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Genome Note

Draft genome sequence of a multidrug-resistant *Escherichia coli* ST189 carrying several acquired antimicrobial resistance genes obtained from Brazilian soil

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ABSTRACT

Objectives: This study reports the draft genome sequence of a multidrug-resistant *Escherichia coli* isolate obtained from a Brazilian soil sample.
Methods: The *E. coli* genome was sequenced using an Illumina MiSeq platform. De novo genome assembly was performed using SPAdes v.3.9. The draft genome sequence was annotated using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP). The resistome, virulome and mobilome were identified using tools available from the Center for Genomic Epidemiology.
Results: The genome presented 5613 protein-coding sequences and a GC content of 50.3%. Resistome analysis showed antimicrobial resistance genes to β-lactams (bla_{TEM-1B}), tetracyclines [*tet*(A) and *tet*(34)], aminoglycosides (*aadA1*, *aadA5* and *aadA24*), phenicols (*floR*), sulfonamides (*sul2* and *sul3*), trimethoprim (*dfrA17*) and macrolides [*mdf*(A)]. For quinolone resistance, mutations in the quinolone resistance-determining regions of GyrA (Ser83Leu; Asp87Tyr) and ParC (Ser80Ile; Glu62Lys) were detected. Plasmid incompatibility (Inc) groups were detected, including ColpVC, IncN3, IncP1 and IncF [F113:A8:B20], with IncF113 being a new allele. The isolate belongs to ST189 (CC165), serotype O80:H26-*fimH*54 and presents some virulence genes (*lpfA*, *iss* and *gad*).
Conclusion: This is the first draft genome sequence of an *E. coli* ST189 isolate of serotype O80:H26-*fimH*54 obtained from soil. This draft genome sequence can be used to compare antimicrobial-resistant *E. coli* isolates obtained from different sources.

Escherichia coli is commonly found in the gastrointestinal tract of humans and animals and is also able to survive in environments such as soil and water [1]. Bacterial resistance to antimicrobial agents has become a public-health problem, and several studies have reported multidrug-resistant (MDR) *E. coli* isolates worldwide independent of the source of isolation. The association of different antimicrobial resistance mechanisms leads to a MDR phenotype, which has become extremely common. The aim of this study was to characterise a MDR *E. coli* isolates recovered from a soil sample in Brazil.

In 2017, *E. coli* isolate S366 was obtained from a soil sample of a guava culture in Jardinópolis City, São Paulo State, Brazil. The resistance profile was determined by the disk diffusion method according to Clinical and Laboratory Standards Institute (CLSI) guidelines [2]. The genome of isolate S366 was sequenced on an Illumina MiSeq platform (Illumina Inc., San Diego, CA) using 250-bp paired-end reads. De novo genome assembly was performed using SPAdes v.3.9, and the draft genome sequence was annotated using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v.3.2.

Antimicrobial resistance genes (ARGs), plasmid replicons, multilocus sequence typing (MLST), serotype, *fimH* type and virulence gene analysis were studied using ResFinder 3.0, PlasmidFinder 2.0, MLST 2.0, SerotypeFinder 2.0, FimTyper 1.0 and VirulenceFinder 2.0, respectively, available at the Center for Genomic Epidemiology (http://genomicepidemiology.org/). The phylogenetic group, core genome MLST (cgMLST), whole genome MLST (wgMLST) and ribosomal MLST (rMLST) were analysed using EnteroBase (http://enterobase.warwick.ac.uk/species/index/ecoli).

Isolate S366 presented resistance to ampicillin, cefazolin, cefaclor, cefoxitin, cefuroxime, ceftazidime, ceftriaxone, cefotaxime, cefepime,

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Table 1
Antimicrobial resistance genes (ARGs) and plasmids of multidrug-resistant *Escherichia coli* S366 ST189.

	Identity (%)	Contig
ARGs		
bla$_{TEM-1B}$	100.00	526
tet(A)	100.00	22
tet(34)	84.75	17
aadA1	99.24	126
aadA5	100.00	22
aadA24	89.10	350
floR	99.78	232
sul2	100.00	60
sul3	100.00	124
dfrA17	100.00	22
mdf(A)	99.92	7
Plasmids		
IncFII(pSE11)	93.18	392
IncFIA(pBK30683)	95.59	600
IncFIB(AP001918)	97.94	504
IncN3	100.00	58
IncP1	100.00	31
ColpVC	98.96	106

aztreonam, tetracycline, doxycycline, gentamicin, tobramycin, streptomycin, chloramphenicol, trimethoprim/sulfamethoxazole, trimethoprim, ciprofloxacin, norfloxacin, levofloxacin, ofloxacin, lomefloxacin and nalidixic acid, being classified as MDR [3].

A total of 2 139 972 (2 × 250-bp) paired-end reads were generated with 107× coverage. In total, 5613 protein coding sequences, 265 pseudogenes, 84 tRNAs, 28 rRNAs and 11 ncRNAs were identified, with a GC content of 50.3%. Resistome analysis showed several acquired ARGs to β-lactams (*bla*$_{TEM-1B}$), tetracyclines [*tet*(A) and *tet*(34)], aminoglycosides (*aadA1*, *aadA5* and *aadA24*), phenicols (*floR*), sulfonamides (*sul2* and *sul3*), trimethoprim (*dfrA17*) and macrolides [*mdf*(A)] (Table 1). For quinolone resistance, mutations in the quinolone resistance-determining regions of GyrA (Ser83Leu; Asp87Tyr) and ParC (Ser80Ile; Glu62Lys) were detected.

The plasmid incompatibility (Inc) groups detected were ColpVC, IncN3, IncP1 and IncF [F113:A8:B20] (Table 1). The new allele 113 of IncFII was detected and was submitted and deposited in the Plasmid MLST Databases (https://pubmlst.org/plasmid/). Due to limitations of the sequencing technology, it was not possible to determine the location of the acquired ARGs in the detected plasmids. Isolate S366 was classified as serotype O80:H26-*fimH*54, phylogroup A and belonged to ST189 (CC165), cgMLST 94851, wgMLST 105511 and rMLST 1957. Some virulence genes were detected, including *lpfA* (long polar fimbriae), *iss* (increased serum survival) and *gad* (glutamate decarboxylase).

Since the 1970s, *E. coli* ST189 has been reported in North America, Europe, Asia and Africa; however, there are few isolates belonging to ST189 available in the EnteroBase database (https://enterobase.warwick.ac.uk/) that have been reported in human, animal, food and environmental samples. This clone has been related to a MDR phenotype and is associated with several acquired ARGs, including *dfrA* and *aadA* [4,5]. To our knowledge, this is the first report of an *E. coli* ST189 isolate obtained from soil in Brazil, which is of great concern since this clone is spreading worldwide carrying several ARGs.

In summary, we report the first draft genome sequence of an *E. coli* ST189 isolate of serotype O80:H26-*fimH*54 obtained from soil. This draft genome sequence can be used to compare antimicrobial-resistant *E. coli* isolates harbouring acquired ARGs obtained from different sources.

This Whole Genome Shotgun project has been deposited at DDBJ/ENA/GenBank under the accession no. RQOE00000000. The version described in this paper is version RQOE01000000.

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Competing interests

None declared.

Ethical approval

Not required.

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