

Multidrug resistance in quinolone-resistant *Escherichia coli* isolated from drinking water from the Southeast region of Brazil

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The low microbiological quality of water is associated with an annual mortality rate of about 3 million people worldwide. Among the agents of waterborne diarrheal disease diarrheagenic *Escherichia coli* pathotypes should be highlighted. The species harbors a remarkable phenotypic and genotypic diversity including highly heterogeneous antimicrobial drug resistance profiles. Quinolones (mainly fluoroquinolones) are one of the most commonly prescribed classes of antimicrobial drugs and are largely excreted as active compounds (either unchanged or as an active metabolite). These drugs act as “pseudo-persistent” and immobile compounds and seem to exert a relevant selective pressure in environments such as hospital effluents, sewage sludge, and rivers. Furthermore, a frequent association between ciprofloxacin resistance and multidrug-resistant (MDR) phenotypes suggest that quinolone-resistant bacteria may represent one of the major targets of selective pressure in the environment. Thus, aquatic environments may act as a hot spot for selection of resistance markers and also as a route for dissemination of antimicrobial resistant microorganisms among human populations. This study targeted the investigation of aspects related to antimicrobial drug resistance in *E. coli* isolates (n = 423) obtained from drinking water in the Southeast region of Brazil. Evaluation of the antimicrobial susceptibility profile was performed by disk diffusion and PCR was employed to search for integrons and gene cassettes. The results indicated that 146 (34.5%) isolates showed resistance to at least one antimicrobial drug and among them 35 (24.0%) expressed resistance to some quinolone. The majority of quinolone-resistant isolates (24/68.6%) were classified as multidrug-resistant and two (5,7%) of them presented positive results for class 1 integrons, clinical class 1 integrons, and gene cassettes. Data generated showed that drinking water in the studied locations still poses a threat to public health, considering the selection and dissemination of microorganisms carrying resistance genes and genetic elements associated with the expression of antimicrobial resistance and reinforced the idea that genes coding for quinolone resistance are important targets of this selective pressure. Thus, people in general, mainly children, the elderly, and patients under medical care that consume these waters are at risk considering their low microbiological quality.

Keywords: drinking water, *Escherichia coli*, multidrug resistance, quinolone resistance

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