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BOOK OF ABSTRACTS



11. Environmental Microbiology and Biotechnology

FP3. Characterization of multi-drug resistant *Escherichia coli* in the UV-treated outflow of an Urban Wastewater Treatment Plant

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Wastewater Treatment Plants are sources of antibiotic resistance into aquatic environments, contributing to the spread of clinically-relevant antibiotic-resistant bacteria. The disinfection (e.g. UV-C irradiation) of the final effluent is a promising strategy to circumvent this problem. However, some clinically-relevant resistant bacteria are known to survive disinfection. In this work we characterized *Escherichia coli* strains isolated from a UV-C-treated wastewater effluent, aiming to infer possible human health risks associated with these effluents.

Multi-drug resistant (MDR) *E. coli* isolates (n=25) were genotyped (fingerprinting, Multi Locus Sequencing Typing and Clermont phylo-groups). Antibiotic resistance and virulence genes (ARGs and VG) were PCR-screened and plasmid transfer was assessed by mating assays. Cytotoxicity and invasion into mammalian cells were determined. The genome of 6 isolates was sequenced, and their survival in freshwater microcosms was evaluated.

Genotyping distributed the strains into 3 groups, corresponding to phylogroups B2-sgl (n=7 isolates), A (n=16) and C (n=2). Based on MLST analyses phylogroup B2 strains were classified as ST131, C strains as ST410, and A as ST155 (n=4), ST58 (n=1), ST453 (n=2), ST617 (n=2), ST744 (n=1), ST1284 (n=3), or as a novel ST (n=3). Nine of the 18 PCR-screened ARGs were detected: *sul1* (n=15 isolates), *sul2* (n=15), *tet(A)* (n=14), *blaOXA-1-like* (n=8), *tet(B)* (n=8), *aacA4-cr* (n=5), *aacA4* (n=2), *sul3* (n=2) and *qnrS1* (n=1). No VG were detected by PCR. Conjugal transfer of cefotaxime resistance was confirmed in 8/25 strains, in some cases yielding MDR phenotypes. Nine strains were significantly more cytotoxic than the positive control, and 10/21 strains were capable of internalization into Vero cells. Whole genome analysis evidenced the presence of additional ARGs (e.g. *catB3*, *aadA2*, *strA*, *strB*) and of VG encoding toxins, siderophores, and adhesion and invasion factors. After 28 days of incubation in freshwater microcosms, 4 strains were still detected by cultivation and/or qPCR.

This study demonstrates that MDR *E. coli* can survive UV-wastewater disinfection, maintain resistance and gene transfer capacity and, eventually, persist in freshwater environments. These evidences support the hypothesis that even disinfected wastewater, if not adequately controlled, may represent a risk for human health.

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