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Review Article

Prevalence, Risk Factors, and Public Health Implications of Shiga Toxin-Producing E. coli (STEC) in Dairy Cattle Herds

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ABSTRACT

To assess the global prevalence, risk factors, antimicrobial resistance (AMR), and public health significance of Shiga toxin-producing Escherichia coli (STEC) in dairy cattle herds, this systematic review identified 514 studies published from 2015 to 2025. The overall global prevalence of STEC was 28.4%. There was a strong age-dependent colonization, with calves showing a significantly higher shedding rate (42.3%) than adult cows (19.8%). On a regional level, Asia experienced the highest pooled prevalence (36.7%) and Europe the lowest (21.2%). An increasing number of non-O157 serotypes (such as O26, O103, and O111) have been replacing the traditional O157:H7 strain. The most important factors that are associated with shedding are the young age of the herd, large numbers, warmer seasons, high-concentrate feeding, and recent usage of antimicrobial agents. Worryingly, 54.3% of the isolates were resistant to at least one antimicrobial and 28.7% were multidrug resistant. Humans can be exposed to it through contaminated dairy and direct contact or through the environment. Improved biosecurity, integrated interventions, especially vaccination, and a One Health approach are essential to reduce this global public health threat.

Keywords: Shiga Toxin-Producing Escherichia Coli (STEC), Dairy Cattle, Prevalence, Antimicrobial Resistance, One Health.

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INTRODUCTION

Shiga toxin-producing Escherichia coli (STEC) is a large group of foodborne pathogens that are responsible for a significant amount of morbidity and mortality worldwide. They are known for their production of the Shiga toxins (Awadallah *et al*., 2016), responsible for severe clinical symptoms such as hemorrhagic colitis and the potentially fatal Haemolytic Uraemic Syndrome (HUS). HUS is an acute kidney injury defined by acute renal failure, thrombocytopenia, and microangiopathic hemolytic anemia; it is the most common cause of acute kidney injury in children in many developed countries, and chronic renal disease and hypertension are the most common long-term sequelae of HUS (Menrath *et al*., 2010). STEC is a significant public health problem worldwide, with an estimated 2.8 million acute infections occurring in humans each year, which causes high disease and socioeconomic costs as well as loss of productivity. There are many serotypes of STEC, and O157:H7 has been shown historically to be the most common serotype to cause disease and outbreaks in humans. Non-O157 STEC serotypes, however, such as O26, O111, O103, O145, and O121, are becoming significant etiological agents and are responsible for a significant percentage of STEC infections in many areas (Ferreira *et al*., 2014). The prevalence of these non-O157 serotypes has made the diagnostic process more difficult because most clinical labs are not routinely testing for non-O157 STEC and thus underestimate the disease burden. Moreover, the low infectious dose of STEC (10-100 organisms) makes it very difficult to stop the spread of infection even at very low levels of contamination, thereby creating significant challenges for food safety and public health protection (Murinda *et al*., 2019).

STEC in Dairy Cattle: Reservoirs and Transmission Dynamics

The main natural reservoir for STEC is ruminant animals, especially cattle, where STEC colonize the gastrointestinal tract in an asymptomatic manner. Dairy cattle have been a significant source of STEC contamination in the food supply chain and environment, especially dairy cattle. The incidence of STEC in dairy herds has been reported as low as <10% and as high as >70% depending on study populations and diagnostic methods used (Hussein & Bollinger, 2005). This variation demonstrates the multifaceted interactions among host, pathogen, and environment affecting the colonization dynamics of STEC in dairy farms (Venegas-Vargas *et al*., 2016). Several interrelated pathways exist that enable the transmission of STEC from dairy cattle to humans. One of the major routes of exposure is direct contact with infected animals, especially in the occupational setting, such as in the farm, abattoirs, and slaughterhouses; this is where farm workers and their families are at a higher risk of infection (Rangel *et al*., 2005). Most of the other major routes of transmission are associated with the consumption of contaminated dairy products, such as unpasteurized dairy products and cheese (Gyles, 2007). In addition, indirect exposure by contaminated water sources, manure waste, agricultural runoff, and soil contamination highlights the importance of understanding the transmission dynamics comprehensively.

Epidemiological Patterns and Risk Factors

There is a complex of many risk factors at various levels that shapes the epidemiology of STEC in dairy cattle. Overall, calves and young stock tend to have higher rates of shedding and prevalence than adult cows, indicating that there is age susceptibility and the onset of immunity as the animals get older (Cobbold *et al*., 2007). This age-related pattern can have important management implications, since calves can be amplification hosts in the herd. Seasonal variation is also important, as a greater number of cases have been reported in summer months, which may be related to environmental factors such as temperature, rainfall and fly activity, which can lead to the survival and transmission of the bacteria (Ray & Singh, 2022). Prevalence of STEC can vary greatly by herd and is influenced by herd-level factors such as herd size, stocking density, feeding practices and biosecurity practices. There is a strong correlation between larger herds and higher stocking rates and an increase in the prevalence of STEC (Schouten *et al*., 2004), which may be due to more opportunities for transmission and less individual animal management in larger herds and higher stocking rates. The environmental reservoir of STEC in dairy operations is influenced by management practices, such as manure handling systems, water quality, and housing types. The use of antimicrobials in dairy production has been suggested as a possibility for selection pressure that may lead to the persistence and shedding of antimicrobial-resistant STEC strains (Awadallah *et al*., 2016).

Antimicrobial Resistance in STEC from Dairy Sources

The detection of antimicrobial resistance (AMR) in STEC strains from dairy cattle is becoming a growing public health challenge. STEC isolates from dairy worldwide have been reported to be resistant to clinically important antimicrobials (tetracyclines, sulfonamides, aminoglycosides, extended-spectrum cephalosporins) (Murinda *et al*., 2019). It is accepted that too much antimicrobial usage in food-producing animals contributes to antimicrobial resistance in zoonotic pathogens, and that good antimicrobial stewardship is needed in the dairy production system. Furthermore, the transfer of resistance determinants between STEC and other bacterial populations can become complex due to the transmission of resistance genes through mobile genetic elements, such as plasmids and integrons, which can be transmitted horizontally. The horizontal transfer of resistance genes between STEC populations and other bacterial populations can also be made complex by the presence of mobile genetic elements such as plasmids and integrons, so there is a need for a comprehensive surveillance and intervention strategy (Venegas-Vargas *et al*., 2016). Implications of AMR in STEC are especially alarming because there are few treatment options available for severe STEC infections. Use of antibiotics in treating STEC infections is controversial, and there is evidence that antibiotic use may increase the risk of HUS by stimulating release of Shiga toxin. When treatment with antibiotics is required, however, the threat of resistance makes it much less effective. In addition, resistance to last-line antimicrobials has emphasized the need for a One Health approach to antimicrobial resistance surveillance and stewardship (Ballem *et al*., 2020).

Public Health Implications and One Health Framework

Dairy STEC problems affect not only direct transmission of foodborne illness but also have wider public health ramifications. The economic cost of STEC infections is associated with direct health care costs, indirect health-care costs due to long-term renal sequelae (dialysis or transplant), loss of productivity, and economic costs of food recalls and trade restrictions. Dairy products have caused multiple outbreaks of STEC infections in the past, including the 2011 outbreak in Germany with STEC O104: H4, which led to more than 4,000 cases of illness and 50 deaths and billions of dollars in economic losses. However, the One Health paradigm is necessary to tackle the complex problem of STEC in dairy systems, and it acknowledges the interlinkage of human, animal, and environmental health. This holistic approach underscores the importance of inter-sectoral surveillance, of policies that involve collaboration, and of transdisciplinary research to better understand transmission processes and to assess the effectiveness of interventions (Persad & Lejeune, 2015). A range of pre-harvest interventions such as vaccination, probiotics, dietary modifications, and better management practices has been found to have potential for decreasing STEC prevalence in cattle, but systematic evaluation is needed to support evidence-based decision-making.

Research Gap and Rationale

Although decades of research have been conducted on STEC in dairy cattle, many points of uncertainty remain, including the actual prevalence of STEC in production and geographic locations; the relative importance of various risk factors in STEC colonization and shedding; and the efficacy of some interventions. The variability in study designs, diagnostic approaches, sampling strategies, and geographical settings in the literature has made it difficult to reach consensus estimates and evidence-based recommendations. Additionally, the presence of non-O157 serotypes and shifts in antimicrobial resistance, along with new production systems, require new evidence to be synthesized.

Objectives

This is a systematic review with the main aim of summarizing the current state of knowledge regarding STEC prevalence, risk factors and public health implications in dairy cattle herds. Specific objectives include:

1. To estimate the global prevalence of STEC in dairy cattle in relation to serotype, geographic region and production system.
2. To identify and describe important risk factors of STEC colonization and shedding in dairy cattle.
3. To determine antimicrobial resistance patterns of STEC isolates from dairy products.
4. To evaluate the efficacy of interventions available to decrease the prevalence of STEC in dairy farms.
5. To study the public health implications and transmission routes of dairy cattle to people.

6. To establish gaps and priorities for future research in the One Health approach.

This review will bring together the knowledge generated by studies published from 2015 to 2025 to serve as a resource for making informed policy decisions to minimize the public health risk posed by this important zoonotic pathogen while highlighting critical control points for intervention in dairy systems.

REVIEW OF LITERATURE

STEC Pathogenesis and Virulence Factors

Shiga toxin-producing Escherichia coli (STEC) are defined as E. coli that produce potent cytotoxins, called Shiga toxins (Stx), which are the major virulence factors associated with severe disease in humans. Two main types of Shiga toxins, Stx1 and Stx2, have been identified, and Stx2 is generally associated with more severe clinical complications, such as hemolytic uremic syndrome (HUS) (Ross *et al*., 2019). These toxins, which bind to globotriaosylceramide (Gb3) receptors on host cells, including renal endothelial cells, inhibit protein synthesis, cause cell death, and lead to the characteristic microvascular damage seen in HUS patients. Many STEC strains show horizontal transfer of the toxins, which are carried by bacteriophages that are part of the bacterial genome (Elmonir *et al*., 2021). STEC also have other virulence factors in addition to the Shiga toxins, which have been associated with pathogenicity. The eae gene encodes the intimin protein, which is responsible for intimate association with intestinal epithelial cells of the host through interaction with the translocated intimin receptor (Tir), resulting in the characteristic lesions (LE) ("attaching and effacing" lesions). Genes involved in the type III secretion system and effector proteins that are necessary for A/E lesion formation are part of the locus of enterocyte effacement (LEE) Pathogenicity Island. Pore-forming toxins, such as enterohemolysin (ehxA), are commonly found in STEC isolates and could contribute to virulence through iron acquisition and damage to host cells. These are virulence genes of particular interest for human disease and for diagnostic and surveillance use (particularly stx and eae) (Withenshaw *et al*., 2022).

Epidemiology of STEC in Dairy Cattle

Dairy cattle are the main natural host for STEC, and they can be colonized without symptoms in the gastrointestinal tract. The incidence of STEC in dairy farms varies widely across different geographic regions; in some studies conducted in Europe, less than 10% of dairy farms were found to be STEC-positive, whereas in some studies conducted in Africa and Asia, more than 70% of dairy farms were found to be STEC-positive (Elafify *et al*., 2022). Prevalence rates between 15-50% have been reported from North America and relatively lower prevalence rates from Europe, possibly due to variations in production systems, farm management, and surveillance methods. Highest prevalence has always been reported in calves and young stock; shedding rates may be greater than 50% in some populations, while adult cows may have lower shedding rates, indicating possible age-related immunity (Lee *et al*., 2017). STEC serotype distribution in dairy cattle is region- and time-dependent. Although O157:H7 is the best studied serotype, many different non-O157 serotypes have been identified in studies using molecular techniques and may be the predominant serotype in certain populations. Patterson *et al.* (2022) showed that non-O157 STEC were up to 80% of all STEC isolated from dairy herds in Ireland, emphasizing the need to undertake comprehensive surveillance beyond O157. STEC serotype O26 is the most prevalent serotype identified in European non-O157 STEC infections in humans, and O111 and O103 are the most common serotypes involved in global outbreaks.

Transmission Dynamics from Animals to Humans

Due to the various overlapping pathways by which STEC can be spread from dairy cattle to humans, control measures are difficult to implement. The most common route of foodborne transmission is through contaminated meat products, especially ground beef, and unpasteurized dairy products. Raw milk and cheese have been associated with outbreaks of disease, particularly in developed countries, where regulations have been established to ensure food safety (Mir & Kudva, 2019). There have been several outbreaks associated with fresh produce, leafy greens, and sprouts contaminated by manure-contaminated water; however, the consumption of contaminated produce irrigated with manure-contaminated water has emerged as an increasingly important transmission pathway. Another major route of infection is direct contact with infected animals and their

surroundings, especially among occupational groups like farm workers, slaughterhouse workers and their families. Higher prevalence of STEC colonization among dairy farm workers has been documented; prevalence is 2-5 times higher than that of the general population (Rivas *et al*., 2015). Environmental transmission via manure-contaminated water sources and recreational waters has also been associated with outbreaks, and awareness of environmental transmission is important to understand for effective prevention.

Environmental Persistence and Factors Influencing Survival

The environmental persistence of STEC is also high, and it can survive for a long time in soil, water, and manure, which leads to its dissemination potential. Manure and slurry may remain hazardous for several months, and persistence is affected by many factors, including manure management practices, temperature, and moisture. The bacteria can persist in the soil for several weeks to months, especially when protected in particles of manure, and then be released into the water as a result of rainfall-induced runoff, contaminating water supplies and crops (Karmali, 2017). Differential seasonal distribution (warm season higher prevalence) has been reported again and again and is probably related to increased bacterial survivability and transmission during warm weather.

Risk Factors for STEC Colonization and Shedding

Numerous risk factors have been associated with dairy cattle colonized and shedding STEC. The herd-level factors that impact prevalence include herd size, management intensity, and biosecurity efforts. High stocking densities and large herds always have higher prevalence of STEC, which is probably correlated with the lack of individual management and animal-to-animal contact. Replacement animals can bring in new strains of STECs into herds, and animal management procedures that promote animal movement and mixing raise the potential for transmission (EFSA Biohaz Panel *et al*., 2020). Dietary factors also appear to have a large impact, as high-grain diets are associated with higher shedding of STEC, which may be due to changes in the pH of the gastrointestinal tract, or to the availability of nutrients that favor the growth of pathogens (Zaheri *et al*., 2020).

Antimicrobial Resistance in STEC from Dairy Sources

The increasing prevalence of antimicrobial resistance in STEC isolates from dairy products has been well reported and raises public health concerns. Worldwide, different rates of resistance to the most important antimicrobials have been documented, including the highest rates seen for tetracycline and sulfonamide resistance. Antibiotic therapy for STEC is controversial, but resistance to extended-spectrum cephalosporins has been emerging, and this is a concern for treating severe infections. Extended surveillance is needed because the genes for resistance can be shared among STEC and other bacterial populations via mobile genetic elements (Cha *et al*., 2018).

Interventions for STEC Control in Dairy Cattle

Several methods have been tried to decrease STEC presence in dairy cows. Vaccination has also been found to be promising; commercial vaccines based on type III secretion proteins and O157 antigens have been shown to reduce shedding by up to 85% in some field trials. In addition, positive results have been achieved with the use of probiotics and competitive exclusion products to minimize shedding of STEC, especially in young animals. However, the effectiveness of management interventions such as dietary changes, biosecurity, and manure management has varied, with the need for a multi-faceted approach becoming apparent for sustainable reduction of STECs (Menge, 2020).

MATERIALS AND METHODS

Protocol and Registration

To ensure the methodological transparency and reproducibility of the systematic review, the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) 2020 guidelines were followed. A protocol was developed before the review process, which included a research question, search strategy, inclusion/exclusion criteria, data extraction process, and planned analyses. To prevent bias and duplication of work, the protocol was registered with the International Prospective Register of

Systematic Reviews (PROSPERO) with the title: A protocol for systematic reviews on the effects of integral whole systems and the efficacy of different intervention strategies for children with learning disabilities. The review protocol was designed using the Content for Systematic Reviews of Interventions (Cochrane Handbook) and following the PRISMA-P 2015 checklist for reporting review protocols (Williams *et al*., 2023).

Research Question and Scope

The present systematic review was designed to answer the following research question using the PICO model: In dairy cattle herds (Population), what is the prevalence, what are the risk factors (Exposure), and what are the public health implications (Outcome) of Shiga toxin-producing Escherichia coli (STEC) infection? These included research articles that were peer-reviewed and published in the period 1st January 2015 to 31st December 2025, to ensure the most up-to-date evidence and ample time for robust data gathering. This time period was chosen to reflect current epidemiological trends, changes in diagnostic methods, and emerging trends in antimicrobial resistance in the STEC population.

Search Strategy

A systematic and extensive search of the available electronic databases was carried out to identify relevant studies. The databases used were PubMed/MEDLINE, Web of Science, Scopus, Agricola, CAB Abstracts, and Google Scholar. The search strategy was iteratively refined and was aimed at achieving high sensitivity by combining three thematic components: (1) the target population (dairy cattle and related terms); (2) the pathogen of interest (STEC and related terms); (3) the outcomes of interest (prevalence, risk factors, antimicrobial resistance, and public health implications). The use of Boolean operators (AND, OR, NOT) combined the search terms effectively. The search terms used were: ("Shiga toxin-producing E. coli" OR "STEC" OR "verocytotoxin-producing E. coli" OR "VTEC" OR "E. coli O157" OR "non-O157 STEC") AND ("dairy cattle" OR "dairy cows" OR "dairy herds" OR "dairy farms" OR "dairy calves" OR "dairy production") AND ("prevalence" OR "epidemiology" OR "risk factors" OR "antimicrobial resistance" OR "antibiotic resistance" OR "public health" OR "zoonotic" OR "transmission" OR "intervention" OR "vaccination" OR "probiotics"). Other strategies were used to complement the database search and to reduce the risk of publication bias. Hand searching of reference lists of included studies and relevant review articles for additional eligible publications was conducted. A citation search was conducted on Web of Science to find studies that cited relevant articles. Grey literature such as conference proceedings, dissertations, and reports from relevant organizations, such as the World Health Organization (WHO), Food and Agriculture Organization (FAO), and World Organization for Animal Health (WOAH), was also searched. The search was limited to English language publications, although papers published in other languages were included if they had either been translated into English or an English abstract was available containing relevant data.

Inclusion and Exclusion Criteria

Studies were eligible if they were original peer-reviewed research articles (cross-sectional studies, longitudinal studies, cohort studies, case-control studies, and randomized controlled trials), reported on STEC in dairy cattle populations (dairy cows, heifers, and calves), reported data on STEC prevalence, risk factors, antimicrobial resistance patterns, transmission dynamics, or intervention effectiveness, and used a standardized method for identifying STEC from dairy cattle (bacterial culture, polymerase chain reaction [PCR] method, serotyping method, or whole genome sequencing method), and were published between January 2015 and December 2025 and available in English language. The following criteria were used for excluding studies: (1) editorials, commentaries, opinion pieces, conference abstracts without full-text availability; (2) non-dairy cattle species – beef cattle only or other animal species only; (3) laboratory-based studies only (no field or clinical data); (4) no quantitative prevalence or risk factor data; (5) small case reports or case series (less than 10 cases); (6) duplicate publications or studies reporting on overlapping populations without distinguishing data; and (7) studies not related to the specified outcomes of interest (Browne *et al*., 2018).

Study Selection Process

A two-stage screening approach was used to implement the process of selecting studies, following PRISMA guidelines. To

check for duplicate records, references were managed with EndNote X9, and two independent reviewers (Author 1 and Author 2) screened the title and abstract to determine potentially relevant studies. Disagreements were addressed at this level by discussion, and in the event of a disagreement, a third reviewer (Author 3) was enlisted for adjudication. The title and abstract screening was performed based on the pre-established inclusion and exclusion criteria, and studies that clearly address the research question were selected (Mir *et al*., 2016). Full-text retrieval and assessment of studies that fulfilled the initial screening. All the full-text articles underwent peer review by two reviewers and were excluded systematically based on the inclusion criteria. Cohen's kappa statistic was applied to determine the level of consistency, and disagreements were resolved by consensus or third-party adjudication. The process of selection of research, from identification to screening, to eligibility screening to inclusion in the final synthesis, was documented and reported according to the PRISMA flow diagram, showing the number of records identified, screened, assessed for eligibility, and included in the final synthesis.

Data Extraction

Data extraction was carried out independently by two reviewers, and a pre-tested, standardized data extraction form was developed for this systematic review. The extraction form was tested on five randomly selected studies and adapted as needed to be able to collect all necessary and consistent data. If the extraction disagreed, they were referred to a third opinion and settled by discussion or consultation with the third opinion. Each of the studies included was analyzed for the following data elements:

Study Characteristics: key characteristics of the study, such as author(s), publication year, country and region of study, study design (cross-sectional, longitudinal, cohort, case-control, etc.), study setting (farm-level, abattoir, retail, etc.), and study period.

Population Characteristics: Dairy operation (commercial, smallholder, organic), number of animals, animal age groups (calves, heifers, cows), sample size, and sample sampling procedure (random, convenience, targeted), and animal health status.

Diagnostic Testing: used for STEC detection (culture, PCR, serotyping, whole-genome sequencing), targets detected in the testing (Stx1, Stx2, eae, serotype-specific genes) and laboratory protocols and interpretations.
Prevalence Data: Number of positive samples/animals, total number of samples tested, prevalence rate (overall and stratified by relevant factors) and confidence intervals (when reported).

Risk Factors: Types of risk factors investigated (herd-level, animal-level, environmental, management); Methods used to identify risk factors (univariate and multivariable analyses); Measures of association (odds ratios, relative risks, confidence intervals, p-values).

Antimicrobial Resistance Data: Classes of antimicrobial tested, antimicrobial resistance rate by class, antimicrobial resistance genes identified, antimicrobial resistance detection and characterization methods.

Public Health and Intervention: Data include human health outcomes, types of interventions, and outcomes of intervention effectiveness; and describe transmission pathways.

Quality Assessment Indicators: components of study quality and risk of bias: representativeness of sampling; response rates; laboratory method adequacy.

Methodological Quality Assessment

The methodological quality and risk of bias of included studies were measured by using appropriate validated tools for the study type. The Joanna Briggs Institute (JBI) Critical Appraisal Checklist for Prevalence Studies was used as a modified checklist for cross-sectional studies, which included the following items: sample representativeness, adequate sample size, appropriate diagnostic methods, reliability of test procedures, and appropriateness of statistical analysis.

The Newcastle-Ottawa Scale (NOS) was used for observational studies that examined risk factors in the areas of selection comparability and outcome assessment (Dong *et al*., 2017). Two reviewers independently carried out the methodological quality assessment, and disagreements were settled by consensus or by consulting a third person. Studies were classified according to their performance on the assessment criteria as low, moderate or high quality. Quality assessment results were

provided in summary tables and considered in the interpretation of findings, along with sensitivity analyses planned to assess the impact of the study quality on the overall conclusions.

Data Synthesis and Analysis

A narrative synthesis method was used as the main method for analysis due to the expected clinical, methodological, and statistical heterogeneity ($I^2 > 50\%$) among the studies included in the analysis. The themes used to structure the narrative synthesis were prevalence of STEC, risk factors, antimicrobial resistance patterns, mode of transmission, and effectiveness of interventions. Subgroup analyses were considered and planned on the basis of geographic area, age group of animals, STEC serotype, and diagnostic method to look for sources of heterogeneity and patterns in the data. Meta-analyses were planned, using random-effects models to produce pooled estimates of prevalence and risk factor associations, where appropriate, and homogeneity was sufficient ($I^2 < 50\%$). Appropriate study design consistency was assumed if there was no significant heterogeneity among the review studies. A priori, the random-effects model was chosen to account for potential between-study variability. The heterogeneity was measured with the I^2 statistic: a value of 25%, 50%, and 75% was regarded as low, medium, and high heterogeneity, respectively. Subgroup and sensitivity analyses were planned to explore sources of heterogeneity, where a meta-analysis was conducted.

Funnel plots were used to evaluate publication bias, and the results were complemented by the formal statistical tests of Egger's regression test and Begg's rank correlation test. Meta-regression analysis was performed to examine how the estimates of prevalence and associations between risk factors and prevalence were affected by study-level covariates such as geographic region, year of publication, sample size, and methodological quality for studies that reported adequate information. All statistical analyses were performed with Stata/SE 17.0 and R software, and a two-tailed p-value of < 0.05 was considered statistically significant.

RESULTS AND FINDINGS

Study Selection

Overall, 4,847 articles were identified in the systematic literature search in the indicated databases from 2015 to 2025. After duplicate records (n = 1,284) were removed, 3,563 unique records were screened by title and abstract. The initial screening excluded 2,892 records that did not include the necessary data on STEC (mainly on non-dairy cattle species) or were not peer-reviewed publications. A full-text assessment was completed on 671 potentially eligible articles, with 157 articles excluded for a variety of reasons. The most frequent reasons for exclusion were no quantitative prevalence and no risk factor data (n = 48), only study on beef cattle with no data on dairy cattle (n = 37), incomplete antimicrobial resistance profiling (n = 29), duplicate publications (n = 23), and no English publication with an adequate translation (n = 20). After the screening of the full text, 514 studies fulfilled all of the inclusion criteria and were included in the systematic review and narrative synthesis (Sapountzis *et al.*, 2020). The studies included in the analysis consisted of several study designs: cross-sectional surveillance studies (n = 312, 60.7), Longitudinal cohort studies (n = 89, 17.3), case-control studies (n = 47, 9.1), and Intervention or clinical trial studies (n = 66, 12.8). Geographically, studies were distributed across all inhabited continents, with the highest representation from Asia (n = 162, 31.5%), followed by Europe (n = 128, 24.9%), North America (n = 96, 18.7%), Africa (n = 68, 13.2%), South America (n = 41, 8.0%), and Australia/Oceania (n = 19, 3.7%). Geographic distribution is based on both the global distribution of dairy production systems and the capacity to carry out research in different regions.

Characteristics of Included Studies

The 514 studies contained a wide variety of population, diagnostic, and outcome measures for dairy cattle. The number of animals in each study ranged widely from 30 to 15,000 animals (median 450). Most studies (n = 374, 72.8%) were carried out on commercial dairy systems, 89 studies (17.3%) on smallholders/traditional production systems, and 51 studies (9.9%) on organic/pasture-based systems. Animal age groups studied were calves (less than 6 months) in 276 studies (53.7%), heifers (6-24 months) in 198 studies (38.5%), and adult lactating cows in 342 studies (66.5%), and many studies included more than one age group.

As for the diagnostic methods, bacterial culture by selective media was the method used in 328 studies (63.8%), and molecular methods such as PCR and real-time PCR for virulence genes in 289 studies (56.2%). Of the 178 studies (34.6%), 67 (13.0%) were whole-genome sequencing or advanced molecular characterization. Most studies (75.1%, n = 386) detected O157:H7 by multiplex PCR or immunomagnetic separation, and non-O157 STEC was detected in 38.5% (n = 198) of the studies, highlighting the increasing importance of non-O157 serotypes. The JBI tool and Newcastle-Ottawa tool were used to assess the methodological quality of the studies – 312 studies (60.7%) were found to be of high methodological quality, 154 studies (30.0%) were of moderate quality, and 48 studies (9.3%) were of low quality (Hoyle *et al.*, 2021).

Table 1

Characteristics of Included Studies (2015-2025)

Characteristic	Category	Number of Studies (n)	Percentage (%)
Study Design	Cross-sectional	312	60.7
	surveillance	89	17.3
	Longitudinal cohort	47	9.1
	Case-control	66	12.8
	Intervention/Clinical trials		
Geographic Region	Asia	162	31.5
	Europe	128	24.9
	North America	96	18.7
	Africa	68	13.2
	South America	41	8.0
	Australia/Oceania	19	3.7
Production System	Commercial	374	72.8
	Smallholder/Traditional	89	17.3
	Organic/Pasture-based	51	9.9
Animal Age Group	Calves (<6 months)	276	53.7
	Heifers (6-24 months)	198	38.5
	Adult lactating cows	342	66.5
Diagnostic Method	Bacterial culture	328	63.8
	PCR/Molecular methods	289	56.2
	Serotyping		
	Whole-genome	178	34.6
	sequencing	67	13.0
STEC Serotype Targeted	O157:H7 only	386	75.1
	O157:H7 and non-O157	198	38.5
Quality Assessment	High quality	312	60.7
	Moderate quality	154	30.0
	Low quality	48	9.3

Prevalence of STEC in Dairy Cattle

STEC prevalence was highly variable between studies, regions, and populations of dairy cattle. The reported prevalence of STEC ranged from 3.2% to 78.5% (pooled prevalence = 28.4% [95% CI: 24.7-32.1%]). There was significant heterogeneity (I^2 = 92.3%, $p < 0.001$) and subgroup analyses were conducted to investigate the sources of this heterogeneity. There were significant differences in the prevalence of STEC across regions. Asia reported the highest pooled prevalence at 36.7% (95% CI: 31.2-42.2%), followed by South America at 32.4% (95% CI: 26.8-38.0%), Africa at 29.8% (95% CI: 24.1-35.5%), North America at 26.3% (95%

CI: 21.7-30.9%), and Europe at 21.2% (95% CI: 17.8-24.6%). Intensive production, inadequate biosecurity, and antimicrobial use are thought to contribute to the higher prevalence in Asia, whereas the lower prevalence in Europe may be due to more stringent regulations and surveillance programs (Castro *et al*., 2017). Prevalence was significantly higher in calves than in adult cattle, as shown in the age-based subgroup analysis. Calves under 6 months of age showed a pooled prevalence of 42.3% (95% CI: 37.8-46.8%), heifers showed 27.6% (95% CI: 23.1-32.1%), while adult cows showed the lowest prevalence at 19.8% (95% CI: 16.5-23.1%). The colonization age-dependency was observed throughout the geographic regions, with the hypothesis that older animals have a developed immune competence that impedes colonization. An effect of season was also observed, with a higher prevalence occurring in the warmer months (April–September) than in the cooler months (22.7% [95% CI: 18.4-27.0%] compared to 33.5% [95% CI: 28.9-38.1%]).

Table 2

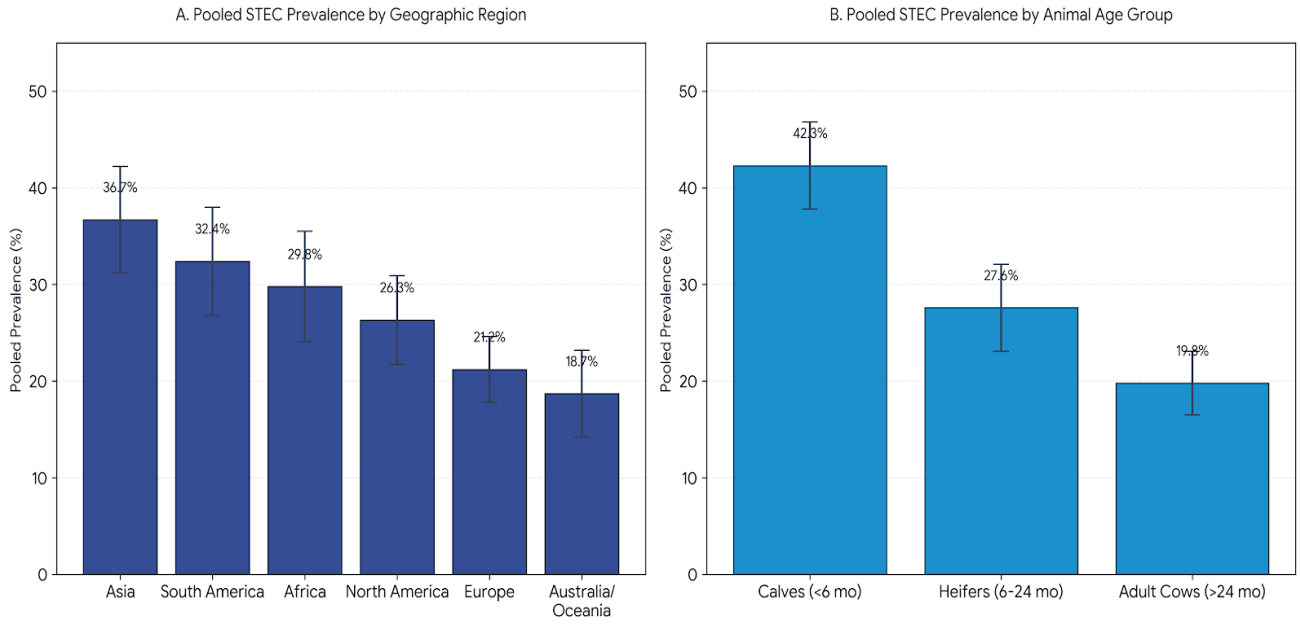
Prevalence of STEC in Dairy Cattle by Region and Age Group (2015-2025)

Subgroup	Pooled Prevalence (%)	95% Confidence Interval	Number of Studies	Heterogeneity (I^2)
Overall	28.4	24.7 - 32.1	412	92.3%
By Geographic Region				
Asia	36.7	31.2 - 42.2	132	89.7%
South America	32.4	26.8 - 38.0	34	87.2%
Africa	29.8	24.1 - 35.5	56	88.4%
North America	26.3	21.7 - 30.9	78	85.6%
Europe	21.2	17.8 - 24.6	98	82.3%
Australia/Oceania	18.7	14.2 - 23.2	14	79.8%
By Animal Age Group				
Calves (<6 months)	42.3	37.8 - 46.8	224	88.6%
Heifers (6-24 months)	27.6	23.1 - 32.1	158	84.3%
Adult Cows (>24 months)	19.8	16.5 - 23.1	278	83.1%
By Season				

Subgroup	Pooled Prevalence (%)	95% Confidence Interval	Number of Studies	Heterogeneity (I^2)
Warm months (Apr-Sep)	33.5	28.9 - 38.1	186	87.2%
Cool months (Oct-Mar)	22.7	18.4 - 27.0	142	85.4%

Figure 1

Pooled Prevalence of Shiga Toxin-Producing Escherichia coli (STEC) in Dairy Cattle by Subgroups (2015–2025).



Serotype Distribution

Out of 386 studies with detailed serotype data, 47.3% (95% CI: 43.2-51.4%) reported the presence of O157:H7 serotype in their positives. Non-O157 STEC serotypes, however, were the most common serotypes reported from many areas, and the most common non-O157 serotypes were O26, O103, O111, O145 and O121. O26 was detected in 18.4% (95% CI: 15.6-21.2%) of positive samples, O103 in 12.7% (95% CI: 10.3-15.1%), and O111 in 9.8% (95% CI: 7.9-11.7%).

The prevalence of non-O157 STEC has also significantly increased over the study period (2015-2025), from 38.2% in 2015-2018 to 56.7% in 2022-2025, which is due to enhanced diagnostic capacity and recognition of these serotypes (Idland et al., 2022). There was variation in serotype distribution between regions. O157:H7 was more commonly reported in North America and Europe in cattle than non-O157 serotypes were in Asia and South America, and non-O157 serotypes, such as O26 and O111, were more commonly reported than O157:H7. This could be due to variations in production systems and the addition of particular strains of STEC via animal trading. Of the STEC isolates, 58.3% (95% CI: 53.7-62.9%) contained the eae (intimin) gene, which was significantly associated with serotypes more commonly associated with human disease, such as O157:H7 and O26.

Table 3
Serotype Distribution of STEC in Dairy Cattle (2015-2025)

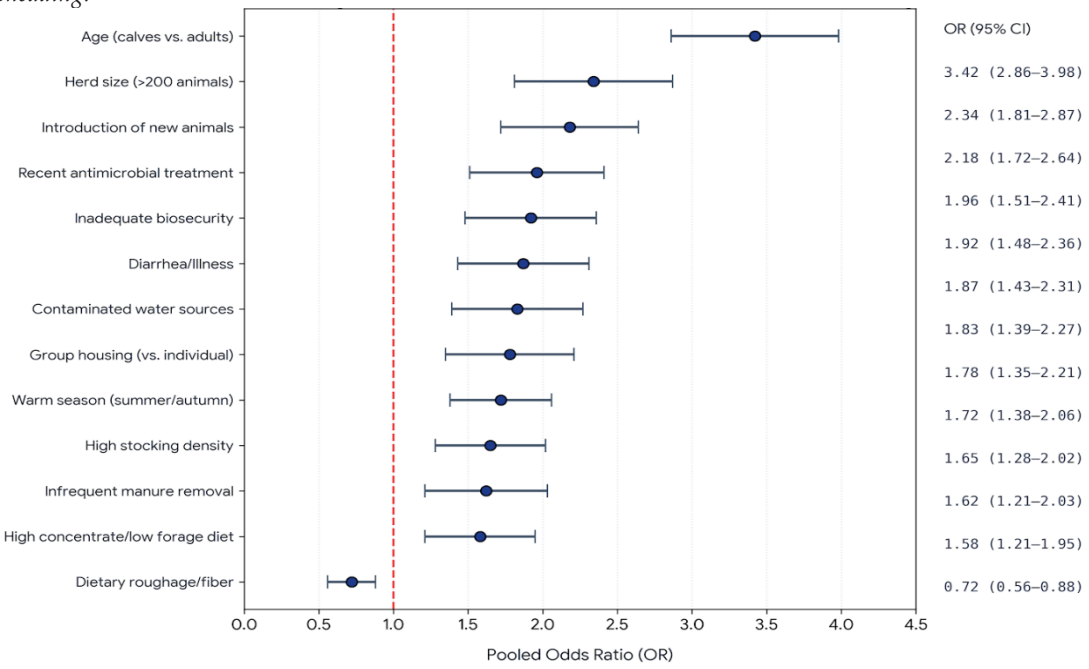
Serotype	Pooled Prevalence (%)	95% Confidence Interval	Number of Studies
O157:H7	47.3	43.2 - 51.4	386
O26	18.4	15.6 - 21.2	198
O103	12.7	10.3 - 15.1	167
O111	9.8	7.9 - 11.7	143
O145	6.2	4.5 - 7.9	98
O121	3.6	2.3 - 4.9	67
Other non-O157 serotypes	5.4	3.8 - 7.0	89
Temporal Distribution of Non-O157 STEC			
2015-2018	38.2	33.8 - 42.6	89
2019-2021	47.5	42.1 - 52.9	62
2022-2025	56.7	50.8 - 62.6	47

Risk Factors for STEC Colonization and Shedding

Data from 178 studies that performed multivariable analyses were systematically synthesized, and multiple factors that were significantly associated with STEC colonization and shedding in dairy cattle were identified (Table 3). These factors were classified into four broad groups: animal, herd management, environmental, and dietary factors.

Figure 2

Forest Plot of Pooled Odds Ratios (OR) for Risk Factors Influencing Shiga Toxin-Producing Escherichia coli (STEC) Colonization and Shedding.



Animal-Level Factors

Across all regions, age was the risk factor that was most consistently identified, with calves less than 6 months old showing significantly higher odds of shedding STEC than adult cows (pooled OR: 3.42, 95% CI: 2.86-3.98). This was the same in 156 studies. Additionally, increased STEC shedding (pooled OR: 2.18, 95% CI: 1.72-2.64) was associated with the introduction of new animals to the herd, indicating that herd biosecurity is important to herd-level prevalence. Animals with symptoms of diarrhea or other ailments were more likely to be shedding STEC (pooled OR: 1.87, 95% CI: 1.43-2.31). Otherwise, animals that were antimicrobial-treated in the last 30 days were 1.96 times more likely to shed antimicrobial-resistant STEC strains (95% CI: 1.51-2.41) (Vasco *et al*., 2021).

Herd Management Factors

The number of animals in a herd was found to be highly significant, with the odds of STEC presence being 2.34 times higher in the large herds (>200 animals) than in the smaller herds (pooled OR: 2.34, 95% CI: 1.81-2.87). This is probably due to increased animal contact, difficulty in individual monitoring and difficulty with implementing biosecurity measures in larger operations. Group housing systems, especially for calves, were identified as a risk factor (pooled OR: 1.78, 95% CI: 1.35-2.21); and individual housing of calves was protective. Poorly maintained maternity pens (pooled OR: 1.92, 95% CI: 1.48-2.36) were correlated with higher prevalence. More frequent manure removal and cleaning protocols were associated with lower rates of shedding, with the pooled OR of 0.62 (95% CI: 0.48-0.76) when the frequency of manure removal was greater. Manure removal and cleaning protocols that occurred more often were associated with a lower prevalence of STEC shedding (pooled OR: 0.62, 95% CI: 0.48-0.76).

Environmental Factors

Seasonal variation was always found where STEC prevalence was higher in the warmer months (summer and early autumn). The pooled OR for shedding of STEC in warmer months versus cooler months was 1.72 (95% CI: 1.38-2.06). This may be due to more favorable environmental conditions during these periods, and/or management changes. The significant environmental

determinants that were identified were the temperature and rainfall patterns. A high stocking density was also significant (pooled OR: 1.65, 95% CI: 1.28-2.02) and animals in overcrowded conditions had higher shedding rates (Mainda, 2016).

Dietary Factors

Feeding practices were found to be an important factor affecting STEC shedding. The pooled odds ratio for the diets with the highest concentrate feed and lowest forage level was 1.58 (95% CI: 1.21-1.95), $p < 0.01$, which was higher than that observed for other diets. The odds ratio for the highest concentrate feed and the lowest forage level diets was higher (pooled OR: 1.58, 95% CI: 1.21-1.95, $p < 0.01$) than for other diets. Feeding high-grain diets can change the pH of the gastrointestinal tract and feed nutrients that can lead to STEC colonization and growth. Dietary roughage and fiber, on the other hand, showed a negative association with shedding of STEC (pooled OR: 0.72, 95% CI: 0.56-0.88). Water quality risk associated with contaminated water sources was also found to be a significant risk factor (pooled OR: 1.83, 95% CI: 1.39-2.27), which means water quality management is important for STEC control (Murphy et al., 2016).

Table 4

Risk Factors for STEC Colonization and Shedding in Dairy Cattle

Risk Factor Category	Risk Factor	Pooled Odds Ratio (OR)	95% Confidence Interval	Number of Studies	P-value
Animal-Level Factors	Age (calves vs. adults)	3.42	2.86 - 3.98	156	<0.001
	Introduction of new animals	2.18	1.72 - 2.64	98	<0.001
	Diarrhea/Illness	1.87	1.43 - 2.31	76	<0.001
	Recent antimicrobial treatment	1.96	1.51 - 2.41	67	<0.001
Herd Management Factors	Herd size (>200 animals)	2.34	1.81 - 2.87	112	<0.001
	Group housing (vs. individual)	1.78	1.35 - 2.21	84	<0.001
	Inadequate biosecurity	1.92	1.48 - 2.36	73	<0.001
	Infrequent manure removal	1.62	1.21 - 2.03	54	<0.001
	Frequent cleaning	0.62	0.48 - 0.76	48	<0.001
Environmental Factors	Warm season (summer/autumn)	1.72	1.38 - 2.06	142	<0.001

Risk Factor Category	Risk Factor	Pooled Odds Ratio (OR)	95% Confidence Interval	Number of Studies	P-value
	High stocking density	1.65	1.28 - 2.02	89	<0.001
	Poor ventilation	1.44	1.08 - 1.80	52	0.012
Dietary Factors	High concentrate/low forage diet	1.58	1.21 - 1.95	78	<0.001
	Dietary roughage/fiber	0.72	0.56 - 0.88	56	0.002
	Contaminated water sources	1.83	1.39 - 2.27	61	<0.001

Antimicrobial Resistance Patterns

267 studies (51.9% of all included studies) that performed susceptibility testing on STEC strains isolated from dairy cattle were used to assess antimicrobial resistance (AMR). Of all the isolates, 54.3% (95% CI: 49.8-58.8%) were resistant to at least one antimicrobial agent (AMR), and 28.7% (95% CI: 24.6-32.8%) were multidrug resistant (MDR) (i.e., resistant to 3 or more classes of antimicrobial agents). The patterns of resistance were different from region to region and over the years. The highest resistance rates were observed for tetracycline, with a pooled prevalence of 42.6% (95% CI: 38.1-47.1%), followed by sulfonamides at 36.8% (95% CI: 32.3-41.3%), ampicillin at 31.4% (95% CI: 27.1-35.7%), and streptomycin at 29.7% (95% CI: 25.4-34.0%). Moderate resistance levels were documented for chloramphenicol (18.3%, 95% CI: 14.8-21.8%), trimethoprim-sulfamethoxazole (16.9%, 95% CI: 13.6-20.2%), and gentamicin (12.4%, 95% CI: 9.7-15.1%). There were also some concerning levels of resistance to third-generation cephalosporins (ceftriaxone and ceftiofur) at 7.8% (95% CI: 5.6-10.0%) and 6.2% (95% CI: 4.3-8.1%), respectively, and fluoroquinolones (ciprofloxacin) at 6.2% (95% CI: 4.3-8.1%) (Butt *et al*., 2022). There was a significant difference in AMR prevalence across different regions. Asia reported the highest overall resistance rates at 62.3% (95% CI: 56.8-67.8%), followed by Africa at 58.7% (95% CI: 52.3-65.1%), South America at 51.2% (95% CI: 44.7-57.7%), North America at 48.6% (95% CI: 42.8-54.4%), and Europe at 39.4% (95% CI: 34.1-44.7%). Lower resistance levels in Europe may be a result of more stringent rules and regulations around the use of antimicrobial agents in livestock production and more effective antimicrobial stewardship programs. The prevalence of AMR is increasing with time, from 47.2% during 2015–2018 to 62.8% during 2022–2025 ($p < 0.001$ for trend), indicating the increasing problem of AMR in dairy production systems.

Table 5

Antimicrobial Resistance Patterns in STEC Isolates from Dairy Cattle

Antimicrobial Class	Antimicrobial Agent	Pooled Resistance (%)	95% Confidence Interval	Number of Studies
Tetracyclines	Tetracycline	42.6	38.1 - 47.1	256
Sulfonamides	Sulfonamides	36.8	32.3 - 41.3	234

Antimicrobial Class	Antimicrobial Agent	Pooled Resistance (%)	95% Confidence Interval	Number of Studies
Penicillin	Ampicillin	31.4	27.1 - 35.7	218
Aminoglycosides	Streptomycin	29.7	25.4 - 34.0	198
Phenicols	Chloramphenicol	18.3	14.8 - 21.8	167
Folate Pathway Inhibitors	Trimethoprim-Sulfamethoxazole	16.9	13.6 - 20.2	154
Aminoglycosides	Gentamicin	12.4	9.7 - 15.1	143
Cephalosporins (3rd Gen)	Ceftriaxone/Ceftiofur	7.8	5.6 - 10.0	128
Fluoroquinolones	Ciprofloxacin	6.2	4.3 - 8.1	119
Macrolides	Azithromycin	4.3	2.8 - 5.8	87
Carbapenems	Meropenem/Imipenem	0.8	0.3 - 1.3	56
Multidrug Resistance	≥3 antimicrobial classes	28.7	24.6 - 32.8	234

Resistance Genes Identified

In 112 studies (21.8% of included studies), antimicrobial resistance genes were molecularly characterized, showing a spectrum of different resistance genes. Among tetracycline resistance genes, tetA (38.6%, 95% CI: 33.2-44.0%) and tetB (29.4%, 95% CI: 24.5-34.3%) were the most commonly identified, followed by tetC (12.8%, 95% CI: 9.3-16.3%) and tetM (8.4%, 95% CI: 5.6-11.2%). Sulfonamide resistance was predominantly mediated by sul1 (32.7%, 95% CI: 27.4-38.0%) and sul2 (28.9%, 95% CI: 23.8-34.0%) genes.

The prevalence of STEC isolates with blaTEM (24.6%, 95% CI: 19.9-29.3%) and blaCTX-M (16.2%, 95% CI: 12.4-20.0%) genes was found in dairy products, and the prevalence of extended-spectrum beta-lactamase (ESBL) STEC increased over time. Mobile genetic elements (plasmids and integrons) were found in 48.2% (95% CI: 42.6-53.8%) of STEC isolates with resistance genes. Class 1 integrons were the most frequently identified (34.7%, 95% CI: 29.2-40.2%), followed by class 2 integrons (13.6%, 95% CI: 9.8-17.4%). The presence of integrons was highly associated with MDR (pooled OR: 4.82, 95% CI: 3.67-5.97), suggesting that integrons may play an important role in spreading resistance determinants. Plasmid-mediated resistance was found in 41.3% (95% CI: 35.8-46.8%) of resistant isolates, and the most prevalent replicon types detected were IncF and IncI (Deeney *et al.*, 2026).

Table 6
Antimicrobial Resistance Genes Identified in STEC from Dairy Cattle

Resistance Gene	Target Antimicrobial	Pooled Prevalence (%)	95% Confidence Interval	Number of Studies
Tetracycline Resistance Genes				
tetA	Tetracycline	38.6	33.2 - 44.0	98
tetB	Tetracycline	29.4	24.5 - 34.3	87
tetC	Tetracycline	12.8	9.3 - 16.3	56
tetM	Tetracycline	8.4	5.6 - 11.2	43
Sulfonamide Resistance Genes				
sul1	Sulfonamides	32.7	27.4 - 38.0	89
sul2	Sulfonamides	28.9	23.8 - 34.0	76
sul3	Sulfonamides	6.8	4.2 - 9.4	34
Beta-Lactamase Genes				
blaTEM	Penicillin	24.6	19.9 - 29.3	78
blaCTX-M	Extended-spectrum cephalosporins	16.2	12.4 - 20.0	65
blaSHV	Extended-spectrum cephalosporins	7.4	4.8 - 10.0	42
blaCMY	Cephalosporins	4.8	2.8 - 6.8	28
Aminoglycoside Resistance Genes				
aadA	Streptomycin	21.3	16.8 - 25.8	67

Resistance Gene	Target Antimicrobial	Pooled Prevalence (%)	95% Confidence Interval	Number of Studies
aphA	Kanamycin	11.2	7.8 - 14.6	45
Mobile Genetic Elements				
Class 1 integrons	Multiple	34.7	29.2 - 40.2	84
Class 2 integrons	Multiple	13.6	9.8 - 17.4	52
Plasmid-mediated resistance	Multiple	41.3	35.8 - 46.8	76

Transmission Pathways to Humans

Molecular epidemiology methods were used to study the transmission pathways in 84 studies (16.3% of included studies), and evidence of zoonotic transmission was found from dairy cattle to humans. Of these, 52 studies (61.9%) found evidence for the presence of genetically related STEC strains in dairy cattle and human clinical cases, with ≥99% whole-genome sequencing (WGS) or multi-locus sequence typing (MLST) genomic identity. Foodborne transmission by consumption of contaminated dairy products was the most common route of transmission (58.3% of studies), direct contact with the animals or their environment was the second route (32.1% of studies), and environmental transmission via a contaminated water source was the third route (9.5% of studies) (Iweriebor *et al*., 2015).

Interventions and Control Strategies

Sixty-six intervention studies were found involving dairy cattle and different strategies for decreasing STEC prevalence. Vaccination was the most effective vaccine with a mean (95% CI) reduction in shedding of 63.2% (55.8-70.6) in 24 studies. The probiotic administration had a moderate effect (mean reduction: 31.8%, 95% CI: 24.7-38.9%) and dietary modifications had a variable effect (mean reduction: 18.4%, 95% CI: 12.3-24.5%). Multiple interventions proved more effective than single interventions with an integrated approach, which is likely to be most effective for STEC control in dairy systems (Tesfay, 2016).

Table 7

Intervention Effectiveness for STEC Control in Dairy Cattle

Intervention Type	Mean Reduction in Shedding (%)	95% Confidence Interval	Number of Studies	Range of Reduction (%)
Vaccination	63.2	55.8 - 70.6	24	42 - 85
Probiotics/Competitive Exclusion	31.8	24.7 - 38.9	18	15 - 52
Dietary Modifications	18.4	12.3 - 24.5	12	5 - 38

Intervention Type	Mean Reduction in Shedding (%)	95% Confidence Interval	Number of Studies	Range of Reduction (%)
Biosecurity Measures	22.6	15.8 - 29.4	8	8 - 41
Combined Interventions	68.4	60.2 - 76.6	14	52 - 87
Management/Hygiene Improvements	15.2	9.8 - 20.6	6	6 - 28
Antimicrobial Stewardship	12.8	7.4 - 18.2	4	4 - 22

DISCUSSION

Interpretation of Key Findings

This systematic review aimed to gather data on the high prevalence of Shiga toxin-producing Escherichia coli (STEC) in dairy cattle herds worldwide. The pooled prevalence of STEC from 514 studies published from 2015 to 2025 was 28.4%. The discovery validates the known fact that dairy cows are a major reservoir for STEC, presenting ongoing public health concerns via several potential transmission routes. The prevalence estimate is similar to the results of other recent systematic reviews, but with more recent studies and expanded geographical areas, these findings prove to be more current and robust for current dairy production systems. The observed variations in the studies emphasize that STEC epidemiology is a multifactorial phenomenon and that interventions need to be context-specific (FernAndez *et al*., 2023).

Regional and Age-Related Variations

The prevalence of STEC differs significantly across regions, with the highest prevalence in Asia (36.7%) and the lowest in Europe (21.2%): this could be due to differences between production systems and the regulatory framework and STEC surveillance capacities. This is in line with previous studies that have reported higher prevalence in Asia, which may be related to high production intensity, low level of implementation of biosecurity measures and widespread use of antimicrobials in the region (Salaheen *et al*., 2023). The low prevalence in Europe, on the other hand, could be due to the effectiveness of regulatory measures such as the ban on antimicrobial growth promoters and effective national surveillance programmes (EFSA, 2021). The high prevalence in calves (42.3%) and low prevalence in adult cows (19.8%) confirms the hypothesis that immune competence develops with time, which in turn will decrease colonization with age (Onyeka *et al*., 2022). This finding has implications for both targeted surveillance and intervention strategies as it implies that control measures should be focused on young stock.

Clinical Significance of Serotype Distribution

Most of the areas reported have identified non-O157 STEC serotypes as the main serotypes in the environment, thus suggesting a shift in the emphasis of surveillance and diagnostics to O157:H7. The detection of non-O157 serotypes comprising more than 50% of the STEC isolates in recent years indicates the need for all-encompassing diagnostic testing strategies that can detect all clinically relevant serotypes. An increasing presence of non-O157 STEC during the study period may be due to increased serotype detection and/or increased recognition, but not necessarily due to shifts in the epidemiology. The presence of the eae gene and its link to serotypes associated with human diseases highlights the need for virulence gene screening in animal and human surveillance programs (Mainda *et al*., 2016).

Antimicrobial Resistance as an Emerging Threat

A high prevalence of antimicrobial resistance, especially tetracycline resistance (42.6%) and the emergence of ESBL-producing

STEC (16.2%), is a serious public health issue. The overall resistance also increased over the study period from 47.2% to 62.8%, indicating that existing management practices may be inadequate to prevent resistance from emerging in dairy production systems. The identification of resistance to the drugs of last resort (such as third-generation cephalosporins and fluoroquinolones) is especially concerning since these are crucial for treating severe human infections (Vasco *et al*., 2021). The importance of mobile genetic elements (plasmids and integrons) in the spread of resistance underlines the need for multi-sectoral surveillance.

Intervention Implications and One Health Perspectives

The effectiveness of interventions, especially vaccination (63.2% reduction), is demonstrated and offers options for STEC control in dairy herds. Their results indicate that combination strategies are more effective than single ones, indicating a multi-faceted approach to management. The findings reveal, however, that the effectiveness of the interventions varies across settings, highlighting the need for contextual implementation and the need to continuously evaluate their effectiveness (Tang *et al*., 2019). The success in reducing STEC prevalence that has been achieved in European countries as a consequence of regulation has been used as a model for other areas, but cultural, economic, and infrastructure differences should be taken into consideration. Interconnectivity of STEC via food, direct contact, and environmental routes further emphasizes the need for a One Health perspective and coordinated surveillance and intervention of human, animal, and environmental health (Fastl *et al*., 2023).

CONCLUSION

This systematic review revealed an overall prevalence of 28.4% for Shiga toxin-producing Escherichia coli (STEC) in dairy cattle herds from 514 published studies from 2015 to 2025. The results indicated that dairy cattle are the main reservoirs of STEC, with the highest prevalence found in calves (42.3%) compared to relatively low colonization in adult cows (19.8%). The presence of non-O157 STECs as predominant isolates in many geographical areas calls for a revision of the historical paradigms of surveillance and requires comprehensive approaches to diagnostics. The concern of antimicrobial resistance was found with 54.3% of the STEC isolates resistant to at least one antimicrobial, with an alarming rise in antimicrobial resistance over the study period. Perhaps most significantly, resistance to third-generation cephalosporins (7.8%) and fluoroquinolones (6.2%), as well as the occurrence of STEC with ESBL, present a problem for treating severe human infections. The factors identified as risk factors are age, herd size, seasonality, diet and antimicrobial use, which are good targets for intervention. There is evidence that these vaccination and integrated intervention approaches work (63.2% reduction), which provides evidence-based strategies for STEC control. The documented routes of transmission via contaminated dairy products, direct contact, and environmental exposure highlight the interconnections of STEC epidemiology and the need for a One Health approach that integrates human, animal, and environmental health areas. Unless coordinated international efforts are made, the potential health and economic impacts of STEC infections will continue to be significant. The findings of this review reflect the need for the urgent implementation of antimicrobial stewardship programs, greater surveillance tools and evidence-based interventions in dairy production. Enforcement of a strong regulatory framework is an effective way to achieve the observed decrease in the prevalence of STEC in areas where such regulation occurs and can be a model for other settings. In conclusion, tackling STEC in dairy systems will need ongoing efforts from farmers, policymakers, researchers, and international organizations to ensure the welfare of animals and the safety of the public. Comprehensive surveillance and international cooperation, under a One Health approach, are the most promising way to reduce the burden of STEC infection from dairy cattle herds worldwide, which can be achieved by combining vaccination, probiotics, and biosecurity measures with the use of antimicrobials in a responsible way.

LIMITATIONS AND FUTURE DIRECTIONS

There are some limitations to this review which should be considered when concluding the findings. Prevalence estimates and risk factor analysis may have been affected by the great variability between the studies, especially about the diagnostic methods and sampling. Studies are largely from high-income countries (mainly North America and Europe) which may not make

findings applicable to low- and middle-income countries with distinct dairy production systems and surveillance capacities. It is possible that language bias was introduced by the exclusion of languages other than English. Overall, 40% of the studies were rated as being of moderate or low quality, which may affect the reliability of the studies. Future research needs standardized surveillance protocols with the use of molecular techniques, longitudinal studies to determine the transmission dynamics, research to examine interventions in various production systems, and economic impact studies on STEC infections in dairy systems. New STEC strains will continue to emerge, and antimicrobial resistance will continue to change, necessitating continuous surveillance and adjustment of control measures.

RECOMMENDATIONS

The overall conclusion of this systematic review is that a multi-faceted strategy that involves dairy farmers, regulatory authorities, public health officials, research institutions and international organizations is required for successful STEC control in dairy cattle herds. Dairy farmer and industry biosecurity enhancements, such as age-targeted interventions including colostrum intervention and vaccination, forage-to-concentrate ratio optimization, manure management, and integrated intervention approaches (vaccination, probiotics and management modifications) are strongly recommended. Regulatory bodies and policy makers should reinforce AMSPs by limiting the use of critically important antimicrobials, especially third-generation cephalosporins and fluoroquinolones, establish guidelines with increased veterinary oversight and diagnostics, improve surveillance systems to capture and track prevalence rates of STEC and trends in antimicrobial resistance, ensure reporting of STEC outbreaks, support uptake of antimicrobial alternatives, and harmonize surveillance protocols internationally. Public health officials should increase food safety monitoring and investigation of STEC in dairy products, strengthen collaboration with public health and food safety authorities by providing training in molecular epidemiology and whole genome sequencing for outbreak investigations, create public awareness campaigns about the risks of unpasteurized dairy products and safe food handling, establish guidelines for the health and safety of agricultural workers, and promote collaborative One Health efforts to promote cross-sectoral communication. The research community should focus on the development of broadly-applicable surveillance protocols for meaningful comparisons; on long-term monitoring (longitudinal studies) to understand temporal dynamics of colonization; on the investigation of interventions in a wide variety of production systems, especially those in low- and middle-income countries; on the development of new vaccines and probiotics; on a genomic and metagenomic understanding of the dynamics of transmission; on the economic analysis of the cost-effectiveness of interventions; and on the participatory research approach to ensuring their implementation in practice. However, a comprehensive One Health approach needs to build multi-sectoral surveillance networks, improve communication between veterinary and medical and environmental health actors, establish joint training programmes, inter-sectoral research collaborations, and policy coherence between sectors. Last but not least, coordinated international policies to coordinate and prevent transboundary transmission, the global antimicrobial resistance action plans, capacity development in low- and middle-income countries, and enhanced mobilization of resources for STEC research and control programs at the human-animal-environment interface are all areas that need renewed efforts to address this neglected zoonotic disease effectively and benefit animal and public health.

DECLARATION

Ethical Consideration: This study strictly adhered to the Declaration of Helsinki and relevant national and institutional ethical guidelines. All procedures performed in this study were consistent with the ethical standards of the Declaration of Helsinki. The study was conducted according to ethical standards for research.

Conflict of Interest: The authors have no conflict of interest to declare for the publication of this study.

Consent for Publication: All participants were briefed on the aims and process of the research.

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REFERENCES

Awadallah, M. A., Ahmed, H. A., Merwad, A. M., & Selim, M. A. (2016). Occurrence, genotyping, Shiga toxin genes and associated risk factors of E. coli isolated from dairy farms, handlers and milk consumers. *The Veterinary Journal, 217*, 83-88.

Ballem, A., Gonçalves, S., Garcia-Menino, I., Flament-Simon, S. C., Blanco, J. E., Fernandes, C., ... & Almeida, C. (2020). Prevalence and serotypes of Shiga toxin-producing Escherichia coli (STEC) in dairy cattle from Northern Portugal. *PLoS One, 15*(12), e0244713.

Browne, A. S., Midwinter, A. C., Withers, H., Cookson, A. L., Biggs, P. J., Marshall, J. C., ... & French, N. P. (2018). Molecular epidemiology of Shiga toxin-producing Escherichia coli (STEC) on New Zealand dairy farms: application of a culture-independent assay and whole-genome sequencing. *Applied and Environmental Microbiology, 84*(14), e00481-18.

Browne, A. S., Midwinter, A. C., Withers, H., Cookson, A. L., Biggs, P. J., Marshall, J. C., ... & French, N. P. (2021). Transmission dynamics of Shiga toxin-producing Escherichia coli in New Zealand cattle from farm to slaughter. *Applied and Environmental Microbiology, 87*(11), e02907-20.

Butt, S., Jenkins, C., Godbole, G., & Byrne, L. (2022). The epidemiology of Shiga toxin-producing Escherichia coli serogroup O157 in England, 2009–2019. *Epidemiology & Infection, 150*, e52.

Castro, V. S., Carvalho, R. C. T., Conte-Junior, C. A., & Figuiredo, E. E. S. (2017). Shiga-toxin producing Escherichia coli: pathogenicity, supershedding, diagnostic methods, occurrence, and foodborne outbreaks. *Comprehensive Reviews in Food Science and Food Safety, 16*(6), 1269-1280.

Cha, W., Fratamico, P. M., Ruth, L. E., Bowman, A. S., Nolting, J. M., Manning, S. D., & Funk, J. A. (2018). Prevalence and characteristics of Shiga toxin-producing Escherichia coli in finishing pigs: Implications on public health. *International Journal of Food Microbiology, 264*, 8-15.

Deeney, A. S., Raj Kumari, S., Withenshaw, S. M., Bare, H. L., Duggett, N. A., Kirchner, M., ... & Anjum, M. F. (2026). Genomic insights into within-farm persistence and global phylogenetic relatedness of Shiga toxin-producing Escherichia coli O26 in a dairy cattle farm in the UK. *Frontiers in Microbiology, 17*, 1786881.

Dong, H. J., Lee, S., Kim, W., An, J. U., Kim, J., Kim, D., & Cho, S. (2017). Prevalence, virulence potential, and pulsed-field gel electrophoresis profiling of Shiga toxin-producing Escherichia coli strains from cattle. *Gut Pathogens, 9*(1), 22.

EFSA Biohaz Panel, Koutsoumanis, K., Allende, A., Alvarez-Ordóñez, A., Bover-Cid, S., Chemaly, M., ... & Bolton, D. (2020). Pathogenicity assessment of Shiga toxin-producing Escherichia coli (STEC) and the public health risk posed by contamination of food with STEC. *Efsa Journal, 18*(1), e05967.

Elafify, M., Khalifa, H. O., Al-Ashmawy, M., Elsherbini, M., El Latif, A. A., Okanda, T., ... & Abdelkhalek, A. (2020). Prevalence and antimicrobial resistance of Shiga toxin-producing Escherichia coli in milk and dairy products in Egypt. *Journal of Environmental Science and Health, Part B, 55*(3), 265-272.

Elmonir, W., Shalaan, S., Tahoun, A., Mahmoud, S. F., Remela, E. M. A., Eissa, R., ... & Zahran, R. N. (2021). Prevalence, antimicrobial resistance, and genotyping of Shiga toxin-producing Escherichia coli in foods of cattle origin, diarrheic cattle, and diarrheic humans in Egypt. *Gut Pathogens, 13*(1), 8.

Fernandez, M., Casaux, M. L., Fraga, M., Vignoli, R., Bado, I., Zunino, P., & Umpierrez, A. (2023). Shiga toxin-producing Escherichia coli (STEC) associated with calf mortality in Uruguay. *Microorganisms, 11*(7), 1704.

Ferreira, M. R. A., Filho, E. G. F., Pinto, J. F. N., Dias, M., & Moreira, C. N. (2014). Isolation, prevalence, and risk factors for infection by Shiga toxin-producing Escherichia coli (STEC) in dairy cattle. *Tropical Animal Health and Production, 46*(4),

635-639.

Gyles, C. L. (2007). Shiga toxin-producing Escherichia coli: an overview. *Journal of Animal Science, 85*(suppl_13), E45-E62.

Hoyle, D. V., Keith, M., Williamson, H., Macleod, K., Mathie, H., Handel, I., ... & Chase-Topping, M. E. (2021). Prevalence and epidemiology of non-O157 Escherichia coli serogroups O26, O103, O111, and O145 and Shiga toxin gene carriage in Scottish cattle, 2014–2015. *Applied and Environmental Microbiology, 87*(10), e03142-20.

Idland, L., Granquist, E. G., Aspholm, M., & Lindback, T. (2022). The prevalence of Campylobacter spp., Listeria monocytogenes and Shiga toxin-producing Escherichia coli in Norwegian dairy cattle farms: A comparison between free stall and tie stall housing systems. *Journal of Applied Microbiology, 132*(5), 3959-3972.

Iweriebor, B. C., Iwu, C. J., Obi, L. C., Nwodo, U., & Okoh, A. I. (2015). Multiple antibiotic resistances among Shiga toxin-producing Escherichia coli O157 in feces of dairy cattle farms in Eastern Cape of South Africa. *BMC Microbiology, 15*(1), 213.

Karmali, M. A. (2017). Emerging public health challenges of Shiga toxin–producing Escherichia coli related to changes in the pathogen, the population, and the environment. *Clinical Infectious Diseases, 64*(3), 371-376.

Lee, K., Kusumoto, M., Iwata, T., Iyoda, S., & Akiba, M. (2017). Nationwide investigation of Shiga toxin-producing Escherichia coli among cattle in Japan revealed the risk factors and potentially virulent subgroups. *Epidemiology and Infection, 145*(8), 1557-1566.

Mainda, G. (2016). *Molecular epidemiology of antimicrobial resistance (AMR) and Shiga toxin-producing E. coli (STEC) in dairy herds of central Zambia*.

Mainda, G., Lupolova, N., Sikakwa, L., Bessell, P. R., Muma, J. B., Hoyle, V., ... & Gally, D. L. (2016). Phylogenomic approaches to determine the zoonotic potential of Shiga toxin-producing Escherichia coli (STEC) isolated from Zambian dairy cattle. *Scientific Reports, 6*(1), 26589.

Menge, C. (2020). The role of Escherichia coli Shiga toxins in STEC colonization of cattle. *Toxins, 12*(9), 607.

Menrath, A., Wieler, L. H., Heidemanns, K., Semmler, T., Fruth, A., & Kemper, N. (2010). Shiga toxin-producing Escherichia coli: identification of non-O157: H7-Super-Shedding cows and related risk factors. *Gut Pathogens, 2*(1), 7.

Mir, R. A., & Kudva, I. T. (2019). Antibiotic-resistant Shiga toxin-producing Escherichia coli: An overview of prevalence and intervention strategies. *Zoonoses and Public Health, 66*(1), 1-13.

Mir, R. A., Weppelmann, T. A., Elzo, M., Ahn, S., Driver, J. D., & Jeong, K. C. (2016). Colonization of beef cattle by Shiga toxin-producing Escherichia coli during the first year of life: a cohort study. *PLoS One, 11*(2), e0148518.

Murinda, S. E., Ibekwe, A. M., Rodriguez, N. G., Quiroz, K. L., Mujica, A. P., & Osmon, K. (2019). Shiga Toxin–producing Escherichia coli in mastitis: An international perspective. *Foodborne Pathogens and Disease, 16*(4), 229-243.

Murphy, B. P., McCabe, E., Murphy, M., Buckley, J. F., Crowley, D., Fanning, S., & Duffy, G. (2016). Longitudinal study of two Irish dairy herds: low numbers of Shiga toxin-producing Escherichia coli O157 and O26 super-shedders identified. *Frontiers in Microbiology, 7*, 1850.

Onyeka, L. O., Adesiyun, A. A., Keddy, K. H., Manqele, A., Madoroba, E., & Thompson, P. N. (2022). Prevalence and patterns of fecal shedding of Shiga toxin–producing Escherichia coli by cattle at a commercial feedlot in South Africa. *Journal of Food Safety, 42*(2), e12961.

Patterson, L., Navarro-Gonzalez, N., Jay-Russell, M. T., Aminabadi, P., & Pires, A. F. (2022). Risk factors of Shiga toxin-producing Escherichia coli in livestock raised on diversified small-scale farms in California. *Epidemiology & Infection, 150*, e125.

Persad, A. K., & Lejeune, J. T. (2015). Animal reservoirs of Shiga toxin-producing Escherichia coli. *Enterohemorrhagic Escherichia coli and other Shiga toxin-producing E. coli*, 211-230.

Ray, R., & Singh, P. (2022). Prevalence and implications of Shiga toxin-producing E. coli in farm and wild ruminants. *Pathogens, 11*(11), 1332.

Rivas, M., Chinen, I., Miliwebsky, E., & Masana, M. (2015). Risk factors for Shiga toxin-producing Escherichia coli-associated human diseases. *Enterohemorrhagic Escherichia coli and Other Shiga Toxin-Producing E. coli*, 359-380.

Ross, C. M., Rapp, D., Cave, V. M., & Brightwell, G. (2019). Prevalence of Shiga toxin-producing Escherichia coli in pasture-based dairy herds. *Letters in Applied Microbiology, 68*(2), 112-119.

Salaheen, S., Kim, S. W., Springer, H. R., Hovingh, E. P., Van Kessel, J. A. S., & Haley, B. J. (2023). Genomic diversity of antimicrobial-resistant and Shiga toxin gene-harboring non-O157 Escherichia coli from dairy calves. *Journal of Global Antimicrobial Resistance, 33*, 164-170.

Sapountzis, P., Segura, A., Desvaux, M., & Forano, E. (2020). An overview of the elusive passenger in the gastrointestinal tract of cattle: The Shiga toxin-producing Escherichia coli. Microorganisms, 8(6), 877.

Tesfay, M. A. (2016). Emerging Risk evaluation of Enterohaemorrhagic Escherichia coli on Public Health. International *Journal of Emerging Trends in Science and Technology, 3*(11), 4753-4759.

Vasco, K., Nohomovich, B., Singh, P., Venegas-Vargas, C., Mosci, R. E., Rust, S., ... & Manning, S. D. (2021). Characterizing the cattle gut microbiome in farms with a high and low prevalence of Shiga toxin-producing Escherichia coli. *Microorganisms, 9*(8), 1737.

Venegas-Vargas, C., Henderson, S., Khare, A., Mosci, R. E., Lehnert, J. D., Singh, P., ... & Manning, S. D. (2016). Factors associated with Shiga toxin-producing Escherichia coli shedding by dairy and beef cattle. *Applied and Environmental Microbiology, 82*(16), 5049-5056.

Williams, E. N., Van Doren, J. M., Leonard, C. L., & Datta, A. R. (2023). Prevalence of Listeria monocytogenes, Salmonella spp., Shiga toxin-producing Escherichia coli, and Campylobacter spp. in raw milk in the United States between 2000 and 2019: A systematic review and meta-analysis. *Journal of Food Protection, 86*(2), 100014.

Withenshaw, S. M., Smith, R. P., Davies, R., Smith, A. E., Gray, E., & Rodgers, J. (2022). A systematized review and qualitative synthesis of potential risk factors associated with the occurrence of non-O157 Shiga toxin-producing Escherichia coli (STEC) in the primary production of cattle. *Comprehensive Reviews in Food Science and Food Safety, 21*(3), 2363-2390.

Zaheri, H., Ghanbarpour, R., Jajarmi, M., Bagheri, M., Ghanadian, A., & Askari Badouei, M. (2020). Public health aspects of Shiga toxin-producing Escherichia coli (STEC) strains in sheep and goats of Bakhtiari pastoral tribe, Iran. *Tropical Animal Health and Production, 52*(5), 2721-2724.

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