Letters in Animal Biology

Journal homepage: www.liabjournal.com

Zoonotic *Escherichia coli* infections: Pathogenic variants, mechanism of disease, transmission routes, and foodborne outbreaks

Abdul Rehman Rafee [1], Monyer Abdulamier Abd Alfatlawi [2], Ali Asad [3], Sarah Noor [4], Shaista Shafiq [4], Iftikhar Ud Din [4], Nida Zainab* [5], Talha Ahmad [6], Sumaira Afzal [7], Muqadas Arshad [8], Silla Ambrose [9], Sahar Mustafa [10]

[1] *Department of Epidemiology and Public Health, Faculty of Veterinary Sciences, University of Veterinary and Animal Sciences, Lahore, Pakistan*
[2] *Department of Microbiology, College of Veterinary Medicine, University of Al-Qadisiyah, Iraq*
[3] *Department of Molecular Biology and Biotechnology, Faculty of Biosciences, Institute of Biochemistry and Biotechnology, University of Veterinary and Animal Sciences, Lahore, Pakistan*
[4] *Department of Biochemistry and Biotechnology, The University of Faisalabad, Pakistan*
[5] *Allama Iqbal Open University, Islamabad, Pakistan*
[6] *School of Engineering and Science, University of Dundee, United Kingdom*
[7] *Department of Zoology, University of Agriculture, Faisalabad, Pakistan*
[8] *Department of Human Nutrition, The University of Agriculture, Peshawar, Pakistan*
[9] *Faculty of Veterinary Science, University of Agriculture, Faisalabad, Pakistan*
[10] *Department of Clinical Medicine and Surgery, University of Agriculture, Faisalabad, Pakistan*

Article info

Received: 24 July 2025
Received in revised form: 16 September 2025
Accepted: 22 September 2025
Published online: 04 October 2025

Keywords

Escherichia coli
Strains
Transmission
Zoonosis
Foodborne outbreaks
One Health

* *Corresponding author:*
Nida Zainab
Email: nidach285@gmail.com

Reviewed by:

Itrat Zahra
Institute of Zoology, University of the Punjab, Lahore, Pakistan

Consent to publish the name of second reviewer could not be obtained

T. Ramasamy
Madras Veterinary College, Tamil Nadu Veterinary and Animal Sciences University, Chennai-600 007, India

Abstract

Escherichia coli is a gram-negative, rod-shaped bacterium with diverse pathogenic strains. Most strains of *E. coli* are motile and capable of causing infections in humans, small and large ruminants, and birds. The zoonotic *E. coli* phenotypes include Shiga toxin-producing *E. coli* (STEC), enteropathogenic *E. coli* (EPEC), enterotoxigenic *E. coli* (ETEC), enterohemorrhagic *E. coli* (EHEC), enteroaggregative *E. coli* (EAEC), and uropathogenic *E. coli* (UPEC), all of which pose a significant threat to public health. These pathogenic variants possess unique virulence factors, including Shiga toxins, adhesins, and enterotoxins, which enable E. coli to colonize host cells and disrupt their functions. The transmission of these pathogenic agents often occurs through direct contact with the infected animal, consumption of unhygienic dairy products, and environmental exposure to fecal material. Foodborne outbreaks due to zoonotic *E. coli*, specifically STEC O157:H7, are most often associated with undercooked meat, unpasteurized dairy, and contaminated water. This review highlights the major zoonotic pathotypes of *E. coli*, delineates their disease mechanisms and transmission routes from animals to humans, along with a summary of prominent foodborne outbreaks in humans and animals. It further emphasizes the importance of adopting an integrated One Health approach for the prevention and effective control of zoonotic *E. coli* infections, thereby reducing their incidence and public health burden.

1. Introduction

Escherichia coli (*E. coli*) is a gram-negative bacterium that colonizes the gastrointestinal tract and other mucosal surfaces of various animals (Puvača and de Llanos Frutos 2021). Most *E. coli* strains cause severe diseases of the gastrointestinal tract, but some also cause extra-intestinal infections (Moxley 2022). The dual nature - a potential deadly disease-causing pathogen and a vital commensal bacterium, makes *E. coli* an intriguing paradox of the human gut microbiota (Hameed et al. 2024). Commensal *E. coli* plays a vital role in gastrointestinal health and is the most ubiquitous facultative anaerobe of the gut (Zhang et al. 2022). It supports the gut microbial balance by competing with harmful bacteria and binding the mucosal membranes without damaging the normal physiological conditions. However, pathogenic strains disrupt the symbiotic balance and cause diseases (Zaada et al. 2019). Interestingly, while these strains cause acute human illness, they often

thrive as asymptomatic commensals in the primary animal reservoirs such as cattle, sheep, and goats, facilitating widespread environmental and foodborne contamination (Peek et al. 2018). Zoonosis, by definition, includes diseases transmissible from animal species to humans, and *E. coli* is one of the leading causes in this group. Zoonotic *E. coli* infections, especially infections triggered by enterohemorrhagic *E. coli* (EHEC) strains such as O157:H7, pose significant risks of animal-to-human transmission (Liu et al. 2023; Nupur et al. 2023). The EHEC strains are long recognized to have a severe adverse impact on the health of humans and animals, often leading to acute diseases like hemorrhagic colitis, diarrhea, and the life-threatening hemolytic uremic syndrome (HUS) (Hwang et al. 2021). Zoonotic *E. coli* infections, particularly STEC infections, are of considerable public health concern because of their profound impact on food safety, the healthcare system, economies, and culture (Majowicz et al. 2014; Ramos et al. 2020).

Based on its virulence and site of infection, *E. coli* is classified into intestinal pathogenic *E. coli* (IPEC) and extraintestinal pathogenic *E. coli* (ExPEC) (Sora et al. 2021). These pathogenic variants have acquired mobile genetic elements, such as plasmids, transposons, and bacteriophages, which encode a wide variety of virulence factors such as toxins and adhesins. These virulence factors enable *E. coli* to cause immune evasion, tissue colonization, and host cell death (Al-Mustapha et al. 2023). IPEC pathotypes, such as enterotoxigenic *E. coli* (ETEC), Shiga toxin-producing *E. coli* (STEC), and enteropathogenic *E. coli* (EPEC), cause various diarrheal diseases, whereas EPEC strains are mainly associated with sepsis, neonatal meningitis, and urinary tract infections (Manges et al. 2019; Cabrera-Sosa and Ochoa 2020; Meena et al. 2021). With nearly 75% of emerging infectious diseases originating from animals, the global incidence of *E.coli* is rising. This emphasizes the urgent need for comprehensive and integrated control to counteract such inter-species pathogen transmission (Chala and Hamde 2021; Rodriguez 2024). Severe loss of economic resources and disease occurrence can be initiated by outbreaks frequently associated with food contamination and result in life-threatening conditions like HUS and hemorrhagic colitis. The acute clinical manifestations of zoonosis, like hemorrhagic colitis and HUS, make them particularly insidious with cattle as most important reservoir and is usually contracted through contaminated food and water (Ramos et al. 2020). The risk of HUS and other long-term complications is disproportionately high in very young, the elderly, and immunocompromised individuals (Christensen et al. 2021).

A very complicated public health problem is the transmission of *E. coli* from the environment to animals and humans. Contaminated water used for drinking and exposure to the environment can transmit *E. coli*, which resides in stool, water, and soil (Laird et al. 2021). Direct contact between people and animals is also vital, particularly in farms. The use of veterinary services and animal manure as compost in horticulture is another condition that could result in transmission (Govers et al. 2024). These dependencies emphasize the need to have a One Health strategy that brings together environmental, animal, and human health programs. Although these modes are extremely important, transmission from human to human poses a very big challenge, especially in dirty, poor environments (Mwafy et al. 2023; Nadi et al. 2024; Denpetkul et al. 2025). Shiga toxin-producing *E.coli* (STEC)-associated foodborne outbreaks across the globe are a public health priority due to the potential to cause severe illness, substantial economic loss, and an erosion of consumer confidence. More than 39,787 cases and 1,343 outbreaks have occurred since 1982 worldwide, including a major outbreak in Germany in 2011 that caused 3,126 illnesses and 46 deaths (Köckerling et al. 2017). Dairy and meat are most often the original sources of contamination and cause 30-31% of European and 35-40% of American infections, respectively. The increased risk was confirmed by studies in which it was identified that 11.1% of animal feed samples were found to be positive for STEC when tested (Venegas-Vargas et al. 2016). Stricter food safety procedures, such as zero-tolerance for STEC in ready-to-eat foods and creating effective interventions such as vaccination in animals, are immensely recommended in a bid to stem this problem. Public health interventions still grapple with the issue of new STEC serotypes arising despite such interventions and heightened public awareness (Mehrdel et al. 2023; Thomas and McAllister 2024).

This review provides a comprehensive and updated overview of zoonotic *E. coli* infections by characterizing major intestinal pathotypes such as EHEC/STEC, EPEC, and ETEC and their clinical outcomes, ranging from simple diarrhea to life-threatening HUS. It will delineate the complex pathways of transmission from animal reservoirs, particularly cattle, through contaminated food, water, and direct contact, while highlighting the emergence of hypervirulent strains and antibiotic resistance. Lastly, the review highlights major foodborne outbreaks to indicate the effect on public health and calls for a "One Health approach" to harmonize the environmental, animal, and human health sciences for an effective surveillance, management, and mitigation of this global threat.

2. Zoonotic *E. coli* pathotypes

As discussed above, *E. coli* constitutes a diverse group of gram-negative bacteria, where some strains are harmless and others cause severe infections affecting humans, animals, and birds (Puvača and de Llanos Frutos 2021; Yu et al. 2021). The disease-causing strains are classified into various pathotypes based on their virulence factors and mechanisms of infection. Some of the important pathotypes of medical and veterinary importance are discussed as follows.

2.1 Enterohemorrhagic *E. coli* (EHEC) or Shiga-toxin producing *E. coli* (STEC)

A highly infectious pathogen whose detrimental effects on the gastrointestinal system are well documented is EHEC, particularly the O157:H7 serotype and non-O157 STEC isolates, such as O26, O111, and O145 (Holzer et al. 2025). Virulence is caused by core virulence determinants such as hemolysin, enteric attachment intimin, and Shiga toxins (stx1, stx2 - of which stx2 is extremely toxigenic) (Pakbin et al. 2021; Ouarroud et al. 2023; Lee et al. 2024). These proteins synergistically cause host cell lysis and enhance disease severity. Clinically, EHEC infection results in profuse diarrhea that can progress to hemorrhagic colitis (Melinte et al. 2024). In vulnerable individuals, it causes HUS, a potentially lethal syndrome characterized by thrombocytopenia, hemolytic anemia, and sudden onset of kidney failure. Though other ruminants such as goats and sheep are also responsible for the perpetuation of EHEC, cattle are the primary asymptomatic reservoir for the disease (Ray and Singh 2022). Effective transmission to humans, primarily through contaminated food or water, is facilitated by the low infectious dose and persistence of the bacteria in the bovine gastrointestinal tract (Edison et al. 2024). Successful control measures call for continued research into the mechanisms of virulence of EHEC and reservoir dynamics, particularly

in the face of the continued emergence of new serotypes with their possible causation of outbreaks (Strzelecki et al. 2025). Cattle, particularly "supershedders" that infect the environment, are the major reservoir of EHEC/STEC in animals. Xenografts, rabbits, and mice are employed by researchers as models of animals to understand infection of these strains. Clinical manifestations of EHEC, e.g., diarrhea and, in others, clinical manifestations which are indistinguishable from human illnesses like hemolytic uremic syndrome (HUS), are studied through these models. Furthermore, Shiga toxins and locus of enterocyte effacement (LEE) enable the bacteria to attach and kill intestinal cells, and these features make the bacteria pathogenic. Though the animal models do not simulate human disease, they do provide information.

2.2 Uropathogenic *E. coli* (UPEC)

It is the most prevalent extraintestinal pathogenic *E. coli* (ExPEC) sub-pathotype, which is primarily implicated in urinary tract infections (Whelan et al. 2023). It causes urinary tract infections in humans, cats, dogs, cattle, and pigs (García et al. 2023; Oh and Park 2025). It possesses certain adhesion genes, such as pyelonephritis-associated pili (PAP) and S fimbria adhesion (SFA), which facilitate robust colonization, toxins such as hemolysin A (hlyA), and efficient iron-acquiring systems such as siderophores (Sroithongkham et al. 2024). They are responsible for various types of diseases, including urethritis, cystitis, pyelonephritis, and urosepsis (Zagaglia et al. 2022). HlyA is a pore-forming exotoxin that induces host cell lysis and iron release, and cytotoxic necrotizing factor (CNF-1) disrupts host cytoskeleton and signaling pathways, which result in inflammation and further tissue damage (Chaoprasid and Dersch 2021; Moxley 2022).

2.3 Avian Pathogenic *E. coli* (APEC)

APEC is a well-recognized cause of colibacillosis in poultry with severe economic implications. This pathotype shares significant virulence factors with UPEC, such as increased serum survival genes (iss), hemolytic fimbriae (hlyF), outer membrane protein (ompA), iron-scavenging siderophores, and temperature-sensitive hemagglutinin (tsh) that facilitate the adhesion, immune evasion, and iron uptake by the pathotype (Kathayat et al. 2021; Hu et al. 2022). APEC is particularly involved in multiple organ damage and causes airsacculitis, pericarditis, perihepatitis, and septicemia, often mediated via virulence and resistance genes carried on colicin V plasmids (Ezzat et al. 2023; Khairullah et al. 2024; Rahayu et al. 2025). These plasmids in APEC not only enhance pathogenicity but also confer multidrug resistance. Its similarity with UPEC and neonatal meningitis *E. coli* (NMEC) raises concern about its zoonotic potential and hence warrants its appropriate diagnosis by bacterial isolation, PCR for virulence genes, and antibiotic sensitivity testing (Nowaczek et al. 2021).

2.4 Other pathotypes of *E. coli*

Septicemia-associated *E. coli* pathotype is strongly linked to potentially fatal septicemia and bacteremia (Al-Quraishi and Jabar 2022). Similarly, NMEC is a significant etiologic agent of neonatal meningitis (Su et al. 2023). Although the virulence determinants responsible for the pathogenicity of NMEC are increasingly well characterized, the intricate patterns of their transmission and the growing risk of antibiotic resistance among zoonotic ExPEC strains continue to pose major challenges to veterinary medicine as well as public health (Mehmood and Ashraf 2023; Edison and Kariyawasam 2025). Compared to Shiga toxin-producing *E. coli* (STEC), the ETEC and EPEC pathotypes are the significant zoonotic variants generally overlooked. ETEC is an important cause of traveler's diarrhea and childhood diarrhea in endemic areas and is transmitted mainly through contaminated food and water via the oro-fecal route with chicken as a typical vector (Kantele and Lääveri 2022; Thani 2023). EPEC, on the other hand, is classically associated with infantile diarrhea, but atypical EPEC strains have shown broader host distribution, which raises its potential zoonotic concerns (Garcia and Fox 2021; Mare et al. 2021). These strains may contain virulence markers typically associated with other *E. coli* pathotypes, representing an increased likelihood of disease production and interspecies transmission (de Castro et al. 2012).

3. General mechanism of pathogenesis of *E. coli*

Though there is variability in virulence factors among different strains, the general mechanism of pathogenesis of most of the *E. coli* pathotypes consists of several uniform key steps, such as adherence and colonization, immune evasion, toxin production, tissue invasion and damage, nutrient acquisition, and dissemination (da Silva Santos et al. 2015; Baby et al. 2016; Martin et al. 2017; Holmes et al. 2021; Saman et al. 2025). Initially, bacteria bind to the host cells through different adhesions, such as fimbriae or pili, Intimin, and afimbrial adhesins (Kaper and Nataro 2004; Eto et al. 2007; Cirl et al. 2008; Baby et al. 2016). Secondly, bacteria use certain mechanisms to avoid detection by the host immune system, such as capsule, LPS modifications, antigenic variation, and secretion systems (Govindarajan et al. 2020; Gao et al. 2024; Halabitska et al. 2024; Saman et al. 2025). Thirdly, *E. coli* strains produce toxins that are of various kinds depending on the strain's type. The release of exotoxins (stx, LT/ST, HlyA, CNF-1) or effector proteins causes host cell dysfunction, apoptosis, and inflammation. Fourthly, the invasion and tissue damage are mediated directly by some strains, such as EIEC and UPEC, which replicate intracellularly and cause host cell lysis or indirectly by certain strains, such as STEC, which release toxins extracellularly (da Silva Santos et al. 2015). The next step is nutrient acquisition, in which siderophores (enterobactin, aerobactin, and yersiniabactin) extract tightly bound iron for host proteins to facilitate bacterial persistence (Khasheii et al. 2016; Martin et al. 2017). Lastly, bacteria disseminate systemically or locally, causing bacteremia and septic shock due to endotoxin release in some cases (Barber et al. 2016; Ma et al. 2017; Holmes et al. 2021). Some invasive and enterotoxigenic strains have plasmid-determined features that enhance their infectiveness in domestic animals. There are evidences which indicate that certain calves might serve as super-shedders, where they disproportionately infect the environment and spread STEC strains in a disproportionate manner. Also, wild animal studies such as those conducted on mountain brushtail possums indicate that physical and social contact, not proximity, are of greater significance in transmission. The general mechanisms of pathogenesis of *E. coli* is given in Fig. 1. Some of the important pathotypes of *E. coli*, along with their virulence factors and mode of pathogenesis, are given in Table 1.

4. Transmission pathways of zoonotic *E. coli*

Direct animal contact, typical of farm work and environments such as farms and petting zoos, significantly enhances the risk of zoonotic transmission of *E. coli*, especially of STEC (Isler et al. 2021). These environments facilitate human-animal proximity and enhance the possibility of disease transmission through contact or contamination of surfaces. For example, research has confirmed significant frequencies of positive fecal samples for STEC in petting zoo-housed animals, such as sheep, goats, cattle, and camels (Nada et al. 2023). Outbreaks of *E. coli*

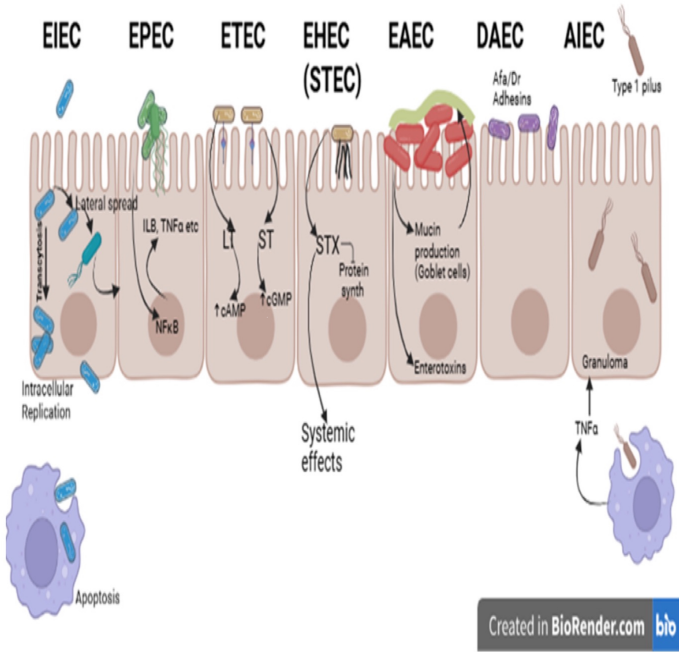

Fig. 1. *General mechanism of pathogenesis of Escherichia coli pathotypes*
EIEC: Enteroinvasive E. coli, EPEC: Enteropathogenic E. coli, ETEC: Enterotoxigenic E. coli, EHEC: Enterohemorrhagic E. coli, STEC: Shiga toxin-producing E. coli, EAEC: Enteroaggregative E. coli, DAEC: Diffusely adherent E. coli, AIEC: Adherent invasive E. coli

O157 have been documented in petting zoo environments, where genetically identical human and animal strains have demonstrated this direct transmission capacity (Bentancor et al. 2023). The transmission risk is exacerbated by poor hygiene practices, such as inadequate handwashing facilities, a lack of readily available hygiene information, and poor facility layouts (Esposito et al. 2023). Agricultural workers are especially vulnerable due to daily exposure to livestock, contaminated environments, insufficient personal protective equipment, and reduced compliance with biosecurity measures (Gambushe et al. 2022). To minimize contamination and promote better hygiene, redesign of high-contact facilities is required while balancing the educational and recreational benefits of such human-animal interactions (Liguori et al. 2023). A significant and longstanding public health issue is the transmission of several *E. coli* strains, most notably O157:H7, through contaminated meat products (Salman and Steneroden 2023). Though chicken, lamb, and pork are potential threats, undercooked ground beef is the most common carrier because cattle are the primary reservoirs (Willis et al. 2023). During slaughter, intestinal contents may contaminate carcasses, which initiates the infection risk. There have been reports of pig derived products associated with *E. coli* O157:H7 outbreaks, warranting the cautious handling of all types of meat. In addition to the primary contamination, cross-contamination of kitchens worsens the issue of disease outbreaks (da Silva et al. 2024). The pathogens may transfer from raw meat juices to other foods or food preparation surfaces if proper hygiene procedures are not adhered to rigorously (Willis et al. 2023). Therefore, there should be adherence to appropriate food safety practices like proper cooking and careful segregation of raw and cooked foods (Kinanti et al. 2024).

Although meat products are a primary concern, *E. coli* can also be transmitted through other sources like contaminated vegetables and unpasteurized milk or dairy products (Hassani et al. 2023; Sarba et al. 2023). A major public health issue is the foodborne transmission of various strains of *E. coli*, particularly via contaminated products and unpasteurized milk (Wada et al. 2025). Leafy greens, sprouts, and fruits can become contaminated with *E. coli* through contaminated soil, irrigation water, and animal feces (Osafo et al. 2022). The threat is worsened by poor sanitation and the use of contaminated water in agricultural operations (Davidova-Gerzova et al. 2023). Raw milk and farm cheeses can also become contaminated with pathogenic types of *E. coli*, such as STEC, which are generally spread by cow feces (Wada et al. 2025). Zoonotic transmission of *E. coli* and other transmission sources are shown in Fig. 2. Both recreational water sources as well as contaminated drinking water constitute an actual threat to public health via waterborne transmission of *E. coli*, particularly virulent strains such as O157:H7 (Osafo et al. 2022; Lenchenko et al. 2024). Although *E. coli* is sensitive to chlorination, it is still challenging to detect low concentrations of the bacterium in water; hence, vigilant and continuous monitoring needs to be practiced. Epidemiological reports have associated recreational water bodies, such as swimming pools and lakes, with intermittent illness, and these environments are also routinely implicated in outbreaks of *E. coli*, owing to fecal contamination from agricultural runoff, livestock presence, or insufficient wastewater treatment (Osafo et al. 2022). For instance, direct and significant correlation between the presences of *E. coli* within well water and the proximity of the septic tanks have been reported, emphasizing the need for improved sanitation and infrastructure (Paruch and Paruch 2022).

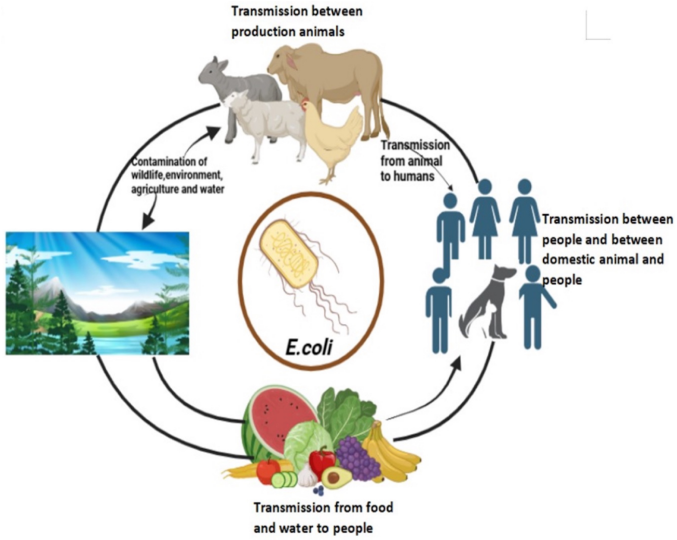

Fig. 2. *Zoonotic transmission of Escherichia coli and its other potential routes of spread to humans*

5. Major foodborne outbreaks in humans

Shiga toxin–producing *Escherichia coli* (STEC) strains (especially O157:H7 and non-O157) cause foodborne outbreaks in humans (Tack et al. 2021). Because of its severity and fatal complications, this strain is the most dangerous. These strains enter humans through contaminated food and water, colonize the intestinal tract, and produce toxins, causing nausea, abdominal cramping, vomiting, and watery to bloody diarrhea (Gambushe et al. 2022; Mansour et al. 2023). Vulnerable groups such as children, the elderly, and immunocompromised individuals are at particular risk of developing HUS (Zhang et al. 2022). In the United

Table 1. Pathotypes of *Escherichia coli* along with their virulence factors and mode of pathogenesis

Pathotype	Virulence factors	Target site	Mode of pathogenesis	Associated diseases	Risk groups	References
Enteropathogenic *E. coli* (EPEC)	Bundle-forming pilus, intimin	Small intestine	Attack and affect lesions	Infantile diarrhea	Infants, lambs, cats, and dogs	(Lee et al. 2022; Ryandini et al. 2024)
Enterotoxigenic *E. coli* (ETEC)	Heat-labile/stable toxins	Small intestine	Toxin-mediated fluid secretions	Traveler's diarrhea and watery diarrhea	Traveler's children, calves, and piglets	(Zhang et al. 2022; Hassan et al. 2023)
Enterohemorrhagic *E. coli* (EHEC)	Shiga toxins (stx1, stx2), intimin	Colon	Cytotoxicity and inflammation	Hemorrhagic colitis and hemolytic uremic syndrome	All ages, especially children, cattle and small ruminants	(Sun et al. 2022)
Enteroinvasive *E. coli* (EIEC)	Invasion plasmid antigens proteins	Colon	Invasion of epithelial cells	Dysentery-like illness	Humans and all age groups	(Ghosh et al. 2025)
Enteroaggregative *E. coli* (EAEC)	Aggrevate adherence fimbria (AAF), enteroaggregative heat-stable enterotoxin (EHSE)	Small intestine	Biofilm formation and persistent colonization	Persistent diarrhea	Children and immunocompromised patients, dogs, and poultry	(Izquierdo-Vega et al. 2023)
Diffusely adherent *E. coli* (DAEC)	Afimbrial and Dr family adhesins	Small intestine	Diffuse adherence	Watery diarrhea	Fewer immune patients	(Hosseininasab et al. 2024)
Uropathogenic *E. coli* (UPEC)	P fimbriae, hemolysin, siderophores	Urinary tract	Ascending infection and inflammation	Urinary tract infections (UTIs)	Female catheterized patients, humans, cats, dogs, cattle	(Whelan et al. 2023)
Neonatal meningitic *E. coli* (NMEC)	K1 polysaccharide capsule, invasion of brain epithelium proteins (ibe)	Meninges	Blood brain barrier invasion	Neonatal meningitis	Neonates, calves, lambs, piglets	(Liu et al. 2021)
Adherent invasive *E. coli* (AIEC)	Adherence and invasion factors	Ileum and colon	Intracellular replication	Crohn's disease	Children with IBD	(Mansour et al. 2023)
Shiga toxin-producing *E. coli* (STEC)	Shiga toxins (stx1 and stx2)	Colon	Toxin-mediated endothelial damage	Hemorrhagic colitis and hemolytic uremic syndrome	All ages groups	(Freedman et al. 2023)
Hybrid strain (e.g., EAHEC)	Shiga toxins, Aggrevate adherence fimbria (AAF), intimin	Colon	EHEC and EAEC mechanisms	hemolytic uremic syndrome (HUS) outbreaks	All ages	(Gomes et al. 2023)
Avian pathogenic *E. coli* (APEC)	Increased serum survival (iss), colicin V, and iron uptake system	Respiratory and systemic	Septicemia and respiratory infections	Colibacillosis in poultry	Poultry, zoonotic potential	(Joseph et al. 2023)
Animal enterotoxigenic *E. coli* (aETEC)	F4, F5, F6 fimbriae, heat-labile and heat-stable toxins	Small intestine	Toxin-mediated fluid loss	Neonatal diarrhea in piglets and calves	Livestock neonates	(Von Mentzer and Svennerholm 2024)
Mastitis-associated *E. coli* (MAEC)	Variable adhesins, iron uptake systems	Mammary gland	Inflammation and colonization	Mastitis in dairy cattle	Dairy cattle	(Meçaj et al. 2023; Ahmed and Nawaz, 2024; Germon et al. 2025)
Septicemic *E. coli* (SEPEC)	Cytotoxins and serum resistance genes	Blood stream	Bacteremia and septicemia	Sepsis in animals and humans	Immunocompromised individuals	(Karbalaei et al. 2025)
Multidrug resistant *E. coli* (MDREC)	Extended spectrum beta lactamases (ESBL), carbapenemases,	Various organs	Resistance to antibiotics	Nosocomial infections and resistant urinary tract infections	Hospitalized and immunocompromised individuals	(Rozwadowski and Gawel 2022)
Zoonotic *E. coli* O157:H7 (ZEC)	Shiga toxins, intimin	Colon	Epithelial destruction and Shiga toxicity	Foodborne outbreaks and hemolytic uremic syndrome	The general population is exposed through contaminated sources	(Farag et al. 2023; Riaz et al. 2023)

States from 2010 to 2017, the health department recorded 466 STEC outbreaks, of which 44% of O157 and 41% of non-O157 outbreaks were observed (Tack et al. 2021). In Germany in 2011, an outbreak of O104:H4 caused 50 deaths, and almost 3,000 cases were seen (Bloch et al. 2012). Another outbreak in the USA affecting 1727 individuals with 144 hospitalizations was linked to non-O157 STEC, including serotypes STEC O111 and O11 of STEC O26, which are mostly associated with dairy products (Luna-Gierke et al. 2014). According to a study in Alberta (Canada) from 2018-2021, 729 overall isolates of non-O157 STEC were identified clinically, from which 42.4% cases were of young people (18years or less) and 31.1% cases of children (0 to 9 years) (Glassman et al. 2022).

6. Major feedborne outbreaks in animals

E. coli is the main cause of systemic and enteric illness in immunocompromised or young animals, and the most commonly prevalent pathotype is enterotoxigenic *E. coli* (ETEC), a major cause of neonatal diarrhea in piglets and calves (Islam et al. 2023). It results in

dehydration, excessive fluid loss, and death if left untreated. While in poultry, the most prevalent strain is avian pathogenic *E. coli* (APEC), which mostly disturbs internal organs and the respiratory system with predominant signs of perihepatitis, airsacculitis, septicemia, and pericarditis in affected birds (Kromann et al. 2021). STEC has also been identified in animal-origin foods, with prevalence rates in swine ranging from 4.4- 68.3% (live swine), 22-86.3% (in slaughtered pigs), and 0.10- 80% (retail pig meat) (Haque et al. 2022). Moreover, in retail pig meat, O157:H7 serotype with different virulence gene combinations have been reported from Africa (O157 + stx2 + eae + ehxa), the United States (O157 + Shiga toxin gene/stx), and Asia (O157 + Shiga toxin 1 gene /stx1 + Shiga toxin 2 gene /stx2 + enterohemolysin A gene /ehxa). While non-O157 serotypes in the U.S. (non-O157 + stx + intimin gene / eae) and unknown serogroups + (stx + eae, stx2 + eae, or stx1 + stx2 + eae) were identified in England (Haque et al. 2022). In Iran from 2008-2016, 75 strains of non-O157 STEC serotypes were identified in humans and animals. O113 serotype was found in cattle (55.5%), goat (22.2%), and red deer (22.2%), whereas, O26, O111, O5, O63, O75, and O128 were isolated from cattle (100%), sheep (100%), pigeon (100%), and from goats (66.6%) and pigeon (33.3%), respectively (Badouei et al. 2023). The prevalence of the top five STEC serotypes in slaughter cattle ranged from 1.0% to 4.5% depending on breed and production system (Badouei et al. 2023). These findings underline the dual relevance of *E. coli* outbreaks for both animal production economics and zoonotic transmission potential.

One health approach is essential to control zoonotic *E. coli* because the bacteria circulate between humans, animals, birds, food, and the environment (Shaheen 2022). In humans, *E. coli* can be controlled by proper hygiene, chlorination of wastewater, avoiding undercooked dairy products, and unpasteurized milk (Slattery and Garvey 2025). In animals, better farm management practices decrease *E. coli* shedding in feces (Kannan et al. 2021). Other than this, vaccination and probiotics can also limit their gut colonization, particularly in poultry birds (Watts and Wigley 2024). In the food chain, better slaughterhouse hygiene, proper pasteurization, and washing of vegetables with clean water are very critical. These approaches can minimize the intensity of *E. coli* infections, but complete removal is quite difficult due to their widespread occurrence as both commensal and pathogenic bacteria.

7. Conclusion

As a one welfare problem of concern, because of its far-reaching implications in food safety, animal welfare, and public health, zoonotic *E. coli* is of serious concern. Acute gastrointestinal and extraintestinal diseases are caused by pathogenic species such as EHEC, EPEC, ETEC, and EAEC. As such, pathogens possess animal reservoirs like cattle and poultry, and are contagious from the reservoirs to human beings or through contaminated food and water, making them the most risky. O157:H7 and other foodborne Shiga toxin-producing *E. coli* (STEC) emphasize the need for additional food safety practices and sanitizing procedures. Treatment is further worsened by increasing antimicrobial resistance of the strains, which points to the significance of using antibiotics responsibly in animal as well as human healthcare. Measures in the future must focus on coming up with new vaccinations for cattle in a bid to stem the spread of the infection at the source and on embarking on improved genomic surveillance in keeping track of emerging strains of *E. coli* and its pattern of resistance. Predictive models based on Artificial Intelligence can also be used to forecast outbreaks, allowing for more proactive and focused responses.

Declarations

Funding: Not applicable

Conflict of interest: Authors declare no conflicts of interest

Acknowledgements: None

References

Ahmed B, Nawaz MA. (2024). Evaluation of anti-bacterial efficacy of nanoparticles against major mastitis-associated pathogens. Continental Veterinary Journal 4(2): 222-230. http://dx.doi.org/10.71081/cvj/2024.030

Al-Mustapha AI, Raufu IA, Ogundijo OA, Odetokun IA, Tiwari A, Brouwer MSM, Heikinheimo A. (2023). Antibiotic resistance genes, mobile elements, virulence genes, and phages in cultivated ESBL-producing *Escherichia coli* of poultry origin in Kwara State, North Central Nigeria. International Journal of Food Microbiology 389: 110086. https://doi.org/10.1016/j.ijfoodmicro.2023.110086

Al-Quraishi MQA, Jabar AD. (2022). Distribution of some virulence factors in septicemic and diarrhoeagenic *Escherichia coli* pathotypes in Iraq. Biochemical and Cellular Archives 22(1): 1435-1440. https://connectjournals.com/03896.2022.22.1435

Baby S, Karnaker VK, Geetha RK. (2016). Adhesins of uropathogenic *Escherichia coli* (UPEC). International Journal of Medical Microbiology and Tropical Diseases 2(1): 10-18.

Badouei MA, Taban H, Nemati A, Dos Santos LF. (2023). Molecular serotyping of Shiga toxin-producing *Escherichia coli* (STEC) of animal origin in Iran reveals the presence of important non-O157 seropathotypes. Veterinary Research Forum 14(5): 267-274. https://doi.org/10.30466/vrf.2022.550618.3416

Barber AE, Norton JP, Wiles TJ, Mulvey MA. (2016). Strengths and limitations of model systems for the study of urinary tract infections and related pathologies. Microbiology and Molecular Biology Reviews 80(2): 351-367. https://doi.org/10.1128/mmbr.00067-15

Bentancor A, Blanco Crivelli X, Piccini C, Trueba G. (2023). New Concepts on Domestic and Wild Reservoirs and Transmission of *E. coli* and Its Environment. In: Torres, A.G. (eds) Trending Topics in *Escherichia coli* Research. Springer, Cham. https://doi.org/10.1007/978-3-031-29882-0_3

Bloch S, Felczykowska A, Nejman-Faleńczyk B. (2012). *Escherichia coli* O104:H4 outbreak—have we learnt a lesson from it? Acta Biochimica Polonica 59(4): 483-488.

Cabrera-Sosa L, Ochoa TJ. (2020). *Escherichia coli* diarrhea. In: Hunter's tropical medicine and emerging infectious diseases. Elsevier, pp. 481-485. https://doi.org/10.1016/B978-0-323-55512-8.00046-6

Chala B, Hamde F. (2021). Emerging and re-emerging vector-borne infectious diseases and the challenges for control: a review. Frontiers in Public Health 9: 715759. https://doi.org/10.3389/fpubh.2021.715759

Chaoprasid P, Dersch P. (2021). The cytotoxic necrotizing factors (CNFs)—a family of Rho GTPase-activating bacterial exotoxins. Toxins 13(12): 1-24. https://doi.org/10.3390/toxins13120901

Christensen H, Bachmeier J, Bisgaard M. (2021). New strategies to prevent and control avian pathogenic *Escherichia coli* (APEC). Avian Pathology 50(5): 370-381. https://doi.org/10.1080/03079457.2020.1845300

Cirl C, Wieser A, Yadav M, Duerr S, Schubert S, Fischer H, Stappert D,

Wantia N, Rodriguez N, WH. (2008). Subversion of toll-like receptor signaling by a unique family of bacterial Toll/interleukin-1 receptor domain-containing proteins. Nature Medicine 14: 399–406. https://doi.org/10.1038/nm1734

da Silva DC, de Oliveira JP, Santos EAR, Tadielo LE, Possebon FS, Pereira JG. (2024). Microbiological assessment of a hospital kitchen before and after Good Manufacturing Practices' intervention. Food Science and Technology 44: e00379. https://doi.org/10.5327/fst.00379%20

da Silva Santos AC, Gomes Romeiro F, Yukie Sassaki L, Rodrigues J. (2015). *Escherichia coli* from Crohn's disease patient displays virulence features of enteroinvasive (EIEC), enterohemorrhagic (EHEC), and enteroaggregative (EAEC) pathotypes. Gut Pathogens 7(1): 2. https://doi.org/10.1186/s13099-015-0050-8

Davidova-Gerzova L, Lausova J, Sukkar I, Nesporova K, Nechutna L, Vlkova K, Kaspar J. (2023). Hospital and community wastewater as a source of multidrug-resistant ESBL-producing *Escherichia coli*. Frontiers in Cellular and Infection Microbiology 13: 1184081. https://doi.org/10.3389/fcimb.2023.1184081

de Castro AFP, Bentancor A, Mercado EC, Cataldi A, Parma AE. (2012). *Escherichia coli* animal reservoirs, transmission route and animal disease. In: Pathogenic *Escherichia coli* in Latin America. Bentham Science Publishers, pp. 223–248. https://doi.org/10.2174/97816080519221100101

Denpetkul T, Srathongneam T, Sittipunsakda O, Tancharoen S, Krabkran P, Mongkolsuk S, Sirikanchana K. (2025). Protective masks reduced gastrointestinal risks of antibiotic-resistant *E. coli* for hospital wastewater treatment plant workers: a quantitative microbial risk assessment. Environmental Pollution 374: 126180. https://doi.org/10.1016/j.envpol.2025.126180

Edison LK, Kariyawasam S. (2025). From the gut to the brain: transcriptomic insights into neonatal meningitis *Escherichia coli* across diverse host niches. Pathogens 14(5): 485. https://doi.org/10.3390/pathogens14050485

Edison LK, Kudva IT, Kariyawasam S. (2024). Host–pathogen interactions during Shiga toxin-producing *Escherichia coli* adherence and colonization in the bovine gut: a comprehensive review. Microorganisms 12(10): 2009. https://doi.org/10.3390/microorganisms12102009

Esposito MM, Turku S, Lehrfield L, Shoman A. (2023). The impact of human activities on zoonotic infection transmissions. Animals 13(10): 1646. https://doi.org/10.3390/ani13101646

Eto DS, Jones TA, Sundsbak JL, Mulvey MA. (2007). Integrin-mediated host cell invasion by type 1-piliated uropathogenic *Escherichia coli*. PLoS Pathogens 3(7): e100. https://doi.org/10.1371/journal.ppat.0030100

Ezzat M, Hassanin AAI, Mahmoud AE, Ismail SM, El-Tarabili RM. (2023). Risk factors, antibiotic profile, and molecular detection of virulence and antibiotic resistance genes of enteric bacteria in diarrheic calves in Egypt. International Journal of Veterinary Science 12(2): 161-168. https://doi.org/10.47278/journal.ijvs/2022.186

Farag AM, Karmi M, Mubarak AG, Younis W, Youseef AG. (2023). Isolation and characterization of non-O157 Shiga toxin-producing *Escherichia coli* in Aswan Governorate with a zoonotic approach. Journal of Advanced Veterinary Research 13(6): 886-894. https://www.advetresearch.com/index.php/AVR/article/view/1312

Freedman SB, Van De Kar NCAJ, Tarr PI. (2023). Shiga toxin–producing *Escherichia coli* and the hemolytic–uremic syndrome. New England Journal of Medicine 389(15): 1402-1414. https://doi.org/10.1056/NEJMra2108739

Gambushe SM, Zishiri OT, El Zowalaty ME. (2022). Review of *Escherichia coli* O157:H7 prevalence, pathogenicity, heavy metal and antimicrobial resistance, African perspective. Infection and Drug Resistance 15: 4645-4673. https://doi.org/10.2147/IDR.S365269

Gao S, Jin W, Quan Y, Li Y, Shen Y, Yuan S, Yi L, Wang Y, Wang Y. (2024). Bacterial capsules: occurrence, mechanism, and function. NPJ Biofilms and Microbiomes 10(1): 21. https://doi.org/10.1038/s41522-024-00497-6

Garcia A, Fox JG. (2021). A one health perspective for defining and deciphering *Escherichia coli* pathogenic potential in multiple hosts. Comparative Medicine 71(1): 3-45. https://doi.org/10.30802/AALAS-CM-20-000054

García V, Lestón L, Parga A, García-Meniño I, Fernández J, Otero A, Mora A. (2023). Genomics, biofilm formation and infection of bladder epithelial cells in potentially uropathogenic Escherichia coli (UPEC) from animal sources and human urinary tract infections (UTIs) further support food-borne transmission. One Health 16: 100558. https://doi.org/10.1016/j.onehlt.2023.100558

Germon P, Foucras G, Smith DGE, Rainard P. (2025). Invited review: mastitis *Escherichia coli* strains: mastitis-associated or mammopathogenic? Journal of Dairy Science 108(5): 4485-4507. https://doi.org/10.3168/jds.2024-26109

Ghosh D, Halder P, Samanta P, Chowdhury G, Shaw S, Bose P, Ramamurthy T. (2025). Lactose fermenting enteroinvasive *Escherichia coli* from diarrhoeal cases confers enhanced virulence. Scientific Reports 15(1): 24040. https://doi.org/10.1038/s41598-025-07232-x

Glassman H, Ferrato C, Chui L. (2022). Epidemiology of non-O157 Shiga toxin-producing *Escherichia coli* in the province of Alberta, Canada, from 2018 to 2021. Microorganisms 10(4): 814. https://doi.org/10.3390/microorganisms10040814

Gomes TAT, Santos ACM, Hernandes RT, Arias-Guerrero MY, Farfán-García AE, Gómez-Duarte OG. (2023). Emergence of hybrid *Escherichia coli* strains. In: Trending topics in *Escherichia coli* research: The Latin American perspective. Springer, pp. 295–315. https://doi.org/10.1007/978-3-031-29882-0_13

Govers SK, Campos M, Tyagi B, Laloux G, Jacobs-Wagner C. (2024). Apparent simplicity and emergent robustness in the control of the *Escherichia coli* cell cycle. Cell systems 15(1): 19-36. https://doi.org/10.1016/j.cels.2023.12.001

Govindarajan DK, Viswalingam N, Meganathan Y, Kandaswamy K. (2020). Adherence patterns of *Escherichia coli* in the intestine and its role in pathogenesis. Medicine in Microecology 5: 100025. https://doi.org/10.1016/j.medmic.2020.100025

Halabitska I, Petakh P, Kamyshna I, Oksenych V, Kainov DE, Kamyshnyi O. (2024). The interplay of gut microbiota, obesity, and depression: insights and interventions. Cellular and Molecular Life Sciences 81(1): 443. https://doi.org/10.1007/s00018-024-05476-w

Hameed H, Sarwar MT, Zafar R, Raza Q, Ain Qu, Younas S, Arshad S. (2024). *E. coli* and the normal microbiota; their interaction and role in health and disease. Frontiers in Microbiology and Biotechnology 2(1): 1–16. https://doi.org/10.54219/fmb.02.2024.161

Haque M, Bosilevac JM, Chaves BD. (2022). A review of Shiga-toxin producing *Escherichia coli* (STEC) contamination in the raw pork production chain. International Journal of Food Microbiology 377: 109832. https://doi.org/10.1016/j.ijfoodmicro.2022.109832

Hassan MA, Batiha GE, Saad SA, Mahrous E. (2023). Study on enterotoxigenic *Escherichia coli* producing extended spectrum beta lactamase (ESBL) from chicken meat and its products. International Journal of Veterinary Science 12(5): 652-658. https://doi.org/10.47278/journal.ijvs/2022.217

Hassani YAE, Ghazi IE, Ahouangninou C, Laziri F. (2023). Microbial contamination of vegetables produced at smallholdings in the urban and peri-urban area of Meknes City, Morocco. International Journal of Agriculture and Biosciences 12(2): 92-97. https://doi.org/10.47278/journal.ijab/2023.049

Holmes CL, Anderson MT, Mobley HL, Bachman MA. (2021). Pathogenesis of gram-negative bacteremia. Clinical Microbiology Reviews 34(2): 0023420. https://doi.org/10.1128/cmr.00234-20

Holzer K, Marongiu L, Detert K, Venturelli S, Schmidt H, Hoelzle LE. (2025). Phage applications for biocontrol of enterohemorrhagic *E. coli* O157:H7 and other Shiga toxin-producing *Escherichia coli*. International Journal of Food Microbiology 439: 111267. https://doi.org/10.1016/j.ijfoodmicro.2025.111267

Hosseininasab SA, Saffari F, Tadjrobehkar O, Zandi H, Ahmadi B, Khoshnood A, Mehboodi M. (2024). Diffusely adherent and cyclomodulin-positive *Escherichia coli* are associated with colon diseases. Jundishapur Journal of Microbiology 17(8): e147563. https://doi.org/10.5812/jjm-147563

Hu J, Afayibo DJA, Zhang B, Zhu H, Yao L, Guo W, Peng H. (2022). Characteristics, pathogenic mechanism, zoonotic potential, drug resistance, and prevention of avian pathogenic *Escherichia coli* (APEC). Frontiers in Microbiology 13: 614963. https://doi.org/10.3389/fmicb.2022.1049391

Hwang Sb, Chelliah R, Kang JE, Rubab M, Banan-MwineDaliri E, Elahi F, Oh DH. (2021). Role of recent therapeutic applications and the infection strategies of Shiga toxin-producing *Escherichia coli*. Frontiers in Cellular and Infection Microbiology 11: 1049391. https://doi.org/10.3389/fcimb.2021.614963

Islam MS, Rahman AMMT, Hassan J, Rahman MT. (2023). Extended-spectrum beta-lactamase in *Escherichia coli* isolated from humans, animals, and environments in Bangladesh: a One Health perspective systematic review and meta-analysis. One Health 16: 100526. https://doi.org/10.1016/j.onehlt.2023.100526

Isler M, Wissmann R, Morach M, Zurfluh K, Stephan R, Nüesch-Inderbinen M. (2021). Animal petting zoos as sources of Shiga toxin-producing *Escherichia coli*, *Salmonella* and extended-spectrum β-lactamase (ESBL)-producing *Enterobacteriaceae*. Zoonoses and Public Health 68(2): 79-87. https://doi.org/10.1111/zph.12798

Izquierdo-Vega JA, Castillo-Juarez RJ, Sánchez-Gutiérrez M, Ares MA, De La Cruz MA. (2023). A mini-review of enteroaggregative *Escherichia coli* with a specific target on the virulence factors controlled by the AggR master regulator. Polish Journal of Microbiology 72(4): 347–354. https://doi.org/10.33073/pjm-2023-037

Joseph J, Zhang L, Adhikari P, Evans JD, Ramachandran R. (2023). Avian pathogenic *Escherichia coli* (APEC) in broiler breeders: an overview. Pathogens 12(11): 1280. https://doi.org/10.3390/pathogens12111280

Kannan G, Mahapatra AK, Degala HL. (2021). Preharvest management and postharvest intervention strategies to reduce Escherichia coli contamination in goat meat: a review. Animals 11(10): 2943. https://doi.org/10.3390/ani11102943

Kantele A, Lääveri T. (2022). Extended-spectrum beta-lactamase-producing strains among diarrhoeagenic *Escherichia coli*—prospective traveller study with literature review. Journal of Travel Medicine 29(1): taab042. https://doi.org/10.1093/jtm/taab042

Kaper JB, Nataro JP, Mobley HL. (2004). Pathogenic *Escherichia coli*. Nature Reviews Microbiology 2: 123–140. https://doi.org/10.1038/nrmicro818

Karbalaei M, Esmailpour M, Oksenych V, Eslami M. (2025). Comprehensive analysis of blaCTX-M1 gene expression alongside iutA, csgA, and kpsMII virulence genes in septicemic *Escherichia coli* using real-time PCR. Microorganisms 13(1): 95. https://doi.org/10.3390/microorganisms13010095

Kathayat D, Lokesh D, Ranjit S, Rajashekara G. (2021). Avian pathogenic *Escherichia coli* (APEC): an overview of virulence and pathogenesis factors, zoonotic potential, and control strategies. Pathogens 10(4): 467. https://doi.org/10.3390/pathogens10040467

Khairullah AR, Afnani DA, Riwu KHP, Widodo A, Yanestria SM, Moses IB, Fauziah I. (2024). Avian pathogenic *Escherichia coli*: epidemiology, virulence and pathogenesis, diagnosis, pathophysiology, transmission, vaccination, and control. Veterinary World 17(12): 2747-2762. https://doi.org/10.14202/vetworld.2024.2747-2762

Khasheii B, Anvari S, Jamalli A. (2016). Frequency evaluation of genes encoding siderophores and the effects of different concentrations of Fe ions on growth rate of uropathogenic *Escherichia coli*. Iranian Journal of Microbiology 8(6): 359-365.

Kinanti AS, Prihanto AA, Jatmiko YD, Kobun R, Xia W, Felicia L. (2024). Harnessing bacteriophages: a promising approach to combat foodborne pathogen biofilms. International Journal of Agriculture and Biosciences 13(4): 656–668. https://doi.org/10.47278/journal.ijab/2024.172

Köckerling E, Karrasch L, Schweitzer A, Razum O, Krause G. (2017). Public health research resulting from one of the world's largest outbreaks caused by entero-hemorrhagic Escherichia coli in Germany 2011: A review. Frontiers in Public Health 5: 332. https://doi.org/10.3389/FPUBH.2017.00332

Kromann S, Olsen RH, Bojesen AM, Jensen HE, Thøfner I. (2021). Development of an aerogenous Escherichia coli infection model in adult broiler breeders. Scientific Reports 11(1): 19556. https://doi.org/10.1038/s41598-021-98270-8

Laird TJ, Abraham S, Jordan D, Pluske JR, Hampson DJ, Trott DJ, O'Dea M. (2021). Porcine enterotoxigenic *Escherichia coli*: antimicrobial resistance and development of microbial-based alternative control strategies. Veterinary Microbiology 258: 109117. https://doi.org/10.1016/j.vetmic.2021.109117

Lee JB, Kim SK, Yoon JW. (2022). Pathophysiology of enteropathogenic *Escherichia coli* during a host infection. Journal of Veterinary Science 23(2): e28. https://doi.org/10.4142/jvs.21160

Lee W, Ha J, Choi J, Jung Y, Kim E, An ES, Kim SH. (2024). Genetic and virulence characteristics of hybrid Shiga toxin-producing and atypical enteropathogenic *Escherichia coli* strains isolated in South Korea. Frontiers in Microbiology 15: 1398262. https://doi.org/10.3389/fmicb.2024.1398262

Lenchenko E, Sachivkina N, Karamyan A, Volobueva O, Neborak E, Avdonina M, Molchanova M. (2024). Characteristics of biofilms formed by pathogenic Enterobacterales isolated from infected gastrointestinal tracts of rabbits. International Journal of Veterinary Science 13(6): 870–877. https://doi.org/10.47278/journal.ijvs/2024.183

Liguori G, Costagliola A, Lombardi R, Paciello O, Giordano A. (2023).

Human-animal interaction in animal-assisted interventions (AAI)s: zoonosis risks, benefits, and future directions—a one health approach. Animals 13(10): 592. https://doi.org/10.3390/ani13101592

Liu CM, Aziz M, Park DE, Wu Z, Stegger M, Li M, Koch BJ. (2023). Using source-associated mobile genetic elements to identify zoonotic extraintestinal E. coli infections. One Health 16: 518. https://doi.org/10.1016/j.onehlt.2023.100518

Liu Y, Zhu M, Fu X, Cai J, Chen S, Lin Y, Lin Z. (2021). *Escherichia coli* causing neonatal meningitis during 2001–2020: a study in eastern China. International Journal of General Medicine 2021: 3007–3016. https://doi.org/10.2147/IJGM.S317299

Luna-Gierke RE, Griffin PM, Gould LH, Herman K, Bopp CA, Strockbine N, Mody RK. (2014). Outbreaks of non-O157 Shiga toxin-producing *Escherichia coli* infection: USA. Epidemiology and Infection 142(11): 2270–2280. https://doi.org/10.1017/S0950268813003233

Ma J, Li N, Liu Y, Wang C, Liu X, Chen S, Sun H. (2017). Antimicrobial resistance patterns, clinical features, and risk factors for septic shock and death of nosocomial *E. coli* bacteremia in adult patients with hematological disease: a monocenter retrospective study in China. Medicine 96(21): e6959. https://doi.org/10.1097/MD.0000000000006959

Majowicz SE, Scallan E, Jones-Bitton A, Sargeant JM, Stapleton J, Angulo FJ, Kirk MD. (2014). Global incidence of human Shiga toxin–producing *Escherichia coli* infections and deaths: a systematic review and knowledge synthesis. Foodborne Pathogens and Disease 11(6): 447–455. https://doi.org/10.1089/fpd.2013.1704

Manges AR, Geum HM, Guo A, Edens TJ, Fibke CD, Pitout JDD. (2019). Global extraintestinal pathogenic *Escherichia coli* (ExPEC) lineages. Clinical Microbiology Reviews 32(3): e00135-18. https://doi.org/10.1128/cmr.00135-18

Mansour S, Asrar T, Elhenawy W. (2023). The multifaceted virulence of adherent-invasive *Escherichia coli*. Gut Microbes 15(1): 2172669. https://doi.org/10.1080/19490976.2023.2172669

Mare AD, Ciurea CN, Man A, Tudor B, Moldovan V, Decean L, Toma F. (2021). Enteropathogenic *Escherichia coli*—a summary of the literature. Gastroenterology Insights 12(1): 28–40. https://doi.org/10.3390/gastroent12010004

Martin P, Tronnet S, Garcie C, Oswald E. (2017). Interplay between siderophores and colibactin genotoxin in *Escherichia coli*. IUBMB Life 69(6): 435–441. https://doi.org/10.1002/iub.1612

Meçaj R, Muça G, Koleci X, Sulçe M, Turmalaj L, Zalla P, Tafaj M. (2023). Bovine environmental mastitis and their control: an overview. International Journal of Agriculture and Biosciences 12(4): 216–221. https://doi.org/10.47278/journal.ijab/2023.067

Meena PR, Yadav P, Hemlata H, Tejavath KK, Singh AP. (2021). Poultry-origin extraintestinal *Escherichia coli* strains carrying the traits associated with urinary tract infection, sepsis, meningitis and avian colibacillosis in India. Journal of Applied Microbiology 130(6): 2087–2101. https://doi.org/10.1111/jam.14905

Mehmood S, Ashraf M. (2023). Antimicrobial resistance and virulence determinants of *E. coli* in bovine clinical mastitis in dairy farms. Continental Veterinary Journal 3(1): 54–59.

Mehrdel B, Yehya AHS, Dheyab MA, Jameel MS, Aziz AA, Nikbakht A, Kareem AA. (2023). The antibacterial and toxicological studies of mycosynthesis silver nanoparticles by isolated phenols from *Agaricus bisporus*. Physica Scripta 98(12): 125007. https://doi.org/10.1088/1402-4896/ad080f

Melinte V, Radu AM, Văcăroiu CM, Cismaru MI, Oprescu Macovei AM, Mihăilă DE, Gheorghiță V. (2024). A successful approach to diagnosing Shiga-like toxin-producing *Escherichia coli*-induced colitis. Diagnostics 14(8): 801. https://doi.org/10.3390/diagnostics14080801

Moxley RA. (2022). Enterobacteriaceae: *Escherichia*. In: McVey DS, Kennedy M, Chengappa MM, Wilkes R, editors, Veterinary Microbiology. Wiley. Pp. 56–74. https://doi.org/10.1002/9781119650836.ch6

Mwafy A, Youssef DY, Mohamed MM. (2023). Antibacterial activity of zinc oxide nanoparticles against some multidrug-resistant strains of *Escherichia coli* and *Staphylococcus aureus*. International Journal of Veterinary Science 12(3): 284-289. https://doi.org/10.47278/journal.ijvs/2022.181

Nada HG, El-Tahan AS, El-Didamony G, Askora A. (2023). Detection of multidrug-resistant Shiga toxin-producing *Escherichia coli* in some food products and cattle faeces in Al-Sharkia, Egypt: one health menace. BMC Microbiology 23(1): 127. https://doi.org/10.1186/s12866-023-02873-2

Nadi WG, Ahmed LI, Awad AAN, Taher EM. (2024). Occurrence and antibiogram of *Escherichia coli* in livestock. International Journal of Veterinary Science 13(2): 218-225. https://doi.org/10.47278/journal.ijvs/2023.079

Nowaczek A, Dec M, Stępień-Pyśniak D, Urban-Chmiel R, Marek A, Różański P. (2021). Antibiotic resistance and virulence profiles of *Escherichia coli* strains isolated from wild birds in Poland. Pathogens 10(8): 1059. https://doi.org/10.3390/pathogens10081059

Nupur MN, Afroz F, Hossain MK, Harun-ur-Rashid SM, Rahman MG, Kamruzzaman M, Ferdous KA, Haque MA. (2023). Prevalence of potential zoonotic bacterial pathogens isolated from household pet birds and their antimicrobial profile in northern Bangladesh. Agrobiological Records 11: 28-38. https://doi.org/10.47278/journal.abr/2023.005

Oh JY, Park HM. (2025). Molecular characterization of uropathogenic Escherichia coli (UPEC) strains isolated from companion dogs and cats in Korea. Journal of Veterinary Science 26(1): e14. https://doi.org/10.4142/jvs.24244

Osafo R, Balali GI, Amissah-Reynolds PK, Gyapong F, Addy R, Nyarko AA, Wiafe P. (2022). Microbial and parasitic contamination of vegetables in developing countries and their food safety guidelines. Journal of Food Quality 2022(1): 4141914. https://doi.org/10.1155/2022/4141914

Ouarroud B, El Maadoudi M, Barakat A, Hasni S. (2024). Shiga toxin-producing *Escherichia coli* (STEC); virulence factors, pathologies caused and foods at risk: review. In: International Conference on Advanced Intelligent Systems for Sustainable Development (AI2SD'2023). AI2SD 2023. Lecture Notes in Networks and Systems, Springer, Cham. https://doi.org/10.1007/978-3-031-52385-4_31

Pakbin B, Brück WM, Rossen JWA. (2021). Virulence factors of enteric pathogenic *Escherichia coli*: A review. International Journal of Molecular Sciences 22(18): 9922. https://doi.org/10.3390/ijms22189922

Paruch L, Paruch AM. (2022). An overview of microbial source tracking using host-specific genetic markers to identify origins of fecal contamination in different water environments. Water 14(11): 1809. https://doi.org/10.3390/w14111809

Peek SF, McGuirk SM, Sweeney RW, Cummings KJ. (2018). Infectious

diseases of the gastrointestinal tract. In: Peek SF, Divers TJ, editors, Rebhun's Diseases of Dairy Cattle, Elsevier. Pp:249-356. https://doi.org/10.1016/B978-0-323-39055-2.00006-1

Puvača N, de Llanos Frutos R. (2021). Antimicrobial resistance in *Escherichia coli* strains isolated from humans and pet animals. Antibiotics 10(1): 69. https://doi.org/10.3390/antibiotics10010069

Rahayu U, Wibisono FJ, Tyasningsih W, Effendi MH, Budiastuti B, Budiarto B, Tang JYH. (2025). Risk of antimicrobial and multidrug resistance on avian pathogenic *Escherichia coli* in public health. Journal of Advanced Veterinary Research 15(3): 414–420. https://advetresearch.com/index.php/AVR/article/view/2236

Ramos S, Silva V, Dapkevicius MdLE, Caniça M, Tejedor-Junco MT, Igrejas G, Poeta P. (2020). *Escherichia coli* as commensal and pathogenic bacteria among food-producing animals: Health implications of extended spectrum β-lactamase (ESBL) production. Animals 10(12): 2239. https://doi.org/10.3390/ani10122239

Ray R, Singh P. (2022). Prevalence and implications of Shiga toxin-producing *E. coli* in farm and wild ruminants. Pathogens 11(11): 1332. https://doi.org/10.3390/pathogens11111332

Riaz A, Shahzad, MA, Ahsan A, Aslam R, Usman M, Rasheed B, Ali A. (2023). Antimicrobial resistance pattern of *Escherichia coli* isolated from poultry in Lahore, Pakistan. International Journal of Veterinary Science 12(6): 832–837. https://doi.org/10.47278/journal.ijvs/2023.046

Rodriguez J. (2024). One health ethics and the ethics of zoonoses: A silent call for global action. Veterinary Sciences 11(9): 1-35. https://doi.org/10.3390/vetsci11090394

Rozwadowski M, Gawel D. (2022). Molecular factors and mechanisms driving multidrug resistance in uropathogenic *Escherichia coli*—an update. Genes 13(8): 1397. https://doi.org/10.3390/genes13081397

Ryandini D, Ma'arif S, Hidayat A, Putri AR, Kusharyati DF, Pratiwi M, Fitriadi RO. (2024). Antibacterial, antiaging, and antiangiogenic activity of Streptomyces sp. SAE4034 extract from mangrove sediment. International Journal of Agriculture and Biosciences 13(4): 574-581. https://doi.org/10.62310/liab.v5i1.201

Salman M, Steneroden K. (2023). Important zoonotic diseases of cattle and their prevention measures. In: Singh A, editor, Zoonoses: Infections Affecting Humans and Animals. Springer, Cham. Pp. 91-111. https://doi.org/10.1007/978-3-031-27164-9_1

Saman QR, Fatima W, Ahmad MR, Malik MI, Ahsan H, Baig A, Shabir M, Ayub M, Siddique AB. (2025). Immune evasion strategies of *E. coli*. In: García-Rubio VG, Alvi MA, Saeed Z, Ahmad M, editors, Foundations of Holistic Healing: Complementary and Alternative Medicine. Unique Scientific Publishers, Faisalabad, Pakistan. Pp. 65-70. https://doi.org/10.47278/book.HH/2025.451

Sarba EJ, Wirtu W, Gebremedhin EZ, Borena BM, Marami LM. (2023). Occurrence and antimicrobial susceptibility patterns of *Escherichia coli* and *Escherichia coli* O157 isolated from cow milk and milk products, Ethiopia. Scientific Reports 13(1): 16018. https://doi.org/10.1038/s41598-023-43043-8

Shaheen MN. (2022). The concept of one health applied to the problem of zoonotic diseases. Reviews in Medical Virology 32(4): e2326. https://doi.org/10.1002/rmv.2326

Slattery M, Garvey M. (2025). Chlorine Disinfection Byproducts: A public health concern associated with dairy food contamination. Dairy 6(2): 18. https://doi.org/10.3390/dairy6020018

Sora VM, Meroni G, Martino PA, Soggiu A, Bonizzi L, Zecconi A. (2021). Extraintestinal pathogenic *Escherichia coli*: Virulence factors and antibiotic resistance. Pathogens 10(11): 1355. https://doi.org/10.3390/pathogens10111355

Sroithongkham P, Nittayasut N, Yindee J, Nimsamer P, Payungporn S, Pinpimai K, Chanchaithong P. (2024). Multidrug-resistant *Escherichia coli* causing canine pyometra and urinary tract infections are genetically related but distinct from those causing prostatic abscesses. Scientific Reports 14(1): 11848. https://doi.org/10.1038/s41598-024-62028-9

Strzelecki P, Karczewska M, Szalewska-Pałasz A, Nowicki D. (2025). Phytochemicals controlling enterohemorrhagic *Escherichia coli* (EHEC) virulence—current knowledge of their mechanisms of action. International Journal of Molecular Sciences 26(1): 381. https://doi.org/10.3390/ijms26010381

Su Y, Ma G, Zheng Y, Qin J, Li X, Ge Q, Liu B. (2023). Neonatal meningitis-causing *Escherichia coli* induces microglia activation which acts as a double-edged sword in bacterial meningitis. International Journal of Molecular Sciences 24(12): 9915. https://doi.org/10.3390/ijms24129915

Sun H, Wang M, Liu Y, Wu P, Yao T, Yang W, Yang B. (2022). Regulation of flagellar motility and biosynthesis in enterohemorrhagic *Escherichia coli* O157: H7. Gut Microbes 14(1): 2110822. https://doi.org/10.1080/19490976.2022.2110822

Tack DM, Kisselburgh HM, Richardson LC, Geissler A, Griffin PM, Payne DC, Gleason BL. (2021). Shiga toxin-producing *Escherichia coli* outbreaks in the United States, 2010–2017. Microorganisms 9(7): 1529. https://doi.org/10.3390/microorganisms9071529

Thani TS. (2023). Characterization of *Escherichia coli* pathotypes and factors associated with well and water contamination in Mombasa County. MSc Thesis, Jomo Kenyatta University of Agriculture and Technology, Mombasa County, Kenya. http://localhost/xmlui/handle/123456789/6010

Thomas KD, McAllister TA. (2024). The science of Shiga toxin-producing (Verotoxin-producing) *Escherichia coli* (STEC): An ongoing one health journey toward improved health and food safety - Editorial summary. Microorganisms 12(2): 344. https://doi.org/10.3390/microorganisms12020344

Venegas-Vargas C, Henderson S, Khare A, Mosci RE, Lehnert JD, Singh P, Manning SD. (2016). Factors associated with Shiga toxin-producing Escherichia coli shedding by dairy and beef cattle. Applied and Environmental Microbiology 82(16): 5049-5056. https://doi.org/10.1128/AEM.00829-16

Von Mentzer A, Svennerholm AM. (2024). Colonization factors of human and animal-specific enterotoxigenic *Escherichia coli* (ETEC). Trends in Microbiology 32(5): 448-464. https://doi.org/10.1016/j.tim.2023.11.001

Wada Y, Muhammad SL, Adeyemi NA, Bolakojo OY, Ibrahim MJ, Jimba JH, Saliu MA, Aliyu AA, Tijani HO. (2025). Occurrence of pathogenic *Escherichia coli* O157:H7 in vegetables, fruit and milk in selected areas of Sabon Gari LGA, Kaduna State, Nigeria: A short communication. Journal of Science Technology and Education 13(1): 233-240.

Watts A, Wigley P. (2024). Avian pathogenic Escherichia coli: an overview of infection biology, antimicrobial resistance and vaccination. Antibiotics 13(9): 809. https://doi.org/10.3390/antibiotics13090809

Whelan S, Lucey B, Finn K. (2023). Uropathogenic *Escherichia coli* (UPEC)-associated urinary tract infections: the molecular basis for challenges to effective treatment. Microorganisms 11(9): 2169.

https://doi.org/10.3390/microorganisms11092169

Willis C, Jørgensen F, Cawthraw S, Aird H, Lai S, Kesby M, Raykova G. (2023). A survey of Salmonella, *Escherichia coli*, and antimicrobial resistance in frozen, part-cooked, breaded, or battered chicken products on retail sale in the UK. Journal of Applied Microbiology 134(5): lxad093. https://doi.org/10.1093/jambio/lxad093

Yu D, Banting G, Neumann NF. (2021). A review of the taxonomy, genetics, and biology of the genus *Escherichia* and the type species *Escherichia coli*. Canadian Journal of Microbiology 67(8): 553-571. https://doi.org/10.1139/cjm-2020-0508

Zaada DSY, Ben-Yosef M, Yuval B, Jurkevitch E. (2019). The host fruit amplifies mutualistic interaction between *Ceratitis capitata* larvae and associated bacteria. BMC Biotechnology 19(2): 92. https://doi.org/10.1186/s12896-019-0581-z

Zagaglia C, Ammendolia MG, Maurizi L, Nicoletti M, Longhi C. (2022). Urinary tract infections caused by uropathogenic *Escherichia coli* strains—new strategies for an old pathogen. Microorganisms 10(7): 1425. https://doi.org/10.3390/microorganisms10071425

Zhang Y, Tan P, Zhao Y, Ma X. (2022). Enterotoxigenic *Escherichia coli*: intestinal pathogenesis mechanisms and colonization resistance by gut microbiota. Gut Microbes 14(1): 2055943. https://doi.org/10.1080/19490976.2022.2055943

Citation

Rafee AR, Abd Alfatlawi MA, Asad A, Noor S, Shafiq S, Ud Din I, Zainab N, Ahmad T, Afzal S, Arshad M, Ambrose S, Mustafa S. (2025). Zoonotic *Escherichia coli* infections: pathogenic variants, mechanism of disease, transmission routes, and foodborne outbreaks. Letters in Animal Biology 05(2): 107 – 117. *https://doi.org/10.62310/liab.v5i2.238*