




Genome Sequences of 34 Shiga Toxin-Producing *Escherichia coli* Isolates from Swine and Other Sources

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ABSTRACT Shiga toxin-producing *Escherichia coli* (STEC) bacteria are foodborne pathogens that can be carried by various animals. The swine STEC population is partially composed of host-specific strains that are often not well characterized. In this work, the genome sequences of a number of swine STEC strains are presented.

Shiga toxin-producing *Escherichia coli* (STEC) bacteria are important foodborne pathogens that are carried in the intestines of endotherms. The majority of STEC bacteria associated with swine carry the Shiga toxin subtype 2e gene, which can provoke edema disease in pigs and mild diarrhea in humans; however, swine may also carry STEC that is highly pathogenic for humans (1). STEC bacteria isolated with healthy pigs are very heterogeneous and belong to a multitude of serotypes, and many are sometimes untypeable or the serotype is difficult to determine (2–4). To increase the inventory of swine STEC genome sequences and better characterize the STEC population in pigs, whole-genome sequencing was performed on 29 strains isolated from asymptomatic swine and 3 beef trim isolates belonging to uncommon or difficult-to-serotype O groups, and 2 strains isolated from swine with postweaning diarrhea or edema disease (Table 1).

The DNeasy blood and tissue kit (Qiagen, Valencia, CA) and the QIAcube instrument (QIAgen) were used on pure cultures to extract genomic DNA, which was then fragmented using microTUBE-15 AFA beads screw-cap (Covaris, Woburn, MA) and an M220 Focused-ultrasonicator (Covaris) with default settings to achieve a 350-bp peak. The sheared DNA was used for library construction using the Accel-NGS 2S Plus DNA library kit (Swift Bioscience, Ann Arbor, MI). Library quality was assessed using the high-sensitivity DNA kit (Agilent Technologies, Santa Clara, CA) on a 2100 Bioanalyzer instrument (Agilent Technologies), while the concentration was determined by quantitative PCR (qPCR) using the KAPA library quantification kit (Kapa Biosystems, Wilmington, MA). Lastly, paired-end sequencing (2 × 250 bp) was performed using an Illumina MiSeq platform with a MiSeq reagent kit v2 (Illumina, San Diego, CA).

The raw data were quality filtered using Trimmomatic v0.36 (5), assembled using SPAdes v3.9.0 (6), and improved with Pilon v1.20 (7). Read and assembly quality was assessed with FastQC v0.11.5 and Quast v4.4 (8), respectively. After removal of contigs shorter than 500 bp or with coverage less than 8×, the assembly N_{50} values ranged from 53.3 to 247.9 kb. Draft genomes were annotated using the NCBI Prokaryotic Genome Annotation Pipeline (9). Genome sizes and coverages of the sequenced strains, including previously reported information, are presented in Table 1.

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TABLE 1 Description of STEC strains sequenced, their determined *in silico* serotype, and previously reported serotypes and Shiga toxin variants

Strain	GenBank accession no.	Genome length (Mb)	Genome coverage (×)	Origin	<i>In silico</i> serotype determined ^a	Previously reported serotype	Previously reported Shiga toxin	Reference(s) or source
2185	NWBG00000000	5.14	205	Swine with postweaning diarrhea	O141ab:H4	O141	Equivocal result (stx not found) ^b	10, TW01530 ^c
65-57	NWBF00000000	5.02	300	Swine with edema disease	O139:H1	O139:H-	Not available (2e) ^b	TW03023 ^c
94-0426	NWBE00000000	5.72	144	Swine	O26:H11	O149	Not available (1a) ^b	TW05926 ^c
C019	NWBD00000000	5.20	117	Swine feces	O155:H21	O59:H21	2e	Unpublished ^d
C040	NWBC00000000	4.95	344	Swine feces	O71:H21	O71:H21	2e	Unpublished ^d
C056	NWBB00000000	4.78	87	Swine feces	O--:H7	O--:H7	2e	Unpublished ^d
C092	NWBA00000000	5.08	163	Swine feces	O100:H30	O--:H30	2e	Unpublished ^d
C104	NWAZ00000000	5.15	169	Swine feces	O174:H2	O174:H2	2e	Unpublished ^d
C114	NWAY00000000	5.10	188	Swine feces	O155:H21	O184:H48	2e	Unpublished ^d
C165	NWAX00000000	5.11	161	Swine feces	O100:H30	O100:H30	2e	Unpublished ^d
C309	NWAW00000000	5.17	281	Swine feces	O86:H32	O86:H32	2e	Unpublished ^d
C316	NWAV00000000	4.95	255	Swine feces	O163:H19	O163:H32	1a	Unpublished ^d
C322	NWAW00000000	5.12	98	Swine feces	O155:H21	O59:H21	2e	Unpublished ^d
C323	NWAT00000000	5.14	183	Swine feces	O155:H21	O59:H21	2e	Unpublished ^d
C336	NWAS00000000	5.12	112	Swine feces	O155:H21	O59:H21	2e	Unpublished ^d
ED-53	NWAR00000000	5.01	262	Swine feces	O89:H9	O101:NM	2e	11, TW05983 ^c
F313	NWAQ00000000	5.02	211	Swine feces	O163:H19	O163:H-	1a	2, 5
F322	NWAP00000000	5.09	243	Swine feces	O--:NH4	O--:H51&24	1a	2, 5
F328	NWAO00000000	5.41	206	Swine feces	O155:H21	O--:H-	2e	2, 5
F339	NWAN00000000	5.35	94	Swine feces	O152:H19	O20:H19	1a	2, 5
F344	NWAM00000000	4.99	191	Swine feces	O100:H30	O--:H30	2e	2, 5
F352	NWAL00000000	5.12	239	Swine feces	O121:H10	O121:H-	2e	2, 5
F426	NWAK00000000	5.32	140	Swine feces	O155:H21	O--:H-	2e	2, 5
F469	NWAJ00000000	5.00	278	Swine feces	O--:H30	O--:H30	2e	2, 5
F498	NWAI00000000	5.07	161	Swine feces	O89:H9	O101:H-	2e	2, 5
F500	NWAH00000000	5.43	111	Swine feces	O159:H16	O159:H4	2e variant	2, 5
IMP 871	NWAG00000000	5.27	249	Beef trim	O163:H19	O163:H19	2 (2a) ^b	12
IMP 886	NWAF00000000	5.13	257	Beef trim	O153/O178:H19	O20:H19	1 (1a) ^b	12
JAN 020	NWAE00000000	4.95	229	Beef trim	O163:H19	O163:H19	2a	13
T025	NWAD00000000	5.33	402	Swine feces	O155:H21	O59:H21	2e	3
T097	NWAC00000000	5.32	230	Swine feces	O155:H21	O--:H21	2e	3
T168	NWAB00000000	5.35	191	Swine feces	O155:H21	O59:H21	2e	3
T186	NWAA00000000	4.91	257	Swine feces	O141ab:H19	O59:H19	2e	3
T297	NVZZ00000000	5.42	133	Swine feces	O155:H21	O59:H21	2e	3

^a*In silico* serotype was obtained using SerotypeFinder (14).

^bShiga toxin subtype was determined using VirulenceFinder (15).

^cThomas S. Whittam STEC Center isolate number.

^dW. Cha, P. M. Fratamico, L. Ruth, A. Bowman, J. Nolting, S. Manning, J. Funk, Prevalence and characteristics of Shiga toxin-producing *Escherichia coli* in finishing pigs: implications on public health, unpublished data.

Accession number(s). GenBank accession numbers of the assemblies are shown in Table 1, and raw data are available at the Sequence Read Archive.

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