

Identification of Associated-Virulence Genes in Quinolone-Resistant *Escherichia coli* Strains Recovered from an Urban Wastewater Treatment Plant

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Abstract : Objective: It has often been reported an association between antibiotic resistance and virulence. However, resistance to quinolones seems to be an exception, it tends instead to be associated with an attenuation of virulence, particularly in clinical strains. The purpose of this study was to evaluate the potential virulence of 28 quinolone-resistant *E. coli* strains recovered from water at the inflow (n=16) and outflow (n=12) of an urban wastewater treatment plant (WWTP). Methods: *E. coli* isolates were selected on Tergitol-7 agar supplemented with 2µg/ml of ciprofloxacin, they were screened by PCR for 11 virulence genes related to Extraintestinal pathogenic *E. coli* (ExPEC): papC, papG, afa/draBC, sfa/foc, kpsMTII, iutA, iroN, hlyF, ompT, iss and traT. The phylogenetic groups were determined by PCR and clonal relationship was evaluated by ERIC-PCR. Results: Genotyping by ERIC-PCR showed 7 and 12 DNA profiles among strains of wastewater (inflow) and treated water (outflow), respectively. Strains were assigned to the following phylogenetic groups: B2 (n = 1, 3.5%), D (n = 3, 10.7%), B1 (n = 10, 35.7%) and A (n = 14, 50%). A total of 8 virulence-associated genes were detected, traT (n=19, 67.8%), iroN (n= 16, 57.1%), hlyF (n=15, 53.5%), ompT (n=15, 53.5%), iss (n=14, 50%), iutA (n=9, 32.1%), sfa/foc (n=7, 25%) and kpsMTII (n=2, 7.1%). Combination of virulence factors allowed to define 16 virulence profiles. The pathotype APEC was observed in 17.8% (D=1, B1=4) and human ExPEC in 7% (B2=1, D=1) of strains. Conclusion: The study showed that quinolone-resistant *E. coli* strains isolated from wastewater and treated water in WWTP harbored virulence genes with the presence of APEC and human ExPEC strains.

Keywords : *E. coli*, quinolone-resistance, virulence, WWTP

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