

Systematic Review

Molecular Identification of *Escherichia coli* Isolated from Street Foods: Global Evidence and Public Health Implications

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Abstract

Escherichia coli (*E. coli*) pathotypes present in contaminated food, street food, or water are major contributors to foodborne illnesses. Polymerase chain reaction (PCR) methods are widely applied to detect and confirm *E. coli* pathotypes in food samples, thereby supporting outbreak prevention efforts. The objective of this study was to provide a comprehensive and reliable review of the molecular identification of *E. coli* isolated from street foods and to examine its public health implications. The review followed the “Preferred Reporting Items for Systematic Reviews and Meta-Analyses” (PRISMA) guidelines and included data retrieved from seven electronic scientific databases covering the period from 1 January 2015, to 15 August 2025. Relevant full-text articles were identified using the search string (“Street food”) AND (*Escherichia coli*), and only those that met established inclusion and exclusion criteria were selected. A total of 23 studies from Asia, Africa, Europe, and Latin America were included. These studies analyzed a wide range of street foods and beverages. MacConkey Agar and Eosin Methylene Blue Agar were the primary culture media used for the growth and isolation of *E. coli*. PCR was employed in 50% of the studies to amplify specific DNA segments, enabling the identification of eight *E. coli* pathotypes: EHEC, ETEC, EAEC (Eagg), EIEC, EPEC, UPEC, DAEC, and APEC. Additionally, a few studies reported phylogroups such as A, B1, B2, C, D, E, and Clade 1. The prevalence of *E. coli* in street foods varied widely, ranging from 0.5% in Chile to 100% in Mexico. Overall, this systematic review provides an updated scientific overview highlighting persistent challenges in street food safety and *E. coli* contamination. Across studies, three recurring issues were identified: (1) inadequate and unhygienic vending locations, (2) poor quality of food, and (3) inappropriate food preparation practices. These findings underscore the need for strategic interventions. The evidence presented could support governments and

the scientific community in advancing research on *E. coli* in street foods and implementing corrective measures at local or regional scales, such as educational campaigns for vendors and consumers.

Keywords: *Escherichia coli*; street food; food safety; molecular typing; *E. coli* pathotypes; PRISMA standardized method

1. Introduction

Street food includes a wide range of foods (meat, poultry, seafood, fruits, vegetables, and grains) and beverages (water, fruit juices, milkshakes, and coffee) that are prepared and sold by street vendors in public sites (streets, marketplaces, train stations, sidewalk stalls, and public transport stops) for immediate consumption without further processing or preparation [1–3]. Approx. 2.5 billion customers worldwide consume street food every day [4] due to their affordability and practicality [5].

Street food micro-industries, which are generally unregulated, informal, or quasi-clandestine, provide employment for rural and urban citizens in many areas of developing countries [6]. However, many street vendors exhibit bad food-handling practices and low hygienic standards (environmental contamination) during their activities [7–11]; consequently, street meals, which are ideal places for the growth of pathogenic microorganisms, are potential vehicles of foodborne bacterial diseases [12]. The pathogens, such as *Klebsiella pneumonia*, *Staphylococcus aureus*, *Salmonella* spp., *Listeria monocytogenes*, and *E. coli*, can cause mild or severe disease symptoms that include fever, headache, nausea, vomiting, abdominal pain, and severe diarrhea [13–16].

In particular, *E. coli* is a Gram-negative, usually motile, non-spore-forming, chemoorganotrophic, facultative anaerobic bacillus belonging to the *Enterobacteriaceae* family [17–19]; the bacteria inhabit the gastrointestinal tracts of the intestines of warm-blooded animals, including humans, forming part of the gut microbiota and protecting the gastrointestinal epithelium from other pathogenic microorganisms [20,21]. However, *E. coli* commensal strains can acquire specific virulence attributes, causing a broad spectrum of diseases [22,23], including cholecystitis, bacteremia, cholangitis, urinary tract infections, and traveler's diarrhea [24].

Based on virulence factors, infection sites, and disease mechanisms, pathogenic *E. coli* have been divided into two main groups: Intestinal Pathogenic *E. coli* (IPEC) and Extraintestinal Pathogenic *E. coli* (ExPEC) [25].

The IPEC group comprises six pathogenic pathotypes that cause different diseases, namely (1) diffusely adherent *E. coli* (DAEC)—diarrhea in children; (2) enteroaggregative *E. coli* (EAEC)—persistent diarrhea; (3) enterohemorrhagic *E. coli* (EHEC)—hemorrhagic colitis and hemolytic-uremic syndrome; (4) enteroinvasive *E. coli* (EIEC)—watery diarrhea and dysentery; (5) enteropathogenic *E. coli* (EPEC)—diarrhea in children and animals; and (6) enterotoxigenic *E. coli* (ETEC)—traveler's diarrhea [26–28].

The ExPEC group comprises five variants that can colonize and induce disease in bodily sites outside of the gastrointestinal tract, namely (1) avian pathogenic *E. coli* (APEC)—colibacillosis in avian species; (2) mammary pathogenic *E. coli* (MPEC)—bovine mastitis; (3) neonatal meningitis *E. coli* (NMEC)—neonatal meningitis; (4) sepsis-associated *E. coli* (SEPEC)—septicemia; (5) uropathogenic *E. coli* (UPEC)—urinary tract infection [29–33]. Four *E. coli* pathotypes: ETEC, EPEC, EHEC, and EIEC, frequently found in contaminated food, street food, or water, are responsible for foodborne illnesses [34].

Pathotypes refer to groups of *E. coli* strains classified according to their virulence factors, mechanisms of infection, and clinical symptoms. These classifications are based

on phenotypic traits and pathogenic behavior in humans or animals [20,25]. In contrast, phylogroups refer to genetically distinct lineages of *E. coli*, determined through molecular analyses of conserved genes, which reflect evolutionary relationships and ecological adaptations [20,35–37].

E. coli is divided into several phylogroups based on genetic diversity, which is closely related to their ecological niches and pathogenic potential. Historically, four main phylogroups (A, B1, B2, and D) were identified [36], but research has expanded this classification, and a more refined classification [37] has described eight phylogroups (A, B1, B2, C, D, E, F, and *Escherichia* cryptic clade I). Additional phylogroups, G and H, have also been identified through whole-genome sequence analyses [38,39]. Recently, a large-scale genome analysis of *E. coli* expanded this further, identifying 14 distinct phylogroups, with each group showing genetic distinctions based on core gene differences and varied gene gain/loss patterns [35]. These phylogroups are not just genetic subdivisions but also align with specific ecological niches and disease-causing potential. For instance, phylogroups B2 and D are more commonly associated with extra-intestinal infections, while groups like A and B1 are more prevalent in commensal strains [35,37]. This refined understanding of phylogroup structure allows for better epidemiological tracking and characterization of *E. coli* strains.

Rapid and accurate molecular methods are currently used to detect or confirm *E. coli* pathotypes in food and other samples [19,40]; the polymerase chain reaction (PCR) methods that are applied in many laboratories include conventional PCR, multiplex PCR, quadruplex PCR, nested PCR, quantitative PCR (qPCR), reverse-transcription PCR (RT-PCR), and Droplet Digital PCR (ddPCR) [41–43].

Molecular *E. coli* characterization in food samples can be confirmed with multiple marker genes such as *adk*, *agg*, *arpA*, *bfpA*, *chuA*, *cyd*, *daeA*, *eagg*, *elt*, *esth*, *estp*, *fliCH7*, *gadA*, *hlyA*, *ipaH*, *lacY*, *lacZ*, *lt*, *malB*, *phoA*, *rbfO157*, *rfbE*, *st*, *stx 1*, *stx 2*, *TspE4.C2*, *uidA*, *uspA*, *yjaA*, and *16SrDNA* [41,44–52].

E. coli is used as a more specific indicator of fecal contamination than other fecal coliform species [19,53–55]. Infection prevention for *E. coli* requires control measures at all stages of the food chain, from agricultural production, manufacturing, to preparation of foods in both commercial establishments, household kitchens, or street food stands [56]. Molecular methods allow for quick analysis of food samples and possible early detection of infection focal points [57].

Scientific studies oriented to analyze primary sources of *E. coli* outbreaks, such as raw or undercooked ground-meat products, raw milk, and vegetables sold in the streets of many cities, are essential activities to achieve food safety and to improve the quality of life and psychophysical health of humans worldwide.

A previous systematic review by Koumassa et al. [58] indicated that bacteria such as *E. coli* are frequently identified in street food sold in developing countries due to poor hygiene practices and knowledge, inadequate preparation methods, substandard packaging, and poor environmental conditions, while Heredia & García [59] suggested that foods of animal origin are potential vehicles of foodborne pathogens. As a further example, *E. coli* exceeded the acceptable limits in 20.8% of grilled-pork samples tested by Anihouvi et al. [60] in Benin. Even the data collected by Salamandane et al. [2] pointed in the same direction: the microbiological quality of water and street food sold in Maputo (Mozambique) was generally unsatisfactory for human consumption due to contamination with *E. coli*.

A complex and multidisciplinary approach based on relevant and recent studies is required to prevent and control outbreaks of foodborne pathogens while at the same time promoting food safety. The objective was to present a comprehensive and reliable report

on the molecular identification of *E. coli* isolated from street foods on a global scale. For the first time, in addition to the standard information (i.e., country, food type, sample size, and *E. coli* prevalence), molecular parameters (i.e., DNA extraction and detection methods, target genes, and product sizes) were also collected and analyzed, offering readers a broader view of this public health problem. Starting from our results, governments and the scientific community could further study *E. coli* in street food and, at the same time, carry out corrective actions or educational hygienic campaigns with vendors and citizens worldwide.

2. Materials and Methods

The systematic review of the literature was performed according to the standardized method of Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) and the statement guidelines and the checklist of Moher et al. [61]. Supplementary File S1 presents the PRISMA checklist for this study.

2.1. Search Strategy

Searching the literature published from 1 January 2015 to 15 August 2025 was carried out by an author (YSG). Seven electronic scientific databases, including ISI Web of Science (Clarivate Analytics, London, UK), EBSCOhost (EBSCO Industries, Birmingham, AL, USA), EMBASE (Elsevier, Amsterdam, The Netherlands), Science Direct (Elsevier, Amsterdam, The Netherlands), SciELO (São Paulo Research Foundation—FAPESP, São Paulo, São Paulo, Brazil), Scopus (Elsevier, Amsterdam, The Netherlands), PubMed (National Library of Medicine of USA—NLM, Bethesda, MD, USA), were searched individually for the relevant full-text articles using the following search string:

((street food [Title/Abstract]) OR (street foods [Title/Abstract])) AND (*Escherichia coli* [Title/Abstract]) OR (*E. coli* [Title/Abstract])) Filters: from 2015–2025.

2.2. Inclusion Criteria

The inclusion criteria applied to full-texts for assessing their eligibility were (a) original articles focusing on the molecular identification of *E. coli* isolated from street foods, (b) articles published from 1 January 2015 to 15 August 2025, (c) articles written in English, (d) studies limited to street food, (e) molecular identification of *E. coli*, and (f) articles published in peer-reviewed journals inserted in the Scimago Quartiles Rankings (SJR) database.

2.3. Exclusion Criteria

The exclusion criteria applied to full-texts for assessing their eligibility were (a) abstracts not associated with the full article, (b) articles published in non-peer-reviewed sources, (c) articles not written in English, (d) reviews of literature or meta-analyses, (e) letter to the editor, (f) data note, (g) short communication, and (h) studies with high risk of bias based on the Joanna Briggs Institute (JBI) tool [62].

2.4. Selection of Studies

The identified articles were compiled using Mendeley Desktop Reference Management System 2.11.0, and the duplicates were removed. Subsequently, two authors (Y.S.-G. and N.G.-V.) independently screened titles and abstracts. Irrelevant titles were removed. A third author (C.F.) made a final decision when two reviewers had differing opinions.

Inclusion and exclusion criteria were subsequently applied to full texts to assess the eligibility of the selected published material. Two authors (Y.S.-G. and N.G.-V.) independently analyzed the full-text papers, and only those that met all criteria were finally selected. Disagreements between the two researchers were resolved through consultation with a third author (C.F.).

2.5. Data Extraction Matrix

Article—level data were extracted from each selected paper; subsequently, it was summarized and tabulated in an analysis matrix developed in MS Excel® (Excel for Microsoft 365). The summarized information was organized in eighteen columns with the following subjects: (a) reference, (b) country, (c) rural/urban, (d) sample collection period, (e) quartile, (f) risk of bias, (g) food type, (h) sample size, (i) sample weight, (j) isolation of *E. coli*, (k) DNA extraction method, (l) detection method, (m) target gene, (n) product size, (o) sample size, (p) positive samples, (q) prevalence, and (r) confidence interval (CI).

2.6. Quality Assessment

The standard tool, JBI, was used to assess the quality and risk of bias of the observational studies [62]. The tool is commonly used as guidance for conducting reviews, qualitative studies, prevalence/incidence analysis, diagnostic tests, mixed-method analyses, and scoping reviews.

The checklist consists of nine questions, each with four possible answers (yes, no, unclear, and not applicable). The JBI tool has a score-rating system to assess the quality of studies: high quality (7–9), moderate (4–6), and low quality (less than 4) (Supplementary File S2). Two researchers (Y.S.-G. and N.G.-V.) separately assessed the risk of bias. Disagreements between the two researchers were resolved through consultation with a third author (CF).

3. Results

3.1. Literature Search

The PRISMA Statement flow diagram that indicates the four phases of the literature search (identification, screening, eligibility, and inclusion) is shown in Figure 1. During the identification phase, a total of 314 articles were recorded. Duplicates were automatically removed via bibliographic management software; the remaining 188 articles were screened for title and abstract pertinence. Only 58 articles that have passed the screening phase were assessed based on pre-established inclusion and exclusion criteria. Finally, 23 articles [63–85] were included in this systematic review.

3.2. Characteristics of the Selected Studies

The basic characteristics of the selected studies, i.e., country, region (rural/urban), sample collection period (months), SJR quartile, and risk of bias (score, moderate/low), are summarized in Table 1.

Table 1. Basic characteristics of selected studies.

Country	Rural/Urban	Sample Collection Period (Months)	Quartile	JBI Score (%)	Risk of Bias	Reference
South Africa	Urban	February 2016–August 2017 (19)	Q3	7/9 (77.7)	Moderate	Asiegbu, Lebelo, & Tabit, 2020 [63]
Portugal	Urban	March 2019–December 2022 (46)	Q2	7/9 (77.7)	Low	Barreira et al., 2024 [64]
Bangladesh	Urban	March–May 2017 (3)	Q4	6/9 (66.6)	Moderate	Bhowmik et al., 2022 [65]
Indonesia	Urban	N.D.	Q3	7/9 (77.7)	Moderate	Budiarso et al., 2021 [66]
Brazil	Urban	April–June, 2019 (3)	Q4	6/9 (66.6)	Moderate	da Silva Oliveira et al., 2021 [67]
Bangladesh	Urban	January–October, 2018 (10)	Q2	7/9 (77.7)	Low	Das et al., 2021 [68]

Table 1. Cont.

Country	Rural/Urban	Sample Collection Period (Months)	Quartile	JBİ Score (%)	Risk of Bias	Reference
Malaysian	Urban	N.D.	Q3	7/9 (77.7)	Moderate	Elexson et al., 2017 [69]
Nigeria	Urban	June–August, 2019 (3)	Q1	9/9 (100)	Low	Fayemi et al., 2021 [70]
India	Urban	N.D.	Q4	6/9 (66.6)	Moderate	Jenifer & Sathiyamurthy, 2020 [71]
Bangladesh	Urban	June, 2018 (1)	Q1	9/9 (100)	Low	Johura et al., 2020 [72]
Egypt	Urban	December 2013–December 2014 (13)	Q1	9/9 (100)	Low	Khalil & Goma, 2016 [73]
Malaysian	Urban	October 2019–February 2020 (5)	Q3	7/9 (77.7)	Moderate	Latchumaya et al., 2021 [74]
Mexico	Urban	2021–2023 (N.D.)	Q1	9/9 (100)	Low	Mora-Coto et al., 2025 [75]
Indonesia	Urban	N.D.	Q4	6/9 (66.6)	Moderate	Novira et al., 2020 [76]
South Africa	Urban	November 2014–February 2015 (4)	Q2	7/9 (77.7)	Low	Plessis et al., 2017 [77]
South Africa	Urban	September 2017–May 2018 (9)	Q1	9/9 (100)	Low	Ritcher et al., 2021 [78]
Ecuador	Urban	N.D.	Q2	7/9 (77.7)	Low	Salazar-Llorente et al., 2021 [79]
Chile	Urban	January–October 2019 (10)	Q2	7/9 (77.7)	Low	Sánchez et al., 2021 [80]
India	Urban	September 2015–May 2017 (21)	Q2	7/9 (77.7)	Low	Sivakumar et al., 2021 [81]
Bangladesh	Urban	N.D.	Q4	6/9 (66.6)	Moderate	Tabassum, Saha & Islam, 2015 [82]
Iraq	Urban	April, 2022 (1)	Q2	7/9 (77.7)	Low	Taha et al., 2023 [83]
Argelia	Urban	February 2013–March 2014 (14)	Q1	9/9 (100)	Low	Yaici et al., 2017 [84]
Ecuador	Urban	November 2016–January 2017 (3)	Q3	7/9 (77.7)	Moderate	Zurita et al., 2020 [85]

Note. N.D.: not declared, JBİ: Joanna Briggs Institute.

Eleven of twenty-three studies (47.8%) were developed in Asian countries, i.e., Bangladesh [65,68,72,82], India [71,81], Indonesia [66,76], Iraq [83], and Malaysia [69,74]. Six studies (26.1%) were performed in African countries, i.e., Algeria [84], Egypt [73], Nigeria [70], and South Africa [63,67,78]. Five studies (21.7%) were implemented in American countries, i.e., Brazil [67], Chile [80], Ecuador [79,85], and Mexico [75]. Only one study was performed in Europe (Lisbon, Portugal) [64].

All studies included in this review were conducted in urban or peri-urban contexts; the length of the sample collection periods varied from one [72,83] to thirty-four months [64].

All selected articles were published in journals belonging to the SJR database; more specifically, six articles (26.1%) were published in Q1 SJR journals [70,72,73,75,78,84], seven articles (30.4%) in Q2 SJR journals [64,68,77,79–81,83], five articles (21.7%) in Q3 SJR journals [63,66,69,74,85], and five articles (21.7%) were found in Q4 SJR journals [65,67,71,76,82].

Thirteen studies (56.5%) had a low risk of bias [64,68,70,72,73,75,77–81,83,84], while ten studies (43.5%) showed a moderate risk of bias [63,65–67,69,71,74,76,82,85].

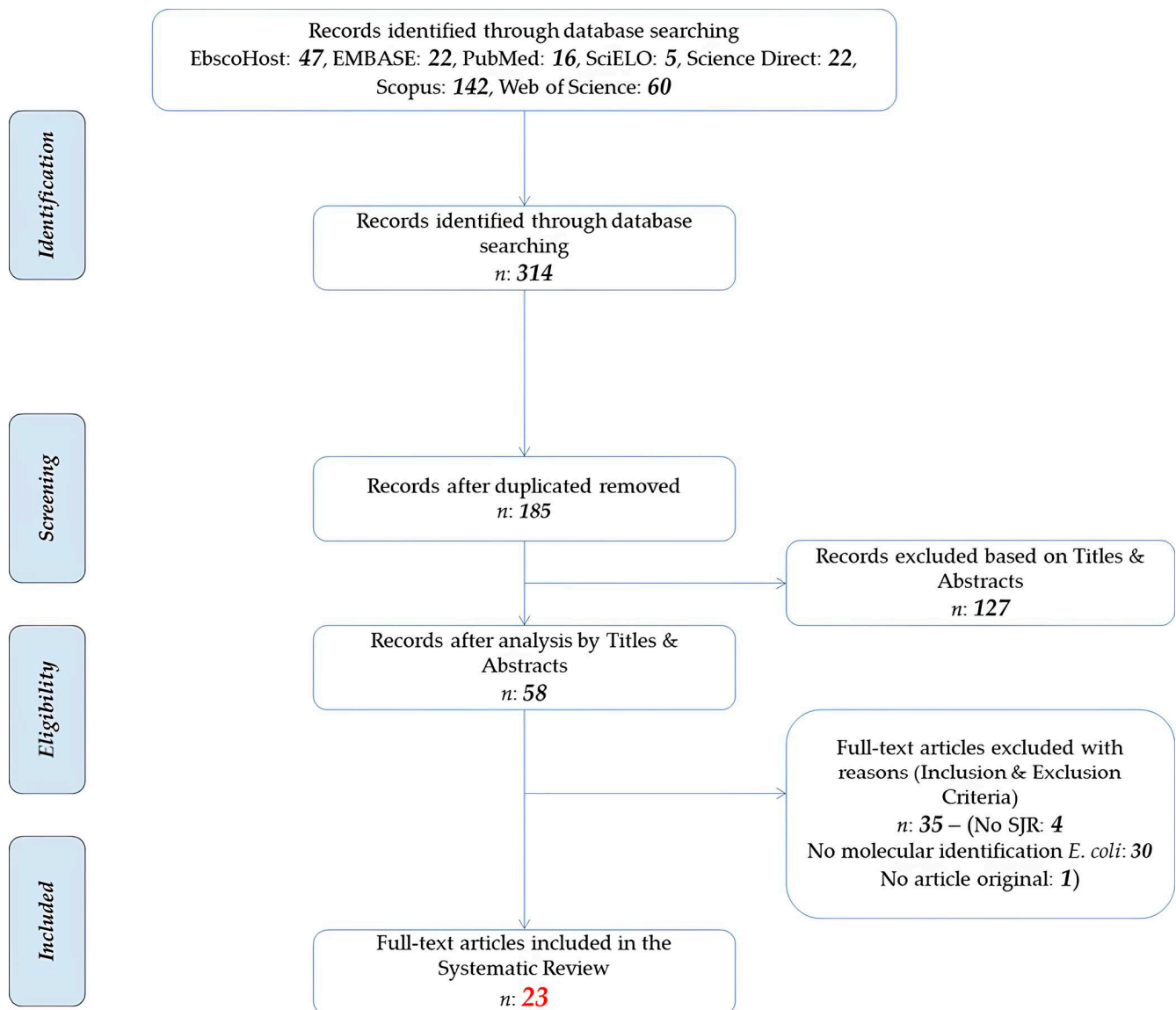


Figure 1. PRISMA flow diagram.

3.3. Pre-Enrichment and Isolation Culture Media

Different types of street foods (beef, poultry, seafood, cheese, eggs, fruits, vegetables, and grains) and beverages (sodas and fruit juices) were analyzed. Collected samples (weight between 1 and 50 g) from various street vendors were mashed or homogenized.

Before molecular identification, most studies used culture-based methods to improve the recovery of *E. coli* from food matrices (Table 2). Frequently, the food samples were inoculated in buffered peptone water medium for pre-enrichment culture; this preliminary methodological step was applied in thirteen of the selected studies (56.5%) [64,66,68,71,73,74,77–81,83,84]. Various culture media, i.e., liquid media (nutrient broths) and solid media (Agar plates), were used for the growth and isolation of *E. coli* in the laboratory. The most commonly used growth media were (1) MacConkey Agar (employed in eleven studies—47.8%) [68,70–73,75,80–84], (2) Eosin methylene blue Agar (employed in nine studies—39.1%) [67–69,71,72,75,78,79,81], and (3) Plate Count Agar (employed in four studies—17.4%) [67,73,74,79]. Most of the studies focused on identifying diarrheagenic *E. coli* pathotypes (IPEC), including EHEC, ETEC, EAEC, EIEC, EPEC, and APEC, confirming the clinical and epidemiological relevance of the isolates.

Table 2. Molecular methods for identification of *Escherichia coli* in this systematic review.

Food Type & Number of Samples	Sample Weight (g or mL)	Culture Media for <i>E. coli</i> Recovery	DNA Extraction Method	Detection Method	Pathotype/Phylogroup	Target Gene	Product Size (bp)	Reference	
Starch Beef Poultry Fish Vegetables Sandwiches 110	25	HiCrome™ enrichment broth (Sigma-Aldrich, Johannesburg South Africa)	ZR Fungal/ Bacterial DNA MiniPrep™ Kit (Zymo Research Irvine, US)	qPCR	EHEC (O15:H7)	16SrDNA	1500	Asiegbu, Lebelo, & Tabit, 2020 [63]	
Patties Salt cod fritters Croissants Donuts Sandwiches Fresh vegetables Fruits Juices 118	25	Peptone water	BioRobot EZ1 automated extraction method (Qiagen, Hilden Germany)	qPCR	EHEC	<i>stx 1</i>	180	Barreira et al., 2024 [64]	
						<i>stx 2</i>	255		
				Multiplex PCR	ETEC	<i>eaeA</i>	384		
						<i>eltB</i>	322		
				PCR	EAEC	<i>estA</i>	147		
				Multiplex PCR	APEC	<i>uspA</i>	884	Bhowmik et al., 2022 [65]	
					N.D.	<i>uidA</i>	166		
				ARDRA	N.D.	16SrDNA	996		
				Quadruplex PCR	A—B1—C—D— E	<i>arpA</i>	400		
						<i>chuA</i>	288		
						<i>yjaA</i>	211		
						<i>TspE4.C2</i>	152		
Skewered meatballs 10	25	Peptone water Chromocult coliform Agar	Wizard® Genomic DNA Purification Kit	PCR	EIEC	<i>ipaH</i>	619	Budiarso et al., 2021 [66]	
						<i>eaeA</i>	384	da Silva Oliveira et al., 2021 [67]	
						<i>stx 1</i>	180		
						<i>stx 2</i>	255		
Handmade juices Salad Chotpoti 78	10	Peptone water MacConkey Agar Eosin methylene blue Agar	N.D.	PCR	N.D.	<i>Adk</i>	536	Das et al., 2021 [68]	
Popiah 15	10	Sterile physiological saline Eosin methylene blue Agar	Manual extraction	PCR	EHEC	<i>stx 1</i>	180	Elexson et al., 2017 [69]	
						<i>stx 1</i>	180	Fayemi et al., 2021 [70]	
						<i>stx 2</i>	255		
						<i>eaeA</i>	384		
						<i>rfbO157</i>	259		
						<i>fliC_{H7}</i>	247		
						<i>stx 1</i>	180	Jenifer & Sathiyamurthy, 2020 [71]	
						<i>stx 2</i>	255		
						<i>eaeA</i>	384		
						<i>rfbE</i>	296		
						<i>fliC_{H7}</i>	247		
						<i>hlyA</i>	534		
						<i>stx 1</i>	180	Khalil & Gomaa, 2016 [73]	
						<i>stx 2</i>	255		
						<i>eaeA</i>	384		
						<i>rfbE</i>	296		
						<i>fliC_{H7}</i>	247		
						<i>hlyA</i>	534		
						<i>stx 1</i>	180	Latchumaya et al., 2021 [74]	
						<i>stx 2</i>	255		
						<i>rfbO157</i>	259		
						<i>fliC_{H7}</i>	247		
						<i>hlyA</i>	534		
						<i>stx 1</i>	180	Mora-Coto et al., 2025 [75]	
						<i>stx 2</i>	255		
						<i>rfbO157</i>	259		
						<i>fliC_{H7}</i>	247		
						<i>hlyA</i>	534		
						<i>stx 1</i>	180	Mora-Coto et al., 2025 [75]	
						<i>stx 2</i>	255		
						<i>rfbO157</i>	259		
						<i>fliC_{H7}</i>	247		
						<i>hlyA</i>	534		
						<i>stx 1</i>	180	Mora-Coto et al., 2025 [75]	
						<i>stx 2</i>	255		
						<i>rfbO157</i>	259		
						<i>fliC_{H7}</i>	247		
						<i>hlyA</i>	534		
						<i>stx 1</i>	180	Mora-Coto et al., 2025 [75]	
						<i>stx 2</i>	255		
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						<i>stx 1</i>	180	Mora-Coto et al., 2025 [75]	
						<i>stx 2</i>	255		
						<i>rfbO157</i>	259		
						<i>fliC_{H7}</i>	247		
						<i>hlyA</i>	534		
						<i>stx 1</i>	180	Mora-Coto et al., 2025 [75]	
						<i>stx 2</i>	255		
						<i>rfbO157</i>	259		
						<i>fliC_{H7}</i>	247		
						<i>hlyA</i>	534		
						<i>stx 1</i>	180	Mora-Coto et al., 2025 [75]	
						<i>stx 2</i>	255		
						<i>rfbO157</i>	259		
						<i>fliC_{H7}</i>	247		
						<i>hlyA</i>	534		
						<i>stx 1</i>	180	Mora-Coto et al., 2025 [75]	
						<i>stx 2</i>	255		
						<i>rfbO157</i>	259		
						<i>fliC_{H7}</i>	247		
						<i>hlyA</i>	534		
						<i>stx 1</i>	180	Mora-Coto et al., 2025 [75]	
						<i>stx 2</i>	255		
						<i>rfbO157</i>	259		
						<i>fliC_{H7}</i>	247		
						<i>hlyA</i>	534		
						<i>stx 1</i>	180	Mora-Coto et al., 2025 [75]	
						<i>stx 2</i>	255		
						<i>rfbO157</i>	259		
						<i>fliC_{H7}</i>	247		
						<i>hlyA</i>	534		
						<i>stx 1</i>	180	Mora-Coto et al., 2025 [75]	
						<i>stx 2</i>	255		
						<i>rfbO157</i>	259		
						<i>fliC_{H7}</i>	247		
						<i>hlyA</i>	534		
						<i>stx 1</i>	180	Mora-Coto et al., 2025 [75]	
						<i>stx 2</i>	255		
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						<i>fliC_{H7}</i>	247		
						<i>hlyA</i>	534		
						<i>stx 1</i>	180	Mora-Coto et al., 2025 [75]	
						<i>stx 2</i>	255		
						<i>rfbO157</i>	259		
						<i>fliC_{H7}</i>	247		
						<i>hlyA</i>	534		
						<i>stx 1</i>	180	Mora-Coto et al., 2025 [75]	
						<i>stx 2</i>	255		
						<i>rfbO157</i>	259		
						<i>fliC_{H7}</i>	247		
						<i>hlyA</i>	534		
						<i>stx 1</i>	180	Mora-Coto et al., 2025 [75]	
						<i>stx 2</i>	255		
						<i>rfbO157</i>	259		
						<i>fliC_{H7}</i>	247		
						<i>hlyA</i>	534		
						<i>stx 1</i>	180	Mora-Coto et al., 2025 [75]	
						<i>stx 2</i>	255		
						<i>rfbO157</i>	259		
						<i>fliC_{H7}</i>	247		
						<i>hlyA</i>	534		
						<i>stx 1</i>	180	Mora-Coto et al., 2025 [75]	
						<i>stx 2</i>	255		
						<i>rfbO157</i>	259		
						<i>fliC_{H7}</i>	247		
						<i>hlyA</i>	534		
						<i>stx 1</i>	180	Mora-Coto et al., 2025 [75]	
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						<i>fliC_{H7}</i>	247		
						<i>hlyA</i>	534		
						<i>stx 1</i>	180	Mora-Coto et al., 2025 [75]	
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						<i>stx 2</i>	255		
						<i>rfbO157</i>	259		
						<i>fliC_{H7}</i>	247		
						<i>hlyA</i>	534		
						<i>stx 1</i>	180	Mora-Coto et al., 2025 [75]	
						<i>stx 2</i>	255		
						<i>rfbO157</i>	259		
						<i>fliC_{H7}</i>	247		
						<i>hlyA</i>	534		
						<i>stx 1</i>	180	Mora-Coto et al., 2025 [75]	
						<i>stx 2</i>	255		
						<i>rfbO157</i>	259		
						<i>fliC_{H7}</i>	247		
						<i>hlyA</i>	534		
						<i>stx 1</i>	180	Mora-Coto et al., 2025 [75]	
						<i>stx 2</i>	255		
						<i>rfbO157</i>	259		
						<i>fliC_{H7}</i>	247		
						<i>hlyA</i>	534		
						<i>stx 1</i>	180	Mora-Coto et al., 2025 [75]	
						<i>stx 2</i>	255		
						<i>rfbO157</i>	259		
						<i>fliC_{H7}</i>	247		
						<i>hlyA</i>	534		
						<i>stx 1</i>	180	Mora-Coto et al., 2025 [75]	
						<i>stx 2</i>	255		
						<i>rfbO157</i>	259		
						<i>fliC_{H7}</i>	247		
						<i>hlyA</i>	534		
						<i>stx 1</i>	180	Mora-Coto et al., 2025 [75]	
						<i>stx 2</i>	255		
						<i>rfbO157</i>	259		
						<i>fliC_{H7}</i>	247		
						<i>hlyA</i>	534		
						<i>stx 1</i>	180	Mora-Coto et al., 2025 [75]	
						<i>stx 2</i>	255		
						<i>rfbO157</i>	259		
						<i>fliC_{H7}</i>	247		
						<i>hlyA</i>	534		
						<i>stx 1</i>	180	Mora-Coto et al., 2025 [75]	
						<i>stx 2</i>	255		
						<i>rfbO157</i>	259		
						<i>fliC_{H7}</i>	247		
						<i>hlyA</i>	534		
						<i>stx 1</i>	180	Mora-Coto et al., 2025 [75]	
						<i>stx 2</i>	255		
						<i>rfbO157</i>	259		
						<i>fliC_{H7}</i>	247		
						<i>hlyA</i>	534		
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						<i>stx 2</i>	255		
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						<i>fliC_{H7}</i>	247		
						<i>hlyA</i>	534		
						<i>stx 1</i>	180	Mora-Coto et al., 2025 [75]	
						<i>stx 2</i>	255		
						<i>rfbO157</i>	259		
						<i>fliC_{H7}</i>	247		
						<i>hlyA</i>	534		
						<i>stx 1</i>	180	Mora-Coto et al., 2025 [75]	
						<i>stx 2</i>	255		
						<i>rfbO157</i>	259		
						<i>fliC_{H7}</i>	247		
						<i>hlyA</i>	534		
						<i>stx 1</i>	180	Mora-Coto et al., 2025 [75]	
					</				

Table 2. Cont.

Food Type & Number of Samples	Sample Weight (g or mL)	Culture Media for <i>E. coli</i> Recovery	DNA Extraction Method	Detection Method	Pathotype/ Phylogroup	Target Gene	Product Size (bp)	Reference
Ice-based beverages 85	10	Brain heart infusion broth	Chelex 100	RT-PCR	ETEC	<i>Lt</i>	450	Novira et al., 2020 [76]
						<i>St</i>	160	
					EHEC	<i>eaeA</i>	384	
						<i>stx 1</i>	180	
						<i>stx 2</i>	255	
Cabbage heads Spinaches 180	25	Peptone water Petrifilm 3 m	Quick-gDNA Miniprep Kit (Zymo Research, Irvine, US)	Multiplex PCR	EHEC	<i>stx 1</i>	180	Plessis et al., 2017 [77]
						<i>stx 2</i>	255	
						<i>eaeA</i>	384	
				Quadruplex PCR	A—C—E— Clade1	<i>arpA</i>	400	
						<i>chuA</i>	288	
						<i>yjaA</i>	211	
						<i>TspE4.C2</i>	152	
						PCR	<i>trpA</i>	
<i>E</i>	<i>arpA</i>	301						
Vegetables 545	50	Peptone water Coliform count plates Agar Eosin methylene blue Agar	Quick-gDNA Miniprep Kit (Zymo Research, Irvine, US)	PCR	ETEC	<i>Lt</i>	450	Richter et al., 2021 [78]
						<i>St</i>	160	
					EPEC	<i>bfpA</i>	324	
						EHEC	<i>eaeA</i>	
					<i>stx 1</i>		180	
					<i>stx 2</i>	255		
					EAEC	<i>Eagg</i>	630	
					EIEC	<i>ipaH</i>	619	
Bolon Encebollado Sauces Ceviche Fruit Fruit juices Cheese Raw chicken Ground beef 405	10	Peptone water Plate count Agar Eosin methylene blue Agar	Boiling	PCR	<i>N.D.</i>	16SrDNA (V3-V4)	465	Salazar-Llorente et al., 2021 [79]
Beef Pork Fish Shrimps Vegetables Hot dogs Fruit juices 3300	25	Peptone water MacConkey Agar	<i>N.D.</i>	Multiplex PCR	EHEC	<i>stx 1</i>	180	Sánchez et al., 2021 [80]
						<i>stx 2</i>	255	
Raw Lassi Rasmalai Burfi Pedha Curd Rasgulla Salad Chutney Masala 430	<i>N.D.</i>	Peptone water MacConkey Agar Eosin methylene blue Agar	Manuel extraction	Multiplex PCR	EHEC	<i>stx 1</i>	180	Sivakumar et al., 2021 [81]
						<i>stx 2</i>	255	
					EPEC	<i>eaeA</i>	384	
						<i>bfpA</i>	324	
					ETEC	<i>Lt</i>	450	
						<i>St</i>	160	
EAEC	<i>Agg</i>	254						
Velpuri 74	<i>N.D.</i>	Nutrient Agar MacConkey Agar	Manual extraction	PCR	<i>N.D.</i>	16SrDNA (V3-V5)	600	Tabassum, Saha & Islam, 2015 [82]
Shawarma Red meat Kebab Burgers 130	10	Peptone water Coliform Agar MacConkey Agar	Boiling	Multiplex PCR	<i>N.D.</i>	<i>uidA</i>	166	Taha et al., 2023 [83]
						<i>Elt</i>	511	
					ETEC	<i>Esth</i>	172	
						<i>Estp</i>	120	
Sandwiches 200	25	Buffered tryptone water MacConkey Agar	Macherey-Nagel NucleoSpin Tissue kit (Macherey-Nagel, Hoerd, France)	Quadruplex PCR	A—B1—D	<i>chuA</i>	288	Yaici et al., 2017 [84]
						<i>yjaA</i>	211	
						<i>TspE4.C2</i>	152	
Sauces Ceviche Salad Cheese 150	1	Brilliant green bile broth ESBL CHROM Agar	Boiling	Quadruplex PCR	A—B1—B2—D	<i>gadA</i>	373	Zurita et al., 2020 [85]
						<i>arpA</i>	400	
						<i>chuA</i>	288	
						<i>yjaA</i>	211	
						<i>TspE4.C2</i>	152	

Note. *E. coli*: *Escherichia coli*; N.D.: not declared; PCR: Polymerase Chain Reaction; qPCR: Quantitative Polymerase Chain Reaction; RT-PCR: Reverse-Transcription Polymerase Chain Reaction; ARDRA: Amplified Ribosomal DNA Restriction Analysis; APEC: Avian Pathogenic *E. coli*; ETEC: Enterotoxigenic *E. coli*; EPEC: Enteropathogenic *E. coli*; EAEC: Enteraggregative *E. coli*; EHEC: Enterohemorrhagic *E. coli*; UPEC: Uropathogenic *E. coli*; DAEC: Diffusely adherent *E. coli*; EIEC: Enteroinvasive *E. coli*.

3.4. Molecular Identification of *E. coli*

The main characteristics of the applied experimental methodologies are presented in Table 2.

All DNA extraction methods performed in the selected studies followed some common procedure steps, i.e., (1) disruption of cytoplasmic and nuclear membranes, (2) denaturation of nucleoprotein complexes, (3) inactivation of nucleases and other enzymes, (4) removal of biological and chemical contaminants (lipids, proteins, and other nucleic acids), and finally (5) DNA precipitation. The selected DNA extraction method depends on multiple factors, including cost, time, and contamination risks. The boiling method was applied to extract the genomic DNA from *E. coli* isolates in seven studies (30.4%) [67,70,72,74,79,83,85], while the DNA manual extraction was realized in four studies (17.4%) [69,71,81,82]. Frequently, DNA extraction was carried out through commercial kits, such as (1) Colony PCR [65,73,75], (2) Quick-gDNA Miniprep kit (Zymo Research, Irvine, USA) [77,78], (3) ZR Fungal/Bacterial DNA MiniPrep™ Kit [63], (4) Wizard® Genomic DNA Purification Kit [66], (5) Macherey-Nagel NucleoSpin Tissue kit (Macherey-Nagel, Hoerd, France) [84]. Only two groups of authors did not declare the DNA extraction method applied in their methodological protocols [68,80].

The polymerase chain reaction (PCR), sometimes called “molecular photocopying”, was used to amplify small segments of *E. coli* DNA in twelve studies (52.2%) [64,66–72,77–79,82]. Multiplex PCR, which is characterized by amplifying multiple sequences in a single reaction, was used in nine studies (39.1%) [64,65,73–75,77,80,81,83]. Quadruplex PCR was implemented in four studies (19.0%) [65,77,84,85]. The qPCR and RT-PCR methods were implemented in a few protocols [63,64,76].

Six different *E. coli* pathotypes were detected, more specifically: (1) EHEC in twelve studies [63,64,67,69,70,73,74,76–78,80,81], (2) ETEC in six studies [64,72,75,78,81,83], (3) EAEC [64,78,81], (4) EIEC [78,81], (5) UPEC [75], (6) DAEC [75], and (7) APEC [65]. Various phylogroups, such as A, B1, B2, C, D, E, and Clade1, were detected in a few studies [65,77,84,85].

All studies complemented PCR-based detection with sequencing to confirm the identity of *E. coli* strains, virulence genes, or to analyze pathogenic gene variants (Table 3). These sequencing studies allowed researchers to confirm the specificity of the PCR amplicons and to assess the genetic diversity among isolates: 16SrDNA—1500 bp [63], 16SrDNA—996 bp [65], 16SrDNA (V3–V4)—465 bp [79], 16SrDNA (V3–V5)—600 bp [82], *adk*—536 bp [68], *agg*—254 bp [81], *arpA*—400 bp [65,77,85], *astA*—110 bp [64], *chuA*—288 bp [65,77,84,85], *estA*—147 bp [64], *caeA*—384 pb [64,67,70,73,76,78,81], *elt*—511 bp [83], *eltB*—322 bp [64], *esth*—172 bp [83], *estp*—120 bp [73], *fliC_{H7}*—247 bp [70,73,74], *gadA*—373 bp [84], *hlyA*—534 bp [73], *ipaH*—619 bp [66,78], *lt*—450 bp [72,75,76,81], *vat*—289 bp [75], *cnf1*—498 bp [75], *hlyA*—1177 bp [75], *afa*—809 bp [75], *rfbE*—296 bp [73], *rfbO157*—259 bp [70,74], *st*—160 bp [72,76,81], *stx 1*—180 bp [64,67,69,70,73,74,76,78,80,81], *stx 2*—255 pb [64,67,70,73,74,76,78,80,81], *TspE4.C2*—152 bp [65,77,84,85], *uidA*—166 bp [65,71,83], *uspA*—884 bp [65], and *yjaA*—211 bp [65,77,84,85].

3.5. Prevalence of *E. Coli* in Street Food

The selected studies indicated different sample sizes, from 10 [66] to 3300 food samples [80]. The street food *E. coli* prevalence (Figure 2a) ranged between 0.5% (Chile) [80] and 100% (Mexico) [75].

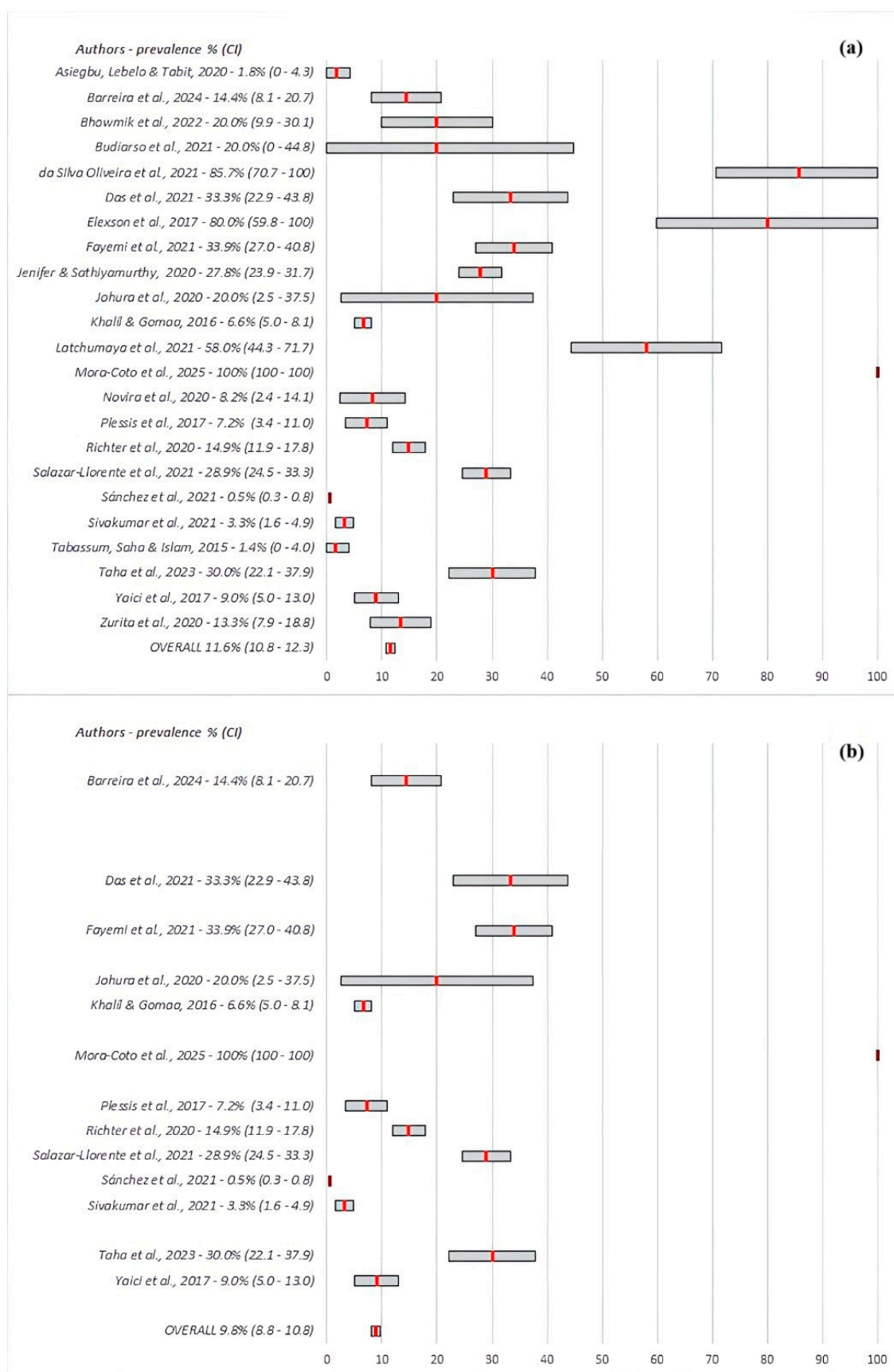


Figure 2. (a) Street food *E. coli* prevalence in the selected studies [63–85]. (b) Street food *E. coli* prevalence in studies with low risk of bias [64,68,70,72,73,75,77–81,83,84]. Note—(CI): Confidence Interval; |: mean *E. coli* prevalence.

Seven studies (30.4%) reported *E. coli* prevalence greater than 30.0% [67–70,74,75,83]. Eight studies (34.8%) reported *E. coli* prevalence between 10.0% and 30.0% [64–66,71,72,78,79,85]. Eight studies (34.8%) reported *E. coli* prevalence less than 10.0% [63,73,76,77,80–82,84].

The *E. coli* overall prevalence (world average) in analyzed street food was 11.6% (901/7795). The greater continental *E. coli* prevalence was calculated based on Asian data (19.6%—285/1452); the street food *E. coli* prevalence in Africa and Latin America street foods were equal to 11.0% (237/2160) and 8.9% (362/4065), respectively (Figure 3). The study carried out in Europe reported an *E. coli* prevalence of 14.4% (17/118) in the analyzed street food sold in Lisbon (Portugal). The overall prevalence decreased from 11.6% to 9.8% when only studies with a low risk of bias were considered (Figure 2b).

At the national level, the *E. coli* prevalence calculated based on data from India and Bangladesh (neighboring countries) was comparable, more specifically 16.5% (India) and 18.5% (Bangladesh).

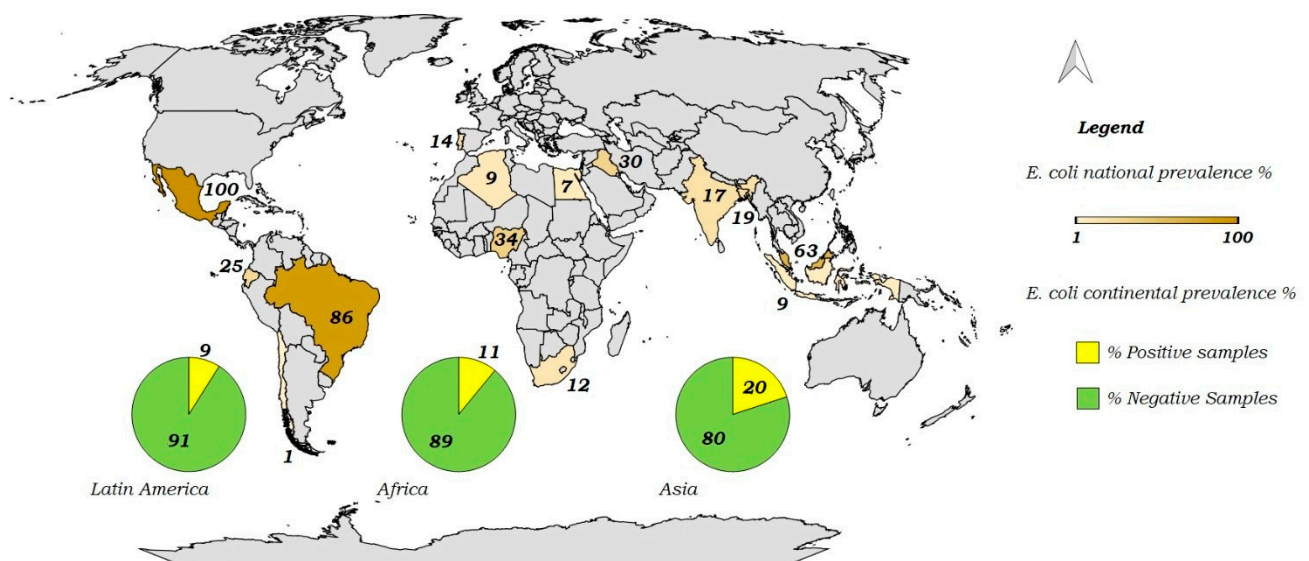


Figure 3. National and continental street food *E. coli* prevalence in the selected studies. *E. coli* national prevalence: Algeria—9%, 18/200 (Yaici et al., 2017 [84]: 18/200); Bangladesh—19%, 43/232 (Bhowmik et al., 2022 [65]: 12/60; Das et al., 2021 [68]: 26/78; Johura et al., 2020 [72]: 4/20; Tabassum, Saha & Islam, 2015 [82]: 1/74); Brazil—86%, 18/21 (da Silva Oliveira et al., 2021 [67]: 18/21); Chile—0.5%, 18/3300 (Sánchez et al., 2021 [80]: 18/3300); Ecuador—25%, 137/555 (Salazar-Llorente et al., 2021 [79]: 117/405; Zurita et al., 2020 [85]: 20/150); Egypt—7%, 62/945 (Khalil & Gomaa, 2016 [73]: 62/945); India—17%, 153/930 (Jenifer & Sathiyamurthy, 2020 [71]: 139/500; Sivakumar et al., 2021 [81]: 14/430); Indonesia—9%, 9/95 (Budiarso et al., 2021 [66]: 2/10; Novira et al., 2020 [76]: 7/85); Iraq—30, 39/130 (Taha et al., 2023 [83]: 39/130); Malaysia—63%, 41/65 (Elexson et al., 2017 [69]: 12/15; Latchumaya et al., 2021 [74]: 29/50); Mexico—100%, 189/189 (Mora-Coto et al., 2025 [75]: 189/189); Nigeria—34%, 61/180 (Fayemi et al., 2021 [70]: 61/180); Portugal 14%, 17/118 (Barreira et al., 2024 [64]: 17/118); South Africa—12%, 96/835 (Asiegbu, Lebelo, & Tabit, 2020 [63]: 2/110; Plessis et al., 2017 [77]: 13/180; Richter et al., 2020 [78]: 81/545). *E. coli* continental prevalence: Asia—20%, 285/1452; Africa—11%, 237/2160; Latin America—9%, 362/4065.

Table 3. Molecular targets used for *E. coli* pathotype identification and characterization in the included studies.

Gene	Associated Pathotype	Function	References
<i>stx 1, stx 2</i>	EHEC	Shiga toxins—cause hemorrhagic colitis and HUS	[64,67,69,70,73,74,76,78,80,81]
<i>eaeA</i>	EHEC, EPEC	Intimin—adherence to intestinal cells	[64,67,70,73,76,78,81]

Table 3. Cont.

Gene	Associated Pathotype	Function	References
<i>lt, st</i>	ETEC	Enterotoxins—cause traveler’s diarrhea	[72,75,76,81]
<i>ipaH</i>	EIEC	Invasion plasmid antigen—intracellular spread	[66,78]
<i>bfpA</i>	EPEC	Bundle-forming pilus—initial adherence	
<i>aggR, astA</i>	EAEC	Aggregative adherence regulator and toxin	[64]
<i>rfbO157, fliCH7</i>	EHEC	O and H antigen markers—serotyping of O157:H7	[70,73,74]
<i>vat, cnf1, hlyA</i>	UPEC	Associated with host cell damage, cytotoxicity, and tissue invasion	[75]
<i>afa</i>	DAEC	Fimbrial adhesins linked to the diffuse adherence pattern	[75]
<i>uspA</i>	APEC	Uropathogenic-specific protein—associated with avian strains	[65]
<i>uidA</i>	N.D.	β-glucuronidase—generic <i>E. coli</i> marker	[65,71,83]
<i>16SrDNA</i>	N.D.	Ribosomal RNA—universal bacterial identifier	[63,65,79,82]

Note. N.D.: not declared; EHEC: Enterohemorrhagic; EPEC: Enteropathogenic *E. coli*; ETEC: Enterotoxigenic *E. coli*; EIEC: Enteroinvasive *E. coli*; EAEC: Enteroaggregative *E. coli*; UPEC: Uropathogenic *E. coli*; DAEC: Diffusely adherent *E. coli*; APEC: Avian Pathogenic *E. coli*.

4. Discussion

Street food is a mass phenomenon that transcends cultural boundaries and geographical distances [86,87] due to its low cost, wide availability, and unique flavor [86,88].

However, the global popularity of street food has raised concerns about its quality and potential bacterial contamination, as foodborne diseases have become more prevalent in recent years and pathogenic bacteria have been linked to street food [12,89,90]. Foods containing bacteria, viruses, fungi, or parasites cause around 200 diseases of variable clinical manifestations, from mild diarrhea to cancer [8,12,91], and nearly 600 million people get sick after eating contaminated food [12,92,93]. According to Pires et al. [94], almost half of foodborne diseases in the United States occur due to agricultural products, and at least one-third of the cases involve pathogenic bacteria. Furthermore, nearly 50% of the foodborne outbreaks in Europe are related to food [95]. At a global level, numerous diseases associated with food pathogens emerge every year, *E. coli* being one of the most frequently found [96].

Although not all *E. coli* strains are pathogenic, nonpathogenic strains can acquire virulent genes through horizontal gene transfer, potentially becoming harmful to human health [20,26,43,48]. These pathogenic strains can cause both extraintestinal and intestinal pathologies. However, human extraintestinal infections have increased lately [20,43,97]. *E. coli* is related to animal products, which, in turn, are a basis for contamination for other products and the environment that surrounds them [22,98]; in many regions worldwide, including America, Europe, Asia, and Africa, various strains related to raw meats, raw milk, ready-to-eat meats, vegetables, poultry, fruits, cereals, among others, have been reported [22,96,98,99].

The results of this systematic review have revealed the widespread presence of *E. coli* in street foods in various urban and peri-urban contexts. The overall prevalence (world average) of *E. coli* in street foods was 11.6% (Figure 2a), demonstrating that a significant proportion of food consumed on public roads is contaminated by this pathogen, posing a risk to public health. This finding is aligned with data reported in regional studies from the United States and Europe, which have indicated that up to 50% of foodborne illness outbreaks are linked to contamination of raw or minimally processed food products by bacterial pathogens, including *E. coli* [94,95].

In addition, the prevalence of *E. coli* varies considerably between continents (Figure 3), with Asia having the highest prevalence (19.6%), followed by Africa (11.0%) and Latin America (8.9%); this variability may be related to multiple factors, including hygienic conditions during food handling, sanitary infrastructure, local regulations, cultural practices in different countries [100–102], as well as the educational level of the sellers [103–107]. These observations reflect patterns documented in international literature, where limited sanitary

infrastructure, informal food economies, and lack of regulatory oversight are associated with increased microbial risks in street foods [8,98].

Likewise, notable differences were observed between the types of food analyzed. The studies reviewed address a wide range of foods, from meat products to fruits and beverages. However, the lack of a standardized approach to sampling and molecular analysis could have influenced the disparity in the results between studies. Heterogeneity in sample collection periods, ranging from one to twenty-one months (Table 1), may also have affected the findings.

Regarding molecular identification methodologies, the PCR technique was widely used in studies to detect *E. coli*, which underscores the importance of this technique as a robust tool for the identification of pathogens in food samples, as well as for the understanding of their genetic diversity and their relationship with different ecological niches and pathogenic potential. The identification of pathotypes and phylogroups not only provides a more detailed view of the genetic structure of *E. coli* but also has practical implications for epidemiology and public health by facilitating better traceability of the strains and their pathogenic capacity. For example, phylogroups B2 and D are commonly associated with extraintestinal infections, while phylogroups A and B1 are usually predominant in commensal strains [35,37].

A recent Mexican study by Mora-Coto et al. [75] provides further evidence on this issue; the researchers analyzed 189 street food samples (vegetables and fruits) collected over three years and found that all of them (100%) were contaminated with *E. coli*. Importantly, both the intestinal (ETEC, DAEC) and the extraintestinal (UPEC) pathotypes were identified, alongside a concerning trend of antibiotic resistance. These findings reinforce the notion that street foods can act not only as vehicles of pathogenic *E. coli*, but also as reservoirs of antimicrobial resistance (AMR), increasing the risk for difficult-to-treat infections and underscoring the urgent need for stricter hygienic practices. Growing evidence indicates that *E. coli* isolated from street food can also harbor AMR, posing an additional threat to public health. Several studies included in this review, such as those by Fayemi et al. [70], Yaici et al. [84], and Zurita et al. [85], reported that *E. coli* isolates from street foods exhibited AMR to commonly used antibiotics, such as ampicillin, tetracycline, and ciprofloxacin. Studies from Latin America and Africa have observed the coexistence of virulence and resistance genes, which highlights the potential for horizontal gene transfer and the emergence of multidrug-resistant pathotypes. These findings emphasize the urgent need to strengthen antimicrobial stewardship, improve hygiene practices, and implement routine surveillance programs targeting foodborne bacteria in informal food markets.

The expanded classification of *E. coli* also allows for a more precise differentiation between pathogenic and non-pathogenic strains, which is crucial for the early detection of infectious outbreaks and the management and control of foodborne illness. It is therefore important to further refine genetic identification techniques to enhance food safety [8,17,35,48].

The prevalence of pathogenic *E. coli* in street foods, such as EHEC, ETEC, and other variants, poses a significant threat to food safety, especially in developing countries, where sanitary control systems may be limited. The detection of various virulent genes in these studies reinforces the need for stricter preventive and control measures to reduce food contamination and protect public health. The widespread occurrence of virulent *E. coli* pathotypes frequently implicated in global foodborne outbreaks is consistent with reports from the WHO and regional surveillance systems [34,96].

The studies reviewed in this study showed that street food is an increasingly popular option, especially for those who view this field as a simple business opportunity. However, it is necessary to understand the influence that the quality of these foods has on

people, taking into account that the number of people affected by the consumption of contaminated food is increasing more and more. In addition, the alarming prevalence of *E. coli* in street foods has been reported in various regions of the world, underscoring the importance of improving hygienic practices in food handling both in urban and peri-urban settings [64,67,69,74]. The high prevalence reported in several Asian countries suggests the importance of strengthening sanitary control systems in these regions.

Molecular techniques, especially PCR, have proven to be key tools in the identification of *E. coli* in food. However, it is critical to adopt standardized procedures for sample collection and molecular identification in order to obtain more comparable results across studies. Conventional PCR was the most frequently used technique for detecting *E. coli* in street foods. It was employed in 52.2% of the selected studies, probably due to its low cost, accessibility, and reliability in limited laboratory conditions [64,66–72,77–79,82]. However, the multiplex and quadruplex PCR variants used in 39.1% and 17.4% of the selected studies, respectively, were more efficient and could detect multiple virulence genes or phylogroups simultaneously, reducing analysis time and the number of false negatives [64,65,73–75,77,80,81,83–85]. In contrast, qPCR showed superior sensitivity and allowed for accurate quantification of gene copies, although its use was limited (8.7% of selected studies) by cost and equipment requirements [63,64]. The use of RT-PCR was marginal (4.3% of selected studies), but it demonstrated strong potential for detecting virulence factors in complex food matrices with high specificity [76]. Overall, the results indicate that, in street food contexts, multiplex PCR and qPCR represent an optimal balance between reliability and applicability, whereas conventional PCR remains the most widely adopted method due to its operational feasibility in resource-limited settings.

Finally, the findings of this review point to the urgent need to implement stricter food safety policies, especially in those countries with a high prevalence of *E. coli* in street foods, and to promote training programs for street vendors to ensure safe food-handling practices.

For instance, the Codex Alimentarius, developed by the FAO and WHO, provides specific hygiene guidelines for preparing and selling food in public places; the regional codes derived from it represent concrete steps towards ensuring food safety and protecting public health worldwide [108,109]. The hygiene rules aim to ensure safe food handling, control chemical and bacterial contamination, maintain proper food temperature preservation, and promote good hygiene practices among handlers and within the environment [3]. We firmly believe that local authorities, particularly in developing countries, should accurately share information about the hygiene standards set out in the Codex with street vendors. At the same time, science-based risk assessments are needed to quickly identify local sources of contamination and outbreaks; surveys are also required to evaluate the level of awareness among both sellers and consumers regarding food safety and hygiene.

To strengthen food safety regulations in the context of street food, practical interventions should focus on three key areas: (1) implementing mandatory certification and regular training programs for street food vendors on hygienic food handling and pathogen prevention, (2) establishing low-cost, mobile microbiological testing units to enable rapid on-site detection of pathogenic *E. coli*, and (3) promoting standardized protocols for food sampling and molecular detection across regions. Additionally, integrating food safety education into public campaigns can improve people's awareness and promote shared responsibility among consumers and vendors. These strategies, when supported by local authorities and adapted to the socio-economic context of each region, can significantly reduce the prevalence of illnesses caused by *E. coli* in street foods.

In summary, the studies analyzed in this review employed diverse methodological approaches: (1) the sample size ranged from 10 to 3300 and the sample weight from 1 to 50 g; (2) the food types included a wide variety of products, e.g., cheeses, meat, sandwiches,

fresh vegetables, fruits, and juices; (3) the collection period ranged from one to 34 months; (4) the culture media for *E. coli* recovery were primarily MacConkey Agar, Eosin methylene blue Agar, and Plate Count Agar; (5) the DNA extraction was carried out through several different methods and commercial kits; (6) the five detection methods were PCR, qPCR, multiplex PCR, quadruplex PCR, and RT-PCR; (7) finally, 33 *E. coli* target genes were employed. Different methods for DNA extraction and different PCR protocols introduced variations in the sensitivity and specificity of the tests to be considered when analyzing the results. For all these reasons, the results are very varied and heterogeneous, making a meta-analysis difficult.

We considered that sampling strategies that involve the use of various types of foods may increase the risk of bias during all stages of analysis. Therefore, we recommend analyzing only one type of food or drink per study and using standard and highly sensitive methods. We also recommend repeating the sampling and molecular analyses at least twice a year, in both the dry and wet seasons. The results of the molecular analyses may differ greatly because the rainwater and the dew can contain a range of parasites, bacteria, and other pathogenic microorganisms due to fecal contamination from animal droppings and other human sources [110]. We are well aware that molecular detection methods depend on various factors, including the availability of instruments and reagents, as well as the budget allocated to the investigation. The qPCR showed greater sensitivity than conventional PCR, but its use is generally limited due to cost and equipment requirements.

5. Conclusions

Street food is a business that grows exponentially worldwide but, at the same time, is a critical public health issue. Increasingly, studies report data on street food contaminated by microorganisms (i.e., bacteria and viruses), chemical agents (i.e., pesticides and heavy metals), and particulate matter (i.e., glass, metal, and plastic). Unhygienic food contaminated by *E. coli* could cause great risks to human health, especially in the developing countries of Asia and Africa.

This systematic review summarizes recent scientific information about the presence of *E. coli* in street food worldwide. For molecular identification, various street foods from each country and different methods were used; for DNA extraction, the most commonly used was manual extraction, and for DNA detection, the most frequently used method was PCR. The street food *E. coli* prevalence ranged between 0.5% (Chile) and 100% (Mexico). Since *E. coli* is widely recognized as an indicator of fecal contamination, its detection in ready-to-eat street foods points to deficiencies in sanitation during food preparation, storage, or vending. Most microbial contamination is attributed to health problems in general.

Food safety regulations play a crucial role in protecting consumers and preserving the integrity, quality, and safety of street food. Legal frameworks of selling food on the street indicate specific requirements for vendors worldwide, specifying food sanitary standards and establishment sanitation procedures. Local authorities have the difficult task of monitoring street food vendors and enforcing hygiene and food safety standards.

Science-based risk assessments (such as molecular and rapid tests) are periodically needed at a local level to promptly identify sources of contamination or outbreaks. Hygiene surveys are also needed to gain a clear picture of the hygiene education among street vendors and consumers.

Based on the results of this systematic review, governments and the scientific community could further study *E. coli* in street food and carry out corrective actions.

Supplementary Materials: The following supporting information can be downloaded at: <https://www.mdpi.com/article/10.3390/microbiolres16120253/s1>, Supplementary File S1: PRISMA Checklist, Supplementary File S2: Quality assessment of included studies.

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