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Y-054. Extended Spectrum Beta-Lactamase Producers at Wastewater Treatment Plant

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Background: The aim of this study was the detection of extended-spectrum *β-lactamases* (ESBL) producing *Enterobacteriaceae* at an urban wastewater treatment plant setting. Our previous work, showed contamination of urban sewage impacted by hospital discharges, with antimicrobial resistant bacteria, namely ESBL producers. This question alerted us to the fate of this contamination. In that way, it was our purpose to look for ESBL producers before, during and after wastewater treatment. **Methods:** Wastewater samples were collected bimonthly in the last trimester of 2005, upstream the wastewater treatment plant, after biological treatment and downstream final u.v. treatment. Isolates were selected by sample spreading and by membrane filtration on Mac Conkey agar and Mac Conkey agar with ceftazidime (2 mg/l) or cefotaxime (2 mg/l). Colonies of lactose fermenters were randomly selected and screened for ESBL production, by the double disc synergy test and by addition of clavulanic acid to cefotaxime and ceftazidime discs, according to the CLSI guidelines. Identification of the selected strains was achieved by classic biochemical tools and ID 32 GN. Susceptibility to antimicrobial agents was determined according to the CLSI. *β - lactamases* were characterized by isoelectric focusing. Conjugation experiments were done in order to study transferability of ESBL genes. **Results:** Sewage treatment is very effective in coliform counts reduction, nevertheless ESBL producers were found upstream, after biological treatment and at the final effluent. A total of 28 samples were studied. From 80 isolates screened, 40 produced ESBLs of different pIs, alone or in association with other *β -lactamases*. Transference of the ESBLs of pI 5,6, 5,9, 8,2, 8,4, genes, by conjugation, was achieved in 7 isolates. **Conclusions:** The input of ESBL producers to natural environments and the transferability of the ESBL genes, by conjugation, might provide a track for environmental dissemination of resistant bacteria and genes that may create a source of transferable traits for environmental bacteria, influencing natural reservoirs of resistance.