



Complete Genome Sequence of a Natural *Escherichia coli* O145:H11 Isolate That Belongs to Phylogroup A

Michelle Qiu Carter,^a Antares Pham^a

^aProduce Safety and Microbiology Research Unit, Western Regional Research Center, Agricultural Research Service, U.S. Department of Agriculture, Albany, California, USA

ABSTRACT *Escherichia coli* O145:H11 strain RM14721 was originally isolated from wildlife feces near a leafy greens-growing region in Yuma, AZ. This strain was initially positive for *stx*₁; however, in subsequent cultures, *stx*₁ was not detected by PCR. Here, we report the complete genome sequence and annotation of RM14721.

The *Escherichia coli* species comprises commensal strains residing naturally in intestinal tracts of their mammalian hosts and pathogenic strains causing diverse intestinal and extraintestinal infections in humans and animals (1, 2). Shiga toxin-producing *Escherichia coli* (STEC) serotype O145, one of the major non-O157 serotypes associated with severe human disease (3, 4), has evolved independently via multiple lineages. Strains linked to the 2010 romaine lettuce-associated outbreak of O145 infections (5) and to the 2007 ice-cream-associated outbreak of O145 and O26 coinfections (6, 7) have a *fliCH28* antigen, share an evolutionary lineage with STEC O157:H7, and belong to phylogroup E (8, 9). However, STEC O145:H25 is genetically more similar to other non-O157 STEC strains, including O111 strain 11128 and O26 strain 11368, which are both in phylogroup B1, than to O145:H28 (10). Strain RM14721 was isolated from wildlife feces near a leafy greens-growing region in Yuma, AZ (11). This strain was initially positive for *stx*₁ genes by PCR; however, in the subsequent cultures, *stx*₁ genes were not detected.

Single-molecule real-time (SMRT) sequencing was performed on a PacBio RS II instrument using the protocol "Procedure & Checklist—Greater Than 10 kb Template Preparation Using AMPure PB Beads" (12), followed with template binding using P6v2 sequencing polymerase and MagBeads. The SMRTbell sequencing libraries were prepared using 8 μg of sheared DNA and the SMRTbell template prep kit 3.0. The SMRT cells were run with a 0.1 nM on-plate concentration, P6/C4 sequencing chemistry, the MB1percV1 collection protocol, and a 360-min data collection mode. A FASTQ file was generated using SMRT Analysis (version 2.3.0), and assembly was performed with RS_HGAP_Assembly.3. The complete genome sequence was submitted to GenBank for annotation using the Prokaryotic Genome Annotation Pipeline.

The genome of *E. coli* strain RM14721 is composed of a 4,620,018-bp chromosome and a 106,432-bp plasmid, encoding 4,870 coding sequences (CDSs), 22 rRNAs, and 86 tRNAs. The average GC contents of the chromosome and plasmid are 50.9% and 49.9%, respectively. The serotype of strain RM14721 was confirmed to be O145:H11 by a BLAST search of *E. coli* O-antigen and H-antigen databases (13, 14). The sequence type (ST) was determined to be ST1155 using the Michigan scheme (<http://www.shigatox.net/ecmlst/cgi-bin/scheme>) and ST48 using the Warwick scheme (15). *In silico* phylotyping using the Clermont method (16) placed this strain in phylogroup A. Consistently, the multi-locus sequence typing (MLST)-based phylogenetic analysis clustered strain RM14721 with other *E. coli* A strains, including REL606 and enterotoxigenic *E. coli* (ETEC) strain H10407 when more than 400 *E. coli* strains with a complete genome available in GenBank as of January 2018 were included in the analysis. No homologs of genes

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encoding the heat-labile (LT) or heat-stable (ST) enterotoxin were identified in RM14721. PHASTER (17, 18) analysis detected three intact prophages on the chromosome, spanning chromosomal positions 484362 to 507958 (23.5 kb), 1617891 to 1653895 (36.0 kb), and 2334672 to 2375071 (40.4 kb). Although no Shiga toxin genes were identified in the genome of RM14721, several putative integration sites for Stx-converting phages were identified, including AU5Stx1 (GenBank accession number KU977419), PA2 (Stx2a) (NCBI reference sequence NC_028449), and 1717 (Stx2c) (NCBI reference sequence NC_011357), indicating the potential of strain RM14721 to evolve into an STEC strain.

Accession number(s). The genome sequence of *E. coli* O145:H11 strain RM14721 was deposited in GenBank under the accession numbers [CP027105](#) (chromosome) and [CP027106](#) (plasmid).

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