

Poster #1113 High antibiotic resistance patterns of *Escherichia coli* in hospital wastewater in Nicaragua



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Abstract

Antibiotic resistant bacteria have emerged by the selective pressure of antimicrobial use in humans and animals. Water plays an important role for dissemination of these organisms among humans, animals and the environment. We studied the antibiotic resistance patterns among 493 *Escherichia coli* isolates from different aquatic environmental sources collected through October 2008 to May 2009 in León, Nicaragua. High levels of antibiotic resistance were found in *E. coli* isolates in hospital sewage water and in 8 of 87 well water samples. Among the resistant isolates from the hospital sewage, ampicillin, chloramphenicol, ciprofloxacin, nalidixic acid and trimethoprim-sulfamethoxazole was the most common multi-resistance profile. Among the resistant isolates from the wells, 19% were resistant to ampicillin, ceftazidime, ceftriaxone, cefotaxime, chloramphenicol, ciprofloxacin, gentamicin, nalidixic acid and trimethoprim-sulfamethoxazole. *E. coli* producing ESBL and harbouring the genes for CTX-M enzymes were detected in one of the hospital sewage samples and in 26% of the resistant isolates from the well water samples. CTX-M-9 group was more prevalent in *E. coli* isolates from the hospital sewage samples and CTX-M-1 group in the well water samples. CTX-M-1 group was mainly detected in one clone in the well water samples and CTX-M-9 group in one clone from the hospital sewage samples.

Introduction and purpose

The emergence of antibiotic resistant bacteria presents a major threat to public health because it reduces the effectiveness of antibiotic treatment, leading to increased morbidity, mortality and health care expenditure. Resistant bacteria found in the aquatic environment may disseminate among the population and the genes conferring resistance may be introduced in the natural bacterial ecosystems. The aim of this study was to determine the antibiotic resistance patterns of *Escherichia coli* isolates from different aquatic environmental sources in León, Nicaragua.

Results

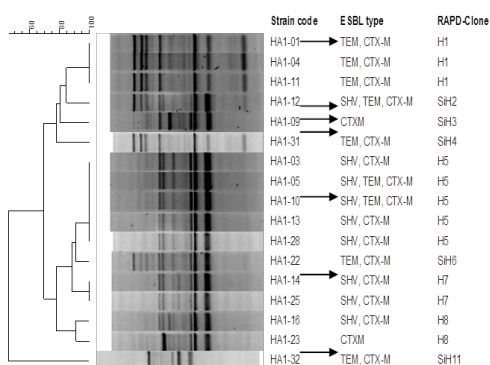


Figure 1. Clonal similarity of *E. coli* from the hospital sewage water sewage by RAPD PCR

Methods

Antibiotic resistance patterns were studied among 493 *E. coli* isolates from different aquatic sources collected through October 2008 to May 2009 (i) household drinking water (n= 20); (ii) well water used for consumption (n= 87); (iii) sewage water from two municipal sedimentation treatment plants (two samples of each influent and effluent, n=8) and (iv) from the sewage effluents of the main hospital in the city (n= 3) in León, Nicaragua.

The following antibiotics were tested: ampicillin, amoxicillin-clavulanic acid, cefotaxime, ceftazidime, ceftriaxone, ciprofloxacin, chloramphenicol, gentamicin, nalidixic acid and trimethoprim-sulfamethoxazole by the agar dilution method.

Phenotypic detection of extended-spectrum beta-lactamase (ESBL) was analysed using the Etest® system.

All ESBL positive *E. coli* strains were screened for the resistance genes by PCR. To identify the beta-lactamase genes, sequencing was performed.

	n(%)	
	HSW (n=32)	WW (n=46)
SHV	17 (53)	10 (22)
TEM	14 (44)	-
OXA	-	26 (57)
CTX-M-1 group	11 (34)	34 (74)
CTX-M-9 group	21 (65)	12 (26)

Table 1. Beta-lactamase gene prevalence in *E. coli* isolates from waste water

High levels of antibiotic resistance were found (Figure 1 and Table 1) in *E. coli* Isolates in all hospital sewage water (HSW) samples and in 8 of 87 well water (WW) samples.

Among the resistant isolates from the hospital sewage, ampicillin, chloramphenicol, ciprofloxacin, nalidixic acid, trimethoprim-sulfamethoxazole showed the most common multi resistance profile. *E. coli* producing ESBL and harbouring the genes for CTX-M enzymes were detected in one of the hospital sewage samples and in 26% of the resistant Isolates from the well water samples.

CTX-M-9 group was more prevalent in *E. coli* isolates from the hospital sewage samples and CTX-M-1 group in the well water samples.

Conclusion

The presence of antibiotic resistant *E. coli* strains was frequent in the environmental water samples. Isolates carrying the CTX-M group of enzymes have become one of the main public health concerns due to their ability to be involved in nosocomial and community acquired infections. In the present study, it was found that CTX-M-15 and CTX-M-9 were the specific beta-lactamases present in the *E. coli* isolates. Our results suggest that multi-resistant ESBL-producing *E. coli* are widely spread in hospital sewage water and in some well water samples in Nicaragua.

References

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