AMERICAN SOCIETY FOR MICROBIOLOGY | Microbiology Resource Announcements

GENOME SEQUENCES

Draft Genomic Sequence of *Escherichia coli* Sequence Type 131, Isolated from Retail Chicken Skin

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ABSTRACT *Escherichia coli* sequence type 131 (ST131) is a foodborne pathogen increasingly associated with urinary tract infections. We report here the draft genomic sequence of ST131 B7S75, isolated from retail chicken skin, including information about its virulence factors and antibiotic resistance.

Urinary tract infections affect ca. 10 million people in the United States annually, with 75% of those being women (1). There is a close relationship between the consumption of retail poultry meat and urinary tract infections in humans (2, 3). Sequence type 131 (ST131) strains, which are often antibiotic resistant, have rapidly emerged to become uropathogenic *Escherichia coli* strains of clinical significance, and they are found ubiquitously in humans, food animals, and the environment (4). Toward this end, *E. coli* ST131 B7S75, recovered from retail chicken skin in our laboratory, was subjected to genomic sequencing.

B7S75 was streaked on a Trypticase soy agar (TSA) plate and incubated at 37°C for 24 h. DNA was isolated from a single colony scraped from the TSA plate. Genomic DNA was extracted using the DNeasy blood and tissue kit (Qiagen, Hilden, Germany) and quantified in a Qubit 3.0 fluorimeter (Life Technologies, Carlsbad, CA, USA). The genomic DNA library was prepared using the Nextera DNA Flex library prep kit (Illumina, San Diego, CA, USA). Libraries were analyzed for concentration, pooled, and denatured for loading onto a flow cell for cluster generation. Denatured libraries were sequenced on the Illumina MiniSeq platform. A total of 6.7×10^6 sequencing reads using 150-bp paired-end sequencing were obtained. Read quality was assessed with FastQC version 1.0.0 (Illumina BaseSpace Labs). The genome was assembled *de novo* using SPAdes (version 3.9.0), and 189 contigs (386-fold coverage) were obtained, the longest of which was 633,173 bp. Annotation was performed using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP; version 4.3) (5). The genome characteristics were genome size, 5.21 Mb; GC content, 50.66%; total genes, 5,457; total coding sequences (CDS), 5,366; number of CDS coding genes, 5,130; number of RNA genes, 91; number of rRNAs, 12; number of tRNAs, 74; number of noncoding RNAs (ncRNAs), 5; and number of pseudogenes, 236. The O and H antigen of B7S75 are O25:H4 (SerotypeFinder 2.0). The multilocus sequence type was sequence type 131 (ST131). The plasmid multilocus sequence type was IncF:F16:A-:B1. Virulence factors of B7S75 associated with urinary tract infections (UTIs) include the enterobactin siderophore receptor gene (*iroN*), increased serum survival gene (*iss*), glutamate decarboxylase gene (*gad*), periplasmic chaperone EcpD gene (*ecpD*), outer membrane protease T gene (*ompT*), intimin-like inverse autotransporter gene (*sinH*), and the type 1 fimbrial protein gene (*T1P*). Antimicrobial resistance (AR) genes include those for aminoglycosides [*aac(3)-IId*] and extended beta-lactamases ($bla_{\text{TEM-1B}}$) (according to the Illumina Bacterial Analysis Pipeline version 1.0.4).

Genomics data are now considered an integral part of risk assessment for food

Citation Xu A, Mackay W, Scullen OJ, Sheen S, Ramos R, Sommers C. 2019. Draft genomic sequence of *Escherichia coli* sequence type 131, isolated from retail chicken skin. Microbiol Resour Announc 8:e01533-18. https://doi.org/10.1128/MRA.01533-18.

Editor Jason E. Stajich, University of California, Riverside

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Received 9 November 2018
Accepted 4 January 2019
Published 14 February 2019

safety and environmental microbiology (6). These genomic data will be useful for understanding the control of *E. coli* ST131 in foods.

Data availability. This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under the accession number RAGZ00000000 and BioProject number PRJNA492277. The raw reads are available in the Sequence Read Archive (SRA) under accession number SRX4723048. The version described in this paper is the first version.

ACKNOWLEDGMENT

This work was supported by the U.S. Department of Agriculture (USDA)-Agricultural Research Service national program project 108, food safety project 8072-42000-078-00D.

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