

Genomics and Systems Biology and Emerging Technologies

P-141 - ANTIBIOTIC-RESISTANT *E. COLI* IN AN UV-TREATED EFFLUENT: TROUBLED WATERS AHEAD?

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Background

Urban wastewater treatment plants (UWTP) are unable to effectively eliminate antibiotic resistance genes (ARGs) and antibiotic-resistant bacteria (ARB), thus important pathways for the dissemination of resistance into aquatic systems. Disinfection, e.g. UV irradiation, might be useful in containing such contaminants, though low amounts of ARGs and ARB still persist in the final effluent. Therefore, it is a priority to assess potential risks associated with the bacterial populations in UWTPs outflow.

In this work, we assessed antibiotic resistance and virulence features of cefotaxime-resistant *E. coli* strains that survived UV treatment.

Method

Non-clonal *E. coli* isolates (n=25) were obtained from the final effluent of a UWTP which included a UV-based tertiary treatment. Phylogroup determination and multilocus sequence typing (MLST) were conducted, followed by PCR screening of ARGs, virulence factors and characterization of integrons content. Plasmid DNA purification and replicon typing were performed, followed by mating assays. Illumina-based genome sequencing was performed for 6 selected isolates.

Results & Conclusions

Most of the 25 *E. coli* strains were multidrug resistant (80%) and harbored *bla*_{CTX-M-15} (n=15), *bla*_{CTX-M-27} (n=4), *bla*_{CTX-M-32} (n=4) or *bla*_{CTX-M-1} (n=2). PCR screening for other ARGs yielded positive results for *bla*_{OXA-1-like} (n=8), *qnrS1* (n=10), *sul1* (n=15), *sul2* (n=15), *sul3* (n=2), *tet(A)* (n=14) and *tet(B)* (n=8). Plasmid DNA was purified from all isolates and restriction analysis resulted in 16 distinct plasmid profiles. *IncF* (n=22), *IncFIB* (n=17), *IncFIA* (n=14) and other six replicons (*Incl1*, *IncP*, *Incl2*, *IncN*, *IncB/O* and *IncX4*) were identified. Mating assays yielded transconjugants for 8 donor strains and co-transfer of tetracycline, gentamicin and sulfamethoxazole/trimethoprim resistance was observed. Strains were affiliated with phylogroups A (n=16), B2 (n=7) and C (n=2). MLST affiliated the strains to ST58 (n=1), ST131 (n=2), ST410 (n=1), ST453 (n=2), ST6897 (n=4), ST1284 (n=1) or unknown MLST types (n=14). *In silico* analyses of selected genomes (n=6) predicted all strains as potential human pathogens. and revealed 4 different serotypes as well as intrinsic and acquired resistance mechanisms previously unidentified by PCR. A variety of virulence factors such as *iss* (n=5), *gad* (n=4), *ipfA* (n=3) and many others (*sat*, *iroN*, *cma*, *iha*, *capU*, *astA*, *senB* and *mchF*) were also observed in these isolates.

UV-surviving strains were shown to possess determinants involved in pathogenicity, antimicrobial resistance and plasmid transfer, highlighting the need for improvements of wastewater disinfection to mitigate the risks associated with UWTP discharge.

Keywords: Urban wastewater treatment plants, UV-C radiation, Extended-spectrum beta-lactamases, *Escherichia coli*