

TITLE: Molecular characterization of multidrug-resistant CMY-producing *Escherichia coli* obtained from a swine farm

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ABSTRACT:

Diarrheagenic *Escherichia coli* (DEC) cause diarrheal diseases, a public health problem, and are classified into different well-defined pathotypes. Multidrug-resistant (MDR) bacteria have become a global public health problem since are already disseminated in several sources, including animal and environment and DEC MDR have been reported worldwide. The objective of this study was to characterize MDR *E. coli* isolates obtained from a swine farm regarding to acquired antimicrobial resistance genes (ARGs), plasmids, diarrheagenic virulence genes, phylogenetic groups, genetic relatedness, sequences types, and *fimH*-type. *E. coli* isolates were obtained using fecal and soil samples from a swine farm and 34 antimicrobials were tested. Acquired ARGs, plasmids, diarrheagenic virulence genes and phylogenetic groups were determined by PCR. Pulsed-field gel electrophoresis (PFGE), Multilocus sequence typing (MLST) and sequencing of the *fimH* gene were used for determining the genetic relatedness, sequences types (ST) and *fimH*-type, respectively. A total of 17 MDR *E. coli* isolates were obtained. These isolates presented several acquired ARGs (*bla*_{CMY}, *bla*_{SHV}, *bla*_{OXA-1-like}, *aadA*, *aac*(6')-Ib, *aph*(3')-Ia, *tetA*, *tetB*, *sul1*, *sul2*, *sul3*, *cmlA* and *floR*) and plasmids (IncF, IncFIA, IncFIB, IncFIC, IncY, IncHI1, IncN and ColE-like). Mutations in the quinolone-resistance determining region of GyrA (Ser83Leu; Asp87Asn) and ParC (Glu84Asp) were also detected. Diarrheagenic virulence genes (*ipaH*, *stx2*, *aaiC*) were found, which belong to Enteroinvasive *E. coli* (EIEC), Shiga toxin-producing *E. coli* (STEC) and Enteroaggregative *E. coli* (EAEC), respectively. The majority of isolates was classified as phylo-group A, followed by Unknown and B1. PFGE results showed high genetic diversity (33.6% to 64.7%) and MLST analyses revealed several STs (10, 56, 761, 942, 1634, 1684, 1716, 2394, 2491, 2600, 3274, 4055, 6217, 6396, 7424, 6658, 8067). Subtyping using the *fimH* gene showed different *fimH*-type (23, 25, 54, 86, 566, 946). This study reports high genetic diversity of MDR *E. coli* carrying several acquired ARGs belonging to EIEC, EAEC and STEC pathotypes, which is of concern.

Keywords: DEC; *Escherichia coli*; MDR; Soil; Swine.

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