



Draft Genome Sequences of 158 *Listeria monocytogenes* Strains Isolated from Black Bears (*Ursus americanus*) in the United States

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ABSTRACT *Listeria monocytogenes* is responsible for severe foodborne disease and major economic losses, but its potential reservoirs in natural ecosystems remain poorly understood. Here, we report the draft genome sequences of 158 *L. monocytogenes* strains isolated from black bears (*Ursus americanus*) in the southeastern United States between 2014 and 2017.

Listeria monocytogenes is a facultative intracellular Gram-positive bacterial pathogen responsible for the severe foodborne disease listeriosis (1). Three serotypes (i.e., 1/2a, 1/2b, and 4b) predominate in human listeriosis, with 4b being the leading contributor and including all major hypervirulent clones (1, 2). *L. monocytogenes* is notorious for its persistence in food processing environments (FPEs), but the actual sources of the strains that colonize FPEs remain poorly understood (3). Food animals and agricultural environments have been extensively investigated, while potential reservoirs in natural ecosystems such as wildlife remain underexplored.

We found that wild black bears (*Ursus americanus*) in the southeastern United States were frequently colonized by *L. monocytogenes* without apparent disease symptoms, with 12% of the samples yielding serotype 4b (4). A significant portion of 4b strains exhibited the multiplex PCR profile IVb-vI encountered in emerging clones such as ST382 and 554 (3, 4). Here, we report the whole-genome sequence (WGS) data of 158 *L. monocytogenes* strains from these black bears, including 84 and 57 of serotype 1/2a and 4b, respectively (Table 1). WGS analysis revealed 68 sequence types (STs) based on the multilocus sequence typing (MLST) scheme. Surprisingly, the generally-ubiquitous STs 1, 2, 4, and 6 (5) were markedly uncommon, with only four strains of ST1 and none of ST2, ST4, or ST6. Lineage III, frequently encountered in nonhuman animals (6), was encountered in only nine strains. Dominant groups were clonal complex 554 (CC554) (serotype 4b; $n = 28$), CC388 (serotype 4b; $n = 11$), and CC20 (serotype 1/2a; $n = 9$). The majority of the STs (42/68, ca. 62%) were novel (Table 1).

Fecal samples and rectal and nasal swabs were enriched for *Listeria* using the ISO method with a Half Fraser primary enrichment at 30°C for 24 to 48 h followed by a Full Fraser

Editor David Rasko, University of Maryland School of Medicine

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The authors declare no conflict of interest.
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Received 9 April 2023

Accepted 13 May 2023

Published 5 June 2023

TABLE 1 Characteristics of the 158 *Listeria monocytogenes* strains from black bears (*Ursus americanus*) described in this report

Strain name	Serotype	ST*	CC	Yr	Isolation		City, state, country	Identifier	Capture coordinates	Sample type	No. of contigs	GC content (%)	Total length (bp)	N ₅₀ (bp)	Coverage (x)	No. of reads	Sequencing method	Read quality control and trimming tools	GenBank	BioSample	Assembly	Sequence Read Archive
					Bear	Accession no.																
SK839	1/2a	788	7	2014	NC, USA	UNK1	Unknown	Unknown	Feces	14	37.9	2,886,019	1,493,457	78	534,583	illumina M5Seq	CLC Genomics	AZACD0000000000	SAMN17815015	GCA_017121895.1	SRR13642977	
SK8109	1/2a	900	7	2014	NC, USA	UNK Caswell	Unknown	Unknown	Feces	18	37.9	2,909,257	1,481,159	93	665,817	illumina M5Seq	Workbench 7.5.1	AZCLO0000000000	SAMN17815130	GCA_017120345.1	SRR13643217	
SK8403	1/2a	365	14	2016	Ashville, NC, USA	N056	35-584599 N, 82-6231004 W	Orphan	Nasal swab	67	37.9	2,932,209	428,130	1,170	13,346,689	illumina NextSeq 500	CLC Genomics	AZCLO0000000000	SAMN08183176	GCA_004626455.1	SRR6394897	
SK8557	1/2a	1388	14	2016	Ashville, NC, USA	N131	35-648864 N, 82-470985 W	USA	Feces	30	37.9	2,902,022	339,136	484	4,857,222	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXD0000000000	SAMN08183176	GCA_004626455.1	SRR6392039	
SK8560	1/2a	1388	14	2016	Ashville, NC, USA	N131	35-648864 N, 82-470985 W	USA	Rectal swab	23	37.8	2,953,489	1,504,505	60	461,506	illumina M5Seq	CLC Genomics	AZCFA0000000000	SAMN17814197	GCA_017123355.1	SRR13642676	
SK8165	1/2a	20	20	2015	Ashville, NC, USA	N061	35-581790 N, 82-518469 W	USA	Rectal swab	18	37.9	2,970,085	525,811	424	4,304,067	illumina M5Seq	Workbench 7.5.1	AZAS4000000000	SAMN17815064	GCA_017069151.1	SRR13643076	
SK823	1/2a	20	20	2014	Ashville, NC, USA	N024	35-581683 N, 82-518469 W	USA	Feces	18	37.9	2,858,149	583,919	65	397,990	illumina M5Seq	CLC Genomics	AZCOC0000000000	SAMN17814492	GCA_017122155.1	SRR13642960	
SK847	1/2a	20	20	2014	Marion, GA, USA	UGA169	Unknown	Unknown	Rectal swab	23	37.8	3,028,268	299,142	48	303,351	illumina M5Seq	Workbench 7.5.1	AZCOT0000000000	SAMN17815018	GCA_017121245.1	SRR13642985	
SK8612	1/2a	20	20	2016	Ashville, NC, USA	N087	35-603350 N, 82-527849 W	USA	Feces	18	37.8	3,039,614	378	562,688	183	1,915,619	illumina M5Seq	CLC Genomics	AZAZG0000000000	SAMN17814371	GCA_017059255.1	SRR13642909
SK8217	1/2a	1384	20	2015	Ashville, NC, USA	N043	35-499100 N, 82-530667 W	USA	Rectal swab	15	37.9	2,972,380	525,813	119	1,215,566	illumina M5Seq	Workbench 7.5.1	AZAZA0000000000	SAMN17815039	GCA_017069215.1	SRR13643125	
SK8362	1/2a	1384	20	2015	Ashville, NC, USA	N095	35-517192 N, 82-573830 W	USA	Rectal swab	19	37.9	2,973,852	525,813	247	2,582,252	illumina M5Seq	CLC Genomics	AZAZA0000000000	SAMN17815131	GCA_017068775.1	SRR13643229	
SK8455	1/2a	1384	20	2016	Ashville, NC, USA	N116	35-517192 N, 82-573830 W	USA	Nasal swab	21	37.9	2,892,383	583,956	1,170	12,258,689	illumina NextSeq 500	Workbench 7.5.1	AAAXL0000000000	SAMN08183153	GCA_004623875.1	SRR6395536	
SK8528	1/2a	1384	20	2016	Ashville, NC, USA	N125	35-648864 N, 82-470985 W	USA	Feces	22	37.9	2,848,312	583,887	1,027	10,377,382	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXE0000000000	SAMN08183182	GCA_004622345.1	SRR6397281	
SK8740	1/2a	1484	20	2017	Ashville, NC, USA	N151	35-591109 N, 82-479895 W	USA	Rectal swab	16	37.9	2,936,976	573,660	105	1,049,569	illumina M5Seq	Workbench 7.5.1	AZAZG0000000000	SAMN17814274	GCA_017059075.1	SRR13642884	
SK8690	1/2a	321	321	2016	Ashville, NC, USA	N145	35-684397 N, 82-538996 W	USA	Feces	18	37.8	3,000,799	489,037	190	1,938,787	illumina M5Seq	CLC Genomics	AZAZG0000000000	SAMN17814134	GCA_017059375.1	SRR13642851	
SK8197	1/2a	1370	570	2015	Ashville, NC, USA	N059	35-646382 N, 82-576257 W	USA	Nasal swab	27	37.9	2,848,964	570,292	456	4,617,926	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXZ0000000000	SAMN08183171	GCA_004625055.1	SRR6395184	
SK8116	1/2a	1362	787	2014	Ashville, NC, USA	N049	35-520216 N, 82-492551 W	USA	Rectal swab	12	37.9	2,976,860	544,553	102	721,551	illumina M5Seq	CLC Genomics	AZACP0000000000	SAMN17814358	GCA_017122695.1	SRR13642907	
SK8117	1/2a	1362	787	2014	Ashville, NC, USA	N049	35-520216 N, 82-477618 W	USA	Rectal swab	11	37.9	2,939,966	526,146	124	860,770	illumina M5Seq	Workbench 7.5.1	AZACP0000000000	SAMN17814323	GCA_017123095.1	SRR13642767	
SK8100	1/2a	838	838	2014	Ashville, NC, USA	N040	35-496265 N, 82-503329 W	USA	Swab	126	37.9	2,870,294	43,622	60	596,869	illumina NextSeq 500	Workbench 7.5.1	DAKHK0000000000	SAMN31891312	GCA_056470765.1	SRR22428071	
SK8137	1/2a	838	838	2014	Ashville, NC, USA	N058	35-625244 N, 82-535214 W	USA	Feces	24	37.9	2,891,928	436,201	70	497,362	illumina M5Seq	CLC Genomics	AZACP0000000000	SAMN17814481	GCA_017122395.1	SRR13642946	
SK8140	1/2a	838	838	2014	Ashville, NC, USA	N059	35-627214 N, 82-498245 W	USA	Feces	42	37.9	2,875,338	292,529	35	348,942	illumina M5Seq	Workbench 7.5.1	AZAZQ0000000000	SAMN17815088	GCA_017069155.1	SRR13643175	
SK8144	1/2a	1368	906	2014	VA, USA	VT BBRC 119	Unknown	Unknown	Rectal swab	16	37.9	2,917,963	525,325	139	957,279	illumina M5Seq	CLC Genomics	AZACD0000000000	SAMN17814324	GCA_017123075.1	SRR13642766	
SK8187	1/2a	1368	906	2015	VA, USA	VT BBRC 119	Unknown	Unknown	Nasal swab	22	37.9	2,871,959	524,454	929	10,194,404	illumina NextSeq 500	Workbench 7.5.1	AAAXD0000000000	SAMN08183180	GCA_004627565.1	SRR6392095	
SK8190	1/2a	1368	906	2015	VA, USA	VT BBRC 119	Unknown	Unknown	Nasal swab	26	37.9	2,867,340	517,587	487	4,564,458	illumina NextSeq 500	Workbench 7.5.1	AAAXD0000000000	SAMN08183173	GCA_004625795.1	SRR6396393	
SK8427	1/2a	912	912	2016	Ashville, NC, USA	N110	35-584093 N, 82-531423 W	USA	Rectal swab	25	37.8	2,933,152	299,475	1,265	13,648,343	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXD0000000000	SAMN08183175	GCA_004626441.1	SRR6394294	
SK8429	1/2a	912	912	2016	Ashville, NC, USA	N110	35-584093 N, 82-531423 W	USA	Swab	56	37.9	2,951,097	147,691	71	718,963	illumina NextSeq 500	Workbench 7.5.1	DAKCD0000000000	SAMN31788316	GCA_026352655.1	SRR22336611	
SK8397	1/2a	1383	912	2016	Ashville, NC, USA	N095	35-517192 N, 82-573830 W	USA	Nasal swab	26	37.8	2,961,311	271,119	772	8,477,955	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXD0000000000	SAMN08183169	GCA_004623015.1	SRR6394323	
SK8398	1/2a	1383	912	2016	Ashville, NC, USA	N095	35-517192 N, 82-573830 W	USA	Nasal swab	34	37.8	2,967,471	186,234	76	774,220	illumina NextSeq 500	Workbench 7.5.1	DAKCD0000000000	SAMN31788315	GCA_026352635.1	SRR22336613	
SK8593	1/2a	913	913	2016	Ashville, NC, USA	N136	35-635396 N, 82-573830 W	USA	Rectal swab	18	37.8	3,054,992	439,804	245	2,573,081	illumina M5Seq	CLC Genomics	AZAZH0000000000	SAMN17814125	GCA_017059535.1	SRR13642643	
SK8599	1/2a	920	920	2016	Ashville, NC, USA	N137	35-526243 N, 82-595264 W	USA	Feces	17	37.9	3,011,733	437,579	253	2,627,535	illumina M5Seq	Workbench 7.5.1	AZAZG0000000000	SAMN17814127	GCA_017059395.1	SRR13642645	
SK8632	1/2a	920	920	2016	Ashville, NC, USA	N061	35-517192 N, 82-573830 W	USA	Nasal swab	19	37.9	2,925,003	1,478,054	81	637,413	illumina M5Seq	CLC Genomics	AZAZR0000000000	SAMN17814180	GCA_017123395.1	SRR13642670	
SK8719	1/2a	920	920	2016	Ashville, NC, USA	N138	35-517192 N, 82-573830 W	USA	Nasal swab	18	37.8	3,050,966	437,585	193	2,017,452	illumina M5Seq	Workbench 7.5.1	AZAZR0000000000	SAMN17815012	GCA_017069475.1	SRR13642975	
SK8285	1/2a	935	935	2015	Ashville, NC, USA	N084	35-625251 N, 82-535369 W	USA	Rectal swab	18	37.8	2,943,324	433,614	59	598,692	illumina M5Seq	Workbench 7.5.1	AZAZR0000000000	SAMN17815069	GCA_017069195.1	SRR13643130	
SK8333	1/2a	935	935	2015	Ashville, NC, USA	N015	35-511962 N, 82-529787 W	USA	Rectal swab	17	37.8	3,102,371	498,362	375	3,990,037	illumina M5Seq	Workbench 7.5.1	AZAZO0000000000	SAMN17815091	GCA_017068535.1	SRR13643193	
SK8339	1/2a	935	935	2015	Ashville, NC, USA	N093	35-619101 N, 82-507734 W	USA	Rectal swab	23	37.9	2,967,758	297,084	716	7,488,147	illumina NextSeq 500	Workbench 7.5.1	AAAXE0000000000	SAMN08183158	GCA_004626155.1	SRR6395469	
SK8343	1/2a	935	935	2015	Ashville, NC, USA	N093	35-619101 N, 82-507734 W	USA	Nasal swab	14	37.8	3,052,216	526,690	410	4,276,797	illumina M5Seq	CLC Genomics	AZAZO0000000000	SAMN17815093	GCA_017068555.1	SRR13643188	

(Continued on next page)

TABLE 1 (Continued)

Table with columns: Strain name, Serotype, ST, CC, Yr, City, state, country, Isolation, Bear, Identifier, Capture coordinates, Sample type, No. of contigs, Total length (bp), GC content (%), Coverage (x), No. of reads, Sequencing method, Read quality control and trimming tools, GenBank, BioSample, Assembly, Sequence Read Archive. Rows include strains like S48473, S48751, S48114, etc.

(Continued on next page)

TABLE 1 (Continued)

Strain name	Serotype	ST ^a	CC	Yr	Isolation		Identifier	Capture coordinates	Sample type	No. of contigs	Total length (bp)	GC content (%)	N ₅₀ (bp)	Coverage (x)	No. of reads	Sequencing method	Read quality control and trimming tools	GenBank	BioSample	Assembly	Sequence Read Archive
					City, state, country	Bear															
SK8353	1/2a	1381	1381	2015	Ashville, NC, USA	USA	35.619101 N, -82.507734 W	Rectal swab	25	2,935,652	37.8	356,741	70	716,619	illumina NextSeq 500	FastQC v0.11.5, BBDuk v38.89	AAZADQ000000000	SAMN17815115	GCA_017068835.1	SRRI3643212	
SK8545	1/2a	1387	1387	2016	Ashville, NC, USA	USA	35.619101 N, -82.507734 W	Nasal swab	23	2,828,993	37.9	568,823	572	5,665,666	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAAXEN000000000	SAMN08183155	GCA_004627075.1	SRR6395801	
SK8699	1/2a	1389	1389	2016	Ashville, NC, USA	USA	35.517418 N, -82.575864 W	Rectal swab	20	2,963,264	37.8	459,921	86	690,705	illumina NextSeq 500	FastQC v0.11.5, BBDuk v38.89	AAZCRC000000000	SAMN17814182	GCA_017123815.1	SRRI3642669	
SK8149	1/2a	1475	1475	2014	VA, USA	USA	35.566479 N, -82.589689 W	Feces	38	2,863,550	37.9	180,571	31	304,540	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZAGQ000000000	SAMN17815125	GCA_017068755.1	SRRI3643233	
SK8150	1/2a	1476	1476	2014	VA, USA	USA	Unknown	Rectal swab	85	2,920,183	37.8	64,528	22	226,959	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZAOV000000000	SAMN17815194	GCA_017067915.1	SRRI3643294	
SK8209	1/2a	1477	1477	2015	Ashville, NC, USA	USA	35.560815 N, -82.594653 W	Rectal swab	32	2,918,323	37.8	292,789	42	432,109	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZARQ000000000	SAMN17815095	GCA_017069175.1	SRRI3643196	
SK8243	1/2a	1478	1478	2015	Ashville, NC, USA	USA	35.618079 N, -82.378587 W	Feces	14	2,966,718	37.9	524,291	565	5,896,291	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZARQ000000000	SAMN17815036	GCA_017069535.1	SRRI3643070	
SK8293	1/2a	1479	1479	2015	Ashville, NC, USA	USA	35.645548 N, -82.576047 W	Rectal swab	17	2,850,802	37.9	421,556	64	639,119	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZARQ000000000	SAMN17815042	GCA_017069235.1	SRRI3643080	
SK8728	1/2a	1483	1483	2017	Ashville, NC, USA	USA	35.609941 N, -82.557208 W	Feces	14	3,035,504	37.8	527,573	115	1,184,669	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZAEH000000000	SAMN17814285	GCA_017058975.1	SRRI3642695	
SK8231	1/2a	1487	1487	2015	Ashville, NC, USA	USA	35.609941 N, -82.557208 W	Feces	19	3,038,326	37.8	295,311	438	4,598,873	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZARL000000000	SAMN17815040	GCA_017069435.1	SRRI3643067	
SK8701	1/2a	1487	1487	2016	Ashville, NC, USA	USA	35.566479 N, -82.589689 W	Rectal swab	21	3,039,759	37.8	293,870	197	2,056,553	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZAGU000000000	SAMN17814162	GCA_017059275.1	SRRI3642663	
SK8269	1/2b	379	379	2015	Ashville, NC, USA	USA	35.620224 N, -82.519569 W	Nasal swab	48	2,904,273	37.9	173,236	33	339,275	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZAOX000000000	SAMN17815079	GCA_017069035.1	SRRI3643136	
SK8516	1/2b	379	379	2016	Ashville, NC, USA	USA	35.566479 N, -82.519569 W	Feces	31	2,885,571	37.9	345,706	736	7,400,246	illumina NextSeq 500	FastQC v0.11.5, BBDuk v38.89	AAAXFC000000000	SAMN08183145	GCA_004626735.1	SRR6397282	
SK8781	1/2b	736	736	2017	Ashville, NC, USA	USA	35.560815 N, -82.537208 W	Nasal swab	23	3,001,405	37.9	256,949	226	2,303,773	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZAGQ000000000	SAMN17814377	GCA_017059055.1	SRRI3642911	
SK858	1/2b	2973	2973	2014	Macon, GA, USA	USA	32.519241 N, -83.435799 W	Swab	87	3,000,949	37.8	60,186	89	910,060	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZAGQ000000000	SAMN31891309	GCA_026470745.1	SRR22428074	
SK859	1/2b	2973	2973	2014	Macon, GA, USA	USA	32.519241 N, -83.435799 W	Swab	94	3,015,184	37.8	63,864	89	911,078	illumina NextSeq 500	FastQC v0.11.5, BBDuk v38.89	AAZAGQ000000000	SAMN31891310	GCA_026470745.1	SRR22428073	
SK8106	1/2c	789	789	2014	Ashville, NC, USA	USA	35.499100 N, -82.550667 W	Feces	22	2,928,853	37.8	423,378	78	572,235	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZCLT000000000	SAMN17815138	GCA_017120565.1	SRRI3643222	
SK815	1/2c	789	789	2014	Ashville, NC, USA	USA	35.619750 N, -82.519569 W	Feces	18	2,925,154	37.8	423,470	56	339,038	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZCLO000000000	SAMN17814487	GCA_017122035.1	SRRI3642967	
SK8479	1/2c	1385	1385	2016	Ashville, NC, USA	USA	35.592583 N, -82.537208 W	Nasal swab	27	2,851,686	37.9	596,964	716	7,092,281	illumina NextSeq 500	FastQC v0.11.5, BBDuk v38.89	AAAXEM000000000	SAMN08183150	GCA_004626915.1	SRR6396261	
SK8159	4b	1	1	2015	Ashville, NC, USA	USA	35.581200 N, -82.519569 W	Feces	32	2,917,084	37.9	298,032	1,067	11,288,130	illumina NextSeq 500	FastQC v0.11.5, BBDuk v38.89	AAAXD000000000	SAMN08183189	GCA_004622875.1	SRR6391962	
SK8350	4b	1	1	2015	Ashville, NC, USA	USA	35.619101 N, -82.518469 W	Rectal swab	201	2,966,721	37.8	41,544	98	1,005,851	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZCLJ000000000	SAMN17815135	GCA_017120105.1	SRRI3643223	
SK8581	4b	1	1	2016	Ashville, NC, USA	USA	35.589800 N, -82.537208 W	Rectal swab	18	3,028,114	37.9	476,515	244	2,547,440	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZASF000000000	SAMN17814497	GCA_017069395.1	SRRI3642962	
SK8682	4b	1	1	2016	Ashville, NC, USA	USA	35.620987 N, -82.514457 W	Feces	14	2,933,894	37.9	516,971	203	2,033,106	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZAGP000000000	SAMN17814147	GCA_017059355.1	SRRI3642655	
SK8111	4b	1039	2	2014	Ashville, NC, USA	USA	35.618193 N, -82.537208 W	Rectal swab	19	2,975,332	37.9	329,707	75	600,860	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZCLP000000000	SAMN17815132	GCA_017120325.1	SRRI3643220	
SK8112	4b	1039	2	2014	Ashville, NC, USA	USA	35.618193 N, -82.537208 W	Rectal swab	17	3,016,345	37.9	477,787	105	806,060	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZCPV000000000	SAMN17814387	GCA_017122915.1	SRRI3642910	
SK8121	4b	1039	2	2014	Ashville, NC, USA	USA	35.620987 N, -82.514457 W	Rectal swab	19	2,925,293	37.9	477,783	76	509,221	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZCRP000000000	SAMN17814170	GCA_017123735.1	SRRI3642654	
SK8297	4b	1039	2	2015	Ashville, NC, USA	USA	35.625347 N, -82.537208 W	Nasal swab	30	2,900,303	37.9	307,904	870	8,920,502	illumina NextSeq 500	FastQC v0.11.5, BBDuk v38.89	AAAXED000000000	SAMN08183165	GCA_004625335.1	SRR6395255	
SK8461	4b	1039	2	2016	Ashville, NC, USA	USA	35.62593 N, -82.597632 W	Rectal swab	30	2,942,750	38.0	307,907	1,104	11,284,292	illumina NextSeq 500	FastQC v0.11.5, BBDuk v38.89	AAAXEP000000000	SAMN08183152	GCA_004622375.1	SRR6395704	
SK8537	4b	1039	2	2016	Ashville, NC, USA	USA	35.62593 N, -82.597632 W	Feces	32	2,939,836	37.9	307,899	565	5,827,138	illumina NextSeq 500	FastQC v0.11.5, BBDuk v38.89	AAAXEW000000000	SAMN08183140	GCA_004625495.1	SRR6397048	
SK8542	4b	1039	2	2016	Ashville, NC, USA	USA	35.62593 N, -82.597632 W	Feces	31	2,901,866	37.9	307,910	506	5,106,444	illumina NextSeq 500	FastQC v0.11.5, BBDuk v38.89	AAAXEJ000000000	SAMN08183154	GCA_004627615.1	SRR6395509	
SK8134	4b	631	4	2014	Ashville, NC, USA	USA	35.630684 N, -82.597632 W	Feces	14	2,903,802	38.0	593,005	78	483,920	illumina NextSeq 500	FastQC v0.11.5, BBDuk v38.89	ABINSV000000000	SAMN31821589	GCA_026375595.1	SRR2362639	
SK8444	4b	631	4	2016	Ashville, NC, USA	USA	35.517192 N, -82.509554 W	Feces	37	2,874,823	37.9	244,554	1,342	13,828,113	illumina NextSeq 500	FastQC v0.11.5, BBDuk v38.89	AAAXDQ000000000	SAMN08183178	GCA_004625775.1	SRR6394325	
SK8467	4b	631	4	2016	Ashville, NC, USA	USA	35.517192 N, -82.573830 W	Nasal swab	24	3,003,387	37.9	251,638	152	1,556,226	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZAKQ000000000	SAMN17815082	GCA_017068875.1	SRRI3643182	
SK8634	4b	382	183	2016	Ashville, NC, USA	USA	35.517192 N, -82.573830 W	Nasal swab	17	3,006,694	37.9	309,733	60	481,371	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZCRJ000000000	SAMN17814187	GCA_017123255.1	SRRI3642672	
SK8123	4b	388	388	2014	Ashville, NC, USA	USA	35.508438 N, -82.553691 W	Rectal swab	16	2,932,212	37.9	543,959	83	569,106	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZCRK000000000	SAMN17814135	GCA_017123595.1	SRRI3642652	
SK8282	4b	388	388	2015	Ashville, NC, USA	USA	35.508438 N, -82.553691 W	Nasal swab	30	2,887,474	37.9	498,306	814	8,124,789	illumina NextSeq 500	FastQC v0.11.5, BBDuk v38.89	AAAXEF000000000	SAMN08183160	GCA_004623635.1	SRR6395362	

(Continued on next page)

TABLE 1 (Continued)

Strain name	Serotype	ST ^a	CC	Yr	Isolation		Identifier	Capture coordinates	Sample type	No. of contigs	Total length (bp)	GC content (%)	N ₅₀ (bp)	Coverage (x)	No. of reads	Sequencing method	Read quality control and trimming tools	Accession no.		
					City, state, country	Bear												GenBank	BioSample	Assembly
SK8544	4b	388	388	2016	Ashville, NC, USA		35:62024.N -82:519569.W	Feces	26	2,927,480	37.9	538,013	624	6,372,548	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXDF000000000	SAMN08183186	GCA_004627595.1	SR66391880
SK8578	4b	388	388	2016	Ashville, NC, USA		35:6255263.N -82:597632.W	Feces	18	2,942,399	37.9	303,674	54	422,691	illumina MiSeq	CLC Genomics	AAZCR000000000	SAMN17814246	GCA_017123795.1	SR13642678
SK8647	4b	388	388	2016	Ashville, NC, USA		35:6365396.N -82:537394.W	Feces	20	3,008,530	37.9	538,173	174	1,789,146	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZAAHA000000000	SAMN17814124	GCA_017059325.1	SR13642646
SK8676	4b	388	388	2016	Ashville, NC, USA		35:4959556.N -82:525301.W	Rectal swab	19	3,055,291	37.9	538,212	180	1,876,916	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZAGV000000000	SAMN17814142	GCA_017059315.1	SR13642661
SK8698	4b	388	388	2016	Ashville, NC, USA		35:566479.N -82:517875.W	Feces	15	2,934,732	37.9	543,712	66	530,090	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZCLK000000000	SAMN17815133	GCA_017120065.1	SR13643213
SK8769	4b	388	388	2017	Ashville, NC, USA		35:5804093.N -82:589689.W	Rectal swab	25	2,946,457	37.9	498,310	135	1,350,967	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZAGR000000000	SAMN17814282	GCA_017059295.1	SR13642696
SK8776	4b	388	388	2017	Ashville, NC, USA		35:5804093.N -82:531423.W	Rectal swab	24	2,941,322	37.9	498,313	194	1,931,148	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZAGS000000000	SAMN17814426	GCA_017059135.1	SR13642922
SK8860	4b	2145	388	2014	Ashville, NC, USA		35:4680356.N -82:489578.W	Feces	15	2,883,400	37.9	515,701	79	470,837	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZACV000000000	SAMN17815029	GCA_017121425.1	SR13643007
SK8861	4b	2145	388	2014	Ashville, NC, USA		35:4680356.N -82:489578.W	Feces	88	2,902,099	37.9	66,824	82	812,998	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	DAKHKF000000000	SAMN31891311	GCA_026647025.1	SR22428072
SK8103	4b	554	554	2014	Ashville, NC, USA		35:508438.N -82:553691.W	Feces	14	2,913,078	37.9	408,295	83	598,058	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZCY000000000	SAMN17814186	GCA_017123295.1	SR13642673
SK8104	4b	554	554	2014	Ashville, NC, USA		35:508438.N -82:553691.W	Rectal swab	16	2,947,880	37.9	408,295	108	787,268	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZCKY000000000	SAMN17815142	GCA_017120265.1	SR13643242
SK8155	4b	554	554	2015	Ashville, NC, USA		35:5817291.N -82:518469.W	Rectal swab	34	2,911,628	37.9	307,794	1,000	10,851,154	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXDV000000000	SAMN08183187	GCA_004624655.1	SR66394375
SK8361	4b	554	554	2015	Ashville, NC, USA		35:571702.N -82:517830.W	Rectal swab	21	3,029,841	37.9	408,295	181	1,907,733	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZCLO000000000	SAMN17814247	GCA_017123135.1	SR13642680
SK8373	4b	554	554	2015	Ashville, NC, USA		35:648548.N -82:560473.W	Feces	18	2,987,366	37.9	408,295	208	2,161,193	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZCLX000000000	SAMN17815086	GCA_017120615.1	SR13643192
SK8379	4b	554	554	2015	VA, USA		Unknown	Feces	33	2,892,284	37.9	308,144	929	10,067,487	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXDX000000000	SAMN08183174	GCA_004626315.1	SR66394911
SK8441	4b	554	554	2016	Ashville, NC, USA		35:491520.N -82:564499.W	Feces	32	2,899,903	37.9	307,794	1,206	12,519,329	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXDT000000000	SAMN08183167	GCA_004624955.1	SR66394748
SK8494	4b	554	554	2016	Ashville, NC, USA		35:648864.N -82:470985.W	Feces	30	2,955,636	37.8	303,515	1,267	13,087,194	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXDS000000000	SAMN08183149	GCA_004623955.1	SR66394738
SK8513	4b	554	554	2016	Ashville, NC, USA		35:564779.N -82:580689.W	Feces	30	2,889,359	37.9	308,144	1,007	10,132,309	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXEQ000000000	SAMN08183147	GCA_004624395.1	SR66396513
SK8536	4b	554	554	2016	Ashville, NC, USA		35:637463.N -82:495689.W	Feces	30	2,959,942	37.9	295,426	870	9,131,000	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXDO000000000	SAMN08183183	GCA_004625675.1	SR66392040
SK8543	4b	554	554	2016	Ashville, NC, USA		35:627463.N -82:597632.W	Feces	28	2,902,028	37.9	303,515	795	8,056,112	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXFD000000000	SAMN08183144	GCA_004627115.1	SR66397911
SK8558	4b	554	554	2016	Ashville, NC, USA		35:648864.N -82:495689.W	Feces	27	2,957,295	37.8	308,144	691	7,103,431	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXET000000000	SAMN08183185	GCA_004624435.1	SR66396649
SK8614	4b	554	554	2016	Ashville, NC, USA		35:603339.N -82:499895.W	Rectal swab	18	2,933,332	37.9	408,294	65	510,190	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZCND000000000	SAMN17814196	GCA_017123315.1	SR13642675
SK8757	4b	554	554	2017	Ashville, NC, USA		35:570732.N -82:496931.W	Feces	23	2,943,198	37.9	296,833	123	1,228,096	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZCPM000000000	SAMN17814281	GCA_017123215.1	SR13642692
SK896	4b	554	554	2014	Ashville, NC, USA		35:564102.N -82:496931.W	Feces	12	2,915,645	37.9	540,987	70	438,738	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZCFX000000000	SAMN17814398	GCA_017122875.1	SR13642912
SK897	4b	554	554	2014	Ashville, NC, USA		35:564102.N -82:496931.W	Feces	14	2,987,892	37.9	540,897	96	606,506	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZCFY000000000	SAMN17814418	GCA_017122875.1	SR13642918
SK898	4b	554	554	2014	Ashville, NC, USA		35:564102.N -82:496931.W	Rectal swab	15	2,992,035	37.9	408,295	114	822,705	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZCFZ000000000	SAMN17814249	GCA_017123455.1	SR13642679
SK8317	4b	999	554	2015	Ashville, NC, USA		35:566807.N -82:564075.W	Rectal swab	27	2,889,958	37.9	308,152	712	7,127,335	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXE000000000	SAMN08183156	GCA_004626675.1	SR66395721
SK842	4b	999	554	2014	NC, USA		Unknown	Feces	17	2,935,295	37.9	408,287	87	537,195	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZCZV000000000	SAMN17815017	GCA_017121285.1	SR13642978
SK843	4b	999	554	2014	Ashville, NC, USA		35:589511.N -82:498622.W	Swab	70	2,895,361	37.9	85,377	58	579,252	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	DAKHKO000000000	SAMN31891307	GCA_0266470685.1	SR22428076
SK845	4b	999	554	2014	Ashville, NC, USA		35:589511.N -82:498622.W	Rectal swab	15	2,910,935	37.9	408,287	74	443,013	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZCPO000000000	SAMN17814438	GCA_017123435.1	SR13642934
SK846	4b	999	554	2014	Ashville, NC, USA		35:589511.N -82:498622.W	Swab	90	2,907,630	37.9	62,497	82	808,884	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	DAKHM000000000	SAMN31891308	GCA_026647125.1	SR22428075
SK8275	4b	1375	554	2015	Ashville, NC, USA		35:649548.N -82:560473.W	Rectal swab	19	3,073,987	37.9	408,354	126	910,517	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZCZD000000000	SAMN17814271	GCA_017123465.1	SR13642682
SK8321	4b	1378	554	2015	Ashville, NC, USA		35:619101.N -82:507734.W	Feces	31	2,900,741	37.9	307,904	844	8,601,599	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXFA000000000	SAMN08183142	GCA_004627255.1	SR66399033
SK8329	4b	1378	554	2015	Ashville, NC, USA		35:619101.N -82:507734.W	Rectal swab	25	2,902,558	37.9	307,919	1,075	10,918,862	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXEH000000000	SAMN08183159	GCA_004623535.1	SR66395462
SK8337	4b	1378	554	2015	Ashville, NC, USA		35:619101.N -82:507734.W	Rectal swab	30	2,901,161	37.9	303,526	881	8,951,458	illumina NextSeq 500	FastQC v0.11.5, BBduk v38.89	AAAXE1000000000	SAMN08183157	GCA_004624275.1	SR66397297
SK8341	4b	1378	554	2015	USA		Unknown	Nasal swab	20	3,029,015	37.9	303,526	377	3,880,975	illumina MiSeq	CLC Genomics Workbench 7.5.1	AAZCMI000000000	SAMN17815092	GCA_017120251.1	SR13643199

(Continued on next page)

TABLE 1 (Continued)

Strain name	Serotype	ST ^a	CC	Yr	Isolation		Identifier	Capture coordinates	Sample type	No. of contigs	Total length (bp)	GC content (%)	N ₅₀ (bp)	Coverage (x)	No. of reads	Sequencing method	Read quality control and trimming tools	Accession no.			Sequence Read Archive
					City, state, country	Bear												GenBank	BioSample	Assembly	
SKB349 4b	1378	554	2015	Asheville, NC, USA	35,619,101 N, -82,507,734 W	Rectal swab	25	2,911,540	37.9	327,771	589	5,931,561	ILLUMINA_MiSeq	Workbench 7.5.1	AAZCLJ000000000	SAMN17815134	GCA_017120385.1	SRR13643211			
SKB374 4b	801	651	2015	Asheville, NC, USA	35,619,101 N, -82,507,734 W	Feces	20	3,053,097	37.9	498,503	236	2,561,831	ILLUMINA_MiSeq	Workbench 7.5.1	AAZCMB000000000	SAMN17815087	GCA_017120645.1	SRR13643189			
SKB770 4b	801	651	2017	Asheville, NC, USA	35,580,093 N, -82,651,075 W	Rectal swab	17	3,041,941	37.9	544,009	125	1,300,339	ILLUMINA_MiSeq	Workbench 7.5.1	AAZCPJ000000000	SAMN17814423	GCA_017122895.1	SRR13642915			
SKB775 4b	801	651	2017	Asheville, NC, USA	35,580,093 N, -82,551,423 W	Nasal swab	18	2,980,467	37.9	498,505	141	1,432,594	ILLUMINA_MiSeq	Workbench 7.5.1	AAZCPK000000000	SAMN17814424	GCA_017122635.1	SRR13642920			
SKB142 Lineage III	264	264	2014	VA, USA	Unknown	Feces	25	3,030,315	37.9	386,361	841	9,160,449	ILLUMINA_NextSeq 500	FastQC v0.11.5, BBduk v3.8.89	AAAXDL000000000	SAMN08183181	GCA_004624105.1	SRR6392089			
SKB142 Lineage III	1366	434	2014	VA, USA	Unknown	Feces	14	2,960,623	38.1	489,760	117	851,785	ILLUMINA_MiSeq	Workbench 7.5.1	AAZCOE000000000	SAMN17814332	GCA_017123115.1	SRR13642765			
SKB75 Lineage III	1358	1358	2014	Macon, GA, USA	32,466,313 N, -83,576,571 W	Rectal swab	26	2,906,536	38.0	234,666	72	439,480	ILLUMINA_MiSeq	Workbench 7.5.1	AAZCGV000000000	SAMN17814432	GCA_017122535.1	SRR13642928			
SKB118 Lineage III	1363	1363	2014	Macon, GA, USA	32,548,795 N, -83,452,115 W	Rectal swab	20	2,974,737	37.8	541,748	71	456,905	ILLUMINA_MiSeq	Workbench 7.5.1	AAZCCO000000000	SAMN17814346	GCA_017122275.1	SRR13642815			
SKB119 Lineage III	1363	1363	2014	Macon, GA, USA	32,548,795 N, -83,452,115 W	Rectal swab	23	2,985,300	37.8	546,918	68	483,223	ILLUMINA_MiSeq	Workbench 7.5.1	AAZCRM000000000	SAMN17814157	GCA_017123555.1	SRR13642657			
SKB259 Lineage III	1373	1373	2015	Asheville, NC, USA	35,620,224 N, -82,519,569 W	Nasal swab	13	2,934,131	38.0	527,500	119	833,950	ILLUMINA_MiSeq	Workbench 7.5.1	AAZCCO000000000	SAMN17814273	GCA_017123175.1	SRR13642688			
SKB381 Lineage III	1382	1382	2015	VA, USA	Unknown	Feces	13	2,959,658	38.0	588,980	54	405,818	ILLUMINA_MiSeq	Workbench 7.5.1	AAZCRO000000000	SAMN17814248	GCA_017123335.1	SRR13642677			
SKB782 Lineage III	1486	1486	2017	Asheville, NC, USA	35,560,815 N, -82,594,653 W	Nasal swab	25	3,119,481	37.8	522,775	171	1,821,171	ILLUMINA_MiSeq	Workbench 7.5.1	AAZCPJ000000000	SAMN17814430	GCA_017122575.1	SRR13642923			
SKB67 Lineage III	2158	2158	2016	Macon, GA, USA	32,481,646 N, -83,578,157 W	Rectal swab	12	2,996,511	37.9	596,909	90	559,546	ILLUMINA_MiSeq	Workbench 7.5.1	AAZCPH000000000	SAMN17814467	GCA_017122495.1	SRR13642931			

^a Sequence type (ST) designations in bold are novel STs first identified in this study.

secondary enrichment at 37°C for 48 h, as previously described (4). Strains were streaked from frozen stocks (−80°C) on tryptic soy (TS) agar (Becton, Dickinson & Co.) and incubated at 37°C overnight. Genomic DNA was extracted by the DNeasy blood and tissue kit (Qiagen, Valencia, CA) from strains grown overnight at 37°C in brain heart infusion or TS broth. Libraries were prepared using 0.5 to 1 ng of genomic DNA with a Nextera XT DNA library preparation kit (Illumina, San Diego, CA, USA). Genomes were sequenced using either a NextSeq 500 sequencer with the NextSeq 500/550 high-output kit v2.5 (300 cycles, 2 by 150 bp) (Illumina) or a MiSeq desktop sequencer with the MiSeq kit v2 (500 cycles, 2 by 250 bp) (Illumina) according to the manufacturer's instructions (Table 1). Raw sequencing reads were quality controlled by FastQC v0.11.5 (7) and trimmed using BBDuk2 from BBTools v38.89 (<https://sourceforge.net/projects/bbmap/>) or using CLC Genomics Workbench 7.5.1 (CLC Bio, Boston, MA) (Table 1). Reads were deposited into the National Center for Biotechnology Information (<https://www.ncbi.nlm.nih.gov>), and assemblies produced by SKESA v 2.2 (8) were annotated using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v 6.3 (9). STs and CCs were identified using BIGSdb-Lm, hosted by the Institut Pasteur (<https://bigsdb.pasteur.fr/listeria/>) (10). Default parameters were used for all software.

Data availability. This whole-genome shotgun project has been deposited in GenBank under the accession numbers found in Table 1. The versions described in this paper are the first version.

ACKNOWLEDGMENTS

We thank Alexandra Moura and Marc Lecuit at the Institut Pasteur for the novel sequence type (ST) assignments.

This work was partially supported by award no. 2017-67012-26001 and award no. 2018-07464 from the USDA National Institute of Food and Agriculture. Any opinions, findings, conclusions or recommendations expressed are those of the authors and do not necessarily reflect the view of the USDA.

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