



A Review on Public Health Concern Caused by *Escherichia coli* O157:H7

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Abstract

The public health issues related to *Escherichia coli* safety remains a major issue in the 21st century which affects both the advanced and third-world countries. Hemorrhagic fever caused by *E. coli* O157:H7 has become a global public health dilemma. Worldwide incidences cause by *E. coli* particularly O157:H7 make it an important pathogen that occurred in all countries. Infection cause by O157:H7 range from asymptomatic which may become severe in some cases. *Escherichia coli* O157:H7 can cause infections at a very low dose in humans which is a much lower dose than for most other pathogens of the intestines. Its preference to thrive within the warmer-temperature seasons compared to periods with low temperatures make it a novel pathogen in the tropical regions. It can cause infections at a very low dose in humans which is a much lower dose than for most other pathogens of the intestines: Despite the vital community and clinical health hazards pose by *E. coli* O157:H7 worldwide, a very few studies were conducted in developing countries. Continues surveillance to determine the prevalence of the pathogen as well as accurate diagnostic procedures may immensely help in tackling the pathogen

Keywords: *Escherichia coli*, hemorrhagic fever, enteric diseases, foodborne pathogens

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INTRODUCTION

Dr. Theodor Escherich in 1885 discovered what is now known as *E. coli* through his investigation on the cause of infant diarrhea. The stool sample of the infant was shown to contain a pathogenic bacteria which has been highlighted as an important human pathogen since then. The discovery of Shigella dysenteriae as an agent of epidemic bacterial dysentery was reported by Kioshi Shiga in 1898 (Shiga, 1898). In 1955, that hemolytic uremic syndrome (HUS) was first described and defined (Gasser *et al.*, 1955), while Keusch *et al.*, 1972) showed that Shiga toxins contribute to bloody diarrhea. Some bacteria are known for their ability to cause foodborne illnesses, *E. coli* that produce Shiga- toxin (STEC) are among the pathogens linked to such diseases (Kaufmann *et al.*, 2006). *Escherichia coli* that cause infections in humans are classified into 6 main pathotypes: Entero-pathogenic *E. coli* (EPEC), entero-toxigenic *E. coli* (ETEC), diffusely adhering *E. coli* (DAEC), entero-aggregative *E. coli* (EAEC), entero-invasive *E. coli* (EIEC) and EHEC (Enterohaemorrhagic *E. coli*) based on toxin productions and pathogenicity. The aforementioned pathotypes of *E. coli* are identified to adopt what is referred to as multistep systems of pathogenesis which involved series of steps including; evasion of the host defenses, colonization of the mucosal site, multiplication within the animal, and tissue degeneration of the invaded location (Torres *et al.*, 2005 and Nataro & Kaper 1998).

Escherichia coli, a commonly found member of the natural microflora of human and animal intestinal tract, is a Gram-negative facultative organism and a member of the Enterobacteriaceae (Nys *et al.*, 2004, Von Baum and Marre, 2005). They are one of the most commonly isolates found in faecal matter of mammals (Elder *et al.*, 2000; Brown *et al.*, 2001). These bacteria can easily be transferred to cattle carcasses from hides contaminated with fecal matter during slaughtering and beef processing (Reid *et al.*, 2002). Among the enterics, O157:H7 and non O157: H7 serotypes of *E. coli* that produce shiga toxin have been recognized as the causative agents for HC (haemorrhagic colitis) and HUS (haemorrhagic uraemic syndrome) in humans respectively (Von Baum and Marre, 2005). The two serotypes are of medical importance due their role in outbreaks globally, their ability to cause severe illness and also very minimal number of cells required to trigger an infection among susceptible human population (Duffy and Garvey, 2001).

PUBLIC HEALTH CONCERN

A total 5220 deaths in 28 616 *E. coli* bacteraemia patients, a mortality rate of 18.2% was reported in a United Kingdom (Abernethy *et al.*, 2015). Previously, *Salmonella* and *E. coli* were estimated to cause 1.3 million deaths and 62,000 incidence of gastroenteritis respectively per annum in the US (Mead *et al.*, 1999). However, among the two, the O157:H7 strain was identified as the most important in terms of pathogenicity which

was epidemiologically found to be responsible for many outbreaks due to food ingestion in Japan and Europe. *Escherichia coli* O157:H7 causes 73,000 illnesses in the United States annually based on reported data in 2005 which indicated a significant decrease in number of incidences (Josefa et al, 2005). Similarly, Non O157:H7 food-borne outbreaks have also been reported and the common isolated serotypes in these cases were O26 and O111. According to estimations by the CDC, O157:H7 caused about 73,000 illness and a total of 61 deaths per annum in the United States while non-O157 STEC account for an additional 37,740 illnesses with 30 deaths (White, 2002). After hemorrhagic colitis was found to be caused by *E. coli* as a cause of hemorrhagic colitis the CDC reassessed samples collected between 1973-1983, the report showed that only one isolate have been identified as O157:H7 out of 3,000 *E. coli* strains serotyped. Similar reassessment in United Kingdom public Laboratory conducted between 1978 and 1982 also isolated only 1 O157:H7 serotype out of 15,000 *E. coli* isolates.

However, between 1978 and 1982 the Canadian CDC reassessed 2,000 isolates found in stool samples out of which six isolates were confirmed to be O157:H7 (Griffin and Tauxe, 1997). For that reason, it seems that the occurrence of O157:H7 strains has actually raised during the last decades and the data about its prevalence in some countries remained intact since its discovery. According to records, the largest outbreak caused by O157:H7 serotype was reported in 1996 from Japan, about nine thousand citizens were affected and the implicated source of infection was contaminated radish sprout (Michino et al., 1998). Transmission of the O157:H7 can also occur through person to person. Waterborne and person-person being transmissions were reported to be increasing (Meng et al., 2001). In Malaysia, 22.6-88% prevalence has been reported for *Escherichia coli* in agricultural products (Adzitey, 2011). In addition, incidence of O157:H7 serotype was reported to be 28.6% for the Southern, 38.8% for the Central, 36.5% for the Eastern and 35.6% for the Northern region (Chey et al., 2004). Recently, surveillance data from Sweden, Finland and Canada showed a 2961 30-day deaths in 30,923 incident *E. coli*. (Melissa et al, 2021)

PERIODIC INFECTIONS

Periodic infection caused by O157:H7 are frequently isolated in Canada compared to the USA, but such infection has been reported to have increased in some regions within the USA. However, geographical pattern of spread of diseases appeared to be less frequent in southern compared to northern region of the US and in Canada it was found to be less common in southern compared to western region. Many studies have reported seasonal effect on prevalence of Salmonella and O157:H7 serotype ((Nataro et al., 1998) (Griffin, 1995). Armstrong, 1996, Dargatz et al, 2003, Rivera-Betancourt et al., 2004 and Edrington et al., 2006). Other report indicated seasonal variations have no effect on prevalence of O157:H7 serotype. Various infection routes have been described; transmission via food and human contact. Animal reservoirs were found to be the major source of infections for humans in the United Kingdom (Dayna et al, (2008); Locking et al, 2001; O'Brien et al., 2001). Worldwide incidences cause by STEC particularly O157:H7 make it an important pathogen that occurred in all countries but are most frequent in some parts of the United States, Canada and United Kingdom. Based on estimates about 73,480 cases of O157:H7 infections are recorded each year in the United States ((Altekruse et al., 1999; Nataro and Kaper, 1998; Tauxe, 1997; Mead et al, 1999). On the other hand, from 2000-2005, 24 countries in the European Union have documented 62% cases of O157 infections out of 14,000 incidences (Fisher and Meakins, 2006). About 90 outbreaks were reviewed in Scandinavia, UK, USA, Japan, Ireland and Canada and results have shown that secondary sources were responsible for approximately 20% of

the total outbreak episodes. In addition, the time interval for episodes of the incidences revealed that there was sustained spread of the pathogen after the outbreak among communities affected and it seems to be sporadic (Snedeker et al, 2009).

Several analyses have determined the occurrence rate of O157 in bovine and assessments on documented results suggested some wide discrepancies among results provided by researchers. Fecal samples analysis collected from cattle indicated a prevalence of 0.28-48.8% in dairy farms. Similarly, a prevalence of 0.4% to 40% in calves in the United States while 1.7% to 48.8% were documented in other countries from North America, Europe and Asia. The occurrence rate of O157:H7 seems to be higher within the warmer-temperature seasons compared to periods with low temperatures (Hussain and Bolinger, 2005, Hussain and Sakuma, 2005). Moreover, O157 serotypes is also found in smaller mammals such as sheep researchers have shown. Bovine and sheep intestinal contents samples were reported to harbor about 4.7% and 0.7% respectively of O157:H7 serotypes after slaughtering in the United Kingdom (Milnes, 2008). However, variability tend to be higher between various cattle carriages as prevalence appeared to be higher in one place totally absent in another place (Mathews et al, 2006). The distribution of prevalence is highly affected by external and internal factors in the farmlands and of course the animal origins. Sometimes many herds showed positive fecal samples while others were negative (Synge and Paiba, 2000).

Similarly, one of several studies conducted in Scotland which involved 474 cattle herds concluded that joining together dynamic epidemiological paradigm and the documented prevalence, including considerable diversity of shedding from each animal (so-called super shedders, excrete large amount while many shed small number of bacteria), indicated a unique procedure where approximately twenty percent of highly contagious cattle's shed 80% of the bacteria (Chase-Tapping et al, 2008).

Cattle's super shedding is related to the establishment of the bacteria in lymphoid follicle-dense mucosal region near the anal region. Bovines that harbor the bacteria at fore mentioned location release significant amount microorganisms persistently compared to animals that have the bacteria at different locations. The super-shedders can significantly increase prevalence of O157:H7 serotypes among the normal shedder if they coexist on the same farmland and possibly infects another cattle in the same pen. Potential risk associated with mixing super shedders and low-shedders on the same farms have been studied and the report have shown that phage type 21/28 was frequently isolated microorganism which help in cross-infection. Sex and level of stress are some of the risk factors for colonization by the bacteria. The female gender of cattle is more prone to colonization. In addition, weaning and movements were also recognized as risk factors but factors originating the environment including feed and water source were not implicated according to the report (Chase-Tapping et al, 2007).

DISTRIBUTION

Escherichia coli O157:H7 is transmitted to humans primarily through consumption of contaminated foods, such as raw or undercooked ground meat products and raw milk. Faecal contamination of water and other foods, as well as cross-contamination during food preparation (with beef and other meat products, contaminated surfaces and kitchen utensils), will also lead to infection (WHO, 2018). *Escherichia coli* primarily inhabit the intestine of warm-blooded animals and humans where the bacteria exist as the normal flora (Bell, 2002). Transmission is usually via contact with animals, contaminated food or during processing and preparations animal carcass. Enteric pathogens

(enterobacteriaceae) such as the *E.coli* are distributed from livestock to food crops through various routes such as irrigation with polluted water, dissemination by air, application of manures, transmission through biological agents such as insects and wildlife (Janisiewicz et al, 1999). Domestic and wild animals provide a regular source of EHEC in the environment due to persistent dissemination fecal contamination (Bell, 2002). Distribution from human to human has been highlighted on several occasions in children's kindergarten and health care delivery institutions. According to a study, household transmission is most frequent among individuals within the age of <5 years and adolescents (Parry and Salmon, 1998).

Furthermore, assessment of secondary spread in 90 outbreaks that occurred from 1982 to 2006 identified person to person contact as the route of secondary transmission in houses and nurseries (45.6% vs 11.1%) and institutions (4.5%); bathing water 10% and 55% from unknown sources. The maximum mean percentage of 2^o occurrence have been documented in incidences involving patients with average age below six years while the minimum within the age of 17–59 years (Snedeker et al, 2009). Talley et al, 2009 studied the role of biological agents in distribution of the bacteria particularly invertebrates, which are commonly found on fields of leafy plants and neighboring farmlands, in produce contamination.

During the investigation, a confinement was formed for house flies on a medium containing O157:H7 serotype marked with green fluorescent protein (GFP) followed by testing their ability to transmit the pathogen to spinach plants. The insects were capable of transmitting the GFP-tagged bacteria on outer layer of 50–100% of leaves viewed using fluorescence microscopy and in 100% of samples tested by PCR. Obviously, flies are capable of contaminating leafy vegetables, and this confirms the significance of the role played by insects in the transmission and subsequent contamination of fresh produce. Agricultural production environments and animals including cattle and poultry are noted sources of *E coli* and *Salmonella*. Mode of transmission of these pathogens were linked to ground beef in a number of food-borne out-breaks (CDC, 2002).

Numerous investigations on the microbiological hygiene of cattle at slaughter have indicated that hide contamination is highly associated with cross-contamination to animal carcasses which possibly results from slaughtering and processing (Bell et al, 1997, Elder et al, 2000, McEvoy et al, 2000; Omisakin, 2003 and Arthur et al, 2007). The route of transmission of *E.coli* is shown below in fig. 1.

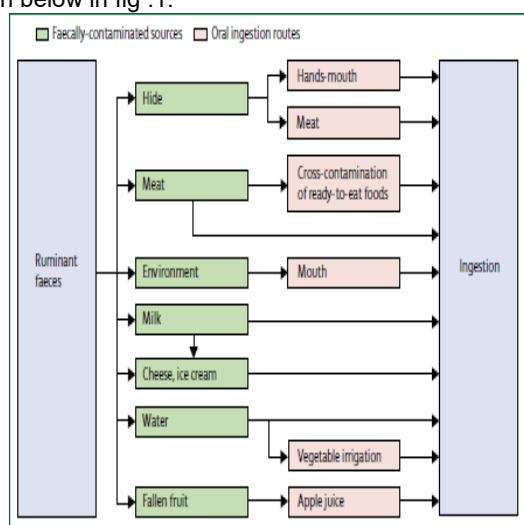


Figure 1 Route of Distribution for *Escherichia coli* (Hugh, 2010)

DISEASES CAUSED BY *E.COLI* O157:H7

More than 70 distinct types of STEC which trigger human diseases globally have been identified (Brooks et al., 2005; Armstrong et al., 1996; Nataro and Kaper 1998). It can cause an illness that begins with minor diarrhea to a severe diarrhea with blood, in some cases results in hemorrhagic form of the disease. Among the serotypes, O157:H7 seems to be frequently related to aggressive infections (Brooks et al., 2005, Rivero et al., 2010 and Tozzi et al., 2003). The disease has been related to contact with animals and their products, animal manure and contamination of vegetables; drinking water and edible fruits have also been implicated (Swerdlow et al., 1992). Partially-cooked meat which harbored *E.coli* O157H7 have been implicated in 50% of foodborne outbreaks in the US (Gansheroff and O'Brien 2000). Healthy cattle may harbor O157:H7 serotype of *E.coli* which can be disseminated transiently and occasionally via feces (Cray & Moon 1995).

Escherichia coli O157:H7 can cause infections at a very low dose (1 and 100 CFU) in humans which is a much lower dose than for most other pathogens of the intestines (Paton and Paton, 1998). The bacteria can get attached to human intestine cells prior to infection for subsequent invasion and multiplication in the human host (Welinder-Olsson and Kaijser, 2005). Several human infection including HS and some forms of diarrhea have been associated with the pathogen since its first identification. It is also associated with severe forms of the infections - Hemolytic Uremic Syndrome. Generally, O157:H7 serotype cause infection that is self-limiting which depends on strain type and extent of the disease may vary. Hemolytic colitis is the most important disease related to O157:H7, its clinical symptoms include bloody diarrhea and abdominal pain which may subsequently develop to HUS or renal failure (Paton and Paton, 1998; Griffin and Tauxe, 1991; Johnson et al., 2006). Based on estimations about 8% of people harboring O157:H7 may eventually develop Hemolytic Uremic Syndrome (McNabb et al., 2008 and Tarr, 2009). Morbidity and mortality due to EHEC is mainly caused by diarrhea-associated HUS, resulting in death in up to 5% of cases and frequent permanent renal injury at a rate of 25% (Garg et al., 2003). This leads to platelet activation and local intravascular thrombosis or thrombotic microangiopathy, blood clot formation within the vasculature, and ultimately, a reduction in platelet counts.

Infection caused by O157:H7 range from asymptomatic which may become severe in some cases. Most information obtained on the infection are usually obtained from outbreaks and sometimes these data may not be reliable or seems to be biased (Manning et al, 2008). However, outbreak data such as those obtained from outbreak in Japan and the 2006 outbreak associated with spinach in the USA (more than 50% people hospitalized) are chosen by most researchers for epidemiological studies (Hataya, 1997 and CDC, 2006). Higher incidence of HUS seemed to occur mostly in infants <5 years old. According to the reports, levels Gb3 receptor sites are higher in children which bound to Shiga toxin that possibly circulate. Malfunctions of the renal cells can lead to azotemia- identified by the increase of nitrogenous compounds resulting from poor filtration by the kidneys (Inward et al., 1997, Tarr, 2009 and Tarr et al., 2005). In patients with post-diarrheal kidney failure, no prophylaxis was known to be effective (Machado et al, 2009).

Despite the vital community and clinical health hazards pose by *E.coli* O157:H7 worldwide, a very few studies were conducted in developing countries. Stringent policies dealing with improper food supplies and agricultural practices will be urgently required to tackle some potential menace associated with distribution of the pathogen. Epidemiological investigation may play a crucial

role in providing useful data for interventions and decision making in health planning.

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