

Diarrheagenic *Escherichia coli* O157 from Libya: recent perspectives and challenges

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Diarrheal pathogens persist as a primary cause of high morbidity – and mortality – gastrointestinal illnesses worldwide particularly in the developing world.^{1,2} Rotaviruses are a major cause of diarrheal illnesses, and a seasonal infection transmitted by the fecal-oral route. The increased incidence of rotavirus infection among human populations has been attributed to its wide-range presence in animals and ability to exchange genetic determinants between strains affecting animal and human hosts.³ Bacteria pathogens are also a leading cause of diarrhea, especially among children, and are reported to be responsible for significant morbidity, mortality, and economic losses, particularly in underdeveloped countries.² In Libya, for instance, research studies of diarrheagenic agents have focused on bacteria and the pediatric population and different serogroups of *Escherichia coli* have been reported as a major cause of childhood diarrhoea.⁴⁻¹¹

Enterohemorrhagic *E. coli* [EHEC; also known by the acronyms Shiga toxin-producing *E. coli* (STEC), or verocytotoxin-producing *E. coli* (VTEC)] is one of the most common of the serogroups associated with gastroenteric illnesses and foodborne outbreaks.¹² The Shiga toxins produced by this group of *E. coli* cause an array of complications in humans, ranging from uncomplicated diarrhea to life-threatening conditions such as hemorrhagic colitis, which can progress into hemolytic uremic syndrome (HUS) and severe acute renal failure. The STEC/VTEC encompass hundreds of serotypes capable of causing severe illnesses in humans, among which O157, O26, O111, O103 and O145 (the so-called *top five*) are the most frequently reported serogroups associated with human disease.¹³ The O157 serogroup is the most commonly reported and has been the main cause of serious outbreaks, especially of foodborne infections.¹² As such, *E. coli* O157 has emerged as a particular public health concern.

Ruminants, particularly cattle, are the natural reservoir of *E. coli* O157, which inhabit the intestinal tract of healthy animals. Infection of humans is typically

acquired through contaminated food and drink (*i.e.* undercooked ground meat, raw milk, dairy products, raw vegetables, contaminated fruits) or through direct contact with animals.^{12,14} Generally speaking, publications describing research on the frequency and occurrence of important zoonotic bacterial organisms of public health concern from underdeveloped regions, such as Libya, are few and epidemiological information remains scarce.^{5,14} However, researchers in Libya have begun reporting on the isolation of *E. coli* O157 from a range of animals and animal products. Herein, we summarize the recent peer-reviewed articles on this topic and provide commentary to promote interest in this important public health concern and highlight the research opportunities (Table 1).

In Libya, 24-33% of pediatric diarrheal cases are caused by rotavirus rotavirus.^{4,15,16} In addition, a recent study uncovered an alarming trend in increasing incidence, with these cases estimated to represent up to 57%.¹⁷ Bacterial pathogens are also reported to be a major cause of diarrhea in children and are responsible for an approximate 27% of the clinical samples examined. Several genogroups of *E. coli* have been characterized (*i.e.* EPEC, ETEC, EHEC, EIHC, EAEC) and found to express multidrug-resistant phenotypes.^{4,5,11} However, the epidemiology, phylogenetic relation and zoonotic features of the reported strains isolated from pediatric human cases, and at population level, are largely unknown.

In Libya, the recently reported *E. coli* O157 isolates from food-producing animals and most recently from animal products underscore the serious health concern facing this region (Table 1). Garbage *et al.*, for instance, have reported the isolation of *E. coli* O157 from raw milk and dairy products collected from different animals, with cow origin being predominant (7/11 of total isolates).¹⁸ This particular study has reported raw goat milk as the most contaminated source (*i.e.* 2/7 samples; 28.6%). On the other hand, Abujnah *et al.* have reported a high isolation rate for *E. coli* O157 from fresh white cheese samples (35.6% of tested samples) collected from local factories around Tripoli; however, the animal origin of the samples was not clear.¹⁹

The consumption of raw or undercooked meat of bovine origin has been frequently reported to be the most common source of *E. coli* O157 contamination and infection. A study of raw sausage specimens (locally known as *almergaz*) that had been collected from local markets in Tripoli isolated *E. coli* O157 from 48%, with 60%

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genopositivity for *stx* genes among the isolated strains; however, the animal source of meat samples was not stated.²⁰ Previously, studies have reported the isolation of this pathogen from burger meat specimens of beef and chicken origins. Considering the collective findings from these studies, the rates of isolation/contamination was found to range between 4-5% in cooked meat and from 20-27% in uncooked meat specimens of burgers (Table 1).^{21,22} Unfortunately, most of the previous studies have not determined the possible sources of these contaminant bacteria or the epidemiologic and phylogenetic relation among these strains and/or toward humans (either humans-in-contact or the consumers).

Prevalence of *E. coli* O157 in healthy dairy cows has been studied as well. In suburban areas of Tripoli, the reported rates range from 6-9%.^{14,23} Shedding of *E. coli* O157 from healthy cattle was reported to be significantly associated with signs of diarrhea and source of water-intake (identifying these parameters as risk factors of shedding). Surprisingly, age which is frequently associated with shedding of *E. coli* O157, was not found to be a significant risk factor. Ultimately, healthy dairy cows have been posited as a natural reservoir of *E. coli* O157 in Libya. A regional study from Egypt identified *E. coli* O157 isolates from marine life (seafood and animals from coastal water; 48% of tested samples).²⁴ Thus, there is a

Table 1. Summary of the prevalence and isolation frequencies of diarrheagenic *Escherichia coli* from humans, animals and animal products in Libya.

Sample origin	Origin and source	N. tested samples	Total positivity, %	Identified <i>E.coli</i> group and/or strains	Identification method	Ref.	
Human Stool (Children)	Diarrheic	239	11.2%	EAEC, EPEC, EHEC, EIEC	PCR	4	
	Diarrheic	124	0.7%	O157:H7	Sera	6	
	Diarrheic	157	7.0%	O157:H7	Sera	7	
	Control	157	4.4%	EPEC, ETEC, EAEC			
	Diarrheic	243	8.6%	EPEC	PCR	5	
	Diarrheic	157	0,11		Sera	9	
	Control	157	0,07	EPEC			
	Diarrheic	356	0,04		Sera	10	
	Control	100	0	EPEC, EAEC			
	Diarrheic	157	8.9%		PCR	11,8	
	Control	157	2.5%				
	Cattle	Feaces	97	6.2	O157	Sera	14
		Feaces	200	9	O157	Sera	23
Raw milk		28	3.5	O157	16srDNA-PCR	18	
Dairy products*		49	9.5/21.4	O157	16srDNA-PCR	18	
Burger ^o		15 ^o	5.4/27.1 ^o	O157:H7	Sera	21	
Camel	Raw milk	9	0	O157	16s rDNA-PCR	18	
Goat	Raw milk	7	28.6	1057	16s rDNA-PCR	18	
Chicken	Burger ^o	120 ^o	4.7/20.3 ^o	O157:H7	Sera	22	
Unknown	Raw sausages	100	48	O157:H7	Sera and PCR	20	
	Cheese	87	35.6	O157:H7	Unspecified	19	

ID, identification. *Dairy products [Include cheese (n=21; 9.5%) and fermented milk (n=28; 21.4%)]; ^oBurgers (sample size is presented in total and positive rates are in respect to cooked/raw products).

serious public health threat among important food resources of this region. Interestingly, recent reports have documented the possible association of outbreaks and infections with the new emergent *E. coli* serotype O104:H4 in Europe and travel history to North Africa.¹³ Environmental contaminants and waste materials of urban and suburban sources can harbor pathogenic and infectious agents and therefore pose a significant public health threat. The non-developed sanitary and health systems of underdeveloped regions can play a major role in the dissemination and emergence of infectious pathogens, such as *E. coli* O157.

The collective peer-reviewed literature on this topic highlight the likely role of food-producing animals as a potential source and carrier of public health-threatening pathogens. However, the carriage status of *E. coli* O157 in different food-producing animals and the related epidemiological information still require investigation. Also, information is absent on the most significant diarrheagenic *E. coli* that are frequently reported and associated with global human outbreaks. Documentation of *E. coli* O157 isolates from animal products is necessary, so that appropriate prevention measures can be developed and applied to control risk in the food chain as well as in the environment. Thus, systematic epidemiological studies are required to determine an accurate estimation of the burden of *E. coli* O157 and other diarrheagenic strains, particularly in food-producing animals. This

will require interactive collaboration between human and veterinary medicine professionals at the clinical, public health and research level.

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