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Hybrid Assembly from 75 *E. coli* Genomes Isolated from French Bovine Food Products between 1995 and 2016

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ABSTRACT Here, we report the complete (or near-complete) genome sequences of 75 *Escherichia coli* isolates, including 71 *stx*-positive *E. coli* isolates, isolated in France between 1995 and 2016 from food of bovine origin. Genomes were assembled using a combination of long- and short-read sequencing.

Shiga toxin-producing *Escherichia coli* (STEC) food contamination can lead to severe human symptoms (1). Here, we assembled 75 *E. coli* genomes, including 31 *eae*-positive STEC and 39 *eae*-negative STEC genomes, isolated from food of bovine origin within a 21-year period in France.

E. coli strains were originally isolated on Trypticase soy broth with yeast extract (TSYE) plates overnight at 37°C. Isolates were revived from 20 to 30% glycerol stock on TSYE plates and incubated overnight at 37°C. One colony was cultured overnight at 37°C in brain heart infusion broth (BHI) with rotation. Genomic DNA was extracted from BHI culture (1 mL) using different extraction methods and sequenced using both MiSeq (Illumina, Inc., San Diego, CA, USA) and MinION (Nanopore, Oxford Science Park, Oxford, UK) technologies (2). Default parameters were used for all software unless otherwise specified. Illumina libraries were constructed using Nextera XT kit and sequenced on v2 micro or standard flow cells (2 × 150 bp or 2 × 250 bp). MinION libraries were constructed from unsheared and non-size-selected DNA using the SQK-LSK109 ligation kit and EXP-NBD104 or EXP-NBD114 barcoding kit and sequenced on FLO-MIN106 flow cells using an Mk1B device.

Illumina reads were trimmed and quality checked using the CLC Genomics Workbench v21 (Qiagen). We generated 299,212 to 3,972,904 reads (mean, 1,368,471 ± 720,963.42) with an average read length of 198.08 (±37.99) bases per sample, representing 12 to 174× (mean, 51 ± 22.65) (Table 1). MinION FAST5 files were basecalled and demultiplexed using guppy_basecaller and guppy_barcode v3.4.5+fb1fbfb or v5.0.11+2b6dbff using “-compress-fastq” and “-trim-barcodes” parameters (3). Statistics on raw reads were performed using NanoPlot v1.29.0 (4). Between 14,450 and 1,992,878 reads (mean, 239,919 ± 341,570.565) were generated with N_{50} values ranging from 2,565 bp to 29,351 bp (mean, 16,330 ± 7,056.38). Assemblies were generated using Unicycler v0.4.8 (-min_fasta_length 1,000), Flye v2.6 or v2.8.1-b1676 (-genome-size 5m), and Raven v1.2.2 (5–7). Assembly quality and contiguity were assessed using QUAST v5.0.2 (8) and manual inspection of the assemblies (*stx*-phage and large plasmids integrity). Either the Unicycler-generated assembly was conserved or the Flye and/or Raven assemblies were further polished with short reads using racon v1.4.13, medaka v0.12.1 (optional), and pilon v1.24 polishing tools (3 to 5 rounds) (9, 10; <https://github.com/nanoporetech/medaka>). If none of these strategies produced satisfying assemblies, Canu v1.8 or v2.1.1 (genomeSize 5m) or Unicycler based on Flye or Raven assembly (-existing_long-read_assembly) was generated (11). Because assemblers have different performances regarding plasmid or phage reconstruction, several assemblies

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TABLE 1 Assembly metrics of *Escherichia coli* draft genomes and NCBI accession numbers for each isolate sequenced

NCBI accession no. (ONT, Illumina)	DNA extraction method(s) ^a	Strain	Serotype ^k	stx subtype(s)	ere	Hybrid assembly	MinION read length (N ₅₀ , lbp)	No. of contigs	Genome size (bp)	Assembly N ₅₀ (bp)	GC content (%)	Genome coverage (X)	GenBank accession no.
SRR18191646, SRR18191606	Bead based	1429	O76:H19	1c	–	Unicycler	10,334	3	5,316,065	5,183,674	50.64	107	JAQQMID000000000
SRR18191539, SRR18191528	Salting out	2206	O79:H48	1a, 2a	–	Unicycler	14,002	16	5,528,843	5,270,995	50.64	107	JAOWPQ000000000
SRR18191517, SRR18191506	Salting out	06QMA126.1	O153/O178:H19	1a, 2a, 2d	–	Flye	17,384	7	5,257,865	5,088,236	50.71	184	JAOWPFO000000000
SRR18191495, SRR18191580	Salting out	06QMA140.2	O149:H1	1d	–	Flye ^d	7,397	4	5,348,285	4,589,384	50.59	179	JAQQMNG000000000
SRR18191569, SRR18191644	Bead based, salting out	06QMA181.1a	O91:H14	1a, 2b, 2b	–	Unicycler	28,527	13	5,618,742	5,174,383	50.74	242	JAQQME000000000
SRR18191633, SRR18191566	Salting out	06QMA227.3	O116:H48	2a	–	Raven ^d	13,538	5	5,602,836	5,378,985	50.76	242	JAOWWJU000000000
SRR18191555, SRR18191544	Salting out	07HMPA386	O46/O134:H38	1a, 2a	–	Unicycler	18,809	5	4,943,051	4,790,646	50.57	150	JAQQMCO000000000
SRR18191613, SRR18191610	Salting out	07HMPA903	O113:H21	2a, 2a	–	Flye ^b	22,124	10	4,965,900	4,764,076	50.63	150	JAOWPDD000000000
SRR18191609, SRR18191608	Salting out, bead based	07HMPA966	O91:H10	2a	–	Unicycler	7,440	6	5,144,288	4,966,076	50.73	238	JAQQMB000000000
SRR18191607, SRR18191605	Salting out	09QMA299.3B	O175:H16	2a	–	Unicycler	25,581	7	5,331,927	5,145,461	50.76	706	JAOWPCC000000000
SRR18191604, SRR18191603	Salting out	09QMA303.1	O8H19	2g	–	Raven ^b	20,236	4	5,088,106	4,812,392	50.73	207	JAQQMA000000000
SRR18191602, SRR18191601	Salting out	09QMA311.2.3	O175:H16	2d	–	Unicycler	23,479	3	5,087,513	4,862,173	50.73	207	JAOWNI000000000
SRR18191600, SRR18191599	Salting out	09QMA33.1	O2H27	2a	–	Unicycler	20,366	11	5,575,342	5,185,943	50.72	706	JAOWPP000000000
SRR18191542, SRR18191541	Salting out	09QMA47.1	O6H10	1c	–	Flye ^d	17,841	7	5,382,235	5,226,869	50.66	223	JAOWPBC000000000
SRR18191540, SRR18191538	Salting out	1890-4	O26:H11	1a	+	Unicycler	22,209	4	5,283,406	4,794,423	50.53	215	JAQQLW000000000
SRR18191537, SRR18191536	Salting out	2011-026	O26:H11	1a	+	Raven ^d	17,173	17	5,268,782	4,794,913	50.54	215	JAOWPAA000000000
SRR18191535, SRR18191534	Salting out	2026-0145	O145:H28	2c	+	Unicycler	23,580	2	5,801,088	4,709,082	50.64	272	JAQQLV000000000
SRR18191533, SRR18191532	Salting out	2039-026	O26:H11	1a	+	Unicycler	9,087	33	5,834,018	5,743,918	50.68	272	JAOWNH000000000
SRR18191531, SRR18191530	Salting out	2048-0145	O145:H28	2c	+	Flye ^c	18,920	9	5,891,761	2,948,002	50.45	262	JAQQLU000000000
SRR18191529, SRR18191527	Salting out	2142-0103	O103:H25	2 ^m	+	Unicycler	22,773	11	5,509,245	4,447,030	50.60	295	JAOWOZ000000000
SRR18191526, SRR18191525	Salting out	2149-0103	O103:H11	1a	+	Unicycler	14,099	5	5,826,806	5,487,952	50.58	295	JAOWPO000000000
						Raven ^d	9,087	3	5,582,748	5,434,794	50.60	295	JAOWNG000000000
						Raven	18,920	3	5,815,566	5,670,366	50.63	151	JAOWNF000000000
						Unicycler	22,773	21	5,735,378	3,340,315	50.52	151	JAQQLS000000000
						Unicycler	14,099	15	5,526,494	5,203,884	50.57	250	JAQQLR000000000
						Flye ^d	22,773	10	5,628,166	5,402,071	50.59	250	JAOWOY000000000
						Raven	22,773	10	5,661,007	5,368,150	50.51	174	JAOWNE000000000
						Unicycler	14,099	27	5,844,869	5,519,265	50.69	153	JAQQLO000000000
						Unicycler	14,099	12	5,758,941	5,122,111	50.69	153	JAOWNX000000000

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TABLE 1 (Continued)

NCBI accession no. (ONT, Illumina)	DNA extraction method(s) ^a	Strain	Serotype ^k	stx subtype(s)	ere	Hybrid assembly	MinION read length (N ₅₀ , lbp)	No. of contigs	Genome size (bp)	Assembly N ₅₀ (bp)	GC content (%)	Genome coverage (X)	GenBank accession no.
SRR18191524	Salting out	2236-3b	O26:H11	1a	+	Flye ^c	16,957	23	5,997,576	5,003,748	50.63	154	JAOWOX0000000000
SRR18191523						Flye		30	6,044,444	5,011,133	50.61	154	JAOWNW0000000000
SRR18191522	Bead based	2918-O145	O145:H28	2a	+	Raven ^b	6,716	7	5,553,909	3,535,429	50.63	72	JAOWND0000000000
SRR18191521						Unicycler		28	5,492,229	1,347,297	50.54	72	JAOQLP0000000000
SRR18191520	Salting out	3273-O103	O103:H2	1a	+	Flye ^d	20,998	22	5,769,060	5,373,151	50.72	238	JAOWOW0000000000
SRR18191519								7	5,570,495	5,272,882	50.63	90	JAOWOV0000000000
SRR21721513	Bead based, salting out	3313-O111	O111:H8	1a	+	Flye ^b	4,229	17	5,489,297	3,617,166	50.55	90	JAOQLO0000000000
SRR18191516						Unicycler	10,277	19	5,488,508	1,232,028	50.55	398	JAOWNV0000000000
SRR18191518	Salting out	3313-O111	O111:H8	1a	+	Unicycler	21,079	18	5,719,857	4,395,063	50.65	128	JAOWOU0000000000
SRR18191515	Salting out	3382-O103	O103:H2	1a	+	Flye ^f	13,920	3	5,540,746	5,463,884	50.67	128	JAOWNL0000000000
SRR18191514						Unicycler		18	5,719,857	4,395,063	50.65	671	JAOWNU0000000000
SRR18191513	Bead based	3383-O103	O103:H2	1a	+	Flye ^b	5,882	5	5,542,730	5,454,423	50.65	671	JAOWOT0000000000
SRR18191512						Flye ^a		6	5,838,831	5,709,619	50.59	778	JAOWNT0000000000
SRR18191511	Bead based	3383-O26b	O26:H11	1a	+	Flye	6,945	9	5,822,451	5,697,780	50.62	778	JAOWOS0000000000
SRR18191510						Flye ^e		5	5,557,311	4,743,383	50.73	259	JAOWOR0000000000
SRR18191509	Bead based	3430-O103	O103:H2	1a	+	Flye ^e	8,683	6	5,558,675	4,744,103	50.72	259	JAOWNS0000000000
SRR18191508						Flye ^b		37	5,728,320	1,975,710	50.56	270	JAOQLN0000000000
SRR18191507	Bead based, salting out	429-O26	O26:H11	1a	+	Unicycler	12,758	12	5,805,978	3,820,369	50.73	148	JAOWOC0000000000
SRR21721511						Flye ^f	12,758	28	5,659,566	1,082,226	50.60	148	JAOWNR0000000000
SRR18191505	Salting out	429-O26	O26:H11	1a	+	Unicycler	25,662	4	5,972,468	5,737,945	50.75	71	JAOWOP0000000000
SRR18191504	Salting out	4712-O26	O26:H11	1a	+	Flye ^b		39	5,664,587	2,049,284	50.56	148	JAOQLM0000000000
SRR18191503	Salting out	4747-O26	O26:H11	1a	+	Unicycler	12,482	6	5,856,627	5,621,430	50.64	148	JAOWPN0000000000
SRR18191502	Salting out	4747-O26	O26:H11	1a	+	Canu ^d		6	5,714,135	5,609,626	50.62	148	JAOWOC0000000000
SRR18191501	Salting out	6423-O26	O26:H11	1a	+	Flye ^f	19,317	5	5,992,428	5,821,752	50.66	264	JAOWPM0000000000
SRR18191500	Salting out	97HMP449	O3:H12	1a	-	Canu ^d	5,941	6	5,371,299	5,104,752	50.51	334	JAOQLL0000000000
SRR18191499	Bead based	97HMP449	O3:H12	1a	-	Unicycler	5,941	7	5,472,012	3,671,848	50.47	334	JAOWPL0000000000
SRR18191497	Salting out	97HMP473	O3:H12	1a	-	Canu ^d	15,334	6	5,309,043	5,043,017	50.54	185	JAOQLK0000000000
SRR18191496	Salting out	97HMP473	O3:H12	1a	-	Unicycler	15,334	4	4,862,109	4,701,590	50.71	141	JAOQLJ0000000000
SRR18191590	Bead based, salting out	97HMP650	O110:H9	1c	-	Unicycler	28,759	1	4,849,707	4,849,707	50.71	141	JAOWNC0000000000
SRR18191588						Raven ^b		3	4,864,116	4,850,996	50.71	238	JAOQLI0000000000
SRR18191587	Bead based, salting out	97HMP652	O110:H9	1c	-	Unicycler	22,595	9	5,439,851	5,167,313	50.67	175	JAOWNQ0000000000
SRR18191586	Bead based, salting out	97HMP657	O136:H12	1a	-	Unicycler	21,241	44	5,655,428	5,156,955	50.68	125	JAOWON0000000000
SRR21721510	Salting out	97HMP657	O136:H12	1a	-	Flye ^d	21,241	2	5,247,946	5,142,912	50.78	805	JAOQLH0000000000
SRR18191585	Bead based, salting out	97HMP657	O136:H12	1a	-	Unicycler	8,149	2					
SRR18191584	Salting out	97HMP657	O136:H12	1a	-	Flye ^d	21,241	2					
SRR18191583	Bead based	97HMP657	O136:H12	1a	-	Unicycler	8,149	2					
SRR18191582	Bead based	97HMP657	O136:H12	1a	-	Unicycler	8,149	2					

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TABLE 1 (Continued)

NCBI accession no. (ONT, Illumina)	DNA extraction method(s) ^a	Strain	Serotype ^b	stx subtype(s)	ere	Hybrid assembly	MinION read length (N ₅₀ , lbp)	No. of contigs	Genome size (bp)	Assembly N ₅₀ (bp)	GC content (%)	Genome coverage (X)	GenBank accession no.
SRR18191581, SRR18191579	Bead based	98HMP1324	O174:H21	2c	–	Raven ^d	5,263	4	5,214,333	5,042,330	50.76	908	JAOWNB0000000000
SRR18191578, SRR18191577	Salting out	98HMP1325	O17/O44/O77:H18	2d	–	Canu	1,4916	6	5,317,997	5,045,734	50.79	908	JAOWPK0000000000
SRR18191576, SRR18191575	Bead based	98HMP1475	O110:H9	1c	–	Unicycler	4,854	6	5,373,540	5,090,743	50.71	199	JAOQLG0000000000
SRR18191574, SRR18191573	Salting out	98HMP1479	O91:H14	1a, 2b, 2b	–	Unicycler	8,894	13	5,831,137	5,558,854	50.68	152	JAOQLE0000000000
SRR18191572, SRR18191571	Salting out	98HMP1487	O136:H12	1a	–	Canu ^d	20,281	2	6,118,277	5,606,901	50.72	152	JAOWPJ0000000000
SRR18191570, SRR18191568	Salting out	Crl154393	O157:H7	2a, 2c	+	Unicycler	21,282	11	5,430,616	5,174,002	50.58	191	JAOQLD0000000000
SRR18191567, SRR18191598	Salting out	Crl154395	O157:H7	2c	+	Unicycler	21,865	17	5,744,891	5,126,924	50.47	134	JAOQLC0000000000
SRR18191597, SRR18191596	Salting out	Crl154397	O157:H7	2c, 2c	+	Flye ^e	20,389	3	5,807,355	5,666,998	50.47	134	JAOWOM0000000000
SRR18191595, SRR18191594	Salting out	Crl169922	O82:H8	–	–	Unicycler	20,244	6	5,780,274	5,273,188	50.49	134	JAOWNA0000000000
SRR18191593, SRR18191592	Salting out	Crl169937	O51:H41	–	–	Unicycler	13,654	4	5,720,557	4,991,949	50.39	129	JAOQLB0000000000
SRR18191591, SRR18191643	Salting out	CrlO103	O103:H2	–	–	Unicycler	16,776	4	5,644,625	5,555,517	50.48	129	JAOWOL0000000000
SRR18191642, SRR18191641	Salting out	CrlO157	O157:H7	2c	+	Unicycler	22,759	19	5,749,327	5,423,006	50.49	240	JAOQLA0000000000
SRR18191640, SRR18191639	Bead based, salting out	<i>E. coli</i> 12-1	O157:H7	2a, 2c	+	Flye ^e	25,609	10	4,868,876	2,456,854	50.78	225	JAOQKZ0000000000
SRR18191638, SRR18191637	Salting out	EC14	O174:H21	2c	–	Unicycler	20,105	4	4,976,199	4,761,119	50.80	225	JAOWOK0000000000
SRR18191636, SRR18191635	Salting out, bead based	ECA135	O22:H16	2b, 2c, 2d	–	Canu ^d	29,351	5	4,958,903	4,892,016	50.63	95	JAOQKY0000000000
SRR18191634, SRR18191632	Bead based, salting out	ECA15	O79:H48	1a, 2a	–	Raven ^b	19,793	5	5,090,231	4,969,612	50.57	144	JAOQKX0000000000
SRR18191631, SRR18191630	Salting out	ECA193	O8H21	1a, 2c	–	Unicycler	20,554	9	5,624,392	4,232,969	50.43	278	JAOQKW0000000000
SRR18191629, SRR18191628	Bead based	ECA194	O179:H8	1a, 2a	–	Unicycler	15,826	3	5,642,849	5,231,425	50.52	278	JAOWOJ0000000000
SRR18191627, SRR18191626	Bead based	ECA279	O174:H2	1a, 2d	–	Unicycler	2,565	7	5,909,043	5,747,499	50.44	284	JAOWPJ0000000000
SRR18191625, SRR18191624	Bead based, salting out	ECA329	O91:H21	2a, 2d	–	Unicycler	15,119	5	5,807,203	5,689,286	50.50	284	JAOWOI0000000000
SRR18191625, SRR18191625	Salting out	ECA329	O91:H21	2a, 2d	–	Flye ^c	15,119	25	5,082,783	4,945,157	50.83	219	JAOQKV0000000000
SRR18191565, SRR18191564	Salting out	ECA34	O5H9	1a	+	Flye ^e	6,208	14	5,155,830	4,911,711	50.83	219	JAOWOH0000000000
									5,459,604	5,386,935	50.63	276	JAOWPH0000000000
									5,313,712	5,313,712	50.70	276	JAOWOG0000000000
									5,326,335	4,303,608	50.71	58	JAOWMZ0000000000
									5,596,707	5,158,603	50.69	222	JAOQKU0000000000
									5,094,287	4,913,760	50.72	154	JAOQKT0000000000
									5,126,030	2,145,451	50.72	199	JAOQKS0000000000
									5,167,400	5,037,956	50.76	199	JAOWOF0000000000
									5,167,518	5,016,862	50.71	235	JAOWNP0000000000
									5,342,559	4,901,208	50.76	167	JAOWOE0000000000
									5,341,159	4,796,583	50.64	86	JAOWOD0000000000

(Continued on next page)

TABLE 1 (Continued)

NCBI accession no. (ONT, Illumina)	DNA extraction method(s) ^f	Strain	Serotype ^k	stx subtype(s)	ere	Hybrid assembly	MinION read length (N ₅₀ , lbp)	No. of contigs	Genome size (bp)	Assembly N ₅₀ (bp)	GC content (%)	Genome coverage (X)	GenBank accession no.
SRR18191623, SRR18191564	Salting out	ECA34	O5:H9	1a	+	Raven ^d	24,947	4	5,414,456	4,637,316	50.68	115	JAOWMY0000000000
SRR18191563, SRR18191562	Bead based, salting out	ECA36	O5:H9	1a, 1a	+	Unicycler	22,228	14	5,418,653	4,566,021	50.66	100	JAOWNN0000000000
SRR18191561, SRR18191560	Bead based, salting out	ECA37	O5:H9	1a, 1a	+	Flye ^b	24,413	11	5,403,523	5,306,942	50.69	112	JAOWOC0000000000
SRR18191559, SRR18191558	Bead based	ECA399	O174:H21	2c	-	Unicycler	3,390	5	5,141,946	3,448,145	50.78	479	JAOCKR0000000000
SRR18191557, SRR18191556	Salting out	ECA400	O6:H10	2d	-	Canu ^d	24,727	2	5,061,078	5,053,258	50.68	200	JAOWPG0000000000
SRR18191554, SRR18191553	Bead based	ECA447	O22:H16	1a, 2b, 2d	-	Unicycler	6,419	5	5,351,044	5,298,558	50.63	121	JAQKQK0000000000
SRR18191552, SRR18191551	Salting out	ECA89	OgN-RRK2:H16	1c	-	Flye	18,224	52	5,336,292	4,922,938	50.72	180	JAOWMY0000000000
SRR18191550, SRR18191549	Salting out	ECA97	O113:H4	2d	-	Unicycler	17,597	4	5,163,781	4,943,802	50.76	180	JAOWNK0000000000
SRR18191548, SRR18191547	Salting out	HSVR03	O157:H7	2c	+	Raven ^b	22,885	40	5,585,011	1,473,641	50.49	67	JAOWMW0000000000
SRR18191546, SRR18191545	Salting out	HSVR04	O157:H7	2c	+	Flye ^b	22,926	11	5,843,094	5,515,994	50.43	113	JAOWOB0000000000
SRR18191543, SRR18191622	Bead based	NC672:mucus	Ox13:H2		-	Flye ^e	6,632	3	5,323,626	5,187,741	50.66	381	JAOWOA0000000000
SRR18191621, SRR18191620	Salting out	NC809	O41:H7		-	Unicycler	19,581	8	5,227,833	4,891,608	50.51	230	JAQKQK0000000000
SRR18191619, SRR18191618	Bead based	NV34	O168:H8	2d	-	Unicycler	6,450	6	5,269,996	4,249,978	50.77	402	JAQKKN0000000000
SRR18191617, SRR18191616	Bead based	NV36	O75:H8	1c,2b	-	Unicycler	6,484	8	5,575,909	5,306,095	50.65	468	JAOWMY0000000000
SRR18191615, SRR18191614	Salting out	Slk8430761	O177:H25	2c, 2d	+	Unicycler ^f	20,113	11	5,577,269	5,301,141	50.65	113	JAOWNN0000000000
SRR18191612, SRR18191611	Salting out	Slk8430767	O177:H25	2c, 2d	+	Flye ^b	17,583	30	5,639,340	5,231,455	50.58	180	JAOWNO0000000000
						Unicycler	17,583	12	5,658,335	5,248,496	50.58	180	JAOWNZ0000000000
						Raven ^d	17,583	3	5,420,630	5,017,089	50.54	150	JAQOKL0000000000
									5,458,939	5,276,849	50.57	150	JAOWML0000000000

^a Long-read assembly polished with pilon.
^b Long-read assembly polished with racon and medaka.
^c Long-read assembly polished with racon (2 rounds) and medaka.
^d Long-read assembly polished with racon, medaka, and pilon.
^e Long-read assembly polished with racon, medaka, and pilon, and contigs <1 kb were removed.
^f Long-read assembly polished with racon (3 rounds), medaka, and pilon, and contigs <1 kb were removed.
^g Long-read assembly polished with racon (4 rounds), medaka, and pilon, and contigs <1 kb were removed.
^h Long-read assembly polished with racon (3 rounds), medaka, and pilon, and contigs <1 kb were removed.
ⁱ Long-read assembly polished with racon (3 rounds), pilon, and contigs <1 kb were removed.
^j If two methods were used for DNA extraction, the first one corresponds to the DNA extraction method used for sequencing using Illumina and the second for MinION sequencing.
^k Serotypes were determined using *in silico* analysis.
^l 50 × subsampling.
^m - are used to describe bash arguments/options.

were retained for some of the samples. Whenever possible, Unicycler performed the circularization of the replicons (5).

Assemblies from 1 to 52 contigs (mean, 10.33 ± 9.73) with a total assembly length between 4,849,707 and 6,118,277 bp (mean, $5,468,530.42 \pm 292,599.77$ bp) and mean GC content of 50.64% (± 0.13) were generated. N_{50} values ranged from 1,082,226 to 5,821,752 bp (mean, $4,759,454.32 \pm 1,018,105.98$ bp). The main sample characteristics, including serotype, *stx* and *eae* gene presence (determined using abricate [-min-cov 60 -min-id 80]), genome coverage, and accession numbers are reported in Table 1. All genomes were annotated using the National Center for Biotechnology Information (NCBI) Prokaryotic Genome Annotation Pipeline (PGAP) v6.3 at http://www.ncbi.nlm.nih.gov/genome/annotation_prok (12).

Data availability. Short and long raw reads were deposited in the NCBI SRA database under BioProject accession number [PRJNA808207](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA808207). Additionally, assembled genomes were deposited in GenBank under accession numbers as referred to in Table 1 within BioProject accession numbers [PRJNA808207](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA808207), [PRJNA885284](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA885284), [PRJNA884285](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA884285), [PRJNA884276](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA884276), and [PRJNA883638](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA883638).

REFERENCES

- Karmali MA. 2004. Infection by Shiga toxin-producing *Escherichia coli*: an overview. *Mol Biotechnol* 26:117–122. <https://doi.org/10.1385/MB:26:2:117>.
- Jaudou S, Tran ML, Vorimore F, Fach P, Delannoy S. 2022. Evaluation of high molecular weight DNA extraction methods for long-read sequencing of Shiga toxin-producing *Escherichia coli*. *PLoS One* 17:e0270751. <https://doi.org/10.1371/journal.pone.0270751>.
- Wick RR, Judd LM, Holt KE. 2019. Performance of neural network basecalling tools for Oxford Nanopore sequencing. *Genome Biol* 20:129. <https://doi.org/10.1186/s13059-019-1727-y>.
- De Coster W, D'Hert S, Schultz DT, Cruts M, Van Broeckhoven C. 2018. NanoPack: visualizing and processing long-read sequencing data. *Bioinforma Oxf Engl* 34:2666–2669. <https://doi.org/10.1093/bioinformatics/bty149>.
- Wick RR, Judd LM, Gorrie CL, Holt KE. 2017. Unicycler: resolving bacterial genome assemblies from short and long sequencing reads. *PLoS Comput Biol* 13:e1005595. <https://doi.org/10.1371/journal.pcbi.1005595>.
- Kolmogorov M, Bickhart DM, Behsaz B, Gurevich A, Rayko M, Shin SB, Kuhn K, Yuan J, Polevikov E, Smith TPL, Pevzner PA. 2020. metaFlye: scalable long-read metagenome assembly using repeat graphs. *Nat Methods* 17:1103–1110. <https://doi.org/10.1038/s41592-020-00971-x>.
- Vaser R, Šikić M. 2021. Time- and memory-efficient genome assembly with Raven. *Nat Comput Sci* 1:332–336. <https://doi.org/10.1038/s43588-021-00073-4>.
- Gurevich A, Saveliev V, Vyahhi N, Tesler G. 2013. QUAST: quality assessment tool for genome assemblies. *Bioinforma Oxf Engl* 29:1072–1075. <https://doi.org/10.1093/bioinformatics/btt086>.
- Vaser R, Sović I, Nagarajan N, Šikić M. 2017. Fast and accurate de novo genome assembly from long uncorrected reads. *Genome Res* 27:737–746. <https://doi.org/10.1101/gr.214270.116>.
- Walker BJ, Abeel T, Shea T, Priest M, Abouelliel A, Sakthikumar S, Cuomo CA, Zeng Q, Wortman J, Young SK, Earl AM. 2014. Pilon: an integrated tool for comprehensive microbial variant detection and genome assembly improvement. *PLoS One* 9:e112963. <https://doi.org/10.1371/journal.pone.0112963>.
- Koren S, Walenz BP, Berlin K, Miller JR, Bergman NH, Phillippy AM. 2017. Canu: scalable and accurate long-read assembly via adaptive k-mer weighting and repeat separation. *Genome Res* 27:722–736. <https://doi.org/10.1101/gr.215087.116>.
- Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, Ostell J. 2016. NCBI prokaryotic genome annotation pipeline. *Nucleic Acids Res* 44:6614–6624. <https://doi.org/10.1093/nar/gkw569>.