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PROKARYOTES

Draft Genome Sequences of Four Uropathogenic *Escherichia coli* Serotype O4:H5 Isolates (ATCC 700414, 700415, 700416, and 700417)

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ABSTRACT Uropathogenic *Escherichia coli* serotype O4:H5 isolates (ATCC 700414, 700415, 700416, and 700417) were recovered from women with first-time urinary tract infections. Here, we report the draft genome sequences for these four *E. coli* isolates, which are currently being used to validate food safety processing technologies.

Uropathogenic *Escherichia coli* (UPEC) is responsible for 75% to 95% of the 10.5 million urinary tract infections (UTI) in the United States each year, which primarily affect women (1). UTI may be considered a form of foodborne illness, as UPEC is routinely found in food animals and retail food products (2) and food isolates have been shown to cause UTI in animal model systems (3). In addition, recent research has implicated UPEC in ulcerative colitis associated with inflammatory bowel disease (4). After consumption of UPEC-contaminated food by these patients, UPEC colonization of the distal gastrointestinal (GI) tract and integration of UPEC into GI ulcers can exacerbate the inflammatory response (4). The pathogenesis of UTI is due to accidental transfer of UPEC-contaminated feces from the GI tract to the urethra (1). The *E. coli* isolates associated with UTI are commonly a genetic match to those found in the individual's feces (5). These four O4:H5 clinical UPEC isolates (6), obtained from women with first-time UTI, are currently being used to validate food safety intervention technologies along with other UPEC (7, 8).

Genomic DNA was extracted using the DNeasy blood and tissue kit (Qiagen, Hilden, Germany) and quantified in a Qubit 3.0 fluorometer (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 and then pooled and denatured for loading onto a flow cell for cluster generation. Denatured libraries were sequenced on an Illumina MiniSeq platform with a 2 × 150-bp read paired-end protocol with 30× coverage. Two Illumina reads from separate DNA preparations were assembled *de novo* using SPAdes (version 3.9.0). Virulence factors, antibiotic resistance genes, genome size, N_{50} values, multilocus sequence type (MLST), mRNA, rRNA, tRNA, genes, pseudogenes, and coding sequences (CDS) were determined using the Illumina Bacterial Analysis Pipeline (version 1.0.4) and the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (version 4.3). The accession numbers and assembly metrics are listed in Table 1.

Genomics data are now considered an integral part of risk assessment for food safety and environmental microbiology (9). These genomic data will be useful for understanding UPEC pathogenesis and should provide novel insights regarding the persistence of UPEC in foods and effective food safety practices for UPEC detection, control, and elimination.

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TABLE 1 Accession numbers and assembly metrics of draft whole-genome sequences of four *E. coli* serotype O4:H5 isolates

ATCC isolate no.	GenBank accession no.	Genome size (bp)	G+C content (%)	BioProject no.
700414	POSZ00000000	5,242,372	50.47	PRJNA429583
700415	POTA00000000	5,300,806	50.37	PRJNA429606
700416	POSX00000000	5,121,072	50.36	PRJNA429461
700417	POSY00000000	5,336,843	50.37	PRJNA429467

Accession number(s). The whole-genome shotgun projects reported here have been deposited in DDBJ/ENA/GenBank under the accession and BioProject numbers listed in Table 1. The versions described in this paper are the first versions.

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