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P03 Prevalence and molecular characterization of CTX-M-producing *Escherichia coli* isolates from wastewaters of a couple slaughterhouse / wastewater treatment plant

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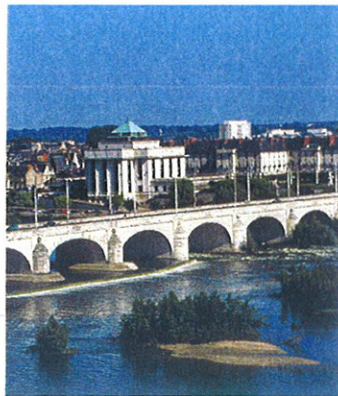
The emergence and spread of Extended-Spectrum Beta-Lactamase (ESBL)-producing *Enterobacteriaceae* is an increasing threat for human health. We investigated the prevalence of ESBL-producing *Escherichia coli* in effluents of a municipal wastewater treatment plant (WWTP): input effluent from the slaughterhouse, input effluent from the city and output treated effluent. Six campaigns of sampling were performed at two-months intervals. Cefotaxime and/or ceftazidime resistant (C3G-R) *E. coli* were looked for and a total of 318 C3G-R isolates were selected. ESBL production was screened by using the double-disk synergy test and ESBL Etest. *bla*_{CTX-M} genes were detected by PCR and sequencing.

The prevalence of C3G-R *E. coli* among total *E. coli* was lower than 3% and 174 of the 318 selected isolates were confirmed to produce ESBL. Among the ESBL-producing isolates from wastewater of the slaughterhouse (n=55), *bla*_{CTX-M} genes identified were *bla*_{CTX-M-1} (n=44), *bla*_{CTX-M-15} (n=8) and *bla*_{CTX-M-14} (n=1). Among the isolates from wastewater of urban origin (n=46), *bla*_{CTX-M} genes identified were *bla*_{CTX-M-1} gene (n=16), *bla*_{CTX-M-15} (n=14), *bla*_{CTX-M-32} (n=2), *bla*_{CTX-M-3} (n=1), *bla*_{CTX-M-14} (n=1) and *bla*_{CTX-M-2} (n=1). In the WWTP output effluent, the *bla*_{CTX-M} genes distribution was similar to that shown in the urban input effluent.

Pulsed-Field Gel Electrophoresis (PFGE) was used to establish genetic relatedness of CTX-M-producing *E. coli* isolates from input effluents. Among 50 PFGE patterns identified, 34 included a single clone, and the others included two or more genetically indistinguishable isolates. The majority of these isolates transferred a large plasmid (~120 bp) together with the co-transfer of ESBL genes, by in vitro conjugation.

The present study showed that CTX-M-producing *E. coli* isolates were present in wastewaters from animal and human origin in the same WWTP. PFGE analysis showed the polyclonal spread of CTX-M-producing *E. coli* in human and animal ecosystem. The analysis of plasmid should help us to explore the possibilities of exchange of plasmids between these ecosystems.

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