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Phylogenetic diversity of quinolone resistant *Escherichia coli* isolated from wastewaters

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Antibiotic resistance dissemination has become more important in the last decades. The species *Escherichia coli* comprises different subgroups which may have different roles in antimicrobial resistance dissemination. In previous studies, wastewater treatment was observed to promote an increase on quinolone resistance, presumably due to the differential removal rates of distinct genotypic groups (Figueira et al., 2011). The current work aimed at investigating the relationship between quinolone-resistance genes and the phylogenetic group of the bacteria. Seventy *Escherichia coli* strains isolated from raw and treated municipal wastewaters were characterized based on a multi locus sequence typing (MLST) approach. The presence of quinolone resistance determinants was assessed based on the detection of mutations in the *gyrA* and *parC* genes and on the presence of the genes *qnrA*, *qnrB*, *qnrS*, *aac6*, *qepA*, *qnrC*. The distribution of the MLST groups and the type of quinolone resistance genetic determinants is discussed.