Diversity, virulence and antibiogram traits of *Escherichia coli* recovered from potable water sources in Gharbia, Egypt

Walid Elmonir, Etab Mohamed Abo Remela and Yasmine Alwakil

ABSTRACT

This study aimed to assess the public health risk of coliforms and *Escherichia coli* contamination of potable water sources in Egypt. A total of 150 water samples (100 tap and 50 well) were collected from five districts in Gharbia governorate, Egypt. High rates of coliforms contamination were recorded in 52 and 76% of examined tap and well water samples, respectively. *E. coli* strains were detected in 16% of the water samples (15% tap water and 18% well water; 23.7% rural and 8.1% urban). Rural water sources were 3.5 times more likely to be contaminated than urban sources ($P = 0.01$). Eight (33.3%) *E. coli* isolates were Shiga toxin-producing *E. coli* (STEC). Multiple drug resistance (MDR) was observed for 62.5% of the isolates. Seven (29.2%) *E. coli* isolates harboured at least one of the extended-spectrum beta-lactamase (ESBL) genes. The majority (87.5%) of the STEC isolates were MDRs and harboured ESBL genes. STEC isolates were significantly more likely to resist six classes of antibiotics than non-STEC isolates. This is the first report of potable water contamination with MDR-STEC in Egypt. This study highlights an alarming public health threat that necessitates preventive interventions for public and environmental safety.

Key words | Egypt, *Escherichia coli*, multi-drug resistance, potable water, STEC

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INTRODUCTION

Waterborne diseases are a major public health problem, particularly in developing countries. More than 500,000 deaths each year in middle- and low-income countries can be attributed to unsafe drinking water; around 65,000 of these deaths occur in Middle Eastern countries (WHO 2014).

Escherichia coli is an indicator of faecal contamination of water (Hunter 2003); this species is also a good predictor of the risk of waterborne diarrhoeal diseases (Grilc *et al.* 2015). Virulent strains of this pathogen are associated with several waterborne outbreaks (Hunter 2003). Shiga toxin-producing *E. coli* (STEC), in particular, is apparently one of the most important diarrhoeal diseases in this century, given the global distribution of STEC, the severity of the signs, and the high number of fatalities, especially among the elderly and children (Hunter 2003). STEC outbreaks are responsible for thousands of cases of infection in both developed (Hoshina *et al.* 2001) and developing countries (Isaacson *et al.* 1993). Water-borne STEC outbreaks are usually associated with contaminated ruminant manure as the primary reservoir of these pathogens (Isaacson *et al.* 1993; Hoshina *et al.* 2001; Madec *et al.* 2016). Hussein (2007) reported that cattle faeces harboured more than 300 STEC serotypes; more than 120 of these serotypes were associated with human clinical cases (Hussein 2007). Community water source contamination with animal faecal matter is apparently more ubiquitous than contamination with human faecal matter, especially in rural dwellings (Schriewer *et al.* 2015), which highlights the high risk of human exposure to zoonotic

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STEC pathogens via water, especially in rural communities. Another major impact of water contamination with *E. coli* is the transmission of antibiotic resistance. Contaminated drinking water is an important vehicle for the spread of antibiotic-resistant *E. coli* from the environment to humans or for the transfer of the mobile resistance genes of these strains to gastrointestinal pathogens (Madec *et al.* 2016). Contamination of water with antibiotic-resistant *E. coli* is an emerging global concern, with an increasing number of cases reported in both high- and low-income countries (Madec *et al.* 2016). This problem is usually potentiated by inadequate or defective infrastructure for water sanitation and waste treatment along with minimal control of antibiotic usage (Madec *et al.* 2016).

In Egypt, water contamination is an emerging crisis. The reasons underlying this crisis include the inadequacy of the public sewer system that covers only approximately one-third of rural households, leaving 42 million people with frequently overflowing septic tanks in their dwellings (World Bank 2015) and, the deficient wastewater treatment infrastructure that resulted in direct discharge of over 100 million m^3 of untreated sewage each year into fresh waterways (El Tahlawi *et al.* 2008). These conditions have contributed to the prevalence of water-related diseases that accounted for 5.1% of annual total deaths and 6.5% of the annual total disease burden in Egypt (Prüss-Üstün *et al.* 2008).

Despite this alarming crisis, studies on the extent and public health risks of water contamination in Egypt are very limited. Therefore, the current study aimed to gain insights into the occurrence of coliforms and diversity of *E. coli* strains in the two most common sources of drinking water in Egypt – wells and taps – in samples collected from five districts in Gharbia province in the middle of the Nile Delta in Egypt. We also assessed the virulence and antibiotic resistance traits of the detected waterborne *E. coli* isolates.

MATERIALS AND METHODS

Study area and sampling

The study was carried out in Gharbia governorate in the middle of the Nile Delta in northern Egypt (30° 52′ 31.28″ N and 31° 2′ 0.636″ E). Gharbia governorate is the tenth largest governorate (1942.34 km^2) in Egypt according to the Central Agency for Public Mobilization and Statistics (CAPMAS 2018). Gharbia is inhabited by 5,066,000 residents, who occupy the whole area of the governorate (100%) with an inhabitation rate of 2583.8/km^2 (CAPMAS 2018), making Gharbia one of the most densely populated governorates in Egypt. The majority of the residents of Gharbia (3,620,000, i.e. 71.5%) live in rural dwellings; this governorate is among the least urbanized governorates (28.5% urbanization rate) in Egypt (CAPMAS 2018).

Water samples were collected from five districts in the governorate: Tanta (the capital), Zefta, Qotor, Basyon and Elsanta. These districts are located across the governorate between the two branches of the Nile River: the Rashid and Damietta branches (Figure 1). Between October and December 2017, a total of 150 water samples (100 tap and 50 well) were randomly collected from five cities and 17 villages in the chosen districts. Thirty water samples (1 L each) were collected in each district (20 tap and 10 well). Sodium thiosulphate was added to tap water samples (18 mg/L) for dechlorination. All the water samples were transported chilled to the laboratory for further analysis.

Coliform and *E. coli* detection

Coliform and *E. coli* count was conducted using a multiple fermentation tube technique as previously described (APHA 1998). A loopful of presumptive positive coliform tubes were inoculated in EC broth (Oxoid, Hampshire, UK) and incubated for 20 h at 44 °C for selective selection of faecal *E. coli* isolates. A loopful of positive EC culture (gas production) was cultivated on Levine's eosin methylene blue agar (Oxoid, Hampshire, UK) and incubated for 20 h at 35 °C. Suspected *E. coli* isolates were identified according to the following biochemical profile: indole (+), methyl red (+), voges-proskauer (−), citrate utilization (−), urease (−), H_2S production (−), and nitrate reduction (+). Serotyping was conducted using somatic (O) and flagellar (H) antisera (Denka Seiken Co., Tokyo, Japan) according to the manufacturer's instructions.

Coliforms and *E. coli* count were categorized as: Conformity coliform count: MP*N* = >1–3 cfu/100 mL; Conformity

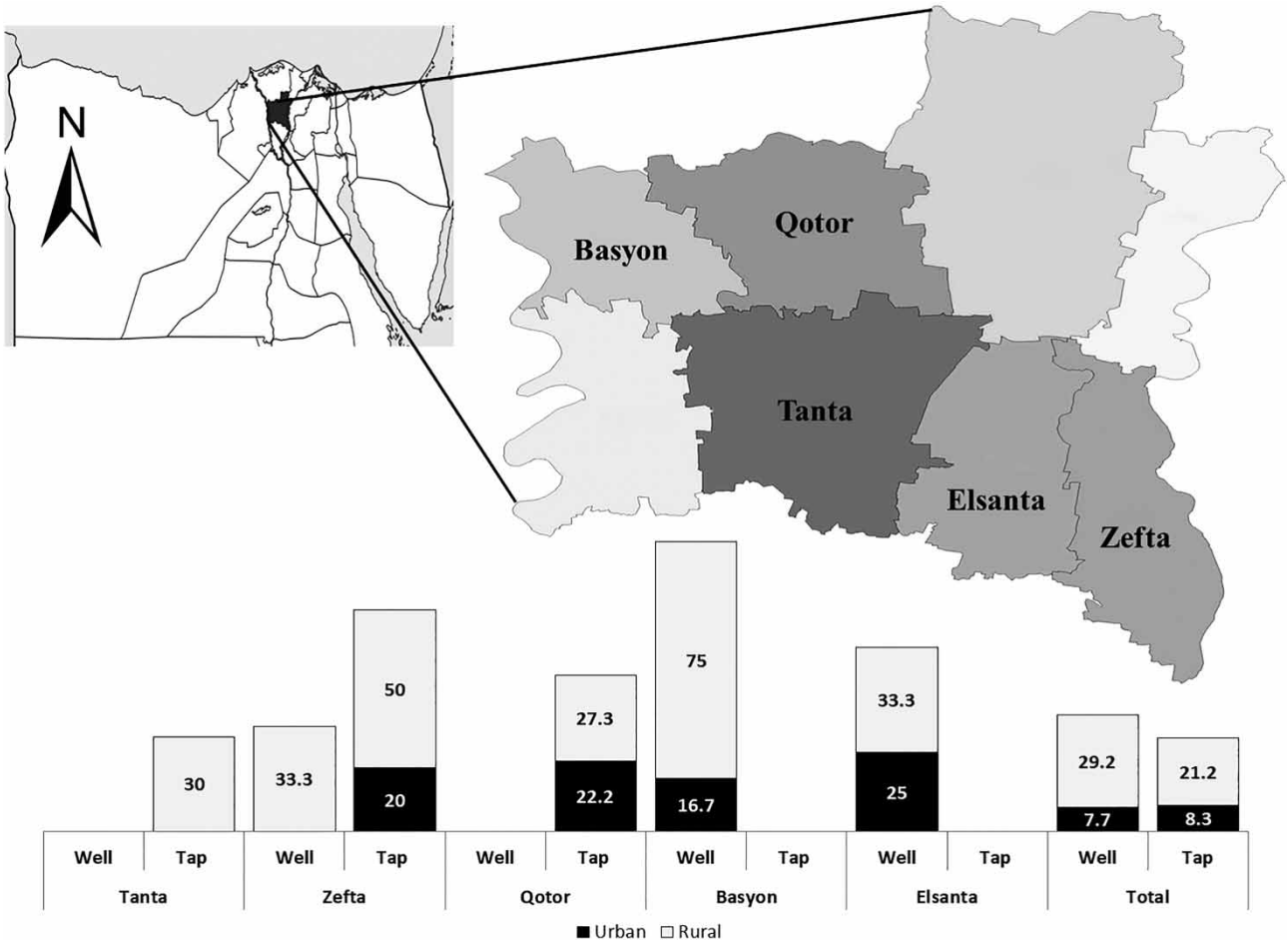

Figure 1 | Frequency distribution and geographical locations of *E. coli* isolates in different water samples collected from Gharbia governorate, Egypt.

E. coli count: MP*N* = >1 cfu/100 mL; Low contamination: MP*N* = >3–10 cfu/100 mL; Intermediate contamination: MP*N* = 11–100 cfu/100 mL; High contamination: MP*N* = >100 cfu/100 mL (WHO 2006; Singh *et al.* 2019).

Antibiotic sensitivity testing of isolated *E. coli*

Antibiotic sensitivity tests were conducted using a standard disc diffusion method according to the instructions of the Clinical and Laboratory Standards Institute (2016). Ten antibiotic discs (Oxoid, Hampshire, UK) were used: ampicillin (10 μg), cefotaxime (30 μg), nalidixic acid (30 μg), ciprofloxacin (5 μg), gentamicin (10 μg), streptomycin (10 μg), kanamycin (30 μg), chloramphenicol (30 μg), tetracycline (30 μg), and sulphamethoxazole/trimethoprim (25 μg).

Molecular characterization of isolated *E. coli*

DNA extraction from broth culture was conducted using the QIAamp DNA Mini Kit (Qiagen, Hilden, Germany) according to the company's instructions.

For testing of virulence genes, *E. coli* isolates were examined using multiplex PCR detection of Shiga toxin genes (*stx1* and *stx2*) and the intimin gene (*eaeA*) as described by Fagan *et al.* (1999). Multiplex PCR was conducted using a 50-μL reaction mixture that contained 5 μL of DNA template (100 ng), 1 μL (20 pmol) of each primer, 25 μL of EmeraldAmp MAX PCR master mix (Takara Bio, Kusatsu, Japan) and water (up to the final reaction volume). The cycling conditions were as follows: initial denaturation at 94 °C for 10 min; 35 cycles of 95 °C for 20 s, 58 °C for 40 s, and 72 °C for 90 s; and a final extension

at 72 °C for 7 min. The reference strains were *E. coli* O157: H7 Sakai (harbouring the *eaeA*, *stx1*, and *stx2* genes) as a positive control and *E. coli* K12DH5α (no virulence genes) as a negative control.

For testing of antibiotic resistance genes, *E. coli* isolates were examined for the detection of β-lactamase resistance genes (bla_{SHV}, bla_{TEM}, $bla_{CTX\text{-}M\text{-}1}$, and $bla_{OXA\text{-}1}$). Multiplex PCR was conducted using the same reaction mixture as that used for virulence genes. Amplification was conducted as previously described (Ogutu *et al.* 2015): 94 °C for 10 min; 30 cycles of 94 °C for 30 s, 61 °C for 35 s, and 72 °C for 1 min; and, finally, 72 °C for 7 min. An *E. coli* isolate positive for β-lactamase genes (bla_{SHV}, bla_{TEM}, $bla_{CTX\text{-}M\text{-}1}$, and $bla_{OXA\text{-}1}$) was included as positive control; this control isolate was kindly provided by the Food Control Department, Veterinary Medicine, Benha University, Egypt. All the primers (Metabion, Steinkirchen, Germany) used in this study are listed in Table S1 in Supplementary Materials.

Statistical analysis

Statistical associations and odds ratio were estimated using Fischer's exact and risk analysis using SPSS v19 (IBM, Armonk, New York). Significant associations were recorded at $P < 0.05$.

RESULTS

A total of 100 tap water and 50 well water samples were assessed for extent and public health risks of water contamination with coliforms and pathogenic *E. coli* in five districts of Gharbia governorate, Egypt. Coliforms and *E. coli* were detected in 92 and 16% of examined water samples, respectively (Table 1). There was no significance difference in coliform counts between tap and well water ($P = 0.4$). There was no association between positive coliforms and positive *E. coli* water samples ($P = 0.1$). High coliforms and *E. coli* contamination rates (>100 cfu/100 mL) were reported by 60 and 9.3% of the examined water samples, respectively (Table 1).

E. coli strains were detected in 16% of examined water samples; 15% of tap and 18% of well water samples (Tables 1 and 2). Additionally, the *E. coli* prevalence rates in the rural and urban samples were 23.7 and 8.1%, respectively (Table 2). There was no association between type of water samples (tap or well) and prevalence of *E. coli* isolates ($P = 0.6$) (Table 2). However, rural water sources were 3.5 times more likely to be contaminated with *E. coli* than urban sources ($P = 0.01$) (Table 2). Among the districts, the highest contamination rates for tap (35%) and well (40%) water were recorded in Zefta and Basyon, respectively (Figure 1). Zefta was the only district with *E. coli* contamination in both water sources (tap and well) (Figure 1).

Twenty-four *E. coli* isolates belonging to six serotypes were detected in the examined water samples: O26:H11 (12 isolates), O128:H2 (5 isolates), O91:H21 (2 isolates), O45:H0 (2 isolates), O124:H0 (2 isolates), and O103:H2 (1 isolate). Molecular characterization of the *E. coli* isolates showed that 8 (33.3%) isolates harboured at least one virulence gene – *stx1* (20.8%), *stx2* (33.3%) and *eaeA* (12.5%)

Table 1 | Frequency distribution and MPN counts of coliforms and *E. coli* in examined water samples in this study

Pathogen	Categories		Well $N = 50$	Tap $N = 100$	Total $N = 150$
Coliforms	Positive		47 (94)	91 (91)	138 (92)
	MPN	Conformity[a]	4 (8)	12 (12)	16 (10.7)
		Low[b]	0 (0)	9 (9)	9 (6)
		Intermediate[c]	8 (16)	27 (27)	35 (23.3)
		High[d]	38 (76)	52 (52)	90 (60)
E. coli	Positive		9 (18)	15 (15)	24 (16)
	MPN	Conformity[e]	41 (82)	85 (85)	126 (84)
		Low[b]	0 (0)	1 (1)	1 (0.7)
		Intermediate[c]	0 (0)	9 (9)	9 (6)
		High[d]	9 (18)	5 (5)	14 (9.3)

MPN, Most probable number count by cfu/100 mL. Numbers in brackets denote percentage.
[a]MPN = >1–3 cfu/100 mL.
[b]MPN = >3–10 cfu/100 mL.
[c]MPN = 11–100 cfu/100 mL.
[d]MPN = >100 cfu/100 mL.
[e]MPN = >1 cfu/100 mL.

Table 2 | Association of *E. coli* prevalence with source and location of water samples

Variable	Category	Percent	OR	95% CI	P
Source	Tap	15	–	–	**0.6**
	Well	18	1.2	0.5–3.1	
0.01	Urban	8.1	–	–	
	Rural	23.7	3.5	1.3–9.4	

Table 3 | Virulence and antibiotic resistance traits of detected *E. coli* serotypes in this study

			Antibiotic resistance patterns										β-Lactamase			Virulence		
Source	P	Ser	S	NA	SXT	TE	CTX	C	AMP	K	CIP	CN	*Tem*	*SHV*	*CTX*	*Stx1*	*Stx2*	*eaeA*
Tap $N=15$	P1	O26	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
	P2	O26	+	+	+	+	+	+	+	+	+		+	+	+	+	+	+
	P3	O26	+	+	+	+	+	+	+	+		+	+	+	+	+	+	+
	P4	O103	+	+	+	+	+	+	+		+	+	+	+		+	+	
	P5	O26	+	+	+	+	+	+		+	+	+						
	P6	O128	+	+	+	+	+	+	+	+	+		+	+			+	
		O128	+	+	+	+	+	+	+	+	+		+	+			+	
	P7	O26	+	+	+	+	+	+										
	P8	O26	+	+	+	+		+										
	P9	O26		+	+	+	+	+										
	P10	O26	+	+		+	+	+										
	P11	O26	+	+	+													
	P12	O26	+	+														
	P13	O26	+															
	P14	O26																
Well $N=9$	P1	O91	+	+	+	+	+	+	+						+	+	+	
	P2	O91	+	+	+	+	+		+									
	P3	O128	+	+	+													
	P4	O128	+	+														
		O124	+	+														
	P5	O124	+															
		O128	+															
	P6	O45															+	
	P7	O45																
Total		N	20	18	14	14	12	12	8	6	6	4	6	6	4	5	8	3
		%	83.3	75	58.3	58.3	50	50	33.3	25	25	16.6	25	25	16.6	20.8	33.3	12.5

AMP, Ampicillin; CTX, Cefotaxime; NA, Nalidixic acid; CIP, Ciprofloxacin; CN, Gentamicin; S, Streptomycin; K, Kanamycin; C, Chloramphenicol; TE, Tetracycline; SXT, Sulphamethoxazole/Trimethoprim.

– as shown in Table 3. Virulence genotypes [*stx1* + *stx2* + *eaeA*], [*stx1* + *stx1*], and [*stx2*] were presented by 37.5, 25 and 37.5% of the isolates, respectively.

Antibiotic sensitivity tests showed that 21 (87.5%) isolates were resistant to at least one antibiotic. Fifteen (62.5%) isolates exhibited multi-drug resistance. The highest resistance rates (58.3–83.3%) were recorded for streptomycin, nalidixic acid, sulphamethoxazole/trimethoprim, and tetracycline, while the lowest rates (16.6–25%) were recorded for gentamicin, ciprofloxacin, and kanamycin (Table 3). Seven (29.2%) *E. coli* isolates harboured at least one of the extended-spectrum beta-lactamase (ESBL) genes: bla_{TEM} (25%), bla_{SHV} (25%) and bla_{CTX} (16.6%) (Table 3). None of the isolates harboured the $bla_{OXA\text{-}1}$ gene. The resistance genotypes among the isolates included 42.9% [$bla_{TEM} + bla_{SHV} + bla_{CTX}$], 42.9% [$bla_{TEM} + bla_{SHV}$], and 14.3% [$bla_{CTX}$].

STEC isolates were significantly more likely to resist the six examined classes of antibiotics (ampicillin, cefotaxime, tetracyclines, kanamycin, chloramphenicol and ciprofloxacin) than non-STEC isolates ($P = 0.03$ to >0.0001) (Table 4). There was no significant difference between tap and well water *E. coli* isolates in terms of the detection frequencies of ESBL genes ($P = 0.2$) and STEC genes ($P = 0.7$).

DISCUSSION

Water safety is a major public health concern in developing countries, particularly Egypt. The overall prevalence of coliforms and *E. coli* in the examined potable water samples was 92 and 16%, respectively. However, there was no association between positive coliforms and positive *E. coli* water samples. Lower rates (27–44.7%) of coliforms

Table 4 | Associations of antibiotic resistance among STEC vs. non-STEC isolates

Variable	Category	Percent	OR	95% CI	P
S	STEC	87.5	–	–	0.6
	Non-STEC	81.3	0.6	0.05–7.1	
NA	STEC	87.5	–	–	0.3
	Non-STEC	68.8	0.3	0.03–3.3	
SXT	STEC	87.5	–	–	0.05
	Non-STEC	43.8	0.1	0.01–1.1	
T	STEC	87.5	–	–	0.03
	Non-STEC	37.5	0.09	0.01–0.9	
CTX	STEC	87.5	–	–	0.01
	Non-STEC	31.3	0.07	0.01–0.7	
C	STEC	87.5	–	–	0.01
	Non-STEC	31.3	0.07	0.01–0.7	
AMP	STEC	87.5	–	–	> 0.001
	Non-STEC	6.3	0.01	0.001–0.2	
K	STEC	62.5	–	–	0.007
	Non-STEC	6.3	0.04	0.003–0.5	
CIP	STEC	62.5	–	–	0.007
	Non-STEC	6.3	0.04	0.003–0.5	
CN	STEC	37.5	–	–	0.09
	Non-STEC	6.3	0.1	0.009–1.3	

C, Categories; OR, Odd ratio; CI, Confidence interval.

contamination were reported elsewhere (Pathak & Gopal 2008; Abera *et al.* 2017), while higher rates of *E. coli* contamination (20–29%) have been reported in Malaysia (Desmarchelier *et al.* 1992), India (Pathak & Gopal 2008) and Ethiopia (Abera *et al.* 2017).

E. coli was detected in 15% of the examined tap water samples, which was higher than the value in another report from Malaysia (7%) (Desmarchelier *et al.* 1992) and lower than the values in other reports (20.2–29%) from India (Pathak & Gopal 2008) and Ethiopia (Abera *et al.* 2017). *E. coli* contamination of tap water is an alarming public health concern and reflects either heavy microbial contamination of source water, which interferes with efficient water treatment, or defects in distribution pipelines post treatment (Pathak & Gopal 2008; Madec *et al.* 2016). It was estimated that 85% of the agricultural drains used as source water for tap water treatment in Egypt have higher coliform counts than permissible by Egyptian legal standards (van Achthoven *et al.* 2004). This may have contributed to our findings.

E. coli was detected in 18% of the well water samples, which was lower than the values in other reports from Malaysia (42%) and Ethiopia (52%) by Desmarchelier *et al.* (1992) and Abera *et al.* (2017), respectively. The source of well water in Gharbia governorate is the Nile aquifer, which is a shallow aquifer that is filled by infiltration from irrigation water drawn from the Nile River (El Tahlawi *et al.* 2008). Hence, the use of animal manure as organic fertilizer and the discharge of animal and human waste into agricultural drains (van Achthoven *et al.* 2004; ESER 2016) could contribute directly to the contamination of well water in the study area.

Rural water sources exhibited significantly higher contamination rates than urban sources ($P = 0.01$). Moreover, odds estimates showed that rural water sources are 3.5 times more likely to be contaminated with *E. coli* than urban sources. These findings are expected because it was previously estimated that children in rural Egypt are 8.7 times less likely to have access to safe water than those residing in urban dwellings (World Bank 2015). This difference could be attributed to several factors. There is a disparity in the distribution of the public sewer system, which covers 37% of rural dwellings compared to 89% of the urban sector in Egypt. This major deficit in the rural sewer system is compensated by the use of household septic tanks that are usually emptied by the private sector. Overflows or leaks of these septic tanks could lead to transmission of faecal pathogens, including *E. coli*, to the nearby shallow ground water table (World Bank 2015). Additionally, when emptying the tanks, the private sector discharges the waste directly into drains and sometimes even into river canals designed for irrigation and recycling as tap water (van Achthoven *et al.* 2004; World Bank 2015). All of these factors could contribute to the high rate of contamination in rural water sources in the study region.

STEC is a major human pathogen that is usually associated with bloody diarrhoea, haemolytic uremic syndrome (HUS) and high fatality rates, especially among children and the elderly (Hunter 2003). Eight (33.3%) of the *E. coli* isolates harboured the *stx2* gene, either alone or with the *stx1* gene, and were thus considered STEC. To the best of our knowledge, this is the first report of STEC in potable water in Egypt. The value observed in our study was higher than a previous report (4%) of STEC in water samples from Brazil (Lascowski *et al.* 2013). In contrast, all the *E. coli* isolates from water samples in France lacked

the *stx* virulence genes (Madec *et al.* 2016). Five of the six identified serotypes (O26:H11, O91:H21, O103:H2, O128:H2, and O45:H0) were identified as STEC. Serogroups O26, O91 and O103 are very common in ruminants and have been implicated in human clinical cases (Hussein 2007). Additionally, the O26:H11 serotype was associated with a water-borne STEC outbreak in Japan that was linked to contamination of a source water with cattle manure (Hoshina *et al.* 2001). Thus our findings highlight the potential role of animals as sources of water contamination with zoonotic STEC in the study region. This finding is consistent with previous studies that reported the important role of animals and the associated zoonotic pathogens in the contamination of water sources, especially in rural dwellings (Hoshina *et al.* 2001; Schriewer *et al.* 2015).

Twenty-one *E. coli* isolates (87.5%) were resistant to at least one antimicrobial agent, which was higher than the values in other reports (8.9–46.9%) from Tanzania (Lyimo *et al.* 2016) and France (Madec *et al.* 2016). Multi-drug resistance to three or more classes of antibiotics was recorded for 15 (62.5%) isolates. This value was higher than that in a previous report (42%) from Turkey (Ozgumus *et al.* 2007) but lower than that in a report (100%) from India (Pathak & Gopal 2008). The *E. coli* isolates exhibited high resistance rates (58.3–83.3%) for streptomycin, nalidixic acid, sulphamethoxazole/trimethoprim, and tetracycline. These findings were comparable with those of previous reports (Pathak & Gopal 2008; Lyimo *et al.* 2016; Egervärn *et al.* 2017); however, Ozgumus *et al.* (2007) reported relatively low tetracycline resistance (15%). In this study, the lowest resistance rates (16.6–25%) were observed for gentamicin, ciprofloxacin, and kanamycin. Consistent with this finding, low resistance to kanamycin (Lyimo *et al.* 2016; Egervärn *et al.* 2017), ciprofloxacin (Lyimo *et al.* 2016) and gentamicin (Ozgumus *et al.* 2007; Egervärn *et al.* 2017) have been previously reported.

Among beta-lactam antibiotics, 33.3 and 50% of the detected *E. coli* isolates exhibited resistance to ampicillin and cefotaxime, respectively. Lyimo *et al.* (2016) reported a comparable rate of ampicillin resistance; however, a higher rate was recorded by Ozgumus *et al.* (2007). Our findings were also higher than the value reported by Madec *et al.* (2016), who recorded a much lower rate (4.5%) of beta-lactam resistance. Seven (29.2%) *E. coli* isolates harboured at least one of the ESBL genes. The bla_{TEM}, bla_{SHV} and bla_{CTX} genes were detected in 16.6–25% of the *E. coli* isolates. The three ESBL genes detected have been previously detected at varying rates in *E. coli* from water sources worldwide (Lyimo *et al.* 2016; Madec *et al.* 2016; Egervärn *et al.* 2017). There was a significant association between resistance to beta-lactam antibiotics (ampicillin and cefotaxime) and ESBL genes in the examined *E. coli* isolates ($P = 0.002$ to >0.0001). This result was consistent with the findings of Egervärn *et al.* (2017), who reported resistance to all beta-lactams for *E. coli* with ESBL genes. STEC isolates were significantly more likely to resist six of the examined antibiotics than non-STEC isolates ($P = 0.03$ to >0.0001). Consistent with his observation, STEC isolates were seen to be positively associated with resistance to penicillins, cephalosporins, and tetracyclines in a previous report from Egypt (Elmonir *et al.* 2018). Interestingly, seven (29.2%) MDR-STEC isolates belonging to four serogroups (three O26, two O128, one O103, and one O91) harboured both *stx* and ESBL genes. There was no significant difference between tap and well water *E. coli* isolates in terms of the detection frequencies of ESBL genes ($P = 0.2$) and STEC genes ($P = 0.7$), indicating that both sources can pose a health risk for human or animal consumers.

In Egypt, many residents utilize tap and well water directly without any further treatment for many purposes such as consumption, cooking, washing, and also as a water source for their livestock. The presence of the recorded high risk MDR-STEC pathogens in these water sources will increase the chances of transmission of these pathogens to human or animal consumers in the study region. This potential transmission possesses an alarming public and animal health risk as MDR-STEC pathogens are not only able to cause serious illness but also are difficult to treat.

CONCLUSIONS

This study recorded high rates of contamination of potable water with coliforms and *E. coli* in the study region. One-third of the *E. coli* isolates were STEC, and the majority were MDR. Thus, our findings highlight the high health risk for population and livestock in the study region.

Extended surveillance, tracing of contamination sources in distribution systems and assessment of water treatment efficiency are urgently required for community safety in the study region.

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CONFLICT OF INTEREST

The authors declare that they have no conflicts of interest.

SUPPLEMENTARY MATERIAL

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