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Genomic characterization of a uropathogenic Escherichia coli ST405 isolate harboring blaCTX-M-15-encoding IncFIA-FIB plasmid, blaCTX-M-24-encoding IncI1 plasmid, and phage-like plasmid

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Abstract

Statement of the Problem: Escherichia coli sequence type 405 is an emerging antibiotic-resistant clonal group associated with the global dissemination of extended-spectrum β-lactamase-producing E. coli. E. coli ST405 has recently caused several outbreaks in China, raising concerns about its public health threat. Understanding the mechanisms underlying its increasing ability to cause outbreaks requires an in-depth knowledge of the genetic features of ST405. In this study, we report the genome assembly and characterization of a uropathogenic E. coli ST405 strain, SZESBLEC201. Methodology and Theoretical Orientation: The MDR E. coli isolate SZESBLEC201 was recovered from a urine specimen of a patient suffering from a UTI on the fourth day of hospitalization. Antimicrobial susceptibility testing was performed to determine the resistant characteristics. The conjugative transferability of plasmids in SZESBLEC201 was investigated by solid mating conjugation. Plasmids profiles of the donor and recipient were determined by S1-nuclease digestion followed by pulsed-field gel electrophoresis. Whole genome sequencing was performed on the Illumina HiSeq 2500 platform and the Oxford MinIon Nanopore platform. High-quality lone reads were assembled de novo using Canu. Contigs were circularized by Circlator. High-quality short-reads were used to correct circularized contigs. Conclusion and Significance: This is the first study to report E. coli ST405 harboring blaCTX-M-15 and blaCTX-M-24 variants in the same isolate in China. The availability of the complete genome of E. coli ST405 facilitates a further investigation of the underlying mechanisms of becoming a globally successful clone and the potential roles played by its blaCTX-M-bearing plasmids and phage-like plasmid in gene transfer.

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Biography

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