

TITLE: GENOTYPIC AND PHENOTYPIC VIRULENCE POTENTIAL OF A MULTIDRUG-RESISTANT *ESCHERICHIA COLI* ST101 STRAIN BELONGING TO PHYLOGROUP B1 CAUSING BLOODSTREAM INFECTION

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ABSTRACT

The *Escherichia coli* EC121 strain is a multidrug-resistant (MDR) pathogen isolated from bloodstream infection. Differently from the majority of extraintestinal pathogenic *E. coli* (ExPEC) strains, it belongs to phylogenetic group B1 and harbors few known virulence factors that are associated with ExPEC pathogenicity. This work aimed to verify the virulence potential of EC121 as a real ExPEC strain. Whole genome sequencing (WGS) of EC121 was performed using Illumina™ platform, reads were assembled with SPAdes and analyzed *in silico* using online bioinformatic tools. The ability to adhere to biotic and abiotic surfaces and to survive against serum complement was also evaluated *in vitro*. The WGS analyses revealed that EC121 harbors about 50 complete virulence genetic clusters associated with host colonization, escape from the immune system, intracellular spread and resistance, and iron acquisition systems. Interestingly, the virulence genes detected were associated with pathogenicity of both diarrheagenic *E. coli* (DEC) and ExPEC pathotypes. The EC121 strain belongs to ST101 and harbors 14 antimicrobial resistance (AMR) genes, including *bla*_{CTX-M-2}, all of them located in high molecular mass plasmids. Moreover, comparative analysis of 206 genomes belonging to the ST101 complex, most of them deposited in the NCBI, showed that 75% (n=155/206) were MDR and 10% (n=17/206) were pandrug-resistant (PDR) strains. Besides, 28% of such strains were isolated from infections, being 16.5% from human extraintestinal infections. Phenotypically, the EC121 strain was able to adhere to and to invade intestinal and bladder cell lineages (Caco-2 and T24, respectively), to form biofilm on abiotic surfaces, and was resistant to the serum. Few studies focused on characterization of virulence factors among strains that do not fit in the classical ExPEC definition and that are usually considered opportunistic pathogens. In fact, most of the strains sequenced belonging to ST101 complex were MDR isolates, being recovered from microbiota, retail food, and environment. However, the phenotypic and genotypic profile of EC121 revealed that its isolation from an extraintestinal infection was not by chance, since it has the capacity to resist to human serum and to adhere and invade bladder cells. We, therefore, demonstrated its full potential to be an ExPEC strain rather than an opportunist pathogen.

Keywords: *Escherichia coli*; virulence; multidrug-resistant; ExPEC, ST101.

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