Title: EVALUATION OF RESISTANT *ESCHERICHIA COLI* PATHOTYPES ISOLATED FROM PUMP STATION IN RIO DE JANEIRO, BRAZIL

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Abstracts:

The human intestines, as well as for other animals, provide an important reservoir for Gram-negative bacilli, including pathogenic and resistant *Escherichia coli* strains, involved with diarrheiogenic diseases. The frequency of pathogenic and antimicrobial-resistant isolates has increased dramatically in the environment, as a consequence of the wide use of these drugs in hospitals and community, as well as in veterinary and, agriculture activities. Over the last decades, the quality of hydric resources used for human consumption and leisure activities has been of great concern to public health, and it has presented visible signs of degradation. In the present study 98 *E. coli* strains isolated from wastewaters sources were collected by Moore's swabs from two different Pump Stations in Rio de Janeiro City between May and July 2013. All strains were submitted to biochemical identification, evaluated for virulence genes *lt, st, ial, stx1, stx2, eagg* and *eaeA* by PCR and, the resistance profiles were determined using the disk diffusion method according to CLSI using 12 antimicrobial drugs representative of seven classes. The prevalence of strains with virulence factors and antimicrobial resistance was higher in June and July than May. Overall, the highest percentages of resistance (AMR) were observed to Streptomycin (33,7%), Tetracycline (22.4%) Nalidixid acid (11.2%) and Ampicillin (11.2%). The resistance in Enterobacteriaceae has been mostly attributed to modifications in the QRDR of different genes and/or PMQR determinants such as *qnr* and [*aac(6')*-Ib-cr], and integrons. MDR profile was observed in 12 strains (12.2%). One strain (1%) was resistant to Gentamicin and, two strains (2%) to Cefoxitin. In the PCR assays, 25 strains (25.5%) showed amplification products, 11 strains (44%) to *st* gene, 10 strains (40%) to *eae*A gene and four strains (16%) to *lt* gene. The relationship between AMR and virulence genes was observed in seven strains (28%) with higher prevalence in July. The selection of resistant microorganisms in nature may be due not only to the production of these compounds by soil bacteria, but also by the elimination of human and animal faeces. The data point is the same of the population profile which had been circulated during the vacation time and showed the importance of continuous monitoring of wastewater discharge into the environment to evaluate the introduction of strains which export their virulence and resistance characteristics.

keiwords: antimicrobial resistance, *Escherichia coli*, pathotypes, pump station, sewage.