

EP0277

ePoster Session

Travel medicine and international health

Sewage treatment plants cause artificial selection of ESBL-producing *E. coli* threatening public health

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Background: As members of gut microbiome, *E. coli* strains are continually released into the municipal sewage systems via defecation. These strains can have a chance to gain resistance genes via mobile genetic elements leading to emergence of multi-drug resistant strains such as ESBL-producing *E. coli* (ESBLEC) due to the favorable environment of wastewater. ESBLEC are found diversely within the community and hospital environment therefore it has a convoluted epidemiology. Quantitative data about ESBLEC at the inlet and the outlet of community sewage treatment plants (STPs) are scarce, especially in developing countries. These data could be useful to raise awareness about the potential risk of spreading ESBLEC strains in the community. Thus, we analyzed the ESBLEC population and their characteristics at one urban and one rural wastewater treatment plants in Turkey.

Material/Methods: 40 samples were collected weekly over a 10-week period, from the inlet and the outlet of one urban (serving 1×10^7 people and several industrial areas, animal husbandry, hospitals) and one rural (serving 2×10^4 people, without hospital settings) STPs using different treatment techniques. Total *E. coli* and ESBLEC loads were determined for each sample using a membrane filtration system. A collection of 473 ESBLEC isolated from the waste and the treated water samples and they were tested for their resistance to selected antimicrobials. Phylogenetic grouping of these strains were determined using PCR. Representative strains were further tested for the presence of TEM-type, SHV-type, CTX-M-type and OXA-type genes by PCR.

Results: The *E. coli* load was similar in urban and rural untreated wastewater (220000 ± 177828 vs 222600 ± 150421 CFU/mL, respectively) as well as treated water (1071 ± 1013 vs $1096 \pm 1303,2$, respectively). ESBLEC was accounted for 0.58% and 0,12% of the total *E. coli* in urban and rural untreated wastewater respectively. For the treated wastewater, these rates were 0.95% in urban and 0,68% in rural STPs. Treatment process in urban STP eliminated 97,03% of total ESBLEC whereas this rate was 94.03% in rural sewage treatment system. The ratios of resistant strains in both treated wastewater were higher compared to the strains from untrated waste water samples for certain antimicrobials. According to phylogenetic grouping the most common phylogenetic groups were C composing 25.6% of the whole strains, followed by A (24%), B2 (19.9%). CTX-M-type found to be the most common ESBL gene among strains tested.

Conclusions. Municipal waste water receives microbial as well as antimicrobial contribution from several sources including hospitals and animal husbandries. The treatment of these media without microbiological elimination process leads to relative enrichment of ESBLEC. Thus, artificial selection of ESBLEC may have a chance to find their way to reach communities through environment raising public health risk.

