

EVALUATION OF THE CIRCULATION AT RESISTANT PATHOTYPES OF *Escherichia coli* IN BRAZIL BETWEEN 2017 AND 2018

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ABSTRACT:

Escherichia coli are a genetically heterogeneous and continuously evolving group of bacteria. Most strains are commensal, however, some have been implicated in a wide range of diseases affecting humans and animals worldwide, such as diarrheogenics *E. coli* (DEC), which express different mechanisms of virulence according to the pathotype. We sought to evaluate the presence of virulence-specific markers in 914 strains of *E. coli*, isolated from human sources (553), animals (268), environmental (18) and foods (80), received by LRNEB / IOC / FIOCRUZ for conclusive diagnosis, between Jan / 2017 and Dec / 2018. The strains were submitted to biochemical identification, evaluated by Polymerase Chain Reaction - PCR for the presence of the virulence genes *lt*, *st*, *ial*, *stx1*, *stx2*, *eagg* and *eaeA* and resistance profiles were determined in 791 strains, through the diffusion disc technique, according to CLSI, using 12 representative antimicrobials of seven classes. In general, the highest percentages of virulence were observed for the *st* (4.9% - 45 strains), *eagg* (3% - 27 strains) and *eaeA* (1.4% - 13 strains) genes, while the highest percentages of resistance were observed for AMP (34.8% - 275 strains), TCY (30.1% - 238 strains), SXT (28.4% - 225 strains), STR (27.9% - 221 strains) and NAL (24.6% - 195 strains). A multidrug resistance (MDR) profile was observed in 224 strains (28.3%), 65.2% isolated from human sources, with 9.6% showing some virulence gene, 19.6% from animal origin with 9.1 % presenting some virulence gene and 15.2% isolated from foods. The constant evaluation of diarrheogenics agents using classical and molecular laboratory methods of subtyping, such as the determination of antimicrobial susceptibility profiles and the genotypic characterization of virulence, favors better monitoring and represents an important epidemiological measure of prevention.

Keywords: diarrheogenics *Escherichia coli*, mechanisms of virulence, antimicrobial resistance