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Genome Note

Draft genome sequence of a multidrug-resistant *tetA*/IncF-harbouring *Escherichia coli* ST906 obtained from a soil cultivated with jaboticaba (*Plinia cauliflora*)

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ABSTRACT

Objectives: The aim of this study was to report the draft genome sequence of a multidrug-resistant (MDR) *Escherichia coli* isolate obtained from a jaboticaba (*Plinia cauliflora*) culture soil in Brazil.
Methods: The whole genome of *E. coli* strain S376 was sequenced on an Illumina MiSeq platform and was assembled using SPAdes v.3.9. All data analyses were performed using tools from the Center for Genomic Epidemiology and Geneious v.11.1.5 software. The genome was annotated using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v.3.2.
Results: A total of 4854 protein-coding sequences were identified, with a GC content of 50.4%. Resistome analysis showed acquired antimicrobial resistance genes to β-lactams ($bla_{TEM-116}$), tetracyclines [*tetA* and *tet*(34)], aminoglycosides (*aadA1*), trimethoprim (*dfrA1*) and macrolides (*mphA*). Mutations in the quinolone resistance-determining region (QRDR) of GyrA, ParC and ParE were detected. Three plasmid incompatibility groups were detected [IncFII (allele 24), IncFIB (allele 1) and ColRNAI]. In silico analysis showed the *tetA* and *mphA* are located inside the IncF plasmid. This isolate was classified as ST906 (singleton), serotype O156:H23-*fimH*61, commensal phylogroup B1 and presented various virulence genes, including *iroN*, *ipfA*, *cma*, *gad* and *iss*.
Conclusion: This is the first report of a draft genome sequence of a MDR *E. coli* ST906 serotype O156:H23-*fimH*61 obtained from a Brazilian soil. This draft genome sequence can be used to compare MDR *E. coli* isolated from different sources and to better understand the spread of this clone worldwide.

Soils are considered reservoirs of antimicrobial resistance genes (ARGs) and present a greater diversity of ARGs than clinical settings; however, the spread of these genes in soil is not well understood owing to the different factors influencing this environment [1]. Multidrug-resistant (MDR) bacteria, including *Escherichia coli*, have been spread to several sources, which is of great concern. Transmission of ARGs as well as MDR bacteria can occur through the ingestion of contaminated food derived from different sources [2]. Therefore, this study aimed to characterise a MDR *E. coli* isolate obtained from a jaboticaba (*Plinia cauliflora*) culture soil in Brazil.

Soil sample (1 g) was added to brain–heart infusion broth (Oxoid Ltd., Basingstoke, UK) and was then seeded on MacConkey agar (Oxoid Ltd.). *E. coli* isolate S376 was obtained from a soil sample of jaboticaba culture in Jardinópolis City, São Paulo State, Brazil. Antimicrobial susceptibility testing was performed by the disk diffusion method according to the Clinical and Laboratory Standards Institute (CLSI supplement M100, 27th ed). *E. coli* strain S376 was classified as MDR [3] since it had a resistance profile to β-lactams (ampicillin, cefaclor, cefazolin), tetracyclines (tetracycline, doxycycline), aminoglycosides (streptomycin), folate pathway antagonists (trimethoprim), fluoroquinolones and quinolones (ciprofloxacin, levofloxacin, norfloxacin, ofloxacin, lomefloxacin, nalidixic acid).

An Illumina MiSeq platform (Illumina Inc., San Diego, CA) with 250-bp paired-end reads was used for sequencing the genome of strain S376. SPAdes v.3.9 was used for de novo genome assembly and the genome was then annotated using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v.3.2. Chromosomal point mutations and acquired ARGs, serotype, multilocus sequence

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typing (MLST), plasmid replicons, virulence genes and *fimH* type were analysed using ResFinder 3.0, SerotypeFinder 2.0, MLST 2.0, PlasmidFinder 2.0, VirulenceFinder 2.0 and FimTyper 1.0, respectively, available at the Center for Genomic Epidemiology (http://genomicepidemiology.org/). In silico analysis was performed using Geneious v.11.1.5 software (Biomatters Ltd., Auckland, New Zeeland). The *E. coli* phylogenetic group was determined using the Clermont phylotyping method (http://clermontyping.iame-research.center/).

A total of 2 130 538 (2 × 250-bp) paired-end reads were generated with 106× coverage. In total, 4854 protein-coding sequences, 155 pseudogenes, 87 tRNAs, 80 rRNAs and 12 ncRNAs were identified, with a GC content of 50.4%. The presence of various acquired ARGs were observed, including for β-lactam resistance ($bla_{\text{TEM-116}}$), tetracycline resistance [*tetA* and *tet*(34)], aminoglycoside resistance (*aadA1*), trimethoprim resistance (*dfrA1*) and macrolide resistance (*mphA*). Mutations in the quinolone resistance-determining region (QRDR) of GyrA (Ser83Leu; Asp87Tyr), ParC (Glu62Lys; Ser80Ile) and ParE (Ser458Ala) were detected.

Three plasmid incompatibility groups were detected, including IncFII (allele 24) and IncFIB (allele 1) inside in the same plasmid, as well as a ColRNAI. In silico analysis showed the *tetA* and *mphA* genes are located inside the IncF plasmid. Isolate S376 was classified as serotype O156:H23-*fimH*61, commensal phylogroup B1 and belongs to the ST906 (singleton). The virulence genes *iroN* (enterobactin siderophore receptor protein), *ipfA* (long polar fimbriae), *cma* (colicin M), *gad* (glutamate decarboxylase) and *iss* (increased serum survival) were detected.

According to the EnteroBase database (https://enterobase.warwick.ac.uk/), *E. coli* ST906 has been detected since the 1980s in several countries from different sources, namely human, environment, animal and plant; however, there are no reports of environmental *E. coli* ST906 isolated in Brazil. Recently, a surveillance study has shown that pansusceptible *E. coli* ST906 obtained from retail meat was associated with urinary tract infections in humans in the USA [4]. IncF plasmids carrying *tetA*, $bla_{\text{TEM-1B}}$ and *mphA* genes as well as virulence factors have been reported worldwide in bacteria belonging to the Enterobacteriaceae family [5]. Therefore, further studies are needed to better characterise MDR *E. coli* isolated from soil.

This is the first report of a draft genome sequence of an MDR *E. coli* ST906 serotype O156:H23-*fimH*61 obtained from a Brazilian soil. This draft genome sequence can be used to compare MDR *E. coli* isolated from different sources and to better understand the spread of this clone worldwide.

This Whole Genome Shotgun project has been deposited at DDBJ/ENA/GenBank under the accession no. RQSJ00000000. The version described in this paper is version RQSJ01000000.

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Competing interests

None declared.

Ethical approval

Not required.

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