



Prevalence of Escherichia coli O157:H7 among pediatric diarrheal cases at Misurata Central Hospital, Libya

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ABSTRACT

Background: Escherichia coli O157:H7 is a major pathogen transmitted through food; it is associated with severe stomach illnesses such as bleeding in the intestines and kidney failure due to destruction of red blood cells (HUS). Even though this organism plays a critical role in clinical settings, many labs do not identify it on a regular basis. **Aims:** This study aimed to determine the prevalence of E. coli O157:H7 among children with diarrhea in Misurata, Libya.

Methods: A cross-sectional study was conducted in 2024 on 124 children aged five days to thirteen years admitted to Misurata Central Hospital. Specimens were collected from stool samples and rectal swabs. Initial isolation was performed using Sorbitol MacConkey (SMAC) agar to identify sorbitol non-fermenting isolates, followed by biochemical identification. Molecular confirmation was performed using polymerase chain reaction (PCR) to detect stx1 and stx2 genes.

Results: Four isolates (3.2%) were sorbitol-negative, of which only one (0.8%) was confirmed as E. coli O157:H7. The confirmed case was a 26-month-old boy presenting with severe diarrhea and dehydration. Statistical analysis revealed a significant difference between observed and expected regional prevalence.

Conclusion: Although the prevalence of E. coli O157:H7 was low, its potential to cause severe disease highlights the need for improved diagnostic strategies, including molecular methods, as well as strengthened surveillance systems and public health interventions in Libya.

Keywords: *E. coli, O157:H7, Diarrhea, Pediatrics, Misurata, Libya*





1. Introduction

Escherichia coli is a facultative anaerobic, gram-negative bacterium that is frequently found in both human and animal digestive tracts (1, 2). Although the majority of E. coli strains are benign and contribute to gut health, some pathogenic strains can cause serious illnesses. One of the most virulent strains, enterohemorrhagic Escherichia coli (EHEC), specifically serotype E. coli O157:H7, is associated with foodborne outbreaks and severe complications such as hemolytic uremic syndrome (HUS) (3, 4). The ability of EHEC to produce Shiga toxins (Stx1 and Stx2), which are strong cytotoxins that harm intestinal and vascular endothelial cells, is the main factor contributing to its pathogenicity (5). Infection with Escherichia coli O157:H7 can cause a range of gastrointestinal symptoms, from mild diarrhea to hemorrhagic colitis. In some cases, especially in children, it may progress to hemolytic uremic syndrome (HUS), which can lead to acute renal failure (1).

Transmission of EHEC is primarily caused by consuming tainted food and water. Unpasteurized dairy products, tainted vegetables, and undercooked meat are common sources (6, 7). EHEC is largely found in cattle, and it is well known that zoonotic transmission can occur through direct or indirect contact with cattle feces (3, 8). The significance of veterinary interventions in preventing human infections is highlighted by recent developments in vaccination strategies aimed at cattle populations, which have demonstrated promise in lowering the transmission of EHEC (8). E. coli can persist in the environment for long periods, including soil, water, and food processing facilities, which compounds its threat. The necessity of strong environmental monitoring systems is highlighted by this resilience. Additionally, international research on outbreak dynamics shows how important it is to combine molecular tools like whole-genome sequencing and PCR for quick detection and outbreak containment (9, 10).

Despite numerous global outbreaks linked to E. coli O157:H7 and its significant public health burden (11), data on its prevalence in Libya remain sparse. Given the high incidence of diarrheal diseases among children in the region, investigating the role of E. coli O157:H7 in local outbreaks is essential to inform targeted prevention and treatment strategies. Such insights are particularly valuable for developing evidence-based public health measures, including food safety policies and public awareness campaigns (9).

This study aims to address this gap by investigating the prevalence of E. coli O157:H7 among children presenting with diarrhea in Misurata, Libya. By employing advanced diagnostic techniques and situating the findings within a global context, this research seeks to contribute to a deeper understanding of E. coli O157:H7 epidemiology and inform effective public health interventions.

2. Materials and Methods

To find out how common E. coli O157:H7 is in children with diarrhea in Misurata, Libya, a cross-sectional study was carried out. 124 stool samples and rectal swabs were taken from kids ranging in age from five days to thirteen years. These samples were taken from patients who were admitted to Misurata Central Hospital during 2024. To preserve the pathogens' viability, samples were gathered in sterile containers and sent right away to the microbiology laboratory. Sorbitol MacConkey (SMAC) agar, a selective medium that separates EHEC strains according to their incapacity to ferment sorbitol, was used to inoculate specimens before microbiological analysis started. Sorbitol-negative colonies were chosen for additional examination after the plates were incubated for 18 to 24 hours at 35°C.

The Analytical Profile Index (API 20E) system was used to biochemically identify the isolates (12), offering a thorough classification of Enterobacteriaceae. Using particular antisera, agglutination tests were performed to confirm the serotype E. coli O157:H7 (BioMérieux,





France). Furthermore, in accordance with established protocols, Shiga toxin genes (stx1 and stx2) were detected in the isolates using polymerase chain reaction (PCR) assays (13). MINITAB software was used to analyze the data, and descriptive statistics were computed to find the means, medians, and standard deviations. Descriptive statistical analysis was performed, and prevalence estimates were calculated and presented with 95% confidence intervals using the exact binomial method. The appropriate institutional review board granted ethical approval, and the parents or guardians of the participating children provided their informed consent. The precise identification of *E. coli* O157:H7 was guaranteed by this methodological approach and offered trustworthy information to back up the goals of the study.

3. Results and discussion

Four isolates (3.2% of the 124 stool specimens examined) were found to be sorbitol-negative on SMAC agar. One isolate (0.8%) was identified as *E. coli* O157:H7 by biochemical testing. The Shiga toxin genes stx1 and stx2 were detected in this isolate, which was taken from a 26-month-old boy who was exhibiting severe diarrhea and dehydration. These virulence factors support the isolate's pathogenicity and are consistent with earlier research showing that Shiga toxins play a significant role in determining the serious consequences of EHEC infections (5, 13). The number of sorbitol-negative isolates four and the confirmed *E. coli* O157:H7 case one is displayed in Figure 1. For clarity, percentages are labeled above the bars.

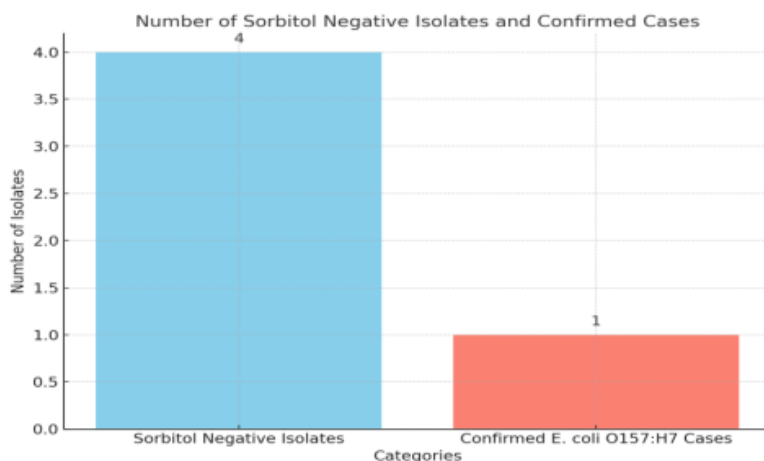


Figure 1: The number of sorbitol-negative isolates and confirmed *E. coli* O157:H7 cases

Despite the seemingly minimal occurrence rate of 0.8%, *E. coli* O157:H7 underscores its significant impact on public health. This is mainly due to its ability to instigate outbreaks and severe conditions such as hemolytic uremic syndrome (HUS). The 95% confidence interval for this rate, derived using the precise binomial method, spans from a mere 0.02% to 4.43%. This interval accounts for the statistical uncertainty inherent in the small sample size and avoids the illogical negative lower bounds observed in previous calculations. Figure 2 displays the



proportion of confirmed *E. coli* O157:H7 cases (representing 0.8%) in relation to other samples.

Studies from neighboring regions report similar prevalence rates, ranging from 0.5% to 1.5%, with sporadic outbreaks noted in areas with limited public health infrastructure (6, 7). These findings highlight the sporadic nature of EHEC infections, often tied to environmental and zoonotic factors.

The role of cattle as primary reservoirs of EHEC is well-established, with improper handling and consumption of undercooked meat identified as major risk factors (3). Additionally, environmental persistence of *E. coli* O157:H7 in water sources, agricultural fields, and food processing environments further facilitates its transmission. Such resilience necessitates stringent food safety measures, regular monitoring of water supplies, and proper disposal of animal waste to mitigate contamination risks.

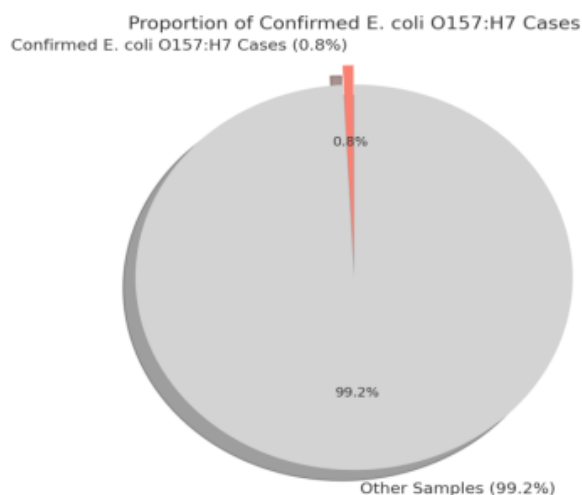


Figure 2: Proportion of confirmed *E. coli* O157:H7 cases relative to other samples.

The detection of sorbitol-negative isolates also underscores the limitations of conventional diagnostic approaches. While SMAC agar is a useful initial screening tool, it lacks specificity, leading to false positives. Incorporating molecular diagnostics such as PCR for Shiga toxin genes significantly enhances detection accuracy (13). These advanced tools should become standard practice in clinical microbiology laboratories, especially in resource-limited settings.

Preventive strategies must prioritize public health education, focusing on hygienic food preparation, proper handwashing, and safe water consumption. Public awareness campaigns can help reduce the burden of EHEC infections, especially in high-risk populations such as children and immunocompromised individuals (14). Moreover, vaccination efforts targeting cattle could offer a promising avenue for reducing zoonotic transmission (15).

Future studies should build on these results by examining seasonal differences in the prevalence of EHEC, analyzing patterns of antibiotic



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resistance, and determining the genetic diversity of isolates. It will be essential to set up strong surveillance networks throughout Libya in order to detect outbreaks early and plan responses efficiently. To reduce the negative effects of E on public health, cooperation between public health organizations, the agricultural industry, and healthcare providers will be essential. E. coli O157:H7.

4. Conclusion

According to this study, E. coli O157:H7 is present in pediatric diarrheal cases in Misurata, Libya, with a confirmed prevalence of 0.8%. The clinical significance of this pathogen cannot be overstated, despite its low prevalence, because it can cause outbreaks and serious complications like hemolytic uremic syndrome (HUS). These results highlight how critical it is to close gaps in public awareness, diagnostic capabilities, and preventative strategies in order to lessen the public health burden of E. coli O157:H7.

To improve public health outcomes in Libya, several measures are needed. Expanding the use of molecular diagnostics, particularly PCR, in clinical laboratories would enhance detection accuracy, provided that trained staff and adequate resources are available. Establishing a national surveillance system is also important to monitor the occurrence and potential outbreaks of E. coli and other intestinal pathogens, with coordination between public health authorities and healthcare facilities. In addition, public awareness efforts should promote safe food handling, proper hygiene, and access to clean water, especially for children. Further long-term studies are required to explore strain diversity, antibiotic resistance, and seasonal trends.

ETHICAL STATEMENT:

Approval for this study was obtained from the hospital administration. Informed consent was secured from the parents or legal guardians of all participating children prior to sample collection. All procedures involving sample collection and handling were conducted in accordance with established clinical and laboratory guidelines to ensure patient safety and data confidentiality. No personally identifiable information was recorded, and all data were analyzed anonymously.

CONFLICT OF INTEREST

There is no conflict of interest to be declared.

AUTHORS' CONTRIBUTIONS

All authors contributed equally to this work

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