AMERICAN SOCIETY FOR MICROBIOLOGY | Microbiology Resource Announcements

| Food Microbiology | Announcement

Draft genome sequences of nine non-O157 Shiga toxin-producing *Escherichia coli* in ready-to-eat food from supermarkets in Argentina

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ABSTRACT Non-O157 Shiga toxin-producing *Escherichia coli* (STEC) are recognized as an important group of bacterial enteropathogens. Here, we report the draft genome sequence of nine strains of non-O157 STEC isolated from ready-to-eat foods in Argentina. The whole-genome sequence data provide a better understanding of these isolates and will aid epidemiological investigation during outbreaks.

KEYWORDS non-O157 STEC, *Escherichia coli*, food, *stx*

Escherichia coli is a predominant component of the intestinal flora of humans and other mammals. However, some *E. coli* strains represent primary pathogens with an enhanced potential to cause diseases, particularly diarrhea and urinary tract infection (1). Due to busy lifestyles, people are forced to consume ready-to-eat foods such as cheese, salad, and fruit, which pose a potential risk to consumers due to contamination by different pathogenic bacteria, including Shiga toxin-producing *Escherichia coli* (STEC) (2). The Ministry of Health of Argentina reported 500 cases of hemolytic uremic syndromes annually between 2000 and 2010 (3).

Five hundred food samples, soft cheese, cottage cheese, salad with cream or mayonnaise, chicken, and meat with sauce (2 g each), were randomly collected from supermarkets in Rosario, Argentina, from June 2000 to December 2001 (4). Samples were homogenized in peptone water, inoculated into Luria broth (Thermo Fisher Scientific, Waltham, MA), and incubated at 37°C for 16 hours. Turbid cultures were streaked onto MacConkey agar plates (Thermo Fisher Scientific) and incubated overnight at 37°C. Non-O157 STEC isolates were confirmed with Vitek GNI+ card (bioMérieux, Durham, NC) and fatty acid methyl ester analysis (MIDI, Newark, DE).

Genomic DNA was extracted from bacterial cultures using the DNeasy blood and tissue kit (Qiagen, Valencia, CA). DNA libraries were constructed using the Nextera XT prep kit (Illumina, San Diego, CA). Whole genome sequencing (WGS) was performed using an Illumina MiSeq platform (Illumina). A 2 × 251 bp-paired-end trimming assembly was performed using the CLC Genomics Workbench, version 11 (Qiagen, Redwood City, CA).

Draft genomes were annotated initially using the Pathosystems Resources Integration Center (PATRIC) software version 3.6.12 and submitted to the NCBI for final annotation by the Prokaryotic Genome Automatic Annotation Pipeline (5) under the accession numbers shown in Table 1. The average G + C content of these strains is estimated to be approximately 50.56%, as examined by the PATRIC database. Default parameters were used for all softwares unless otherwise specified. Table 1 shows the number of contigs, sequence assembly size, biosamples, and SRA accession numbers.

Editor Vincent Michael Bruno, University of Maryland School of Medicine, Baltimore, Maryland, USA

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The authors declare no conflict of interest.

Received 17 May 2023
Accepted 27 August 2023

Published 18 October 2023

TABLE 1 Summary of genome sequence analysis of the non-O157 Shinga toxin-producing *Escherichia coli* isolated from ready-to-eat foods in Argentina[a]

Isolate	Source	Serotype	Genome size (bp)	No. of reads	No. of contigs	Contig N50 (bp)	Coverage (×)	G+C content (%)	NCBI accession no.			Illumina sequencer
									BioSample	SRA	GenBank	
ARG 5468	Cottage cheese	044	5,105,992	2,819,890	241	65,270	131.07	50.32	SAMN14115320	SRR13307203	JAAIWJ000000000	MiSeq
ARG 5266	Cottage cheese	079	5,007,325	5,991,774	190	103,071	278.51	50.89	SAMN14115321	SRR13307202	JAAIWI000000000	MiSeq
SRG 20	Vegetables with mayonnaise	ONT	4,605,243	3,094,080	150	88,652	143.82	48.68	SAMN14115322	SRR13307201	JAAIWH000000000	MiSeq
ARG 177	Soft cheese	08	4,658,353	3,584,302	179	70,176	166.60	50.86	SAMN14115323	SRR13307200	JAAIWG000000000	MiSeq
ARG 4827	Soft cheese	018	4,773,544	4,059,140	233	55,976	188.67	50.97	SAMN14115324	SRR13307199	JAAIWF000000000	MiSeq
ARG 4828	Soft cheese	ONT	4,959,027	1,956,380	236	70,103	90.94	50.92	SAMN14115325	SRR13307198	JAAIWE000000000	MiSeq
ARG 4627	Soft cheese	018	5,174,490	2,574,964	307	43,097	119.69	50.66	SAMN14115326	SRR13307197	JAAIWD000000000	MiSeq
ARG 2379	Soft cheese	128	4,831,383	3,055,814	264	59,200	142.04	50.85	SAMN14115327	SRR13307196	JAAIWC000000000	MiSeq
ARG 4824	Meat with sauce	ONT	4,903,466	2,645,246	223	79,920	122.95	50.69	SAMN14115329	SRR13307194	JAAIWA000000000	MiSeq

[a] ONT= nontypeable.

ACKNOWLEDGMENTS

We thank Dr. Huizhong Chen for critical review of the manuscript.

This manuscript reflects the views of the authors and does not necessarily reflect those of the Food and Drug Administration.

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DATA AVAILABILITY

All sequenced genome data have been deposited at DDBJ/ENA/GenBank under BioProject accession number PRJNA545531 (see Table 1) and BioSample accession numbers SAMN14115320, SAMN14115321, SAMN14115322, SAMN14115323, SAMN14115324, SAMN14115325, SAMN14115326, SAMN14115327, and SAMN14115329.

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