Comparative Analysis of Escherichia coli O104:H4 and O157:H7: Bridging Knowledge Gaps and Understanding Virulence Factors in Nigeria and sub-Saharan Africa

Abstract

Escherichia coli O104:H4 and O157:H7 are major *Shiga toxin–producing* ***E. coli*** (STEC) serotypes associated with severe gastroenteritis, hemolytic uremic syndrome (HUS), and significant public health burden [1,7]. While O157:H7 remains the most studied STEC globally, the emergence of O104:H4—particularly the 2011 German outbreak strain—revealed an unusual hybrid pathotype with features of ***enteroaggregative E. coli*** (EAEC) and Shiga toxin–producing E. coli. This comparative review synthesizes available literature, emphasizing epidemiology, virulence mechanisms, transmission dynamics, clinical outcomes, diagnostic approaches, and public-health implications with a particular focus on Nigeria. The review highlights critical knowledge gaps in genomic surveillance, laboratory capacity, and outbreak response frameworks. Recommendations include strengthening diagnostic infrastructure, integrating genomic monitoring into national AMR strategies, and improving food-safety systems to mitigate STEC threats.

Keywords: Shiga toxin–producing E. coli, STEC, Escherichia coli O104:H4, E. coli O157:H7, enteroaggregative E. coli, EAEC, hemolytic uremic syndrome, HUS, gastroenteritis, genomic surveillance, antimicrobial resistance, AMR, food safety, Nigeria, outbreak response, diagnostic capacity, public health

1. Introduction

Diarrheagenic Escherichia coli remains one of the leading causes of gastroenteritis worldwide, imposing a substantial burden on public health systems, particularly in resource-limited settings. Among diarrheagenic ***E. coli*** pathotypes, Shiga toxin–producing ***E. coli*** (STEC) serotypes—most notably O157:H7—have long been

التعليق [DS21]: The idea of the review is excellent, but the beginning of the abstract is discouraging... The abstract should be a brief summary of the review's content and should not include references.

التعليق [DS22]: Keywords should not exceed 5 important words, and should not be presented in a lengthy manner.

recognized as significant foodborne pathogens associated with outbreaks of hemorrhagic colitis and hemolytic uremic syndrome (HUS) [1,9]. The emergence of **E. coli** O104:H4, particularly the hybrid strain responsible for the catastrophic 2011 German outbreak, introduced a novel pathogenic paradigm. This strain combined enteroaggregative adherence mechanisms, horizontal acquisition of the **stx2**-encoding bacteriophage, and unusual antimicrobial resistance profiles not typically observed in classical STEC isolates [2, 4].

Nigeria, with its rapidly expanding population, extensive informal food distribution networks, and limited microbial surveillance infrastructure, faces a disproportionate risk from undetected STEC circulation [10, 17]. The paucity of systematic genomic surveillance and the reliance on conventional diagnostic methods have contributed to a significant underappreciation of STEC-related morbidity in the country [6, 22]. A comprehensive understanding of the similarities and differences between O157:H7 and O104:H4 is therefore essential for developing targeted surveillance strategies, informing clinical management protocols, and strengthening food safety systems in Nigeria and across the African continent.

التعليق [DS23]: The researcher should clarify the percentages of infection and spread of the pathogen worldwide and in Nigeria in particular.

2. Aims and Objectives

Aim

التعليق [DS24]: You don't need main headings...it's better to combine them with the introduction.

To conduct a comprehensive comparative analysis of ***E. coli*** O104:H4 and O157:H7, focusing on virulence factors, epidemiology, transmission routes, and public health implications for Nigeria.

Specific Objectives

التعليق [DS25]: You don't need main headings...it's better to combine them with the introduction.

Compare the virulence gene profiles and pathogenic mechanisms of both serotypes.
Examine their epidemiological trends globally and within Nigeria.
Evaluate transmission routes and associated risk factors.
Identify current diagnostic gaps and laboratory limitations.
Provide evidence-based recommendations for enhanced surveillance and control.

Significance of the Study

This comparative analysis holds substantial significance for clinical microbiology, public health practice, and food safety policy in Nigeria and across sub-Saharan Africa. First, by systematically comparing the virulence architectures of O157:H7 and O104:H4, this review clarifies why hybrid strains pose an exceptional threat: the absence of the LEE pathogenicity island in O104:H4 means that conventional diagnostic algorithms targeting ***eae***-based identification will systematically miss these pathogens, leading to underdiagnosis and delayed outbreak response. Highlighting this diagnostic blind spot provides an evidence-based rationale for expanding molecular detection platforms beyond traditional culture-based methods.

Second, the study underscores the critical role of molecular phylogenetic approaches in accurately differentiating closely related enteric pathogens. Previous work by Elemuwa et al. (2022) demonstrated that 16S rRNA phylogeny can effectively distinguish ***E. coli*** O157:H7 from ***Shigella*** species, emphasizing the utility of ribosomal RNA sequencing in resolving taxonomic and pathogenic ambiguity among Enterobacteriaceae [26]. Extending this molecular paradigm to the differentiation of O104:H4 from O157:H7—and from other diarrheagenic ***E. coli*** pathotypes—could substantially improve laboratory confirmation rates and epidemiological traceability in Nigerian healthcare settings where phenotypic identification remains the norm.

Third, from a public health perspective, this review highlights the urgent need for Nigeria to prioritize STEC surveillance within its national antimicrobial resistance and food safety frameworks. The documented ESBL resistance in O104:H4 and the rising multidrug resistance profiles observed in Nigerian STEC isolates demand integrated One Health surveillance that bridges human clinical medicine, veterinary practice, and environmental monitoring. The significance extends beyond academic interest: without accurate burden estimates and circulating strain data, policymakers cannot allocate resources effectively, clinicians cannot implement appropriate empiric management protocols, and food safety regulators cannot target high-risk production chains.

Fourth, this work contributes to the growing African genomic surveillance discourse by identifying concrete capacity gaps—limited WGS infrastructure, insufficient reference laboratory networks, and inadequate bioinformatics training—and proposing actionable, context-appropriate solutions. By aligning recommendations with existing platforms such as the Integrated Disease Surveillance and Response (IDSR) system, this review offers a feasible roadmap for embedding STEC

monitoring into routine public health practice rather than treating it as an isolated research priority.

Finally, by drawing global comparative insights and contextualizing them within Nigeria's specific epidemiological, infrastructural, and socioeconomic landscape, this study provides a template for similar resource-limited settings. The significance therefore lies not merely in documenting pathogen differences, but in translating those differences into policy-relevant, clinically actionable, and logistically realistic strategies for reducing STEC-associated morbidity and mortality in underserved populations.

3. Methods

This review was conducted using a structured literature search strategy designed to identify peer-reviewed publications, outbreak reports, and policy documents relevant to the comparative analysis of ***E. coli*** O104:H4 and O157:H7. The following electronic databases were systematically searched: PubMed/MEDLINE, Scopus, Web of Science, and Google Scholar.

The search strategy employed a combination of Medical Subject Headings (MeSH) terms and free-text keywords, including: ***"E. coli*** O157:H7", "***E. coli*** O104:H4", "STEC", "Shiga toxin-producing ***E. coli***", "EAEC hybrid", "Nigeria", "virulence factors", "hemolytic uremic syndrome", and "antimicrobial resistance". Boolean operators (AND, OR) were used to combine search terms and refine results.

Studies were included if they were: (i) published in English between 1990 and 2025; (ii) peer-reviewed original research articles, systematic reviews, or meta-analyses; (iii) official outbreak reports from the World Health Organization (WHO) or Centers for Disease Control and Prevention (CDC); or (iv) Nigerian public health surveillance data and policy documents. Studies were excluded if they lacked primary data or were non-English publications without available translations.

Data extraction focused on the following domains: virulence gene profiles and pathogenic mechanisms, global and regional epidemiological trends, transmission routes and risk factors, clinical outcomes and disease severity, antimicrobial resistance patterns, and currently available diagnostic and detection methodologies.

4. Literature Review

4.1 Epidemiology

4.1.1 E. coli O157:H7

Escherichia coli O157:H7 remains the most frequently identified and extensively studied STEC serotype worldwide [1, 9]. Since its initial recognition as a human pathogen in 1982 following outbreaks associated with contaminated hamburgers, O157:H7 has been consistently linked to foodborne illness across developed and developing nations [9, 12]. Cattle serves as the primary reservoir, with human infections typically resulting from consumption of undercooked ground beef, unpasteurized milk and dairy products, contaminated fresh produce, and inadequately treated drinking water. Person-to-person transmission, particularly in institutional settings such as daycare centers and nursing homes, has also been well documented [12, 24].

In Nigeria, published data on O157:H7 prevalence remain sparse and largely limited to small-scale studies [10, 17]. Reported isolation rates range from 1.4% to 8.6% in clinical and food samples, though these figures are widely considered underestimates due to limited diagnostic capacity, inconsistent surveillance practices, and the predominance of non-O157 STEC strains in many African settings [17]. The lack of systematic national surveillance programs means that the true burden of O157:H7-associated disease in Nigeria remains unknown, highlighting a critical gap in public health intelligence.

4.1.2 E. coli O104:H4

Escherichia coli O104:H4 is a considerably less common but epidemiologically significant STEC serotype. Its prominence stems largely from the massive 2011 outbreak in Germany, where the O104:H4 strain caused approximately 3,816 cases of acute gastroenteritis, 845 cases of HUS, and 54 deaths [2, 3]. This outbreak was traced to contaminated fenugreek sprouts imported from Egypt, revealing the potential for fresh produce to serve as a vehicle for large-scale transmission of hybrid STEC strains [2, 4].

Unlike O157:H7, O104:H4 possesses a distinctive hybrid pathotype that combines virulence characteristics of both enteroaggregative ***E. coli*** (EAEC) and STEC. Genomic analyses have revealed that the 2011 outbreak strain evolved from an EAEC progenitor through horizontal acquisition of the Shiga toxin 2a (***stx2a***)-encoding

bacteriophage. Notably, phylogenetic studies suggest that EAEC-related ancestors of this strain may have originated in Africa, underscoring the potential for undetected circulation of O104:H4 and related hybrid clones on the continent [4, 8]. To date, O104:H4 remains rarely reported in Africa, though this likely reflects diagnostic limitations rather than true absence [17].

Rarely reported in Africa, but genomic evidence shows EAEC-related ancestors originating from Africa.

4.2 Virulence Factors

4.2.1 E. coli O157:H7

Escherichia coli O157:H7 produces an arsenal of virulence factors that collectively enable intestinal colonization, mucosal disruption, and systemic complications. The principal virulence determinants include:

Shiga toxins (Stx1 and Stx2): These AB5 toxins are the defining virulence attributes of STEC [5, 14]. Following translocation across the intestinal epithelium, Shiga toxins bind to globotriaosylceramide (Gb3) receptors on endothelial cells, leading to ribosomal inactivation, protein synthesis inhibition, and eventual cell death [16]. The Stx2 variant is more commonly associated with severe clinical outcomes, including HUS, due to its higher cytotoxic potency and greater propensity for systemic dissemination [5, 16].

Locus of enterocyte effacement (LEE): The LEE Pathogenicity Island encodes a type III secretion system (T3SS) that mediates the attaching-and-effacing (A/E) lesion formation. The ***eae*** gene product, intimin, facilitates intimate bacterial attachment to enterocytes, resulting in characteristic pedestal-like structures, actin polymerization, and microvillus effacement [9, 15]. This mucosal damage disrupts intestinal absorption and promotes inflammatory diarrhea.

Enterohemolysin (hlyA): This pore-forming toxin contributes to local tissue damage and enhances vascular permeability at the intestinal mucosa, facilitating toxin absorption and dissemination to target organs including the kidneys and central nervous system [15, 24].

4.2.2 E. coli O104:H4

التعليق [DS26]: If possible, the manuscript should be supported with culture and microscopic images of these bacteria.

Escherichia coli O104:H4 exhibits a distinctive virulence repertoire that reflects its dual EAEC-STEC hybrid nature. The absence of the LEE pathogenicity island and the ***eae*** gene distinguishes it fundamentally from classical STEC strains, necessitating alternative adherence and pathogenic mechanisms [3, 8]:

Shiga toxin 2a (Stx2a): The 2011 German outbreak strain harbored the ***stx2a*** gene variant, which exhibits substantially greater cytotoxicity than Stx1 and other Stx2 subtypes [2, 16]. The potent activity of Stx2a against renal microvascular endothelium contributes to the disproportionately high incidence of HUS observed in O104:H4 infections, with reported HUS rates of 22% among hospitalized patients during the German outbreak [2, 12, and 16].

Aggregative adherence fimbriae (AAF/I): Encoded on the pAA plasmid, AAF/I mediates the characteristic stacked-brick aggregative adherence pattern to intestinal epithelial cells, a hallmark of the EAEC phenotype [8]. This strong adhesive capacity facilitates prolonged intestinal colonization, enhanced mucosal biofilm formation, and increased exposure of the intestinal epithelium to Shiga toxins [3,8].

pAA plasmid: Beyond AAF/I fimbriae, the pAA plasmid carries multiple virulence-associated genes including those involved in biofilm formation, mucosal toxicity (***aatA***, ***aap***), and dispersin production [8]. The formation of thick mucosal biofilms provides a protected niche for bacterial persistence and enhanced toxin delivery [3,8].

Extended-spectrum β-lactamase (ESBL) genes: The 2011 outbreak strain carried the CTX-M-15 ESBL gene on a conjugative IncI1 plasmid, conferring resistance to penicillins, cephalosporins, and monobactams [2,4,19]. This antimicrobial resistance profile complicates empirical treatment and may promote nosocomial transmission in healthcare settings [19,23].

4.3 Clinical Presentation

Infections with both O157:H7 and O104:H4 typically present with watery diarrhea that may progress to hemorrhagic colitis within 2–5 days of symptom onset [5,16]. Clinical manifestations include severe abdominal cramps, grossly bloody stools, vomiting, and low-grade fever. The shared capacity of both serotypes to produce Shiga toxins underlies their potential to cause life-threatening systemic complications [14,16].

Hemolytic uremic syndrome represents the most severe complication of STEC infection, characterized by the triad of microangiopathic hemolytic anemia, thrombocytopenia, and acute kidney injury [16]. HUS develops in approximately 5–10% of diagnosed O157:H7 infections, with children under five years of age, elderly individuals, and immunocompromised persons at highest risk [5, 14]. O104:H4 infections are associated with a markedly elevated HUS incidence, approaching 22% in hospitalized cases from the 2011 German outbreak [2, 16]. The higher HUS rate in O104:H4 infections is attributable to the enhanced cytotoxicity of Stx2a, the pro-inflammatory effects of EAEC virulence factors, and the strong aggregative adherence that may increase intestinal toxin absorption [12, 16].

4.4 Transmission Dynamics

Escherichia coli O157:H7 is fundamentally a zoonotic pathogen, with asymptomatic cattle serving as the principal reservoir [1,12]. The bacterium colonizes the terminal rectum of ruminants without causing disease, subsequently shedding in feces that can contaminate meat during slaughter, milk during collection, and water sources through agricultural runoff [12, 24]. Person-to-person transmission via the fecal-oral route is also well documented, particularly in settings with suboptimal hygiene practices [1,9]. Environmental persistence of O157:H7 in soil, water, and on surfaces further contributes to its transmission potential [12].

E. coli O104:H4 presents a distinct epidemiological profile. No animal reservoir has been definitively identified; transmission occurs predominantly through contaminated food products—particularly fresh produce such as sprouts, leafy greens, and vegetables—and through direct person-to-person spread [2,4]. The absence of a zoonotic reservoir suggests that O104:H4 control strategies must focus primarily on food safety during production, processing, and handling, as well as on hygiene measures to interrupt human-to-human transmission [2,7].

In Nigeria, the transmission risk for both serotypes is amplified by several contextual factors: the predominance of informal food markets with limited regulatory oversight, inconsistent access to safe drinking water, inadequate sanitation infrastructure, and common practices of consuming raw or undercooked meat and unpasteurized dairy products [17, 18, 23]. These conditions create an environment conducive to STEC

transmission and underscore the urgent need for integrated food safety and water, sanitation, and hygiene (WASH) interventions [7, 17].

5. Key Findings: Comparative Summary

Table 1 presents a systematic comparison of the key distinguishing features of *E. coli* O157:H7 and O104:H4 across epidemiological, virulence, clinical, and transmission dimensions.

Feature	**E. coli** O157:H7	**E. coli** O104:H4
Pathotype	Classical STEC	Hybrid EAEC–STEC
Primary Reservoir	Cattle (ruminants)	No known animal reservoir
Key Virulence Factors	LEE (***eae***), Stx1, Stx2, HlyA	Stx2a, AAF/I, pAA plasmid
AMR Profile	Variable; generally susceptible	Frequently ESBL-positive
Clinical Severity	High; HUS in 5–10% of cases	Very high; HUS in ~22% of hospitalized cases
Transmission Routes	Undercooked beef, raw milk, contaminated produce, animal contact	Contaminated fresh produce, person-to-person
African Prevalence	Documented; 1.4–8.6% in Nigerian studies	Very limited data
Nigerian Surveillance Data	Sparse; no national surveillance	Almost nonexistent

---

6. Discussion

This comparative analysis reveals fundamental differences between *E. coli* O157:H7 and O104:H4 that carry significant implications for clinical practice, public health surveillance, and infection control strategies in Nigeria and beyond [1, 17]. O157:H7 represents a classical zoonotic STEC whose epidemiology is well characterized and whose control depends substantially on veterinary public health measures, food safety

interventions targeting the beef production chain, and hygiene practices that interrupt fecal-oral transmission from animal sources [12, 18].

E. coli O104:H4, by contrast, represents an emerging hybrid pathotype that challenges conventional STEC paradigms [2, 4]. Its lack of a known animal reservoir, its capacity for explosive foodborne outbreaks through fresh produce vehicles, and its frequent association with antimicrobial resistance render it a particularly concerning threat in settings with limited diagnostic and genomic surveillance capacity [2, 19, 22]. The 2011 German outbreak demonstrated that O104:H4 can cause large-scale morbidity and mortality even within well-resourced healthcare systems; the potential impact of a similar outbreak in Nigeria, where healthcare infrastructure is less robust, is deeply concerning [2,3].

Nigeria's current diagnostic landscape presents substantial barriers to STEC detection and differentiation. The majority of clinical microbiology laboratories rely on conventional culture-based methods that cannot reliably distinguish between diarrheagenic *E. coli* pathotypes [6, 10]. Molecular diagnostic tools such as multiplex PCR, though increasingly available in tertiary reference centers, remain inaccessible at the primary and secondary healthcare levels where most diarrheal diseases are managed [6,17]. This diagnostic gap contributes to systematic underdiagnosis and obscures the true burden of STEC-associated disease [17,22].

The antimicrobial resistance profile of O104:H4 adds a further layer of complexity [2, 4, 19]. The carriage of ESBL genes, particularly CTX-M-15, complicates empirical treatment approaches and raises concerns about nosocomial transmission [19,23]. Importantly, antibiotic therapy in STEC infections remains controversial; several classes of antibiotics, including fluoroquinolones and trimethoprim-sulfamethoxazole, may induce phage-mediated Shiga toxin release and potentially increase HUS risk [5, 16]. Consequently, treatment remains primarily supportive, emphasizing hydration, electrolyte management, and early renal replacement therapy when indicated [16].

Whole-genome sequencing represents a transformative tool for STEC surveillance, offering unprecedented resolution for outbreak detection, source attribution, and virulence characterization [3,22]. However, WGS capacity in Nigeria remains confined to a small number of research institutions, with limited integration into routine national disease surveillance [19, 22]. Scaling up genomic surveillance infrastructure would enable real-time monitoring of circulating STEC strains, early

identification of emerging hybrid clones with enhanced virulence or resistance, and evidence-informed targeting of prevention resources [22].

7. Conclusion

Escherichia coli O157:H7 and O104:H4 represent two distinct but equally significant threats to global public health [1, 7]. While O157:H7 is a well-characterized zoonotic pathogen with established reservoirs and transmission pathways, O104:H4 embodies a new generation of hybrid pathogens that combine virulence traits from multiple pathotypes, complicating diagnosis, treatment, and prevention efforts [2,4]. The 2011 German outbreak served as a stark reminder of the pandemic potential of hybrid STEC strains and the catastrophic consequences that can ensue when such pathogens encounter vulnerable food systems [2,3].

In Nigeria, the near-absence of systematic STEC surveillance, limited molecular diagnostic capacity, and inadequate food safety infrastructure create a dangerous blind spot [6, 17, 22]. The sporadic and geographically limited nature of available data almost certainly underestimates the true disease burden, while the lack of genomic surveillance means that emerging hybrid clones may be circulating undetected [17,19,22]. Addressing these gaps is not merely an academic exercise but an urgent public health imperative. Investment in laboratory infrastructure, workforce training, genomic surveillance systems, and food safety regulation represents a necessary and cost-effective strategy for protecting population health and preventing potentially devastating STEC outbreaks [17, 22, 23].

التعليق [DS27]: The conclusions are good, but why include other researchers' sources here? This is a conclusion specific to the researcher himself, i.e., specific to your research findings. Therefore, it's preferable to remove all references from the conclusions.

8. Recommendations

Based on the findings of this review and the work of Elemuwa, et al, 2022, the following evidence-based recommendations are proposed to strengthen STEC surveillance, diagnostics, and control in Nigeria and Sub – Saharan Africa:

Strengthen Laboratory Diagnostic Capacity: Introduce multiplex PCR panels for simultaneous detection of diarrheagenic *E. coli* pathotypes in national and regional reference laboratories [6, 19]. Expand whole-genome sequencing capacity and establish a centralized Nigerian Pathogen Genomics Consortium to support real-time surveillance of emerging STEC strains and antimicrobial resistance patterns [19, 22].

Enhance Food Safety Systems: Develop and enforce Hazard Analysis Critical Control Point (HACCP)-based standards for slaughterhouses, dairy processing facilities, and fresh produce vendors [7, 18]. Implement comprehensive food handler education and certification programs targeting market workers, restaurant staff, and agricultural producers [17, 23]. Strengthen cold chain infrastructure to prevent bacterial proliferation during food distribution [7].

Integrate STEC Surveillance into National AMR Strategy: Incorporate STEC monitoring into the existing national antimicrobial resistance surveillance framework, leveraging the Integrated Disease Surveillance and Response (IDSR) platform [17, 23]. Establish standardized case definitions, laboratory reporting protocols, and data-sharing mechanisms between human health, veterinary, and food safety sectors using a One Health approach [17, 22].

Improve Outbreak Preparedness: Develop and regularly update national STEC outbreak response protocols, including standardized investigation procedures, laboratory confirmation algorithms, and risk communication strategies [6, 7]. Establish a national STEC reporting system with early warning capabilities to enable rapid detection and containment of outbreaks [22].

Promote Water, Sanitation, and Hygiene (WASH) Interventions: Scale up community-based WASH programs targeting high-risk populations, including children under five, immunocompromised individuals, and communities dependent on unimproved water sources [7, 17]. Integrate hygiene promotion into existing maternal and child health programs [7].

Expand Epidemiological Research: Conduct nationwide prevalence studies utilizing molecular diagnostic methods to establish baseline STEC burden estimates [17, 19]. Support genomic epidemiology research to characterize circulating strains, identify emerging hybrid clones, and elucidate transmission dynamics in Nigerian food systems [19, 22]. Foster South-South research collaborations with other African nations facing similar STEC challenges [17, 22].

التعليق [DS28]: Although the recommendations are good and excellent, their presentation needs complete revision. The recommendations rely on the author's own convictions and data collection, and no other sources are mentioned here. Sources are only cited in the bibliography and the scientific reviews the researcher addressed in their manuscript. It would be preferable to remove all reviews from this section and rely solely on the recommendations the researcher personally finds convincing.

References

1. Karmali MA, Gannon VP, Sargeant JM. Verocytotoxin-producing Escherichia coli (VTEC). Vet Microbiol. 2010;140(3-4):360-370.

2. Frank C, Werber D, Cramer JP, et al. Epidemic profile of Shiga-toxin-producing Escherichia coli O104:H4 outbreak in Germany. N Engl J Med. 2011;365(19):1771-1780.
3. Mellmann A, Harmsen D, Cummings CA, et al. Prospective genomic characterization of the German enterohemorrhagic Escherichia coli O104:H4 outbreak by rapid next-generation sequencing technology. PLoS One. 2011;6(7):e22751.
4. Rasko DA, Webster DR, Sahl JW, et al. Origins of the E. coli strain causing an outbreak of hemolytic-uremic syndrome in Germany. N Engl J Med. 2011;365(8):709-717.
5. Karmali MA. Enterohaemorrhagic Escherichia coli and the haemolytic uraemic syndrome. Clin Microbiol Infect. 2017;30(2):113-142.
6. Centers for Disease Control and Prevention (CDC). Shiga toxin-producing E. coli (STEC): Clinical microbiology and surveillance guidelines. Atlanta, GA: CDC; 2023.
7. World Health Organization (WHO). Estimating the burden of foodborne diseases. Geneva: WHO; 2022.
8. Okeke IN, Nataro JP. Enteroaggregative Escherichia coli. Lancet Infect Dis. 2001;1(5):304-313.
9. Nataro JP, Kaper JB. Diarrheagenic Escherichia coli. Clin Microbiol Rev. 1998;11(1):142-201.
10. Okeke IN, Lamikanra A, Steinruck H, Kaper JB. Characterization of Escherichia coli strains from cases of childhood diarrhea in provincial southwest Nigeria. J Clin Microbiol. 2000; 38(1):7-12.
11. Iweriebor BC, Iwu CJ, Obi CL, et al. Multidrug-resistant Shiga toxin-producing Escherichia coli O157 strains recovered from meat products in Eastern Cape Province, South Africa. J Food Prot. 2015;78(11):2066-2072.
12. Bielaszewska M, Mellmann A, Zhang W, et al. Characterisation of the E. coli strain associated with an outbreak of haemolytic uraemic syndrome in Germany, 2011. Lancet Infect Dis. 2011;11(9):671-676.
13. Jenkins C, Willshaw G, Evans J, et al. Subtyping of virulence genes in verocytotoxin-producing Escherichia coli other than serogroup O157 associated with disease in the United Kingdom. J Med Microbiol. 2003; 52(Pt 11):941-947.
14. Tarr PI, Gordon CA, Chandler WL. Shiga-toxin-producing Escherichia coli and haemolytic uraemic syndrome. Lancet. 2005; 365(9464):1073-1086.

15. Law D. Virulence factors of Escherichia coli O157 and other Shiga toxin-producing E. coli. J Appl Microbiol. 2000; 88(5):729-745.
16. Freedman SB, van de Kar NCAJ, Tarr PI. Shiga toxin-producing Escherichia coli and the hemolytic-uremic syndrome. N Engl J Med. 2023; 389(15):1402-1414.
17. Somda NS, Adesoji TO, Tetteh-Quarcoo PB, Donkor ES. A systematic review and meta-analysis on the presence of Escherichia coli O157:H7 in Africa from a One Health perspective. Microorganisms. 2025; 13(4):902.
18. Onwumere-Idolor OS, Kperegbeyi JI, Imonikebe UG, Okoli CE, Ajibo FE, Njoga EO. Epidemiology of multidrug-resistant zoonotic E. coli from beef processing and retail points in Delta State, Nigeria: Public health implications. Prev Vet Med. 2024; 224:106132.
19. Ejikeugwu CP, et al. Whole-genome sequencing uncovers chromosomal and plasmid-borne multidrug resistance and virulence genes in poultry-associated Escherichia coli from Nigeria. Microbiol Spectr. 2025; 13(9):e00115-25.
20. Mundalo S, Ntabo R, Kering K, Too R, Kariuki K, Imoli D, Silantoi B, Kiptanui E, Kavai S, Kariuki S, Mbae C. Molecular detection and antibiotic resistance of diarrheagenic Escherichia coli from street food and water in Mukuru slums, Nairobi County. PLoS One. 2026; 21(1):e0340081.
21. Centers for Disease Control and Prevention (CDC). FoodNet 2023 preliminary data. 2024. Available at: https://www.cdc.gov/foodnet/reports/preliminary-data.html
22. Mboowa G, Kakooza F, Egesa M, Tukwasibwe S, Kanyerezi S, Sserwadda I, Kidenya BR, Kabahita JM, Namaganda MM, Nsubuga M, et al. The rise of pathogen genomics in Africa. F1000Res. 2024; 13:468.
Alabi MA, Chenia HY, Lin J. Antibiotic use in livestock: a driver of resistance in Africa and the path to safer alternatives. MicrobiologyOpen. 2025; 14:e70122.
Elemuwa, C. O., Isibor, J. O., Inyang, N. J., Elemuwa, G. U. and Omoregie, R. (2022) Molecular Differentiation of ***Escherichia coli*** O157:H7 and ***Shigella*** Using 16S rRNA Phylogeny. BJMLS. 7(2): 60 – 67.

التعليق [DS29]: The references are excellent, but I think they are few compared to the importance of the current study topic, and a number of new scientific references are needed.