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Draft Genome Sequences of *Escherichia coli* O113:H21 Strains Recovered from a Major Produce Production Region in California

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ABSTRACT Shiga toxin-producing *Escherichia coli* is a foodborne and waterborne pathogen and is responsible for outbreaks of human gastroenteritis. This report documents the draft genome sequences of seven O113:H21 strains recovered from livestock, wildlife, and soil samples recovered from a major agricultural region for leafy greens in California, USA.

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Shiga toxin-producing *Escherichia coli* (STEC) is a foodborne and waterborne pathogen and is responsible for outbreaks of human gastroenteritis with diverse clinical spectra, ranging from watery and bloody diarrhea to hemorrhagic colitis (1–3). In some cases, the infection progresses to more severe conditions such as the hemolytic uremic syndrome, and the onset of the life-threatening disease symptoms has been associated with the production of Shiga toxins (Stx). Serotype O157:H7 has been commonly associated with the development of severe disease symptoms; however, non-O157 serotypes have been implicated in human outbreaks from waterborne and foodborne sources (3–5). In particular, serotype O113:H21 has been shown to be also responsible for cases of hemolytic uremic syndrome (6, 7). Surveillance studies have indicated cattle to be the main reservoir of O113:H21 strains lacking the adhesin intimin but still harboring Stx gene subtypes, frequently implicated in human infections and severe illnesses (8, 9). The increased detection of STEC O113:H21 and its links to severe clinical cases highlight the importance of this serotype as a relevant emerging foodborne pathogen (4, 10, 11). This report documented the draft whole-genome sequences of seven *E. coli* O113:H7 strains, previously recovered from livestock, wildlife, and soil samples collected in a major agricultural region for leafy-green production in California's Central Coast (12).

Genomic DNA of the sequenced strains was extracted from 1 mL of overnight culture using the Wizard genomic DNA purification kit (Promega Corp., Madison, WI). The purity of the DNA was assessed by fluorometric measurement using the Quant-iT PicoGreen DNA assay kit (Invitrogen, Carlsbad, CA). For the O113:H21 strain RM7806, whole-genome sequencing and 12-kb insert paired-end 454 sequencing libraries were prepared and sequenced using the GS-FLX Genome Sequencer (Roche, Indianapolis, IN). For the remaining O113:H21 strains, whole-genome sequencing was performed on an Illumina MiSeq sequencer (Illumina, Inc., San Diego, CA). DNA sequencing libraries with 575-bp to 675-bp inserts were prepared using the KAPA LTP library preparation kit (KAPA Biosystems, Wilmington, MA). The pooled amplicon libraries were loaded into a MiSeq system and sequenced using a MiSeq reagent kit v2 with 2 × 250 cycles (Illumina, Inc.). Draft genomes were assembled using Newbler assembler (verson 2.6, Roche) to generate a contig graph file (13). For each sequenced O113:H21 genome, the contig with the *stx* gene subtype, stx_{2a}, was identified, and Sanger DNA sequencing of

TABLE 1 Genome characteristics of *Escherichia coli* O113:H21 from produce production regions in California

Strain	Serotype	Source	stx_{2a} integration locus	Genome size (bp)	No. of contigs	G+C content (%)	GenBank accession no.
RM7788	O113:H21	Water	*potC, serT*	5,029,620	179	50.6	NWVS00000000
RM7806	O113:H21	Pig	*potC, serT*	5,155,541	18	50.6	NWVR00000000
RM7807	O113:H21	Pig	*potC, serT*	5,032,176	202	50.6	NWVQ00000000
RM9244	O113:H21	Cattle	*potC, yehV*	5,375,282	279	50.5	NWVP00000000
RM9245	O113:H21	Cattle	*potC, yehV*	5,295,742	311	50.5	NWVO00000000
RM9246	O113:H21	Cattle	*potC, yehV*	5,293,811	294	50.5	NWVN00000000
RM10940	O113:H21	Cattle	*yehV*	5,036,463	131	50.6	NWVM00000000

contig-bridging amplicons was performed to close the scaffold into a single contig to identify the insertion loci of the stx_{2a}-encoding prophage. The stx_{2a} in all O113:H21 strains was located downstream of the antiterminator *Q* gene in the late gene region of the prophage. The average genome size in the examined strains was about 5,175,000 bp with either a 50.5% or 50.6% G+C content. The sequencing data of these O113:H21 strains will aid in a better understanding of the pathogenic potential of STEC strains recovered from a major produce production region in the United States.

Accession number(s). The whole-genome sequences have been deposited at GenBank under the accession numbers listed in Table 1.

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