TITLE: International high-risk clones of *Escherichia coli* carrying *qnr* genes in Brazil

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ABSTRACT:

The misuse of antibiotics has a decisive role in the continuous growth of global levels of antimicrobial resistance, and its importance is highlighted by the difficulty in developing new antibiotic agents. *Escherichia coli* is one of the most prominent multiresistant bacteria, due to its low susceptibility to a wide range of antibiotics, including highly prescribed drugs such as fluoroquinolones, widely used for the treatment of urinary tract infections. In this scenario, the best understanding of how bacteria develop and maintain their resistance mechanisms is crucial. Multilocus Sequence Typing (MLST) is a molecular typing technique, based on an on-line and global database, that allows the analysis of bacterial phylogeny, and so, the gain of a greater knowledge of the bacterial evolutionary dynamics, using the Sequence Type (ST) of each isolate. The *housekeeping* genes of three *qnr-carrying Escherichia coli* strains were sequenced and deposited in the MLST database, and so, the strains were assigned as ST10 (n = 2) and ST131 (n = 1), which ones correspond to about 6% and 3% of all allelic profiles identified in Brazil, respectively. By the use of the eBURST algorithms, ST10 and ST131 were identified as founding genotypes of their corresponding groups and were correlated to others sequence types of Brazilian strains. Despite of the Brazilian data shortage related to *qnr-carrying E. coli* strains characterized by MSLT, this study evidenced the presence of pandemic sequence types associated to that kind of resistance mechanism and to strains isolated from inpatients and patients with community-acquired urinary tract infection. Furthermore, new data from Brazilian strains were inserted in a global scenario.

KEYWORDS: *Escherichia coli*, MLST, antimicrobial resistance, *qnr* genes, ST 10, ST 131.