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## Genome Note

Draft genome sequence of a CTX-M-15-producing *Escherichia coli* ST345 from commercial chicken meat in Brazil

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## ABSTRACT

*Escherichia coli*, the main host of the CTX-M-15 extended-spectrum  $\beta$ -lactamase (ESBL) enzyme, is widely distributed and exchanged between the environment, animals and humans. Therefore, identification of *bla*<sub>CTX-M-15</sub>-positive lineages in food has a significant impact on public health. In this regard, until the end of 1990s, ESBL-producing isolates were mainly associated with hospital-acquired infections, with a predominance of SHV- and TEM-type enzymes. In recent years, a new trend has been observed among ESBL-producers, where most isolates now harbour CTX-M-type, being further isolated from community-acquired infections. Nowadays, CTX-M-15 has been recognised as the most important ESBL variant, invading virtually all human and animal compartments, leading to a global pandemic. Thus, whilst the rapid emergence and dissemination of CTX-M-15 among *E. coli* isolates has generated a large genetic reservoir from which other members of the Enterobacteriaceae family can easily acquire this resistance gene, there are an increasing number of new reservoirs and transmission mechanisms that must be investigated. In this study, we present the draft genome sequence of a CTX-M-15-producing *E. coli* ST345 isolated from commercial chicken meat in Brazil. This draft genome can be used as a reference sequence for comparative analysis among CTX-M-15-producers.

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Extended-spectrum  $\beta$ -lactamases (ESBLs) remain the most important mechanism conferring resistance to broad-spectrum cephalosporins (BSCs) in *Escherichia coli*. Spread of ESBL-producing bacteria to humans through food products is a matter of concern, especially through retail meat [1]. In particular, chicken meat has recurrently been pointed out as a non-human source of ESBLs worldwide, whereas ceftiofur use has resulted in the selection of BSC-resistant bacteria from chickens [2]. During slaughtering, enteric bacteria from the animal's gut may contaminate the carcass and may then reach the human gut through consumption of contaminated meat or foods that come into contact with

contaminated meat or kitchen utensils [3]. Indeed, a few ESBL-producing *E. coli* isolates from human clinical samples were also identified from food-producing animals [1]. In Brazil, previous studies have reported the presence of *E. coli* producing CTX-M-type enzymes in retail chicken meat [4]. Since Brazil is the greatest chicken meat exporter in the world [5], there is an urgent need to strengthen epidemiological surveillance owing to public health concerns.

In 2014, during a surveillance study conducted to assess the occurrence of ESBL-producing bacteria in commercial chicken meat [4], a BSC-resistant CTX-M-15-producing *E. coli* isolate (Ec39764) was recovered from a sample collected at a marketplace located in São Paulo state, Southeastern Brazil.

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The total genomic DNA of Ec39764 was sequenced using the NextSeq Platform (Illumina Inc., San Diego, CA). A total of 12 514 906 paired-end reads (150 × 150 bp) were generated with 375× coverage. In brief, the sequence reads were initially assembled de novo using Velvet v.1.2.10 (<https://www.ebi.ac.uk/~zerbino/velvet/>), and contigs were curated using Geneious software v.R10 (Biomatters Ltd., Auckland, New Zealand). Finally, the draft genome sequence was automatically annotated using PROKKA (<http://www.vicbioinformatics.com/software/prokka.shtml>).

In total, 5028 coding sequences, 288 pseudogenes, 58 tRNAs and 1 rRNA (5S) were identified in Ec39764, with a G + C content of 50.4%. Multilocus sequence typing (MLST), serotypes, plasmid replicons, acquired antimicrobial resistance genes and *E. coli* virulence genes were identified using the services MLST 1.8, SeroTypeFinder 1.1, PlasmidFinder 1.3, ResFinder 2.1 and VirulenceFinder 1.5, respectively, available from the Center for Genomic Epidemiology (<http://genomicepidemiology.org/>).

*E. coli* isolate Ec39764 belongs to ST345, and resistome analysis revealed the presence of aminoglycoside resistance genes [*aph(3')-Ia*, *aadA1*, *aadA2*, *strA* and *strB*], β-lactam resistance genes (*bla*<sub>TEM-1B</sub> and *bla*<sub>CTX-M-15</sub>), the fluoroquinolone resistance gene *qnrS1*, the phenicol resistance gene *cmlA1*, sulphonamide resistance genes (*sul2* and *sul3*), the tetracycline resistance gene *tet(A)* and the trimethoprim resistance gene *dhfrA12*. Plasmids of incompatibility (Inc) groups X1, FIB, I1, FII and Q1 were identified, and the *bla*<sub>CTX-M-15</sub> gene was harboured by an IncX1 plasmid since both are present in the same contig. Finally, Ec39764 carried *iroN*, *cma*, *lpfA*, *iss*, *astA* and *gad* virulence genes.

In summary, here we report the first draft genome sequence of a CTX-M-15-producing *E. coli* ST345 isolate from commercial chicken meat, which can be used as a reference sequence for comparative analysis among CTX-M-15-positive lineages of *E. coli* isolated from human, animal and environmental samples.

This Whole Genome Shotgun project has been deposited at DDBJ/ENA/GenBank under the accession MUFZ000000000. The version described in this paper is version MUFZ010000000.

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## Competing interests

None declared.

## Ethical approval

Not required.

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