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Full Length Research

Isolation of E*scherichia coli* o157:h7 from water sources in the livestock complex, Mando, Kaduna

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ABSTRACT: Failure in understanding the importance of water quality exposes humans and animals to the risk of diseases. Microbial contamination remains a critical risk factor in useable water in many parts of the world. This study was aimed at investigating *Escherichia coli* contamination of water samples. Fifty water samples were analysed to detect the occurrence of potentially pathogenic bacteria of Enterobacteriaceae family. All isolates detected were screened biochemically using Microbact GNB 12E and serotyped for the virulence antigens O and H. The results showed 14% (7/50) of the samples were positive for *Escherichia coli, Salmonella arizonae, Enterobacter gergoviae, Enterobacter aerogenes*, and *Hafnia alvei*. Out of which 3 samples were positive for *Escherichia coli* isolates which were collected from borehole (2 samples) and well water (1 sample) sources. All 2 isolates were serotyped for virulence antigen O157: H7 in which only 2 serotypes were identified for O157:H7 (2%) and O157:H^- (4%). Hence, it could be concluded that water may be an important reservoir for *E. coli* infection and thus, the risk of contracting Enterohaemorrhagic *Escherichia coli* (EHEC) infection from contaminated water have been clearly established.

Key words: EHEC, *Enterobacteriaceae*, reservoir, water, O157:H7.

INTRODUCTION

Water plays a significant role for the sound pathogen that has emerged as a major cause of health of every person and is essential for plant life. About 75% of the earth's crust is covered with water and the human body comprises approximately 70 % of water (Pant, 2004). Therefore, water is the most urgent for life and essential for good health of human beings. In Europe and America, much attention has been paid to the problem of water purity (Pant, 2004). The people of developing countries are attacked by water-borne diseases than those in developed countries (Simpson et al., 2002). Fecal pollution in water system is expected to originate from human and animal sources and multiple pollution control measures may be necessary to meet the requirement of the Clean Water Act and its amendments (Simpson et al., 2002). *E. coli* is one of the indicator organisms for freshwater systems which have been recommended by the U.S. Environmental Protection Agency (EPA) and it is a sensitive measure for fecal pollution since it is common to almost all warm-blooded animals, including humans (U.S. EPA., 1986). Both Enterotoxigenic *E. coli* (ETEC) and Enterohaemorrhagic *E. coli* (EHEC) infections have been associated with the ingestion of food or water contamination with these organisms (Gannon et al., 1992). *E. coli* O157: H7 is a food-borne pathogen that has emerged as a major cause of hemorrhagic colitis. The reservoirs for EHEC O157:H7 are ruminants, particularly cattle and sheep, which are infected asymptomatically and shed the organism in feces. Other animals such as rabbits and pigs can also carry this organism. Humans acquire EHEC O157:H7 by direct contact with animal carriers, their feces, and contaminated

Table 1. Coliforms associated with collected water samples from boreholes and well reservoirs

Type of water	Site of collection	No. examined	No. positive	Identified isolate
Underground water/boreholes	Hostel	5samples	0	NI
	Farm	5samples	1	Salmonella arizonae
	Egege	5samples	2	Escherichia coli
	Fayomi	5samples	1	Acinetobacter lwoffii
	Adeiza	5samples	0	NI
	Jigawa	5samples	2	Hafnia alvei
	Livestock	5samples	2	Escherichia coli
Wells	Balogun	5samples	3	Escherichia coli
	Makeri	5samples	2	Enterobacter gergoviae
	Obgobe	5samples	2	Enterobacter aerogenes

NI; non identified

soil or water, or via the ingestion of undercooked ground beef, other animal products, and contaminated vegetables and fruit. The infectious dose is very low, which increases the risk of disease (Alam and Zurek, 2006). *Escherichia coli* are serotyped based on the O (somatic lipopolysaccharide), H (flagellar) and K (capsular) antigens. Serotype known to contain EHEC includes *E. coli* O157:H7, the non-motile organism *E. coli* O157: H^-, and other serogroups, including members of O26, O91, O103, O104, O111, O113, O117, O118, O121, O128 and O145. *E. coli* O157: H^- is closely related to *E. coli* O157:H7, but it is not simply a non-motile version of this organism; it also has a distinctive combination of phenotypic and virulence features (Buchanan and Dole, 1997). This study was thus designed to investigate *E. coli* O157:H7 contamination in water samples of the livestock complex, Mando, Kaduna.

MATERIAL AND METHODS

Mando livestock complex is a fairly large area stretching about 1500m^2 made up of several federal installations such as the Federal Ministry of Agriculture, College of Agriculture and Animal Science, school of pest control services, an integrated livestock farm, a poultry farm, and a residential quarters. To ensure adequate representation of the area all the samples were collected from all sub-divisions; which includes residential, farm and official areas; and also from the direct reservoir supply (wells) and the storage tanks (boreholes). The study duration was one month from September 2013 to October 2013.

Sample collection

In this study, a total of 50 water samples were collected in sterile sample bottles at early morning. The water samples were collected as described by Duelge and Unruh (2002). Each sample was labeled to show serial number, place of water, type of water as well as time and date of collection.

Sample Processing

Examination of the water samples was completed within 24 hours after collection and inoculation in lactose broth (Cappuccino, 1996). After incubation (37°C±0.5°C for 24hr), the tubes showing growth were inoculated onto MacConkey, and EMB agar plates (Oxoid, Basingstoke, UK). After incubation at 37°C±0.5°C for 24hr ±2hr (Clesceri et al., 1998) suspected *E. coli* colony were identified using Microbact GNB 12E (Oxoid, Basingstoke, UK) and microscopy. The *E. coli* isolates were then subjected to serotyping by slide agglutination test using the Wellcolex® *E. coli* antigen kit (Thermo Fisher Scientific, USA) for identification of EHEC strains, used according to manufacturer's instructions.

RESULTS

In the present study, 50 samples were analysed to detect the occurrence of coliforms among the collected water samples. It is clear that 7 out of 50 water samples were positive for coliform with an incidence of 14 % as shown in Table 1. The highest percentage of coliform detection rate was observed among water samples collected from underground water/boreholes (8%, 4/50) while well water samples had an incidence of 6%, 3/50. For the water samples collected from underground water/borehole the prevalence of *E. coli* was 11% (4/35). While the prevalence of *E. coli* was 20% (3/15) for water samples collected from well water (Table 2). The predominant *E. coli* serotype isolated from the examined water samples was O157:H^- while one isolate was O157:H7.

Table 2. Prevalence of *E.coli* serotypes among the examined water samples

Type of water	No. examined	E. coli positive	E. coli positive (%)	Sources	Serotype	No.
Underground	35	4	11%	Egege	O157:H- O157:H- O157:H7	2 1 1
Wells	15	3	20%	Balogun	O157:H- O157:H- O157:H-	1 1 1

DISCUSSION

Since its discovery in 1982 as a cause of illness, most infections from *E. coli* O157:H7 are believed to have come from eating undercooked ground beef. However, some have been water borne, as WHO estimates that 80% of all sickness in the world can be attributed to inadequate portable water supplies and poor sanitation. Water borne disease attributable to the ingestion of *E. coli* O157:H7 contaminated water has been reported (Geldreich et al., 1992). This study has demonstrated the potential risk of *E. coli* O157:H7 infection through contaminated water consumption with an isolation rate of 2% which is in agreement with the works of Aminu and Saidu, 2015 (3.03%), Chigor et al., 2010 (2.1%), and Sergeant, 2003 (1.5%). Highest proportion of coliform contamination obtained from wells may come from the animal reservoirs (ruminants) within the complex, as has been demonstrated by Emmanuel et al. (2015) and Solomon et al. (2002). These animals are allowed on free grazing and search for water within the complex with no restriction on contact with water sources/reservoirs used by humans (wells and boreholes). The reservoir hosts and epidemiology may vary with the organism. Ruminants, particularly cattle and sheep, are the most important reservoir hosts for *E. coli* O157:H7 (Bidet et al., 2005). A small proportion of the cattle in a herd can be responsible for shedding more than 95% of the organisms. These animals, which are called super-shedders, are colonized at the terminal rectum, and can remain infected much longer than other cattle. Super-shedders might also occur among sheep. Animals that are not normal reservoir hosts for *E. coli* O157:H7 may serve as secondary reservoirs after contact with ruminants (CDC, 2008).

Conclusion

In conclusion, the strain of *E. coli* identified in this study from both the wells and underground water samples are consistent with the strains potentially pathogenic for humans. Identifying the major contributing source of contamination is the critical component for accurate assessment and successful control. Detection of potentially pathogenic *E. coli* O157:H7 in the examined water samples is alarming as many if not all the residents of the livestock complex depend on these water sources daily for bathing, washing, laundry, and for cooking. These individuals are at great risk of contracting *E. coli* O157:H7 infection.

CONFLICT OF INTEREST

The authors declare that they have no conflict of interest.

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