States	In vitro	Chicken-cecal isolate from continuous-flow culture; laboratory amino-acid competition experiments	Species stated; original identification method not reported	Unclear	Intestinal ecology and nutrient competition
(Ha et al., 1995)	United States	In vitro	Chicken-cecal isolate from continuous-flow culture; laboratory nutrient-limited survival experiments	Species stated; original identification method not reported	Unclear	Intestinal ecology and survival under nutrient limitation
(Herráez et al., 2005)	Spain	Case report	Adult farmed/captive ostriches; cecal lesions and systemic tissues	Pure culture, biochemical tests and API 20E	Low	Clinical disease and pathology
(Forgetta et al., 2012)	Canada	Experimental infection	Broiler-derived isolate ECD-227; experimental challenge of 1-day-old chicks	WGS/phylogenomics; MIC testing and experimental reisolation	High	Experimental pathogenicity, AMR and genomics
(Oh et al., 2012)	South Korea	Cross-sectional	Commercial broiler and layer flocks; pooled fresh feces	Selective culture, VITEK 2, LT-gene PCR/sequencing and PFGE	Low	Occurrence, LT enterotoxin and plasmid transfer
(Simmons et al., 2014)	Canada	Diagnostic-method	Commercial broilers aged 28–36 days; cecal and cloacal contents and presumptive isolates	Validated species-specific conventional and real-time duplex PCR	High	Diagnostic accuracy and poultry colonization
(Ferreira et al., 2016)	Brazil	Cross-sectional	Healthy 40-day-old broilers; cefotaxime/ceftazidime-selected cloacal isolates	Biochemical tests/API 20E; resistance-gene PCR and PFGE	Low	ESBL resistance, plasmids and molecular epidemiology

(Simmons et al., 2016)	Canada	Cross-sectional	Commercial broilers aged 28–36 days; PCR-confirmed isolates from the Simmons 2014 population	Species-specific PCR; resistance microarray and PFGE	High	AMR phenotypes/genes and molecular epidemiology
(Ferreira et al., 2018)	Brazil	Cross-sectional	Healthy commercial broilers; ciprofloxacin-selected cloacal isolates	Biochemical/API or VITEK 2 identification; PMQR PCR/sequencing and PFGE	Low	PMQR, AMR and plasmids
(Galetti et al., 2019)	Brazil	Genomic	Healthy commercial broilers; complete-genome follow-up of isolate 40A from Ferreira 2016	Prior phenotypic identification followed by complete PacBio WGS	High	Plasmids, AMR and heavy-metal tolerance
(Huizinga et al., 2019)	The Netherlands	Cross-sectional	Conventional and free-range retail chicken meat; ESBL-selective culture	MALDI-TOF plus WGS-based species confirmation	High	Retail-meat food safety, ESBL and genomics
(X. P. Li et al., 2020)	China	Genomic	Dead broilers submitted to animal hospitals; colistin-selected cecal colonies	MALDI-TOF, mcr-1 PCR, PFGE/MLST and WGS	High	Within-host mcr-1 diversity and plasmid transfer
(Y. Li et al., 2020)	China	Genomic	Chicken-farm fecal isolate HNCF11W	16S rRNA sequencing plus hybrid WGS	High	*tet(X4)*-mediated tigecycline resistance and transferable plasmids
(Tang et al., 2020)	China	Genome announcement	Single chicken-fecal isolate EFCF056	Hybrid Nanopore–Illumina complete WGS	High	Complete genome and mcr-1 multidrug-resistance plasmid
(Ewers et al., 2021)	Europe	Genomic	Healthy chickens in pan-European abattoir surveillance; selected cephalosporin-non-wild-type isolate	MALDI-TOF plus WGS	High	ESBL/AmpC genomic surveillance
(Pontes et al., 2021)	Brazil	Cross-sectional	Broilers on small farms; colistin-selected cloacal isolates	16S rRNA sequencing/species PCR plus Illumina WGS	High	mcr-1, IncHI2 plasmid and One Health
(Saha et al., 2021)	Bangladesh	Genomic	Commercial layer flock; poultry droppings, single isolate OTSVEF-60	Biochemical isolation plus WGS/KmerFinder confirmation	High	Genome, resistome, virulome and biofilm
(Lin et al., 2022)	China	Cross-sectional	Silkie chickens and meat ducks; cecal contents and duck anal swabs	Species-specific PCR plus Illumina/Nanopore WGS	High	Occurrence, mcr-1, virulence and plasmids
(Tang et al., 2022)	China	Surveillance	Food animals at farms/slaughterhouses; separable chicken-source samples	Species confirmation plus short- and long-read WGS	High	Occurrence, AMR, genomics and mcr-1 plasmids
(Kakita, Kudeken, et al., 2023)	Japan	Cross-sectional	Broilers from three Okinawan farms; cecal feces	Species-specific PCR and LT-gene PCR	High	Occurrence and spread of LT-positive strains
(Kakita, Shigemura, et al., 2023)	Japan	Cross-sectional	Broilers from three farms and nine houses; cecal feces and mcr-positive isolates	Species-specific PCR; phenotyping, PFGE and plasmid typing	High	mcr-positive strains, AMR and molecular epidemiology
(Liu et al., 2023)	China	In vitro	Laying-hen cecal contents; cultured ammonia-producing bacteria and in-vitro fermentation	Culture, PCR/Sanger sequencing and BLAST comparison	Moderate	Ammonia-producing ecology and nutritional control
(Okuno et al., 2023)	Japan; UK comparator	Comparative genomic	Public UK poultry-farm genome RHB43-C11 used as a comparator to a human isolate	Hybrid complete WGS and comparative phylogenomics	High	LT1 comparative genomics and One Health

(Srinivas et al., 2023)	India	Comparative genomic	Duck feces and retail chicken samples; six avian isolates	Species-specific PCR plus Illumina WGS	High	Avian comparative genomics, AMR and virulence
(Kakita et al., 2024)	Japan	Genomic	Locally produced retail chicken meat; six new LT-positive isolates	Species-specific PCR plus Illumina/Nanopore WGS	High	Retail-meat occurrence, LT1, AMR and genomics
(Kamel et al., 2024)	Algeria	Cross-sectional	Apparently healthy commercial broilers; cloacal swabs	Conventional biochemical testing and API 20E only	Low	Occurrence and AMR
(Khongthong et al., 2024)	Thailand	Microbiome	Ross 308 broilers under natural heat stress; cecal microbiome	V3–V4 16S rRNA microbiome sequencing	Microbiome inference	Dietary modulation of the cecal microbiome
(Mei et al., 2024)	China	Genomic	Retail chicken-meat isolate XJ19MCE1	mcr-1 PCR/sequencing plus PacBio WGS	High	IncX4 mcr-1 in chicken meat
(Torkan & Askari Badouei, 2024)	Iran	Cross-sectional	Diseased ostrich chicks from seven farms; fecal and cloacal samples	Two molecular PCR protocols plus biochemical characterization	High	Clinical association, virulence and AMR
(Alhassan et al., 2025)	China	Cross-sectional	Chicken manure, eggshell swabs and nearby lake sediments	Culture, partial 16S rRNA sequencing and species-specific PCR	High	Poultry-environment occurrence, AMR and virulence
(Poudel et al., 2025)	United States	Microbiome	Heritage NHC, Ross 308 and Ross 708 broilers; cecal and tracheal microbiome	Full-length 16S rRNA Nanopore microbiome sequencing	Microbiome inference	Genotype-associated microbiome occurrence
(Shi et al., 2025)	China	Genomic	Slaughterhouse chicken; fecal/anal-swab isolate EFSXRJ10	Species-specific PCR plus hybrid Illumina/Nanopore WGS	High	blaNDM-5 IncHI2 plasmid and transferability
(Wang et al., 2025)	Global; China index isolate	Comparative genomic	Global genome collection including 82 avian isolates	Hybrid WGS of index isolate plus analysis of 244 public genomes	High	Global phylogeny and avian-source comparison
(Momoki et al., 2026)	Japan	Surveillance	Healthy poultry; fecal samples in nationwide farm-animal surveillance	Species-specific PCR, selective culture and API32E	High	Nationwide occurrence, diagnostics, virulence and AMR

† Contextual studies (n=6) contributed mechanistic ecological, microbiome, or cross-source comparative genomic evidence relevant to poultry but were not used to estimate poultry occurrence. All unmarked studies were classified as core poultry studies (n=28).
Identification confidence: High, species-specific PCR and/or whole-genome sequencing; Moderate, sequence-supported identification without species-specific PCR/WGS; Low, biochemical/API identification only; Microbiome inference, taxonomic assignment without culture-confirmed isolates; Unclear, original identification method not reported.

(Simmons et al., 2014) and (Simmons et al., 2016) analyzed overlapping Canadian broiler populations. (Galetti et al., 2019) was a complete-genome follow-up of isolate 40A from (Ferreira et al., 2016). The Okinawa LT-positive series included reused comparator isolates; these populations should not be double-counted.

Abbreviations: AMR, Antimicrobial resistance; API, Analytical Profile Index; ESBL, extended-spectrum β-lactamase; LT, heat-labile enterotoxin; MALDI-TOF, matrix-assisted laser desorption/ionization time-of-flight mass spectrometry; MIC, minimum inhibitory concentration; MLST, multilocus sequence typing; PFGE, pulsed-field gel electrophoresis; PMQR, plasmid-mediated quinolone resistance; PCR, polymerase chain reaction; WGS, whole-genome sequencing.

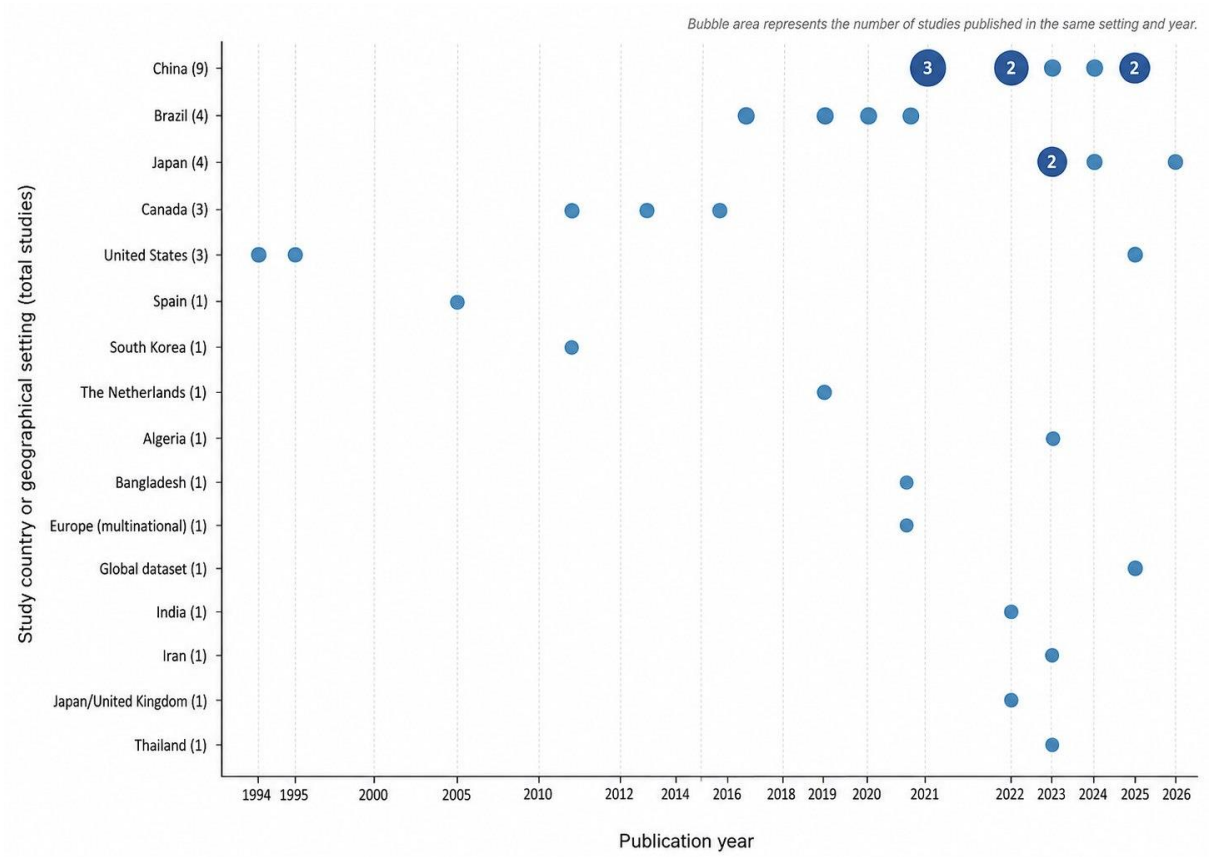


Figure 2. Temporal and geographical distribution of the 34 studies included in the scoping review of poultry-associated *Escherichia fergusonii*. Bubble area represents the number of studies published within the same geographical setting and year, with numbers displayed when more than one study was published. Multinational, global, and cross-country comparative datasets are presented as separate geographical categories.

3.3 Occurrence and distribution in poultry and poultry-associated sources

The occurrence synthesis was restricted to studies with interpretable poultry-related denominators; general detection, targeted selective recovery, and diagnostic or isolate-confirmation measures are presented separately. *Escherichia fergusonii* was detected in commercial broilers, laying hens, ducks, ostriches, slaughterhouse birds, retail chicken meat, and poultry-associated environments. In a nationwide Japanese survey, the organism was recovered from 253 of 548 poultry fecal samples (46.2%) (Momoki et al., 2026). In China, it was identified in 84 of 720 chicken-source samples (11.7%), while another survey recovered 54 isolates from 286 avian samples, including 15 of 50 chicken samples and 39 of 236 duck samples (Lin et al., 2022; Tang et al., 2022). These findings indicate that intestinal carriage may be common in some populations, although variation in sampling design and recovery methods precluded calculation of a pooled prevalence. Across the general, non-antimicrobial-targeted sample-level datasets summarized in Table 2A, 2,078 poultry or poultry-associated samples were examined, of which 430 were positive for *E. fergusonii*. These aggregate counts are provided only to indicate the scale of the available evidence and were not used to calculate a pooled prevalence because of substantial differences in poultry populations, sample sources, study designs, and identification methods.

Studies targeting defined virulence-associated subpopulations also demonstrated broad farm-level distribution. In South Korea, heat-labile enterotoxin-positive *E. fergusonii* was isolated from 43 of 184 commercial chicken flocks (23.4%), all of which were broiler flocks (Oh et al., 2012). In Okinawa, 52 of 346 broiler fecal samples (15.0%) yielded LT-positive isolates (Kakita, Kudeken, et al., 2023). In Canada, species-specific duplex PCR confirmed 268 of 301 presumptive isolates as *E. fergusonii* and identified at least one confirmed isolate on 31 of 32 broiler farms (Simmons et al., 2014). The 268/301 value

represents diagnostic confirmation among presumptive isolates rather than bird- or sample-level occurrence.

Several studies used antimicrobial-supplemented media and therefore estimated selected resistant subpopulations rather than overall carriage. Ciprofloxacin-selective culture recovered 11 isolates from 200 healthy Brazilian broilers, seven of which carried plasmid-mediated quinolone-resistance determinants (Ferreira et al., 2018). Colistin-selective screening yielded three *mcr-1*-positive isolates from 75 Brazilian broilers (Pontes et al., 2021), and one carbapenem-resistant isolate was identified among 25 slaughterhouse chicken samples in China (Shi et al., 2025). Evidence from diseased poultry was more limited; *E. fergusonii* was detected in 10 of 106 samples from ostrich chicks with diarrhea, reduced body weight, or lethargy (Torkan & Askari Badouei, 2024).

Poultry products and environments were additional sources of detection. LT-positive *E. fergusonii* was recovered from six of 60 retail chicken-meat samples in Okinawa, and genomic analysis showed close relatedness between several meat and broiler-fecal isolates (Kakita et al., 2024). An extended-spectrum β-lactamase-selective survey in the Netherlands identified one *E. fergusonii* isolate among 346 retail chicken-meat samples (Huizinga et al., 2019), while a Chinese chicken-meat isolate carried a transferable IncX4 *mcr-1* plasmid (Mei et al., 2024). Environmental sampling identified isolates from chicken manure and an eggshell (Alhassan et al., 2025). The evidence of occurrence is summarized in Table 2.

Table 2. Study-specific detection, recovery, and confirmation estimates for *Escherichia fergusonii* in poultry and poultry-associated sources*

A. General or non-antimicrobial-targeted detection in poultry or poultry-associated samples

Study/ country	Poultry population or source	Selection and identification	Analytical unit	Result	Measure type	Interpretation
(Tang et al., 2022)) China	Chicken-source samples collected at farms and slaughterhouses	Species isolation and confirmation; short- and long-read WGS in selected isolates	Chicken-source samples	84/720 (11.7%)	Sample-level detection	Chicken-specific denominator was separable from the mixed food-animal collection.
(Tang et al., 2022)China	Duck-source samples collected at farms and slaughterhouses	Species isolation and confirmation; short- and long-read WGS in selected isolates	Duck-source samples	20/270 (7.4%)	Sample-level detection	Duck-specific denominator was separable from the mixed food-animal collection.
(Lin et al., 2022)China	Silkie chickens; cecal contents	Differential culture followed by species-specific PCR	Chicken samples	15/50 (30.0%)	Sample-level detection	Species-specific subgroup within the avian survey.
(Lin et al., 2022)China	Meat ducks; cecal contents and anal swabs	Differential culture followed by species-specific PCR	Duck samples	39/236 (16.5%)	Sample-level detection	Species-specific subgroup within the avian survey.
(Srinivas et al., 2023)India	Duck feces and retail chicken products	Selective/differential culture, species-specific PCR, and WGS	Mixed poultry samples	6/48 (12.5%)	Mixed-source sample detection	Four duck-fecal and 44 retail-chicken samples were combined; source-specific positive counts were not reported.
(Torkan & Askari Badouei, 2024)Iran	Diseased ostrich chicks with diarrhea, reduced body weight, and/or lethargy	Biochemical characterization plus two molecular PCR protocols	Ostrich-chick samples	10/106 (9.4%)	Sample-level detection	Cross-sectional association with diseased birds; detection does not establish causality.
(Alhassan et al., 2025)China	Chicken manure, eggshell swabs, and nearby lake sediments	Culture, partial 16S rRNA sequencing, and species-specific PCR	Environmental samples	3/100 (3.0%)	Mixed-source sample detection	Two isolates were from manure and one from eggshell; source-specific denominators were not reported.
(Momoki et al., 2026)Japan	Healthy poultry in nationwide surveillance; fecal samples	Enrichment, species-specific PCR, selective culture, and API32E	Poultry fecal samples	253/548 (46.2%)	Sample-level detection	Broadest poultry-only estimate; poultry species and production categories were not stratified.

B. Virulence- or antimicrobial-resistance-targeted selective recovery

Study/ country	Poultry population or source	Selection and identification	Analytical unit	Result	Measure type	Interpretation
(Oh et al., 2012)South Korea	Healthy commercial broiler and layer flocks; pooled feces	Selective culture, VITEK 2, and LT-gene PCR/sequencing	Flocks	43/184 (23.4%)	Flock-level targeted detection	All positive flocks were broilers; estimates LT-positive *E. fergusonii*, not total species carriage.
(Ferreira et al., 2016)Brazil	Apparently healthy 40-day-old broilers; cloacal swabs	Cefotaxime/ceftazidime-selective culture; biochemical/API 20E identification	Bird samples	2/200 (1.0%)	ESBL-targeted recovery	Estimates recovery of cephalosporin-selected isolates, not general carriage.
(Ferreira et al., 2018)Brazil	Healthy commercial broilers; cloacal swabs	Ciprofloxacin-selective MacConkey culture; API 20E/VITEK 2	Bird samples	11/200 (5.5%)	Quinolone-targeted recovery	Estimates recovery of ciprofloxacin-selected isolates, not general carriage.
(Huizinga et al., 2019)The Netherlands	Conventional and free-range retail chicken meat	ESBL-selective culture; MALDI-TOF and WGS	Retail-meat samples	1/346 (0.3%)	ESBL-targeted recovery	One *bla*TEM-52B-positive isolate; not an estimate of total *E. fergusonii* contamination.
(Y. Li et al., 2020)China	Chicken-farm fecal samples	Tigecycline-resistant *Enterobacterales* screening; 16S rRNA and hybrid WGS	Fecal samples	1/16 (6.3%)	Tigecycline-targeted recovery	Selective detection of the *tet(X4)*-positive isolate HNCF11W.
(Pontes et al., 2021) Brazil	Broilers on small farms; cloacal swabs	Colistin-selective culture; species PCR/16S rRNA and WGS	Cloacal samples	3/75 (4.0%)	Colistin-targeted recovery	Estimates recovery of *mcr-1*-positive colistin-selected isolates.
(Kakita, Kudeken, et al., 2023)Japan	Apparently healthy broilers at slaughter; cecal feces	Selective culture, species-specific PCR, and LT-gene PCR	Broiler samples	52/346 (15.0%)	Virulence-targeted detection	Estimates LT-positive isolates; farm-specific rates were 11.8%, 26.7%, and 6.3%.
(Kakita et al., 2024)Japan	Locally produced retail chicken meat	Species-specific PCR, LT PCR, and complete WGS	Retail-meat samples	6/60 (10.0%)	Virulence-targeted detection	All positives were LT positive and originated from one supermarket chain.
(Shi et al., 2025)China	Slaughterhouse chickens; fecal/anal-swab samples	Carbapenem-resistant screening; species-specific PCR and hybrid WGS	Chicken samples	1/25 (4.0%)	Carbapenem-targeted recovery	Targeted recovery of one *bla*NDM-5-positive carbapenem-resistant isolate.

C. Isolate-confirmation or non-prevalence analytical measures

Study/ country	Poultry population or source	Selection and identification	Analytical unit	Result	Measure type	Interpretation
(Simmons et al., 2014)Canada	Apparently healthy broilers from 32 farms; cecal and cloacal contents	Validated species-specific conventional and real-time duplex PCR	Presumptive cultured isolates and farms	268/301 isolates PCR confirmed; 31/32 farms had ≥1 confirmed isolate	Diagnostic confirmation / farm detection	The 268/301 value is a confirmation proportion among presumptive isolates, not bird- or sample-level occurrence.
(Kamel et al., 2024) Algeria	Apparently healthy commercial broilers; Enterobacteriaceae isolates from 200 cloacal swabs	Conventional biochemical testing and API 20E	Cultured Enterobacteriaceae isolates	8/241 isolates (3.3%)	Isolate-level identification proportion	The denominator is cultured isolates rather than birds; molecular confirmation was not performed.

*The three sections separate general sample- or flock-level detection from virulence- or resistance-targeted selective recovery and from diagnostic or isolate-level confirmation measures. Percentages within and across sections should not be pooled because the analytical units, selection procedures, and identification methods differed substantially. Contextual studies based solely on mechanistic in vitro experiments, microbiome relative abundance, or cross-source comparative genomic analyses were not used to estimate poultry occurrence.

Abbreviations: API, Analytical Profile Index; ESBL, extended-spectrum β-lactamase; LT, heat-labile enterotoxin; MALDI-TOF, matrix-assisted laser desorption/ionization time-of-flight mass spectrometry; PCR, polymerase chain reaction; WGS, whole-genome sequencing.

3.4 *Identification methods and diagnostic challenges*

Identification methods varied substantially and were an important source of uncertainty. Early investigations commonly relied on colony morphology, carbohydrate-utilization profiles, API 20E, VITEK, or other biochemical systems (Forgetta et al., 2012; Herráez et al., 2005; Oh et al., 2012). The close phenotypic relationship between *E. fergusonii* and *E. coli* creates a risk of misidentification when these methods are not supported by molecular confirmation.

The diagnostic discrepancy was demonstrated most clearly in the Canadian broiler study. Among 301 presumptive isolates, validated duplex PCR identified 268 as *E. fergusonii*, whereas API 20E classified only 140 as this species (Simmons et al., 2014). The conventional assay targeted yliE and EFER_1569, and the real-time assay used EFER_3126 together with an *E. coli*-specific target. These assays detected *E. fergusonii* on 31 of 32 farms and showed that reliance on biochemical identification alone may substantially underestimate distribution.

Molecular confirmation became increasingly common in recent surveillance and genomic studies (Momoki et al., 2026; Saha et al., 2021; Shi et al., 2025; Tang et al., 2022; Wang et al., 2025). Whole-genome sequencing provided the highest level of taxonomic confidence while simultaneously characterizing sequence types, resistance genes, plasmids, and mobile elements. Hybrid sequencing enabled complete reconstruction of clinically important plasmids carrying *mcr-1*, *blaNDM-5*, and *tet(X4)* (X. P. Li et al., 2020; Lin et al., 2022; Mei et al., 2024; Pontes et al., 2021; Shi et al., 2025). In contrast, microbiome investigations inferred relative abundance without recovering viable isolates (Khongthong et al., 2024; Poudel et al., 2025). Their ecological findings could not establish strain identity, phenotype, or prevalence, and were independently interpreted of culture-confirmed evidence.

3.5 *Clinical significance and pathogenicity*

Most studies identified *E. fergusonii* in apparently healthy birds, indicating that intestinal carriage can occur without overt disease (Momoki et al., 2026; Oh et al., 2012; Simmons et al., 2014; Tang et al., 2022). Nevertheless, a small group of clinical and experimental studies suggested that particular strains may possess pathogenic potential under specific conditions.

The earliest substantial clinical evidence involved two adult ostriches with fatal fibrino-necrotic typhlitis (Herráez et al., 2005). Both birds had severe cecal inflammation, and *E. fergusonii* was recovered in pure culture from intestinal lesions and internal sites. Although the close association suggested a possible etiological role, identification was primarily phenotypic, and the disease was not experimentally reproduced. More recently, the organism was detected in 10 of 106 ostrich chicks from farms where affected birds exhibited diarrhea, reduced body weight, and lethargy (Torkan & Askari Badouei, 2024). The absence of healthy controls, detailed pathological confirmation, and experimental challenge prevented determination of whether *E. fergusonii* was a primary pathogen, secondary invader, or component of a polymicrobial disorder.

The strongest evidence of pathogenicity was provided by the broiler-derived strain ECD-227 (Forgetta et al., 2012). Experimental inoculation of young chicks caused rapid mortality, reaching approximately 18% at 24 h and 30% at 48 h, and the organism was recovered from internal organs. The strain carried multiple resistance and putative virulence determinants. However, the experimental route, the birds' age, and the use of a single strain limit generalization. Overall, the evidence supports strain-dependent pathogenic potential rather than uniform species-level virulence (Table 3).

Table 3. Clinical and experimental evidence concerning the pathogenicity of *Escherichia fergusonii* in poultry*

Study	Host and health status	Clinical / experimental context	Clinical and pathological findings	Positive sites / recovery	Experimental outcome	Identification	Causality strength	Principal limitation
(Herráez et al., 2005)	Two 2-year-old ostriches; fatal acute enteritis/septicemia	Two affected birds in a 14-ostrich educational/display farm after relocation and management-related stress	Anorexia, prostration, severe hemorrhagic diarrhea, fibrino-necrotic typhlitis,	Pure growth from intestinal lesions, blood, liver, and spleen	No challenge experiment; both affected birds died	Pure culture, biochemical tests, and API 20E	Strong clinical association	Two cases; no molecular confirmation, healthy controls, or experimental

			peritonitis, petechiae, mucosal necrosis, and intralesional Gram-negative colonies					reproduction.
(Forgetta et al., 2012)	One-day-old broiler chicks; experimentally challenged	Forty chicks per strain; comparison with virulent avian *E. coli* and non-virulent *E. coli* K-12	Reduced feed intake, listlessness, ruffled feathers, respiratory distress, disease, and death	ECD-227 recovered from liver, spleen, heart, lung, and internal tissues of diseased/dead birds	Subcutaneous 0.25 mL (~3 × 10^6 CFU); mortality 18% at 24 h and 30% at 48 h	WGS/phylogenomics, MIC testing, and reisolation	Experimental evidence of pathogenicity	Single isolate, neonatal birds, short follow-up, and non-natural inoculation route.
(Torkan & Askari Badouei, 2024)	Ostrich chicks aged 7–40 days with diarrhea, low weight, and/or lethargy	Cross-sectional sampling of 106 chicks from seven farms; positives occurred on three farms	Clinical signs were reported, but detailed gross and histopathological findings were not provided.	Fecal and cloacal samples	No challenge; 10/106 samples positive and 8/10 isolates classified MDR	Biochemical characterization plus two molecular PCR protocols	Possible association	No healthy control group, no lesion-based confirmation of causality, and no experimental reproduction.

*Causality categories reflect the design and directness of evidence: experimental evidence of pathogenicity, strong clinical association, or possible association. Isolation from diseased poultry alone was not considered proof of primary pathogenicity.

Abbreviations: API, Analytical Profile Index; CFU, colony-forming units; MDR, multidrug-resistant; MIC, minimum inhibitory concentration; PCR, polymerase chain reaction; WGS, whole-genome sequencing.

3.6 *Virulence-associated determinants and enterotoxin potential*

Heat-labile enterotoxin was the most consistently documented virulence-associated factor. In South Korea, all 43 isolates recovered from LT-positive broiler flocks carried *eltA* and *eltB*, and 16 transferred the *eltAB*-containing element to *E. coli* J53 by conjugation. The transferable enterotoxin plasmids belonged to the IncF group, and representative sequences were closely related to LT genes of human enterotoxigenic *E. coli* (Oh et al., 2012).

LT-positive lineages were also found in Okinawan broilers and retail chicken meat (Kakita, Kudeken, et al., 2023; Kakita et al., 2024). All six meat isolates carried *elt1AB* on IncFII plasmids, and several were closely related to fecal isolates. Comparative genomic analysis provided additional One Health context: the UK poultry isolate RHB43-C11 carried *elt1* on a plasmid that was highly similar to the LT1-associated element integrated into the chromosome of a human diarrheal isolate (Okuno et al., 2023). Active toxin was demonstrated in the human isolate, not the poultry isolate; therefore, the evidence supports related mobile elements but not direct transmission or confirmed toxin production by the poultry strain.

Other reported determinants were associated with iron acquisition, serum survival, adhesion, invasion, motility, stress tolerance, and biofilm formation. These included *iutA*, *iss*, *traT*, *ompA*, *gadA*, *ecpD*, *ibeB*, *yeeJ*, *fliC*, and the *csg* cluster (Forgetta et al., 2012; Pontes et al., 2021; Saha et al., 2021). The layer-origin strain OTSVEF-60 contained a broad predicted virulence repertoire and formed strong biofilms in vitro (Saha et al., 2021). However, most determinants were inferred from genomic annotation rather than functionally validated. Gene presence should therefore not be equated with expression or disease-causing capacity. Detailed information on the frequency, genetic location, functional evaluation, and interpretation of these determinants is provided in Supplementary Table S4.

3.7 *Antimicrobial-resistance phenotypes*

Antimicrobial resistance was one of the most frequently investigated characteristics of poultry-associated *E.*

fergusonii. Resistance was commonly reported to β-lactams, tetracyclines, aminoglycosides, sulfonamides, trimethoprim, and quinolones. Differences in isolate selection, antimicrobial panels, testing methods, breakpoints, and definitions of multidrug resistance limited direct comparisons. The 20 study/source entries summarized in Table 4 comprised 831 isolate-level antimicrobial-susceptibility observations, with study-specific testing sets ranging from 1 to 253 isolates. This summed denominator does not represent 831 unique poultry isolates because some datasets contained mixed animal sources, overlapping or selected isolate subsets, and reused study populations.

The largest poultry-specific dataset included 253 Japanese poultry isolates, of which 205 were resistant to at least one antimicrobial. Resistance was most frequent to ampicillin, tetracycline, streptomycin, kanamycin, and nalidixic acid, whereas resistance to ciprofloxacin, levofloxacin, imipenem, and meropenem was not detected (Momoki et al., 2026). Among 245 Canadian broiler isolates, resistance was highest to ampicillin, streptomycin, tetracycline, ceftiofur, and amoxicillin-clavulanate (Simmons et al., 2016). Resistance to ciprofloxacin, meropenem, and amikacin was absent, and only one isolate was resistant to imipenem.

High rates of multidrug resistance were reported in several smaller studies. All eight Algerian broiler isolates were multidrug resistant (Kamel et al., 2024); 41 of 54 poultry isolates from chickens and ducks in China were multidrug resistant (Lin et al., 2022); and eight of ten isolates from diseased ostrich chicks were multidrug resistant (Torkan & Askari Badouei, 2024). ECD-227 was resistant to 22 of 28 agents (Forgetta et al., 2012), and OTSVEF-60 was resistant to multiple β-lactam, sulfonamide, tetracycline, aminoglycoside, and quinolone agents (Saha et al., 2021). LT-positive poultry isolates also frequently displayed extensive resistance (Kakita, Kudeken, et al., 2023; Kakita et al., 2024).

Colistin resistance was repeatedly associated with *mcr*-positive poultry isolates. Forty-three chicken-derived isolates from Japan had colistin minimum inhibitory concentrations ranging from 4 to 16 mg/L (Kakita, Shigemura, et al., 2023). Three Brazilian broiler isolates were resistant to colistin, tetracycline, nalidixic acid, and trimethoprim-sulfamethoxazole (Pontes et al., 2021); EFCF056 had a colistin minimum inhibitory concentration of 4 mg/L (Tang et al., 2020); and a chicken-meat isolate carrying IncX4 *mcr-1* had a minimum inhibitory concentration of 8 mg/L (Mei et al., 2024). These studies largely used selective culture or preselected resistant isolates and therefore demonstrated the existence and characteristics of resistant lineages rather than population prevalence.

Resistance to extended-spectrum cephalosporins, carbapenems, and tigecycline was less frequent but clinically important. Brazilian broiler isolates carrying *blaCTX-M-2* displayed multidrug-resistant extended-spectrum β-lactamase phenotypes (Ferreira et al., 2016), a European chicken isolate carried *blaCTX-M-14* (Ewers et al., 2021), and a Dutch retail-meat isolate carried *blaTEM-52B* (Huizinga et al., 2019). A chicken isolate harboring *blaNDM-5* was resistant to several β-lactams and other antimicrobial classes (Shi et al., 2025). Another chicken isolate carried a transferable *tet(X4)* element along with additional resistance genes (Li et al., 2020a). The phenotype findings are summarized in Table 4.

Table 4. Antimicrobial-resistance phenotypes reported in poultry-associated *Escherichia fergusonii*[*]

Study/ source	n tested	Method / standard	Principal resistance phenotype	MDR finding	Interpretive note
(Forgetta et al., 2012)	1	MIC testing; CLSI/CIPARS criteria	ECD-227 was resistant to 22/28 agents; susceptible to ceftriaxone, chloramphenicol, ciprofloxacin, enrofloxacin, amikacin, and trimethoprim-sulfamethoxazole; two intermediate phenotypes	1/1 MDR	Single experimentally pathogenic isolate.
(Simmons et al., 2016)	245	CLSI disk diffusion	Ampicillin 184/245 (75.1%), streptomycin 154/245 (62.9%), tetracycline 140/245 (57.1%), ceftiofur 122/245 (49.8%), amoxicillin-clavulanate 116/245 (47.3%); no resistance to meropenem, amikacin, or ciprofloxacin	Definition: resistance to >2 antibiotics; overall MDR numerator not reported	Largest Canadian phenotype collection; overlaps with Simmons et al. 2014.
(Tang et al., 2024)	133 mixed food-	Broth microdilution	Sulfafurazole 130/133 (97.7%), tetracycline 126/133 (94.7%), ampicillin 112/133 (84.2%), sulfamethoxazole 111/133 (83.5%),	128/133 (96.2%); resistance to ≥4 agents	Phenotypes were pooled across chicken, duck, and pig isolates and

	animal isolates		colistin 25/133 (18.8%); no carbapenem resistance		cannot be attributed specifically to poultry.
(Lin et al., 2022)	54	Broth microdilution; CLSI *E. coli* criteria	Tetracycline 45/54 (83.3%), ampicillin 43/54 (79.6%), trimethoprim-sulfamethoxazole 41/54 (75.9%), florfenicol 40/54 (74.1%), ciprofloxacin 31/54 (57.4%), colistin 4/54 (7.4%); no meropenem or tigecycline resistance	41/54 (75.9%); resistance to ≥3 classes	Chicken and duck isolates combined for phenotype reporting.
(Kakita, Kudeken, et al., 2023)	52	Disk diffusion; CLSI 2020	Tetracycline 50/52 (96.2%), ampicillin 48/52 (92.3%), nalidixic acid 48/52 (92.3%), streptomycin 47/52 (90.4%), kanamycin 41/52 (78.8%); no ciprofloxacin, cefotaxime, meropenem, or aztreonam resistance	No formal MDR definition; 37/52 resisted all five principal agents	LT-positive broiler isolates from three farms.
(Kakita, Shigemura, et al., 2023)	43	Disk diffusion and colistin broth microdilution; CLSI 2020	All 43 were colistin resistant (MIC 4–16 µg/mL); tetracycline 18/43 (41.9%), ampicillin 7/43 (16.3%), trimethoprim-sulfamethoxazole 3/43 (7.0%); no carbapenem, fluoroquinolone, or tigecycline resistance	9/43 (20.9%); resistance to ≥3 classes	mcr-positive subset from the Okinawa broiler surveillance population.
(Kakita et al., 2024)	6	Disk diffusion; CLSI M100-S30	Kanamycin, streptomycin, tetracycline, and nalidixic acid: 6/6; ampicillin 4/6; trimethoprim-sulfamethoxazole 1/6; all susceptible to cefotaxime, meropenem, ciprofloxacin, and chloramphenicol	6/6; resistance in ≥3 classes	Retail-meat LT-positive isolates.
(Kamel et al., 2024)	8	Disk diffusion/broth microdilution; CLSI M100, 30th ed.	Doxycycline and erythromycin 8/8; ampicillin 7/8; ciprofloxacin and trimethoprim-sulfamethoxazole 6/8; cefotaxime, amoxicillin-clavulanate, and kanamycin 5/8; colistin 4/8	8/8; resistance to ≥3 agents	Identification relied on API 20E without molecular confirmation.
(Torkan & Askari Badouei, 2024)	10	Susceptibility-testing method and interpretive breakpoints not reported.	All 10 isolates were susceptible to ciprofloxacin. High resistance to amoxicillin-clavulanate, trimethoprim-sulfamethoxazole, and doxycycline was reported, although exact isolate-level frequencies were not provided.	8/10; resistance to ≥3 classes; four resisted 9–11 agents	Complete isolate-level resistance frequencies were not reported.
(Saha et al., 2021)	1	Kirby-Bauer disk diffusion; standard unclear	Resistant to ampicillin, sulfonamide, trimethoprim, tetracycline, doxycycline, gentamicin, ciprofloxacin, and nalidixic acid; susceptible to nitrofurantoin and chloramphenicol	1/1 MDR	Single layer-derived genomic isolate OTSVEF-60.
(Pontes et al., 2021)	3	MicroScan, broth microdilution, and disk diffusion; EUCAST/Brazilian criteria	All 3 resistant to colistin, tetracycline, nalidixic acid, and trimethoprim-sulfamethoxazole; all susceptible to ciprofloxacin, meropenem, imipenem, and tigecycline	3/3 across four tested categories	Colistin-selective isolation.
(Ferreira et al., 2016)	2	Disk diffusion; CLSI M100-S23	Both isolates resistant to amoxicillin-clavulanate, cefotaxime, cefepime, aztreonam, nalidixic acid, ciprofloxacin, levofloxacin, tetracycline, gentamicin, and trimethoprim-sulfamethoxazole; both susceptible to ertapenem	2/2; non-susceptibility in ≥3 categories	ESBL-selected isolates; same source population later included isolate 40A genomic follow-up.
(Ferreira et al., 2018)	7 PMQR-positive isolates	Disk diffusion; CLSI 2013	All 7 resistant to amoxicillin-clavulanate, cefotaxime, nalidixic acid, ciprofloxacin, levofloxacin, and tetracycline; trimethoprim-sulfamethoxazole 5/7, chloramphenicol 2/7, ceftazidime 1/7	7/7; resistance/non-susceptibility in ≥3 classes	Detailed phenotype was available for the *qnrB19*-positive subset, not all 11 isolates.

(Srinivas et al., 2023)	6	Kirby-Bauer disk diffusion; CLSI 2016	Cefotaxime 6/6, ciprofloxacin 5/6, tetracycline 4/6, co-trimoxazole 4/6, ampicillin 2/6; no imipenem, cefoxitin, ceftazidime, or gentamicin resistance	5/6 by abstract/table; resistance to ≥3 classes	The article text inconsistently stated 4/6 MDR.
(Y. Li et al., 2020)	1	Broth microdilution	HNCF11W was tigecycline resistant and was reported resistant to kanamycin, florfenicol, amoxicillin, and tetracyclines	1/1 MDR	Detailed isolate-specific MICs were mainly in unavailable supplementary material.
(Tang et al., 2020)	1	Susceptibility method as reported in genome announcement	EFCF056 was colistin resistant and resistant to 11 agents; individual results for the remaining ten agents were not completely reported	1/1 MDR	Single complete-genome isolate.
(Mei et al., 2024)	1	Agar/broth dilution; CLSI M100, 30th ed.	Resistant to colistin, ampicillin, streptomycin, tetracycline, chloramphenicol, and florfenicol; susceptible to cefazolin, cefotaxime, aminoglycosides, quinolones, fosfomycin, and trimethoprim-sulfamethoxazole	Multiclass phenotype; formal MDR result not stated	Single chicken-meat isolate.
(Shi et al., 2025)	1	Broth microdilution; CLSI M100-S30	Resistant to ampicillin, amoxicillin-clavulanate, cefotaxime, ceftazidime, meropenem, gentamicin, spectinomycin, apramycin, florfenicol, sulfafurazole, and tetracycline; susceptible to colistin and fluoroquinolones	1/1 MDR	Single *bla*NDM-5-positive chicken isolate.
(Alhassan et al., 2025)	3	Kirby-Bauer disk diffusion; mixed EUCAST/CLSI criteria	All 3 resistant to 19/24 tested agents, including multiple aminoglycosides, β-lactams, macrolides, sulfonamide, tetracyclines, piperacillin, polymyxin B, and imipenem in 2/3	3/3 MDR and XDR; MAR index 0.90	Small environmental isolate set; breakpoint and nomenclature interpretation requires caution.
(Momoki et al., 2026)	253	Disk diffusion; CLSI M100, 35th ed.	Ampicillin 149/253 (58.9%), tetracycline 141/253 (55.7%), streptomycin 138/253 (54.5%), kanamycin 109/253 (43.1%), nalidixic acid 82/253 (32.4%); no ciprofloxacin, levofloxacin, imipenem, or meropenem resistance	205/253 (81.0%) resistant to ≥1 agent; MDR not formally reported	Largest poultry-only phenotype dataset.

*Resistance frequencies are only reported where extractable. Single-isolate genomic studies describe the phenotype of that isolate and should not be interpreted as population frequency. MDR definitions varied across studies; the original study's definition is retained. Selective culture substantially enriched resistant phenotypes in several studies.

Abbreviations: CIPARS, Canadian Integrated Program for Antimicrobial Resistance Surveillance; CLSI, Clinical and Laboratory Standards Institute; EUCAST, European Committee on Antimicrobial Susceptibility Testing; MAR, multiple antibiotic resistance; MDR, multidrug resistant; MIC, minimum inhibitory concentration; PMQR, plasmid-mediated quinolone resistance; XDR, extensively drug resistant.

3.8 *Antimicrobial-resistance genes and mobile genetic elements*

Poultry-associated *E. fergusonii* carried a diverse repertoire of resistance genes, frequently located on conjugative plasmids and other mobile elements. In the Chinese food-animal collection, 25 of 133 isolates carried *mcr-1*, and plasmids from 23 were transferred to *E. coli* J53. IncI2 and IncX1 replicons were common, while complete sequencing revealed IncHI2-IncHI2A and IncI2 plasmids carrying different combinations of resistance genes (Tang et al., 2022). A separate avian survey identified *mcr-1* on transferable IncI2 plasmids (Lin et al., 2022), and IncI2 was also detected among Japanese poultry isolates (Kakita, Shigemura, et al., 2023).

Alternative *mcr-1* plasmid backgrounds were reported in Brazil and China. A Brazilian broiler isolate carried *mcr-1* on a conjugative 182,869-bp IncHI2/ST4 plasmid (Pontes et al., 2021). A chicken-meat isolate carried *mcr-1* on the 33,309-bp IncX4 plasmid pYUXJMC1-MCR (Mei et al., 2024), while EFCF056 contained *mcr-1* together with multiple additional resistance genes on a 204,246-bp plasmid (Tang et al., 2020). Within-host sampling from chicken guts further demonstrated that *mcr-1* could occur in

distinct *E. fergusonii* genotypes and on transferable IncI2 elements within a single host environment (Li et al., 2020b).

Carbapenem and tigecycline resistance involved highly concerning mobile elements. The chicken-derived isolate EFSXRJ10 carried *blaNDM-5* on an approximately 250-kb IncHI2/ST3 plasmid that transferred to *E. coli* (Shi et al., 2025). The chicken isolate HNCF11W carried *tet(X4)* on the transferable 57,105-bp IncX1 plasmid pHNCF11W-tetX4 and a second p0111-like plasmid with additional resistance genes (Li et al., 2020b).

Extended-spectrum β-lactamase, AmpC, and quinolone-resistance genes were also diverse. Brazilian broiler isolates carried *blaCTX-M-2* associated with class 1 integrons and ISCR1 (Ferreira et al., 2016). Among 127 selected Canadian ampicillin-resistant isolates, *blaCMY-2* predominated, with additional *blaTEM*, *blaACT*, *blaSHV*, and *blaCTX-M-15* genes and class 1 integrons (Simmons et al., 2016). Seven ciprofloxacin-selected Brazilian isolates carried *qnrB19* on small ColE-like plasmids (Ferreira et al., 2018), and *qnrS1* was reported in OTSVEF-60 and on the p0111-like plasmid of HNCF11W (Li et al., 2020b; Saha et al., 2021). Common additional determinants included *tet(A)*, *tet(B)*, *aadA*, *strA*, *strB*, *aph* and *aac* variants, *sul1*, *sul2*, *dfrA* variants, *floR*, *catA1*, and *cmlA1* (Kakita et al., 2024; Li et al., 2020b; Saha et al., 2021; Simmons et al., 2016; Tang et al., 2022; Tang et al., 2020).

The mobilome included IncF, IncFII, IncFIB, IncI1, IncI2, IncX1, IncX4, IncHI2, p0111, ColE-like, and non-typeable plasmids. Class 1 and class 2 integrons and insertion or recombination elements such as ISApl1, ISCR1, IS1R, ISEc23, and IS26-associated structures were reported (Ferreira et al., 2016; Pontes et al., 2021; Tang et al., 2022; Torkan & Askari Badouei, 2024). Complete genome analysis also demonstrated extensive insertion sequences, prophages, and heavy-metal-tolerance regions (Galetti et al., 2019; Saha et al., 2021). The repeated experimental transfer of clinically important determinants indicates that *E. fergusonii* can function as an exchange host for mobile resistance elements circulating among poultry-associated *Enterobacterales* (Table 5).

Table 5. Major antimicrobial-resistance genes and mobile genetic elements identified in poultry-associated *Escherichia fergusonii*[*]

Study/ source	Major AMR determinants	Genetic location/ plasmid	Mobile context	Transferability	Accession/ interpretation
(Forgetta et al., 2012)	*aadA*, *aac(3)-VI*, *qacEΔ1-sul1*, *sulI*, *tetA/tetR*, and chromosomal *gyrA* S83L	Class 1 integron/transposon on pECD227_112; five plasmids in ECD-227	Large plasmid-borne resistance and virulence regions	Not tested	Complete genome established a complex multidrug-resistant broiler strain.
(Simmons et al., 2016)	*bla*CMY-2 120/127; *bla*TEM 31/127; *bla*ACT 8/127; *bla*SHV 6/127; *bla*CTX-M-15 4/127; *aadA1*, *strA/B*, *tetA/B/C/E*, *sul1/2*, and *dfr* variants	Locations not resolved	Class 1 integron *intI1* in 35/127; extensive PFGE diversity	Not tested	Selected ampicillin-resistant subset; determinant frequencies should not be generalized to all isolates.
(Tang et al., 2022)	*mcr-1* 25/133; frequent *aph*, *tet(A)*, *bla*TEM-1B, *floR*, *bla*CTX-M-65, *bla*OXA-10, and *gyrA* S83L in the *mcr-1* subset	IncI2 and IncX1 common; representative pTB31P1 and pTB91P1 IncHI2/IncHI2A and pTB44P3 IncI2	Multiple transferable plasmid backgrounds	23/25 *mcr-1* plasmids transferred to *E. coli* J53 (~10^-4–10^-2)	Mixed chicken, duck, and pig collection; AMR results were not fully poultry-stratified.
(Lin et al., 2022)	*mcr-1*, *qnrS1*, *bla*OXA-10, multiple *aph/aad/aac* genes, *cmlA1*, *floR*, *sul3*, *dfrA14*, and *tet(A)* in four sequenced isolates	All *mcr-1* genes on IncI2 plasmids; pEF45-4, 61,140 bp	IncHI2/HI2A, IncI2, IncX1, IncN, IncX4, and p0111 backgrounds	*mcr-1* transferred to *E. coli* J53 (~10^-2–10^-4)	pEF45-4 accession CP086608.

(Ferreira et al., 2016)	*bla*CTX-M-2 in 2/2 isolates	Approximately 250-kb non-typeable plasmid; additional IncI1, IncFIB, and IncF replicons	Class 1 integron and ISCR1; PFGE type K	Conjugation/hybridization supported plasmid localization	Cephalosporin-selected isolates.
(Ferreira et al., 2018))	*qnrB19* in 7/11 isolates	2,989-bp ColE-like plasmid; additional IncI1, IncF, and IncHI1 replicons	ISEcp1-associated region; common PFGE type Ef A	Not reported	Plasmid sequence matched pPAB19-3 (JN985534).
(Galetti et al., 2019)	*bla*CTX-M-2, *aph(4)-Ia*, *aac(3)-IVa*, *strA/B*, *sul1/2*, *tetA/B*, *dfrA7Δ6*, and chromosomal *gyrA* S83L	p150_40A IncI1-ST1 and conjugative p280_40A IncHI2A-ST2; four plasmids total	In1554 class 1 integron; manganese, mercury, nickel, tellurium, copper, silver, and cobalt-zinc-cadmium tolerance loci	p280_40A transferred in vitro	Complete genome CP031282; follow-up of isolate 40A from Ferreira et al. 2016.
(Huizinga et al., 2019)	*bla*TEM-52B	Location not reported; isolate ST8330	WGS-confirmed ESBL determinant	Not tested	BioProject PRJEB33495; single retail-meat isolate.
(Li et al., 2020**a**)	*mcr-1* in two *E. fergusonii* colonies/isolates	IncI2 plasmids	Two distinct sequence types within one broiler gut	Both IncI2 plasmids transferred to *E. coli* C600	BioProject PRJNA434044; selected *mcr-1*-positive broilers.
(Tang et al., 2020)	*mcr-1*, *aac(3)-IId*, *aadA2*, *aph* variants, *bla*TEM-1B, *mph(A)*, *catA1*, *sul1/2*, *tet(A)*, and *dfrA12*	pEF01, 204,246 bp; six plasmids in EFCF056	Multidrug-resistance plasmid carrying all listed determinants	Not reported	Complete-genome accessions CP040806–CP040811.
(Li et al., 2020**b**)	*tet(X4)*, *aadA2*, *lnu(F)*, *tet(A)*, and *bla*SHV-12; second plasmid carried *aadA1*, *floR*, *dfrA14*, *bla*TEM-209, *bla*OXA-10, *cmlA1*, *arr-3*, and *qnrS1*	pHNCF11W-tetX4 IncX1 (57,105 bp) and p0111-like pHNCF11W-130 kb (130,643 bp)	IS26–abh–*tet(X4)*–ISCR2–virD2–*floR*–ΔISCR2 context; ST10543	Both plasmids transferred to *E. coli* C600	BioProject PRJNA625637.
(Ewers et al., 2021)	*bla*CTX-M-14	Location not specified; chicken isolate ST7852	WGS-detected ESBL determinant	Not tested	Single poultry *E. fergusonii* within a wider European food-animal study.
(Saha et al., 2021)	*sul1/2*, *qnrS1*, *mph(A)*, *dfrA12*, *aadA2*, *bla*TEM-1B, and *tet(A)*	Draft genome with IncX1 and p0111 replicons	Class 1 integron dfrA12–ant(3″)-I–qacEΔ–sul; 42 insertion-sequence copies; multiple metal-resistance systems	Not tested	Genome accession JABCUC000000000.1.
(Pontes et al., 2021)	*mcr-1* in 3/3; *sul2*, *tet(B)*, *dfrA1*, *aadA1*, and *sat-2* in additional plasmid contigs	pA12_mcr-1 IncHI2/ST4, 182,869 bp; additional IncB/O, IncX1, and p0111 backgrounds	IS1R, ISEc23, and tellurium-resistance *ter* operon	pA12_mcr-1 transferred to *E. coli* J53; recipient colistin MIC rose to 16 mg/L	Genome accession WYDM00000000.
(Kakita, et al., 2023)	*mcr-1* 43/43 and *mcr-5* 1/43	IncI2 detected in all transconjugants; additional IncHI1, IncF, and IncFIB	Two dominant PFGE types across farms/houses	*mcr-1* transferred from all 43 donors; *mcr-5* did not transfer	No WGS/Southern confirmation of the exact *mcr-1* plasmid when multiple replicons co-transferred.
(Srinivas et al., 2023)	Avian isolates carried broad resistomes, including β-lactam, quinolone, tetracycline, and	Multiple plasmid replicons and mobile elements across six study isolates and public genomes	Comparative pangenome/resistome/mobilome analysis	Not systematically tested	Avian genomes had significantly greater AMR-gene and mobile-element burdens than several non-avian source groups.

	folate-pathway determinants				
(Kakita, Shigemura, et al., 2023)	*tet(A)* and aminoglycoside phosphotransferases in 6/6; *bla*TEM-1B and *mph(A)* in 4/6; *sul2* in 5/6; *aadA5*, *dfrA17*, and *sul1* in 1/6	IncFII, IncFIB/IncI1, IncY, and IncX1 in all six; IncHI2/HI2A in one	Multiple plasmids co-carried resistance and LT-associated virulence regions	Not reported	Complete genomes deposited under PRJDB16297.
(Mei et al., 2024)	*mcr-1* plus *bla*TEM-1B, *aadA1/2*, *cmlA1*, *floR*, *tet(A/M)*, and *dfrA12* on a second plasmid	pYUXJMC1-MCR IncX4 (33,309 bp); pYUXJMC1-2 (82,020 bp)	IS26 downstream of *hha* on the IncX4 plasmid	*mcr-1* plasmid transferred to *E. coli* C600 at 4.17 × 10^-4	BioProject PRJNA967092.
(Shi et al., 2025)	*bla*NDM-5 plus 12 additional genes, including multiple *aph/aad/aac* genes, *cmlA1*, *floR*, *qnrS1*, *sul3*, and *tet(A)*	pSXRJ10-250K IncHI2/ST3, 251,846 bp; second p0111 plasmid carried additional resistance genes	IS3000/ISAba125/IS5/*bla*NDM-5/bleMBL/IS26 composite region	IncHI2 plasmid transferred to *E. coli* J53 at (4.78 ± 0.67) × 10^-5	Single chicken isolate; no detectable fitness cost in the recipient.
(Alhassan et al., 2025)	*sulI/II*, *bla*TEM, *bla*CTX-M-1, *bla*OXA-10/48, *bla*NDM-1, *tetA/B*, *erm(A/B)*, *strA/B*, *aadA15*, and *qnrC*	Genetic locations not resolved	PCR-based determinant panel; no WGS or plasmid typing	Not tested	Three manure/eggshell isolates; nomenclature and phenotype–genotype concordance require cautious interpretation.

*The table summarizes major or epidemiologically important determinants, rather than all genes reported in the extraction workbook. Counts refer to the specific isolate subset tested or sequenced. Absence from a row does not imply that a determinant was tested and found absent. Gene symbols are italicized. Plasmid incompatibility groups, sequence types, and insertion-sequence names are not italicized.
Abbreviations: AMR, antimicrobial resistance; MIC, minimum inhibitory concentration; PFGE, pulsed-field gel electrophoresis; ST, sequence type; WGS, whole-genome sequencing.

3.9 Genomic diversity and phylogenetic relationships

Genomic studies demonstrated substantial heterogeneity among poultry-associated *E. fergusonii*. In South Korea, 43 LT-positive isolates produced 38 PFGE patterns grouped into 17 types, with evidence of both local clonal spread and diversity (Oh et al., 2012). Canadian broiler isolates similarly formed numerous PFGE clusters and unique patterns (Simmons et al., 2016).

Whole-genome studies confirmed broad sequence-type and accessory-genome diversity. Six avian isolates from duck feces and retail chicken meat in India were phylogenetically diverse and carried variable combinations of resistance genes, virulence determinants, plasmids, and mobile elements (Srinivas et al., 2023). In the Chinese food-animal collection, 133 isolates were divided into 41 PFGE subclades, with chicken isolates occurring in 30 of these subclades (Tang et al., 2022). Complete plasmid reconstruction showed that similar resistance determinants could occur on structurally different plasmids, supporting both clonal and horizontal dissemination.

Global and cross-source analyses placed poultry isolates throughout the broader *E. fergusonii* phylogeny rather than in a single avian clade. Substantial genetic heterogeneity is also characteristic of avian *E. coli*, with isolates associated with colibacillosis distributed across multiple phylogenetic groups rather than representing a single uniform pathogenic population (Nakhaee et al., 2015). A global analysis of 244 genomes included 82 avian genomes interspersed with isolates from humans, livestock, food, wildlife, and environmental sources (Wang et al., 2025). In a separate analysis of 196 genomes, a poultry isolate and a human isolate were chromosomally distant but carried closely related *elt1*-associated elements (Okuno et al., 2023). These patterns support ecological connectivity and horizontal gene transfer, but not direct transmission in the absence of coordinated epidemiological data.

Complete-genome reports further illustrated accessory-genome plasticity. The Brazilian isolate 40A contained four plasmids with resistance, heavy-metal tolerance, and mobility functions (Galetti et al., 2019). OTSVEF-60 carried plasmid replicons, a class 1 integron, numerous insertion

sequences, prophages, and CRISPR-associated regions. ECD-227 carried five plasmids, and other isolates harbored complete IncHI2, IncI2, IncX1, IncX4, IncF, or p0111-like plasmids (Forgetta et al., 2012; Lin et al., 2022; Mei et al., 2024; Pontes et al., 2021; Shi et al., 2025; Tang et al., 2020).

3.10 *Poultry products, food safety, and One Health significance*

Retail poultry products provide evidence that *E. fergusonii* can persist beyond the farm. In Okinawa, LT-positive isolates were recovered from six of 60 retail chicken-meat samples. Several were closely related to broiler fecal isolates, all carried *elt1AB* on IncFII plasmids, and all were multidrug-resistant (Kakita et al., 2024). In the Netherlands, one *blaTEM-52B-positiveE. fergusonii* was identified among 346 retail chicken-meat samples screened for extended-spectrum β-lactamase-producing *Enterobacterales* (Huizinga et al., 2019). A Chinese chicken meat isolate carried a transferable IncX4 *mcr-1* (Mei et al., 2024).

Poultry-associated environments may also support persistence and dissemination. *Escherichia fergusonii* was recovered from chicken manure and eggshell samples (Alhassan et al., 2025), while the isolate 40A contained plasmids combining antimicrobial-resistance and heavy-metal-tolerance determinants (Galetti et al., 2019). These findings raise the possibility of maintenance under selective pressures, both antimicrobial and non-antimicrobial, in manure, litter, water, or farm environments, although longitudinal evidence remains limited.

Comparative genomic studies provided further One Health context. Avian genomes were distributed across lineages that included human, livestock, food, wildlife, and environmental isolates (Wang et al., 2025). The close relationship between a poultry *elt1* plasmid and the virulence element of a human diarrheal isolate also supports horizontal exchange across ecological compartments (Okuno et al., 2023). However, no included study documented a confirmed poultry-associated human outbreak or linked a human clinical case to a specific poultry source using both epidemiological and genomic evidence. The evidence therefore supports a plausible food-chain and One Health concern, particularly through contaminated poultry products, poultry-associated environments, and the circulation of mobile resistance and virulence elements. However, poultry-to-human transmission has not been demonstrated through linked epidemiological and genomic evidence.

3.11 *Intestinal ecology and poultry-production relevance*

A smaller group of studies indicated that *E. fergusonii* may influence intestinal ecology and production-related microbial processes independently of pathogenicity and antimicrobial resistance. A chicken cecal isolate showed a competitive advantage over *Salmonella* Typhimurium in serine utilization under defined in vitro conditions (Ha et al., 1994). A subsequent study found that *E. fergusonii* had a longer 50% survival time than two *S.* Typhimurium strains when serine was the limiting nitrogen source and survived longer after aerobic than anaerobic nutrient-limited growth (Ha et al., 1995). These findings suggest that nutrient utilization and persistence could influence survival in poultry houses or intestinal microbial communities, but they do not establish protection against *Salmonella* in live birds.

Microbiome studies suggested that relative abundance may vary with broiler genotype and dietary intervention. Full-length *16S rRNA* sequencing indicated greater cecal abundance in a heritage-type genotype than in commercial genotypes (Poudel et al., 2025). Dietary supplementation with sanguinarine-based isoquinoline alkaloids was associated with reduced relative abundance at 14 days (Khongthong et al., 2024). Because neither study recovered or functionally characterized isolates, the biological implications remain uncertain.

A production-related role was demonstrated in laying hens. Among 287 cultured ammonia-producing cecal isolates, 235 were identified as *E. fergusonii*, which showed the highest ammonia-producing potential. Sodium butyrate reduced its ammonia-generating activity and downregulated *lpdA*, *sdaA*, *gcvP*, *gcvH*, and *gcvT* (Liu et al., 2023). These findings suggest a possible role in intestinal ammonia generation and nutritional modulation, but their generalizability across strains and production systems is unknown. The experimental models, ecological outcomes, and principal limitations of these studies are detailed in Supplementary Table S5.

3.12 *Final Analysis*

This scoping review synthesizes the available evidence on the occurrence, identification, pathogenicity, antimicrobial resistance, genomic diversity, ecological relevance, and One Health significance of *E. fergusonii* in poultry. Collectively, the included studies show that the species is more widely distributed in poultry systems than its limited recognition in routine veterinary bacteriology might suggest. It has been recovered from healthy broilers and

layers, ducks, ostriches with enteric disease, poultry meat, manure, eggshells, and other poultry-associated sources. However, the literature remains methodologically heterogeneous, geographically concentrated, and strongly influenced by selective culture and molecular confirmation. Reported occurrence estimates should therefore be interpreted as study-specific observations rather than as evidence of a single global prevalence. The available data nevertheless identify poultry as a potentially important source and reservoir of *E. fergusonii* lineages carrying clinically relevant virulence and antimicrobial-resistance determinants.

Differences in reported occurrence are likely attributable to both genuine epidemiological variation and differences in study design. Some investigations estimated recovery from individual fecal or cloacal samples, whereas others used pooled flock samples, selected colonies, slaughterhouse specimens, retail products, or resistant subpopulations isolated on antimicrobial-supplemented media (Ferreira et al., 2016; Momoki et al., 2026; Pontes et al., 2021; Simmons et al., 2014). Studies using selective culture for quinolone-, colistin-, carbapenem-, or extended-spectrum cephalosporin-resistant bacteria did not measure general carriage, but rather the occurrence of predetermined resistant phenotypes. Similarly, flock-level positivity cannot be interpreted as individual-bird prevalence, and isolate counts obtained from multiple presumptive colonies cannot be directly converted into animal-level occurrence. Future surveys should explicitly report the sampling unit, distinguish samples from isolates, avoid double-counting colonies from the same host, and provide separate denominators for poultry species, production categories, and sample sources.

Species identification represents an additional source of uncertainty. *Escherichia fergusonii* shares many phenotypic characteristics with *E. coli*, and several early studies relied on biochemical or automated phenotypic identification (Herráez et al., 2005; Oh et al., 2012). The Canadian diagnostic study demonstrated the consequence of this limitation, with species-specific duplex PCR identifying substantially more isolates than API 20E among the same presumptive colonies (Simmons et al., 2014). This discrepancy suggests that routine systems may underestimate occurrence or misclassify the organism as *E. coli*. The increasing use of species-specific PCR and whole-genome sequencing has improved taxonomic confidence, particularly in recent studies of resistance and plasmids (Ewers et al., 2021; Tang et al., 2022; Wang et al., 2025)). Microbiome-based detections should remain analytically separate from culture-confirmed evidence because marker-gene sequencing cannot verify viability, phenotype, or strain-level pathogenic potential (Khongthong et al., 2024; Poudel et al., 2025). Future surveillance should combine differential culture with validated molecular confirmation, and clinically important isolates should ideally undergo whole-genome sequencing.

The pathogenic role of *E. fergusonii* in poultry remains less clearly defined than its role as an intestinal colonizer. Most studies recovered the organism from apparently healthy birds (Momoki et al., 2026; Simmons et al., 2014; Tang et al., 2022). Clinical evidence was concentrated in ostriches and one experimental broiler model. Recovery from severe fibrino-necrotic typhlitis and internal organs of ostriches provided a strong association with enteric and systemic disease, although identification was primarily phenotypic and Koch's postulates were not fulfilled (Herráez et al., 2005). Detection of multidrug-resistant isolates in ostrich chicks with diarrhea, poor growth, and lethargy also indicated a possible clinical role. Still, the absence of healthy controls and experimental reproduction prevented causal attribution (Torkan & Askari Badouei, 2024). In contrast, challenge with ECD-227 demonstrated rapid mortality and systemic recovery (Forgetta et al., 2012). Although this represents the strongest evidence of pathogenicity, a single strain, young birds, and an experimental route of inoculation limit generalization. The current evidence therefore supports strain-dependent pathogenicity rather than a uniform disease phenotype. This distinction has a clear parallel in avian *E. coli*, where pathogenicity is influenced by the broader combination of bacterial characteristics and host-pathogen interactions rather than by the presence of individual virulence-associated traits alone (Peighambari et al., 1995). Experimental models of avian colibacillosis further demonstrate that disease expression is influenced by the bacterial strain, inoculation route, tissue exposure, and host or predisposing conditions rather than bacterial detection alone (Peighambari et al., 2000).

This distinction between colonization and pathogenicity is especially important when interpreting virulence-associated genes. Heat-labile enterotoxin genes were repeatedly identified in poultry isolates. The South Korean study demonstrated plasmid localization and conjugative transfer of *eltAB* (Oh et al., 2012), and subsequent detection in broilers and retail meat suggested persistence of LT-positive strains or plasmids along the production chain

(Kakita, Kudeken, et al., 2023; Kakita et al., 2024). Comparative genomics identified a poultry *elt1* plasmid related to the LT1 element of a human diarrheal isolate (Okuno et al., 2023). However, active toxin was demonstrated only in the human strain, and no poultry-associated human infection was epidemiologically confirmed. Other genes associated with adhesion, iron acquisition, serum survival, invasion, stress tolerance, and biofilm formation were common in genomic reports (Forgetta et al., 2012; Pontes et al., 2021; Saha et al., 2021; Srinivas et al., 2023), but most were not functionally validated. Comparable virulence-associated determinants are well documented in avian *E. coli*, including genes involved in iron acquisition, serum survival, and adhesin-associated functions, such as *iucD*, *iss*, and *tsh*, although their detection alone does not establish pathogenicity (Nikpiran et al., 2019; Yazdani et al., 2013).

Antimicrobial resistance emerged as the most consistent and concerning feature. High resistance frequencies were repeatedly observed for ampicillin, tetracyclines, streptomycin, kanamycin, sulfonamides, and trimethoprim (Kakita, Kudeken, et al., 2023; Kamel et al., 2024; Lin et al., 2022; Momoki et al., 2026; Simmons et al., 2016). Multidrug resistance was common, although frequencies varied according to isolate selection, antimicrobial panels, and definitions. Broader surveillance collections generally retained susceptibility to carbapenems and fluoroquinolones (Momoki et al., 2026; Simmons et al., 2016), indicating that highly resistant isolates coexist with populations showing more limited resistance. The phenotype of selected multidrug-resistant strains should not be generalized to the species as a whole.

Of greater One Health importance was the diversity and mobility of resistance genes. Poultry-associated strains harbored *mcr-1*, *blaNDM-5*, *tet(X4)*, multiple *blaCTX-M* variants, *blaCMY-2*, *blaSHV*, *qnrB19*, *qnrS1*, and numerous aminoglycoside-, tetracycline-, sulfonamide-, trimethoprim-, and phenicol-resistance determinants (Ferreira et al., 2018; Li et al., 2020a; Lin et al., 2022; Mei et al., 2024; Pontes et al., 2021; Shi et al., 2025; Simmons et al., 2016; Tang et al., 2022). These genes occurred on transferable IncI2, IncX1, IncX4, IncHI2, IncF, p0111-like, and ColE-like plasmids. Several studies have demonstrated conjugation in *E. coli*, confirming that *E. fergusonii* can actively participate in horizontal resistance-gene exchange (Pontes et al., 2021; Tang et al., 2022). The occurrence of *mcr-1* on multiple plasmid backbones and in geographically distinct poultry isolates indicates dissemination through both clonal and plasmid-mediated processes. Transferable *blaNDM-5* and *tet(X4)* elements further show that the species can acquire resistance to last-line antimicrobial classes (Li et al., 2020b; Shi et al., 2025).

Co-localization of resistance determinants with integrons, insertion sequences, and heavy-metal-tolerance genes may promote persistence under diverse selective pressures. Class 1 and class 2 integrons, ISCR1, ISApl1, IS26-associated structures, and other insertion sequences were documented (Ferreira et al., 2016; Pontes et al., 2021; Shi et al., 2025; Tang et al., 2022; Torkan & Askari Badouei, 2024). The plasmids of isolate 40A combined antimicrobial-resistance and metal-tolerance determinants, raising the possibility that metals or disinfectants could contribute to plasmid maintenance even when antimicrobial exposure is limited (Galetti et al., 2019). Direct evidence of co-selection on poultry farms remains sparse, but the genetic architecture supports its biological plausibility. Surveillance should therefore assess complete plasmid structures and consider non-antibiotic selective pressures in litter, manure, water, and farm environments.

Genomic studies have consistently demonstrated that poultry-associated *E. fergusonii* is highly diverse rather than dominated by a single avian-adapted lineage. PFGE investigations identified numerous patterns within farm and national collections (Oh et al., 2012; Simmons et al., 2016), while whole-genome analyses revealed multiple sequence types, variable accessory genomes, and broad differences in plasmid and resistance content (Srinivas et al., 2023; Tang et al., 2022; Wang et al., 2025). Poultry isolates were interspersed with human, livestock, food, wildlife, and environmental isolates in global trees (Okuno et al., 2023; Wang et al., 2025). This supports ecological connectivity but does not prove direct transmission. Similar plasmids in chromosomally distant isolates suggest that mobile-element dissemination may be more important than clonal relatedness alone. Future One Health studies should combine core-genome analysis, complete plasmid reconstruction, and detailed epidemiological metadata.

Detection in retail chicken meat, manure, and eggshells extends relevance beyond the live bird. LT-positive and multidrug-resistant isolates were recovered from Japanese retail meat, with some closely related to broiler-fecal isolates (Kakita et al., 2024). ESBL-producing and *mcr-1*-positive strains were also identified in European and Chinese retail products (Huizinga et al., 2019; Mei et al., 2024). These observations provide plausible routes for exposure through food handling, cross-contamination, or inadequate cooking.

Environmental recovery further suggests circulation between birds, housing, waste, and products (Alhassan et al., 2025). However, no included study documented a confirmed poultry-associated human outbreak or linked a clinical isolate to a specific poultry source using epidemiological and genomic evidence. The evidence therefore supports food-chain plausibility and One Health concern, but not confirmed poultry-to-human transmission.

The ecological role of *E. fergusonii* may be broader than pathogenicity and resistance. Early mechanistic studies showed competitive serine utilization and prolonged survival under selected nutrient-limited conditions compared with *S.* Typhimurium (Ha et al., 1995; Ha et al., 1994). These findings suggest that metabolic fitness may influence persistence or participation in competitive-exclusion communities, but do not establish a protective effect in live birds. Microbiome studies found that relative abundances varied with broiler genotype and dietary supplementation (Poudel et al., 2025), although isolate-level function was not confirmed. In laying hens, *E. fergusonii* represented a major proportion of cultured ammonia-producing cecal bacteria, and sodium butyrate reduced ammonia production and expression of nitrogen-metabolism genes (Liu et al., 2023). This indicates a possible production-related role, but its generalizability across strains and management systems is unknown.

The evidence base has important limitations. Many studies were cross-sectional, geographically restricted, based on small isolate collections, or designed to select antimicrobial-resistant organisms. Identification methods varied considerably, poultry-specific denominators were unavailable in several mixed-host studies, and susceptibility results were often pooled across species. Different antimicrobial panels, breakpoints, and multidrug-resistance definitions further limited comparison. Several publications were follow-up molecular analyses of previously described populations, creating a risk of double counting if epidemiological and genomic reports were treated as independent. Clinical studies rarely included healthy controls, and experimental pathogenicity was evaluated for only one well-characterized broiler strain. Finally, the search was restricted to PubMed and Scopus, and reports indexed exclusively in specialized veterinary or agricultural databases may have been missed.

Despite these limitations, the review integrates epidemiological, clinical, diagnostic, genomic, antimicrobial resistance, food safety, and ecological evidence into a poultry-focused synthesis. Future research should move beyond opportunistic isolate characterization toward coordinated surveillance across farms, slaughterhouses, retail products, and human clinical settings. Standardized species-specific identification, representative sampling, harmonized susceptibility testing, complete plasmid sequencing, and open deposition of isolate metadata are needed. Pathogenicity studies should use multiple genetically diverse isolates, natural exposure routes, age-appropriate poultry models, and appropriate controls. Parallel comparison of isolates from healthy and diseased birds would help distinguish commensal carriage from pathogenic lineages, while functional validation of LT production and other predicted virulence traits is essential.

4 Conclusion

Escherichia fergusonii is an underrecognized but increasingly documented poultry-associated bacterium recovered from healthy and diseased birds, poultry meat, and poultry-production environments. Most reported poultry detections were obtained from apparently healthy birds, whereas a smaller number of studies indicate strain-dependent enteric or systemic pathogenic potential. However, the current evidence does not establish *E. fergusonii* as a primary poultry pathogen at the species level. The most consistent concern is its capacity to harbor and transfer clinically important resistance determinants, including *mcr-1*, *blaNDM-5*, *tet(X4)*, extended-spectrum β-lactamase genes, and plasmid-mediated quinolone-resistance genes. Their occurrence on diverse conjugative plasmids, together with recovery of resistant and enterotoxin-positive isolates from retail meat and farm-associated environments, supports the potential role of *E. fergusonii* as a reservoir and exchange host for mobile genetic elements within poultry systems. Direct poultry-to-human transmission has not been established. Representative molecular surveillance, standardized susceptibility testing, plasmid-resolved whole-genome sequencing, coordinated farm-to-food sampling, and controlled natural-route pathogenicity studies are required to define its veterinary, food-safety, and public-health significance.

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During manuscript preparation, the authors used Grammarly to improve English grammar and readability. The authors reviewed and edited all resulting text and take full responsibility for the final manuscript. No generative AI or AI-assisted tools were used to generate or modify images, figures, tables, data, or scientific analyses.

Conflict of Interest

The authors declare no conflict of interest.

Author Contributions

Conceptualization, S.M.P.; methodology, S.M.P.; investigation, S.M.P. and M.B.; literature search, M.B.; formal analysis, S.M.P. and M.B.; data curation, S.M.P.; visualization, S.M.P.; writing—original draft preparation, M.B.; writing—review and editing, S.M.P.; supervision, S.M.P.; project administration, S.M.P. Two reviewers (S.M.P. and M.B.) independently screened titles and abstracts, assessed full texts, and extracted data. All authors have read and agreed to the published version of the manuscript.

Data Availability Statement

Data supporting this scoping review are provided in the article and its Supplementary Materials. The complete extraction dataset is available from the corresponding author on reasonable request.

Ethical Considerations

Ethical approval was not required for this study because it is a scoping review based exclusively on previously published literature and did not involve human participants, live animals, or the collection of new experimental data.

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