



Draft Genome Sequences of 278 *Salmonella enterica* Isolates from Poultry Litter in the Southeastern United States

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ABSTRACT *Salmonella enterica* continues to be a pervasive food safety concern in the poultry industry, contributing to the annual burden of foodborne illnesses in the United States. Poultry litter is a known environmental source for the transmission of *Salmonella* among broiler flocks. Here, we describe the draft genome sequences of 278 *S. enterica* isolates collected from poultry litter in Florida.

Salmonella has been the leading bacterial cause of foodborne illnesses in the U.S. since at least the 1970s (1–8). Each year, *Salmonella* causes approximately 1 million illnesses, 19,000 hospitalizations, and 378 deaths (9, 10). The U.S. poultry industry has struggled for decades to control *Salmonella* contamination among broiler chickens (11). Poultry litter has long been recognized as an environmental source of *Salmonella* dissemination among birds in poultry houses (12–14). Poultry litter is a mixture of poultry excreta, feathers, wasted feed, and bedding materials from poultry houses (15). This report provides a valuable genomic data set of *Salmonella* isolates recovered from poultry litter, which may aid studies on the genomic diversity of *Salmonella* within poultry production environments as well as contribute to future outbreak traceback investigations.

The 278 *Salmonella enterica* isolates were recovered from poultry litter samples collected from 18 commercial poultry farms in Florida between 2017 and 2018. *Salmonella* isolates were isolated using a most probable number (MPN) method (limit of detection of 0.04 MPN/g) and confirmed by PCR (16). Briefly, litter samples were incubated overnight at 37°C in buffered peptone water (BPW) and transferred to Rappaport-Vassiliadis R10 broth for selective enrichment overnight at 42°C. MPN tubes were streaked onto modified lysine iron agar, and two presumptively positive colonies were selected from each plate for *Salmonella* confirmation via PCR targeting the *invA* gene (16). Genomic DNA was extracted after incubation overnight at 35°C in trypticase soy broth (TSB) using the DNeasy blood and tissue kit (Qiagen Inc., Valencia, CA). DNA concentrations were measured using a Qubit 3.0 fluorometer (Life Technologies, MD). Sequencing libraries were prepared according to Nextera XT protocols using 0.2 ng/μL of DNA, and paired-end reads were sequenced on the Illumina (San Diego, CA) MiSeq desktop sequencer using MiSeq reagent V2 or V3 kits (500 cycles) according to the manufacturer's guidelines. Genome coverage and average read quality were estimated from the raw data. Raw data were subjected to genome assembly using Skesa 2.3.0 (17). Taxonomy assignments were performed using Kraken (18). Sequencing records with quality metrics above GenomeTrakr (19, 20) thresholds and correctly identified as *S. enterica* were submitted to the NCBI. Quality control thresholds for *Salmonella* are an average coverage of $\geq 30\times$, average read quality (*Q*) scores for reads 1 and 2 of ≥ 30 , a sequence length of 4.3 to 5.2 Mbp, and a number of contigs of ≤ 300 (20). *Salmonella* serotypes were predicted using SeqSero2 v1.1.0 (21). Default parameters were used for all software. These isolates represented 16 different serovars of *S. enterica*, with most isolates being identified as *S. enterica* serovars Typhimurium ($n = 118$), Mbandaka ($n = 55$), Kentucky ($n = 29$), Enteritidis ($n = 19$),

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TABLE 1 Genome statistics for 278 *Salmonella enterica* isolates recovered from Florida poultry litter between 2017 and 2018

Sample ID	Serotype	No. of contigs	Total length (bp)	N_{50} (bp)	Genome coverage (×)	No. of reads	GC content (%)	No. of genes	SRA accession no.	GenBank accession no.
CFSAN086184 ^a	Typhimurium	58	4,960,245	210,372	60	1,274,398	51.9	4,836	SRR12966968	AAXAED000000000
CFSAN086185 ^a	Typhimurium	63	4,993,312	207,748	70	1,490,216	51.6	4,873	SRR12966969	AAXAEC000000000
CFSAN086186 ^a	Typhimurium	62	4,965,133	208,660	68	1,422,766	51.7	4,847	SRR12967007	AAXACN000000000
CFSAN086187 ^a	Typhimurium	61	4,969,298	238,507	69	1,495,076	51.9	4,857	SRR13407536	AAYUGK000000000
CFSAN086188 ^a	Typhimurium	56	4,968,216	252,441	58	1,227,412	51.8	4,845	SRR12966373	AAXAEW000000000
CFSAN086189 ^a	Typhimurium	55	4,960,737	277,250	55	1,159,634	51.9	4,835	SRR12966160	AAXAFG000000000
CFSAN086190 ^a	Typhimurium	56	4,984,298	252,078	69	1,484,272	51.9	4,860	SRR12966159	AAXAFH000000000
CFSAN086191 ^a	Typhimurium	56	4,959,267	252,078	54	1,135,892	51.8	4,840	SRR12967104	AAXABQ000000000
CFSAN086192 ^a	Typhimurium	58	4,960,503	252,441	57	1,186,918	51.7	4,842	SRR12966771	AAXAEK000000000
CFSAN086193 ^a	Typhimurium	72	4,963,105	188,295	48	1,006,300	51.5	4,857	SRR12966970	AAXAEA000000000
CFSAN086194 ^a	Typhimurium	85	4,957,634	125,307	67	1,398,286	51.3	4,864	SRR12966965	AAXAEG000000000
CFSAN086195 ^a	Typhimurium	62	4,949,342	207,709	56	1,148,826	51.3	4,830	SRR12966136	AAXAGE000000000
CFSAN086196 ^a	Typhimurium	60	4,960,956	207,775	65	1,364,764	51.7	4,837	SRR12966120	AAXAGP000000000
CFSAN086197 ^a	Typhimurium	54	4,976,685	252,441	75	1,599,214	51.6	4,858	SRR12966775	AAXAEI000000000
CFSAN086198 ^a	Typhimurium	62	4,992,359	188,190	68	1,453,000	51.8	4,879	SRR12966967	AAXAEB000000000
CFSAN086199 ^a	Typhimurium	62	4,999,696	207,703	74	1,562,992	51.5	4,892	SRR12966971	AAXADZ000000000
CFSAN086200 ^a	Infantis	29	4,674,371	386,461	54	1,083,234	52.2	4,507	SRR12966964	AAXAEE000000000
CFSAN086201 ^a	Infantis	35	4,658,183	331,268	55	1,103,184	52.2	4,492	SRR12966776	AAXAEF000000000
CFSAN086202 ^a	Typhimurium	57	4,976,773	266,994	60	1,277,004	51.9	4,856	SRR12966773	AAXAEJ000000000
CFSAN086203 ^a	Typhimurium	53	4,967,765	266,994	64	1,357,986	52.0	4,853	SRR12967278	AAWZZD000000000
CFSAN086204 ^a	Typhimurium	53	5,017,894	238,507	105	2,310,200	52.1	4,912	SRR12967263	AAWZZQ000000000
CFSAN086205 ^a	Typhimurium	69	4,941,532	175,199	58	1,225,970	51.9	4,837	SRR12967264	AAWZZM000000000
CFSAN086206 ^a	Typhimurium	69	4,990,349	164,740	63	1,336,008	51.9	4,881	SRR12966774	AAXAEH000000000
CFSAN086207 ^a	Typhimurium	58	4,956,615	196,036	52	1,103,256	51.8	4,836	SRR12967243	AAXAAH000000000
CFSAN086208 ^a	Meleagridis	68	4,892,216	175,379	68	1,693,444	52.1	4,761	SRR13249475	AANZWF000000000
CFSAN086209 ^a	Meleagridis	53	4,878,085	171,637	63	2,050,792	52.1	4,727	SRR13249289	AAOPZO000000000
CFSAN086210 ^a	Meleagridis	50	4,920,962	255,454	77	1,700,962	52.1	4,757	SRR13620978	AAOKFR000000000
CFSAN086211 ^a	Meleagridis	43	4,941,138	464,936	92	2,063,372	51.7	4,774	SRR10827626	AAOQUH000000000
CFSAN086212 ^a	Muenster	53	4,736,397	206,375	90	1,980,158	51.8	4,737	SRR10827812	AANRPL000000000
CFSAN086213 ^a	Muenster	58	4,740,736	204,128	112	2,570,404	51.8	4,742	SRR10827768	AANQBK000000000
CFSAN086214 ^a	Meleagridis	39	4,858,500	398,044	118	2,840,042	51.8	4,803	SRR10854851	AAOKRJ000000000
CFSAN086215 ^a	Muenster	49	4,744,126	289,183	115	2,510,910	51.9	4,740	SRR10827772	AAPNFC000000000
CFSAN086220 ^a	Montevideo	45	4,668,348	297,131	125	2,608,992	51.9	4,613	SRR10827808	AAOKEZ000000000
CFSAN086221 ^a	Montevideo	40	4,684,616	355,176	115	2,490,240	51.9	4,625	SRR10827651	AAQAIZ000000000
CFSAN086222 ^a	Montevideo	43	4,671,158	276,958	105	2,255,084	52.0	4,610	SRR10827755	AAPYBM000000000
CFSAN086223 ^a	Montevideo	44	4,671,060	276,956	81	1,634,014	52.1	4,620	SRR10827636	AAOKEU000000000
CFSAN086224 ^a	Montevideo	42	4,687,041	276,950	68	1,395,922	51.8	4,634	SRR10827638	AAPYBN000000000
CFSAN086225 ^a	Montevideo	42	4,669,071	276,950	56	1,128,438	52.0	4,618	SRR10827759	AAOQRT000000000
CFSAN086226 ^a	Typhimurium	65	4,961,394	208,660	66	1,445,010	51.7	4,958	SRR10825162	AANUNY000000000
CFSAN086227 ^a	Typhimurium	66	4,948,547	186,164	52	1,096,686	51.8	4,942	SRR10825151	AAPRSR000000000
CFSAN086228 ^a	Typhimurium	58	4,950,141	252,441	80	1,787,080	51.6	4,942	SRR10827540	AAOQPT000000000
CFSAN086229 ^a	Typhimurium	55	4,951,744	252,441	86	1,914,304	51.6	4,938	SRR10827558	AAOKEL000000000
CFSAN086230 ^a	Muenster	47	4,718,427	282,249	90	1,893,766	51.6	4,700	SRR10827532	AANZLX000000000
CFSAN086231 ^a	Muenster	41	4,715,352	389,139	110	2,310,096	51.7	4,694	SRR10827535	AANVRB000000000
CFSAN086232 ^a	I--z10:e,n,z15	35	4,698,550	320,992	123	2,584,818	51.9	4,649	SRR10825150	AAOPZC000000000
CFSAN086233 ^a	Mbandaka	34	4,665,901	276,631	99	2,045,486	52.0	4,598	SRR10824940	AANRJK000000000
CFSAN086234 ^a	Mbandaka	44	4,779,451	211,298	84	1,750,728	51.6	4,766	SRR10824941	AAOPZH000000000
CFSAN086235 ^a	Mbandaka	49	4,778,256	171,113	71	1,461,498	51.4	4,769	SRR10828022	AANVPP000000000
CFSAN086237 ^a	Typhimurium	52	5,002,540	282,036	75	1,614,482	52.0	4,881	SRR12820387	AAYEWC000000000
CFSAN086238 ^a	Mbandaka	63	4,986,886	139,409	125	2,678,228	51.9	4,850	SRR12898986	AAWRMT000000000
CFSAN086239 ^a	Mbandaka	41	5,111,037	276,631	100	2,177,498	52.1	4,947	SRR12898924	AAWRBX000000000
CFSAN086240 ^a	Typhimurium	55	5,082,684	252,441	118	2,564,296	52.1	4,973	SRR12903810	AAWREK000000000
CFSAN086241 ^a	Kentucky	75	5,167,973	148,261	106	2,342,264	51.8	5,005	SRR12903804	AAWRET000000000
CFSAN086242 ^a	Typhimurium	50	5,069,882	282,032	95	2,046,376	52.1	4,958	SRR12903790	AAWREU000000000
CFSAN086243 ^a	Typhimurium	52	5,024,860	252,441	78	1,687,286	52.1	4,908	SRR12903902	AAWRDX000000000
CFSAN086244 ^a	Typhimurium	56	5,043,717	249,800	88	1,876,570	52.0	4,939	SRR12903414	AAWRGN000000000
CFSAN086245 ^a	Typhimurium	55	5,076,714	252,441	98	2,098,848	52.1	4,965	SRR12903801	AAWRSE000000000
CFSAN086246 ^a	Kentucky	95	5,164,887	116,362	106	2,352,648	51.4	5,016	SRR12903418	AAWRGG000000000
CFSAN086247 ^a	Kentucky	74	5,164,226	148,261	94	2,078,638	51.6	5,005	SRR12903318	AAWRHW000000000
CFSAN086248 ^a	Kentucky	70	5,163,787	235,822	99	2,161,438	51.8	4,998	SRR12903314	AAWRHB000000000

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TABLE 1 (Continued)

Sample ID	Serotype	No. of contigs	Total length (bp)	N_{50} (bp)	Genome coverage (x)	No. of reads	GC content (%)	No. of genes	SRA accession no.	GenBank accession no.
CFSAN086249 ^a	Typhimurium	51	5,166,447	282,032	98	2,153,578	52.1	5,050	SRR12901896	AAWRIQ000000000
CFSAN086250 ^a	Typhimurium	82	4,932,652	130,777	46	1,013,152	51.4	4,831	SRR10484704	AAPMVY000000000
CFSAN086251 ^a	Typhimurium	226	4,898,930	44,019	35	733,860	51.3	4,930	SRR10483541	AAQPSA000000000
CFSAN086252 ^a	Kentucky	146	4,980,657	81,147	36	758,372	51.6	4,891	SRR10484068	AAQHJE000000000
CFSAN086253 ^a	Kentucky	90	4,989,170	118,003	61	1,402,450	51.2	4,865	SRR10484086	AAPMGB000000000
CFSAN086254 ^a	Typhimurium	65	4,932,002	196,034	49	1,040,286	51.5	4,811	SRR10483547	AAQJEL000000000
CFSAN086255 ^a	Typhimurium	80	4,927,661	142,927	34	716,700	51.6	4,809	SRR10484103	AAPMWZ000000000
CFSAN086256 ^a	Typhimurium	69	4,933,305	150,467	61	1,490,166	51.2	4,821	SRR10484106	AAQFZR000000000
CFSAN086257 ^a	Typhimurium	72	4,931,049	150,468	54	1,374,634	51.4	4,818	SRR10483501	AAQHCE000000000
CFSAN086258 ^a	Typhimurium	58	4,936,274	252,441	63	1,594,138	51.2	4,815	SRR10484098	AAPVFR000000000
CFSAN086259 ^a	Typhimurium	71	4,934,667	150,467	71	1,884,086	51.1	4,830	SRR10484067	AAPCOV000000000
CFSAN086260 ^a	Typhimurium	96	4,912,131	115,146	60	1,440,148	51.2	4,821	SRR10484069	AAPBGV000000000
CFSAN086261 ^a	Typhimurium	58	4,912,246	238,507	75	2,127,322	51.6	4,786	SRR10484326	AAQXYU000000000
CFSAN086262 ^a	Typhimurium	73	4,918,299	161,553	41	885,486	51.6	4,797	SRR10483545	AAQHIV000000000
CFSAN086263 ^a	Typhimurium	75	4,922,751	149,742	41	907,964	51.5	4,805	SRR10483480	AAOXIA000000000
CFSAN086264 ^a	Kentucky	70	4,841,309	227,586	54	1,191,746	51.3	4,689	SRR10483526	AAPMVS000000000
CFSAN086265 ^a	Kentucky	60	4,840,528	227,586	61	1,415,800	51.3	4,684	SRR10483542	AAQGOL000000000
CFSAN086266 ^a	Kentucky	72	4,837,708	166,433	71	1,916,112	50.8	4,688	SRR10483503	AAQKKR000000000
CFSAN086267 ^a	Kentucky	83	4,838,523	147,917	44	1,131,282	51.1	4,698	SRR10483505	AAQKNV000000000
CFSAN086268 ^a	Typhimurium	68	4,936,212	208,660	74	1,744,100	51.6	4,818	SRR10483513	AAQJVW000000000
CFSAN086269 ^a	Typhimurium	73	4,934,491	188,062	84	2,401,192	51.3	4,823	SRR10483523	AAQKYU000000000
CFSAN086270 ^a	Typhimurium	59	4,911,808	249,800	88	2,336,890	51.5	4,780	SRR10484070	AAQHYF000000000
CFSAN086271 ^a	Typhimurium	60	4,917,284	196,037	78	2,275,534	51.5	4,794	SRR10484099	AAPRGG000000000
CFSAN086272 ^a	Kentucky	87	4,905,756	159,786	71	2,072,600	51.0	4,760	SRR10484644	AAOSRX000000000
CFSAN086273 ^a	Kentucky	120	4,901,773	94,649	38	1,036,214	50.9	4,774	SRR10484658	AAPMGC000000000
CFSAN086274 ^a	Kentucky	83	4,909,075	145,182	61	1,534,866	51.2	4,750	SRR10484683	AAPCQQ000000000
CFSAN086275 ^a	Kentucky	93	4,906,723	131,446	51	1,158,292	51.4	4,763	SRR10484699	AAPBZZ000000000
CFSAN086276 ^a	Typhimurium	73	4,933,661	150,334	61	1,419,314	51.5	4,821	SRR10484645	AAQKBA000000000
CFSAN086277 ^a	Typhimurium	77	4,934,252	168,030	46	1,052,296	51.5	4,826	SRR10484656	AAQYGX000000000
CFSAN086278 ^a	Typhimurium	60	4,937,379	252,441	64	1,419,542	51.8	4,807	SRR10484612	AAQKAT000000000
CFSAN086279 ^a	Typhimurium	64	4,938,210	204,339	69	1,537,472	51.9	4,815	SRR10484640	AAPAQB000000000
CFSAN086280 ^a	Typhimurium	64	4,935,453	208,660	70	1,638,648	51.4	4,818	SRR10484598	AAPUXW000000000
CFSAN086281 ^a	Typhimurium	58	4,941,817	187,584	64	1,389,580	51.6	4,818	SRR10484527	AAPMXA000000000
CFSAN086282 ^a	Typhimurium	83	4,946,678	149,552	44	903,638	51.4	4,860	SRR12967241	AAXAAK000000000
CFSAN086283 ^a	Typhimurium	63	4,957,193	187,935	50	1,044,874	51.4	4,846	SRR12967262	AAWZZR000000000
CFSAN086284 ^a	Typhimurium	59	4,976,298	276,437	71	1,524,242	51.4	4,864	SRR12967251	AAWZZX000000000
CFSAN086285 ^a	Typhimurium	60	4,948,765	226,447	50	1,042,438	51.7	4,829	SRR12967252	AAXAAA000000000
CFSAN086286 ^a	Typhimurium	54	4,966,994	282,036	51	1,064,636	51.6	4,852	SRR12967242	AAXAAI000000000
CFSAN086287 ^a	Typhimurium	54	4,961,880	252,441	58	1,215,424	51.6	4,840	SRR12967240	AAXAAJ000000000
CFSAN086288 ^a	Typhimurium	58	4,980,666	282,036	46	952,906	51.2	4,871	SRR12967237	AAXAAO000000000
CFSAN086289 ^a	Typhimurium	57	5,004,547	271,187	55	1,155,526	51.3	4,903	SRR12966113	AAXAGQ000000000
CFSAN086290 ^a	Infantis	30	4,786,382	375,508	53	1,073,286	51.9	4,678	SRR12966110	AAXAGR000000000
CFSAN086291 ^a	Infantis	33	4,742,404	335,807	59	1,169,406	51.9	4,637	SRR12965892	AAXAGZ000000000
CFSAN086292 ^a	Infantis	35	4,776,365	335,807	65	1,298,982	51.9	4,666	SRR12965890	AAXAHC000000000
CFSAN086293 ^a	Infantis	41	4,745,631	259,315	71	1,410,336	51.9	4,651	SRR12965889	AAXAHB000000000
CFSAN086294 ^a	Infantis	42	4,771,230	259,212	40	803,256	51.7	4,678	SRR12966111	AAXAGT000000000
CFSAN086295 ^a	Infantis	47	4,762,780	333,002	33	664,084	51.7	4,678	SRR12966108	AAXAGU000000000
CFSAN086296 ^a	Kentucky	55	4,865,752	237,368	50	1,042,280	49.8	4,695	SRR12965893	AAXAGW000000000
CFSAN086297 ^a	Kentucky	54	4,871,567	318,462	53	1,093,210	49.2	4,702	SRR12965891	AAXAHA000000000
CFSAN086298 ^a	Falkensee	27	4,939,334	388,082	63	1,328,982	52.0	4,735	SRR12965795	AAXAHD000000000
CFSAN086299 ^a	Falkensee	27	4,912,537	387,881	60	1,259,062	51.9	4,709	SRR12965763	AAXAHH000000000
CFSAN086300 ^a	Kentucky	56	4,856,787	333,317	50	1,016,860	49.5	4,687	SRR12966377	AAXAET000000000
CFSAN086301 ^a	Kentucky	52	4,864,696	237,359	46	951,178	49.5	4,690	SRR12966146	AAXAFS000000000
CFSAN086302 ^a	Kentucky	50	4,861,584	333,317	45	920,956	49.9	4,690	SRR12966144	AAXAFU000000000
CFSAN086303 ^a	Kentucky	55	4,875,967	341,107	55	1,154,692	50.4	4,709	SRR12966143	AAXAFY000000000
CFSAN086304 ^a	Typhimurium	61	4,967,903	208,660	55	1,152,716	51.8	4,854	SRR12966138	AAXAGC000000000
CFSAN086305 ^a	Typhimurium	93	4,908,210	125,315	48	971,944	51.4	4,851	SRR12966376	AAXAEU000000000
CFSAN086306 ^a	Typhimurium	55	4,967,195	276,616	46	963,906	51.7	4,850	SRR12967562	AAWZVR000000000
CFSAN086307 ^a	Typhimurium	57	4,963,378	276,424	37	765,832	51.7	4,845	SRR12967665	AAWZUI000000000
CFSAN086308 ^a	Typhimurium	58	4,945,355	271,187	36	742,728	51.7	4,822	SRR12967664	AAWZUM000000000

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TABLE 1 (Continued)

Sample ID	Serotype	No. of contigs	Total length (bp)	N_{50} (bp)	Genome coverage (x)	No. of reads	GC content (%)	No. of genes	SRA accession no.	GenBank accession no.
CFSAN086309 ^a	Typhimurium	52	4,973,263	277,250	42	868,546	51.8	4,858	SRR12967633	AAWZVP000000000
CFSAN086310 ^a	Enteritidis	24	4,751,240	400,836	45	895,802	51.9	4,623	SRR12967629	AAWURO000000000
CFSAN086311 ^a	Enteritidis	25	4,751,762	401,316	45	907,638	51.9	4,620	SRR12967529	AAWZWP000000000
CFSAN086312 ^a	Mbandaka	56	4,768,692	258,839	36	715,336	51.9	4,647	SRR12967292	AAWZYP000000000
CFSAN086313 ^a	Mbandaka	61	4,772,621	322,049	45	914,388	52.0	4,656	SRR12967287	AAWZYS000000000
CFSAN086314 ^a	Braenderup	25	4,835,298	445,305	61	1,245,218	52.1	4,665	SRR12967663	AAWZUK000000000
CFSAN086315 ^a	Braenderup	40	4,785,607	353,145	68	1,387,212	52.1	4,636	SRR12967518	AAWZVW000000000
CFSAN086316 ^a	Braenderup	85	4,699,470	131,222	66	1,319,192	51.8	4,598	SRR12967627	AAWZVN000000000
CFSAN086317 ^a	Braenderup	38	4,733,776	232,639	63	1,261,608	52.0	4,588	SRR12967650	AAWZUW000000000
CFSAN086318 ^a	Braenderup	26	4,743,417	445,345	64	1,272,548	52.0	4,588	SRR12967557	AAWZVV000000000
CFSAN086319 ^a	Braenderup	23	4,751,431	445,357	72	1,446,340	52.2	4,589	SRR12967558	AAWZVT000000000
CFSAN086320 ^a	Braenderup	24	4,728,023	445,348	55	1,093,982	52.1	4,568	SRR12967520	AAWZWX000000000
CFSAN086321 ^a	Montevideo	39	4,891,673	397,312	87	1,815,890	52.3	4,729	SRR12966357	AAXACZ000000000
CFSAN086322 ^a	Montevideo	40	4,766,621	397,426	69	1,406,856	52.3	4,604	SRR12965762	AAXAHG000000000
CFSAN086323 ^a	Montevideo	35	4,688,891	499,474	66	1,353,054	51.6	4,537	SRR12967150	AAXAAX000000000
CFSAN086324 ^a	Montevideo	38	4,828,360	397,450	87	1,759,786	52.3	4,664	SRR12967006	AAXACO000000000
CFSAN086325 ^a	Montevideo	38	4,814,055	390,914	71	1,449,564	52.3	4,648	SRR12966123	AAXAGN000000000
CFSAN086326 ^a	Typhimurium	54	5,000,568	277,250	76	1,611,520	52.1	4,880	SRR12967238	AAXAAL000000000
CFSAN086327 ^a	Typhimurium	52	5,113,879	277,250	115	2,509,634	52.2	4,999	SRR13252874	AAWLRY000000000
CFSAN086328 ^a	Typhimurium	50	5,088,230	277,250	96	2,078,426	52.2	4,988	SRR13252863	AAXXB000000000
CFSAN086329 ^a	Typhimurium	51	5,027,966	277,250	86	1,851,202	52.2	4,915	SRR13249712	AAXYCT000000000
CFSAN086330 ^a	Muenster	39	4,786,310	349,276	74	1,505,010	52.1	4,668	SRR13249687	AAXYDI000000000
CFSAN086331 ^a	Muenster	37	4,725,790	349,525	81	1,650,876	51.8	4,698	SRR10854819	AAOQXH000000000
CFSAN086332 ^a	l-z10:e,n,z15	34	4,701,594	272,822	90	1,809,394	52.2	4,641	SRR10854794	AANCIY000000000
CFSAN086333 ^a	Mbandaka	24	4,671,682	296,510	86	1,739,094	52.2	4,592	SRR10854875	AANUPN000000000
CFSAN086334 ^a	Mbandaka	33	4,784,241	276,631	91	1,869,112	52.1	4,769	SRR10827795	AAPNEP000000000
CFSAN086335 ^a	Mbandaka	40	4,786,993	295,490	88	1,805,270	52.0	4,767	SRR10827776	AAOQSZ000000000
CFSAN086336 ^a	Typhimurium	74	4,931,084	145,313	36	745,014	51.6	4,925	SRR10827627	AANUCL000000000
CFSAN086337 ^a	Typhimurium	62	4,931,438	188,042	42	870,738	51.6	4,915	SRR10827650	AAOQPV000000000
CFSAN086338 ^a	Typhimurium	48	4,959,178	276,474	85	1,804,652	51.9	4,947	SRR10827773	AAOPXW000000000
CFSAN086339 ^a	Typhimurium	54	4,936,252	252,441	37	759,972	51.7	4,914	SRR10827637	AAOKFW000000000
CFSAN086340 ^a	Typhimurium	56	4,961,613	240,486	45	956,966	51.5	4,952	SRR10827929	AAPVEQ000000000
CFSAN086341 ^a	Typhimurium	53	4,973,144	271,163	50	1,047,434	51.5	4,968	SRR10827813	AAOKFT000000000
CFSAN086342 ^a	Typhimurium	46	4,924,597	277,250	67	1,360,572	51.7	4,903	SRR10827761	AAQAIC000000000
CFSAN086343 ^a	Typhimurium	48	4,941,047	282,036	73	1,503,602	51.7	4,918	SRR10827756	AAOPZQ000000000
CFSAN086344 ^a	Typhimurium	53	5,098,999	282,036	116	2,476,802	51.6	4,983	SRR12967628	AAWZVQ000000000
CFSAN086345 ^a	Typhimurium	51	4,950,630	276,462	92	1,898,506	51.6	4,937	SRR10827769	AAOKFV000000000
CFSAN086346 ^a	Typhimurium	52	4,945,227	277,250	87	1,774,270	51.6	4,927	SRR10827935	AAOKFC000000000
CFSAN086347 ^a	Typhimurium	52	4,942,275	252,441	78	1,609,794	51.5	4,928	SRR10822922	AAOUYZ000000000
CFSAN086348 ^a	Typhimurium	57	4,985,896	276,437	61	1,267,074	51.5	4,975	SRR10822921	AANWQX000000000
CFSAN086349 ^a	Typhimurium	51	4,907,917	276,498	58	1,203,678	51.5	4,915	SRR10822920	AAOKDR000000000
CFSAN086350 ^a	Typhimurium	47	4,922,987	282,036	63	1,317,854	51.6	4,897	SRR10823794	AANVQZ000000000
CFSAN086351 ^a	Typhimurium	48	4,935,202	282,036	73	1,628,536	51.6	4,915	SRR10825166	AAOKEJ000000000
CFSAN086352 ^a	Typhimurium	49	4,933,433	282,036	68	1,390,848	51.8	4,919	SRR10824939	AAOKEI000000000
CFSAN086353 ^a	Typhimurium	48	4,929,844	277,250	55	1,148,458	51.7	4,911	SRR10823736	AAQAHK000000000
CFSAN086354 ^a	Typhimurium	49	4,944,380	277,250	60	1,231,866	51.7	4,929	SRR10823734	AAPYAF000000000
CFSAN086355 ^a	Typhimurium	49	4,936,259	277,250	59	1,212,902	51.8	4,919	SRR10827536	AAOQAE000000000
CFSAN086356 ^a	Mbandaka	54	4,752,869	322,049	82	1,631,566	52.0	4,730	SRR10828021	AAOPZZ000000000
CFSAN086357 ^a	Mbandaka	57	4,752,189	322,049	81	1,601,576	52.0	4,738	SRR10827554	AAOQUN000000000
CFSAN086358 ^a	Kentucky	49	4,845,149	381,542	87	1,767,972	51.8	4,800	SRR10827545	AAOKER000000000
CFSAN086359 ^a	Kentucky	60	4,844,553	158,810	76	1,658,378	52.4	4,803	SRR10827639	AAOPZG000000000
CFSAN086360 ^a	Mbandaka	86	4,728,297	117,221	70	1,480,970	52.2	4,748	SRR10827531	AAOKEY000000000
CFSAN086361 ^a	Kentucky	57	4,800,212	127,914	68	1,460,742	52.3	4,749	SRR10824113	AANUMN000000000
CFSAN086362 ^a	Kentucky	49	4,892,880	239,664	75	1,555,552	52.1	4,720	SRR12967530	AAWZWO000000000
CFSAN086363 ^a	Kentucky	50	4,881,334	332,500	52	1,062,462	51.8	4,716	SRR12967561	AAWZVU000000000
CFSAN086364 ^a	Typhimurium	44	4,896,854	273,330	66	1,375,546	52.1	4,770	SRR12967649	AAWZUZ000000000
CFSAN086365 ^a	Typhimurium	143	4,858,300	94,275	50	1,034,456	51.4	4,818	SRR12967288	AAWZYV000000000
CFSAN086366 ^a	Mbandaka	432	4,645,909	21,789	57	1,124,084	50.8	4,891	SRR12967286	AAWZYY000000000
CFSAN086367 ^a	Mbandaka	55	4,713,335	167,154	57	1,160,548	51.7	4,575	SRR12967556	AAWZVZ000000000
CFSAN086368 ^a	Mbandaka	41	4,730,177	235,125	47	933,866	51.7	4,580	SRR12967662	AAWZUL000000000

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TABLE 1 (Continued)

Sample ID	Serotype	No. of contigs	Total length (bp)	N_{50} (bp)	Genome coverage (x)	No. of reads	GC content (%)	No. of genes	SRA accession no.	GenBank accession no.
CFSAN086369 ^a	Mbandaka	31	4,731,144	322,340	45	911,342	51.7	4,568	SRR12967634	AAWZVM000000000
CFSAN086370 ^a	Mbandaka	35	4,692,652	261,721	45	888,884	52.0	4,527	SRR12967622	AAWZVS000000000
CFSAN086371 ^a	Mbandaka	28	4,732,990	336,543	59	1,183,172	52.0	4,572	SRR12967495	AAWZXW000000000
CFSAN086372 ^a	Mbandaka	31	4,700,632	261,566	66	1,310,824	52.0	4,535	SRR12967492	AAWZXW000000000
CFSAN086373 ^a	Mbandaka	80	4,749,220	117,254	53	1,059,592	51.5	4,638	SRR12967493	AAWZXW000000000
CFSAN086374 ^a	Meleagridis	95	4,915,482	93,604	60	1,246,854	51.3	4,805	SRR12967358	AAWZYA000000000
CFSAN086375 ^a	Meleagridis	175	4,929,803	56,775	66	1,387,022	51.1	4,899	SRR12967521	AAWZWY000000000
CFSAN086376 ^a	Mbandaka	58	4,666,599	164,207	47	938,170	51.9	4,600	SRR10140519	AALGDI000000000
CFSAN086377 ^a	Mbandaka	58	4,666,526	161,559	39	770,130	51.8	4,597	SRR10140522	AALGDJ000000000
CFSAN086378 ^a	Mbandaka	38	4,707,246	321,993	64	1,459,282	51.3	4,633	SRR10269955	AALWWO000000000
CFSAN086379 ^a	Mbandaka	30	4,705,878	336,386	42	845,762	51.9	4,619	SRR10166206	AALBYO000000000
CFSAN086380 ^a	Mbandaka	43	4,739,762	278,414	40	821,452	51.8	4,703	SRR10166143	AALBYB000000000
CFSAN086381 ^a	Mbandaka	38	4,739,077	336,385	53	1,069,794	51.9	4,694	SRR10140567	AALGDP000000000
CFSAN086382 ^a	Mbandaka	40	4,740,670	336,464	52	1,062,878	51.9	4,699	SRR10140564	AALGDU000000000
CFSAN086383 ^a	Mbandaka	39	4,703,598	278,963	62	1,229,028	51.8	4,650	SRR10140554	AALGDW000000000
CFSAN086384 ^a	Mbandaka	40	4,738,241	236,501	50	1,013,030	51.8	4,696	SRR10140553	AALGDT000000000
CFSAN086385 ^a	Mbandaka	45	4,740,251	336,276	51	1,038,030	51.9	4,704	SRR10140545	AALGDR000000000
CFSAN086386 ^a	Mbandaka	40	4,701,822	325,300	35	697,552	52.0	4,626	SRR10140541	AALGDK000000000
CFSAN086387 ^a	Mbandaka	67	4,699,536	160,282	62	1,328,064	51.5	4,647	SRR10140543	AALGDM000000000
CFSAN086388 ^a	Mbandaka	112	4,728,826	119,051	67	1,516,304	51.3	4,747	SRR10140498	AALGDL000000000
CFSAN086390 ^a	Mbandaka	52	4,737,683	235,125	79	1,686,002	51.6	4,698	SRR10140482	AALGDG000000000
CFSAN086391 ^a	Mbandaka	37	4,739,856	336,370	63	1,312,338	51.8	4,699	SRR10140484	AALGDF000000000
CFSAN086392 ^a	Mbandaka	44	4,740,415	322,050	65	1,330,202	51.8	4,697	SRR10165145	AALBUV000000000
CFSAN086393 ^a	Mbandaka	28	4,705,905	335,615	63	1,267,928	52.1	4,621	SRR10165152	AALBUZ000000000
CFSAN086394 ^a	Meleagridis	30	4,867,199	335,155	58	1,216,682	51.9	4,780	SRR10165030	AALBUK000000000
CFSAN086395 ^a	Mbandaka	29	4,675,025	335,919	74	1,453,554	52.2	4,581	SRR10165134	AALBUR000000000
CFSAN086396 ^a	Mbandaka	38	4,740,437	235,125	46	943,850	52.0	4,697	SRR10140520	AALGDN000000000
CFSAN086397 ^a	Mbandaka	51	4,737,402	248,197	51	1,032,358	51.8	4,704	SRR10140523	AALGDO000000000
CFSAN086398 ^a	Mbandaka	91	4,727,827	108,291	57	1,141,860	51.7	4,732	SRR10166213	AALBYX000000000
CFSAN086399 ^a	Mbandaka	62	4,739,253	202,832	56	1,225,238	51.7	4,710	SRR10166232	AALBYR000000000
CFSAN086400 ^a	Mbandaka	53	4,738,002	230,198	35	737,460	51.8	4,703	SRR10166210	AALBYP000000000
CFSAN086401 ^a	Mbandaka	50	4,739,115	276,631	54	1,149,812	51.7	4,700	SRR10166211	AALBYS000000000
CFSAN086402 ^a	Illa -z4,z24:-	48	4,558,832	191,822	51	1,020,596	51.1	4,537	SRR10166207	AALBYT000000000
CFSAN086403 ^a	Illa -z4,z24:-	47	4,558,658	186,926	59	1,196,110	51.0	4,534	SRR10140575	AALGDV000000000
CFSAN086405 ^a	Typhimurium	53	4,897,816	282,036	58	1,211,344	52.3	4,814	SRR10140568	AALGDS000000000
CFSAN086408 ^a	Typhimurium	63	4,891,814	192,274	55	1,133,246	52.1	4,815	SRR10140517	AALGDH000000000
CFSAN086409 ^a	Typhimurium	59	4,892,726	252,441	58	1,224,836	51.6	4,819	SRR10140518	AAKXTQ000000000
CFSAN086410 ^a	Enteritidis	28	4,724,629	406,451	65	1,301,324	51.9	4,669	SRR10140505	AAKXTO000000000
CFSAN086411 ^a	Typhimurium	185	4,873,238	43,364	38	833,682	52.2	4,866	SRR10165193	AALBWM000000000
CFSAN086412 ^a	Mbandaka	70	4,708,953	181,795	45	973,594	51.6	4,671	SRR10165146	AALBT000000000
CFSAN086413 ^a	Mbandaka	66	4,712,217	235,125	44	941,698	51.6	4,669	SRR10155288	AALAGV000000000
CFSAN086414 ^a	Mbandaka	72	4,753,278	199,234	44	934,532	51.8	4,719	SRR10155277	AALAKT000000000
CFSAN086415 ^a	Mbandaka	69	4,751,579	247,872	45	1,008,360	51.6	4,722	SRR10155276	AALAKY000000000
CFSAN086416 ^a	Typhimurium	77	4,891,377	129,565	66	1,545,472	52.5	4,822	SRR10156281	AALAJY000000000
CFSAN086417 ^a	Typhimurium	73	4,896,423	187,568	51	1,092,498	52.5	4,823	SRR10156262	AALAJW000000000
CFSAN086418 ^a	Mbandaka	62	4,708,866	197,157	31	641,328	51.9	4,658	SRR10156261	AALAJU000000000
CFSAN086419 ^a	Mbandaka	67	4,713,399	187,862	50	1,054,254	52.0	4,670	SRR10156247	AALAJR000000000
CFSAN086420 ^a	Typhimurium	90	4,887,889	130,776	47	1,022,382	51.9	4,835	SRR10156260	AALAJQ000000000
CFSAN086421 ^a	Typhimurium	126	4,881,937	83,010	48	1,041,544	51.9	4,858	SRR10156197	AALAJL000000000
CFSAN086422 ^a	Typhimurium	96	4,883,375	119,214	46	984,222	52.3	4,838	SRR10156068	AALAHF000000000
CFSAN086423 ^a	Typhimurium	68	4,907,464	193,833	47	987,406	52.8	4,842	SRR10194577	AALFPX000000000
CFSAN086424 ^a	Typhimurium	56	4,881,712	196,036	55	1,150,354	52.4	4,810	SRR10194552	AALFPW000000000
CFSAN086425 ^a	Typhimurium	57	4,893,095	277,250	55	1,119,116	52.4	4,811	SRR10194549	AALFPY000000000
CFSAN086426 ^a	Mbandaka	53	4,756,131	235,125	75	1,496,794	52.1	4,717	SRR10194308	AALFOC000000000
CFSAN086427 ^a	Mbandaka	51	4,751,790	236,501	62	1,251,728	52.1	4,712	SRR10194323	AALFOP000000000
CFSAN086429 ^a	Typhimurium	65	4,902,059	226,339	41	836,472	52.5	4,832	SRR10194626	AALFPZ000000000
CFSAN086431 ^a	Typhimurium	91	4,893,600	110,053	32	657,032	52.4	4,838	SRR10194537	AALFPS000000000
CFSAN086432 ^a	Typhimurium	74	4,887,653	187,569	39	806,104	52.3	4,826	SRR10194531	AALFPA000000000
CFSAN086434 ^a	Mbandaka	58	4,817,234	336,370	68	1,292,840	51.5	4,690	SRR12967357	AALWWI000000000
CFSAN086435 ^a	Mbandaka	86	4,760,515	169,007	58	1,164,028	50.9	4,661	SRR12967293	AALZHT000000000

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TABLE 1 (Continued)

Sample ID	Serotype	No. of contigs	Total length (bp)	N_{50} (bp)	Genome coverage (×)	No. of reads	GC content (%)	No. of genes	SRA accession no.	GenBank accession no.
CFSAN086436 ^a	IIIa 4:z4,z24:-	50	4,579,560	191,822	59	1,598,828	50.9	4,468	SRR12967519	AALWWF000000000
CFSAN086437 ^a	IIIa -z4,z24:-	41	4,571,927	247,531	73	1,627,010	51.8	4,456	SRR12967517	AALZHR000000000
CFSAN086438 ^a	Typhimurium	58	4,964,940	277,053	70	1,980,652	51.9	4,823	SRR12967508	AALZHQ000000000
CFSAN086439 ^a	Typhimurium	60	4,914,856	217,232	64	1,387,200	51.9	4,776	SRR12967494	AALZHP000000000
CFSAN086440 ^a	Typhimurium	63	4,911,001	208,660	74	1,270,218	51.7	4,771	SRR12967491	AALWWB000000000
CFSAN086441 ^a	Typhimurium	162	4,890,774	67,687	64	1,580,114	51.5	4,849	SRR12967354	AALZHU000000000
CFSAN086442 ^a	I 4,[5],12:i:-	67	4,934,939	185,354	48	805,890	51.2	4,871	SRR12967559	AALZHO000000000
CFSAN086443 ^a	IIIa -z4,z24:-	61	4,526,291	149,905	84	825,452	51.6	4,408	SRR12967623	AALWWG000000000
CFSAN086444 ^a	Typhimurium	66	4,903,780	252,441	65	927,660	51.7	4,770	SRR12967621	AALZHZ000000000
CFSAN086445 ^a	Typhimurium	76	4,899,541	149,552	51	1,344,416	51.3	4,816	SRR10321182	AAMMBZ000000000
CFSAN086446 ^a	Typhimurium	58	4,897,688	282,036	110	2,302,540	52.4	4,852	SRR10827527	AAOAA000000000
CFSAN086447 ^a	Typhimurium	61	4,911,875	225,667	93	1,953,686	52.7	4,876	SRR10827534	AAOVAC000000000
CFSAN086448 ^a	IIIa -z4,z24:-	45	4,558,171	212,176	122	2,386,342	51.7	4,556	SRR10823790	AAOKEM000000000
CFSAN086449 ^a	IIIa -z4,z24:-	44	4,558,958	216,344	111	2,163,870	51.7	4,559	SRR10823778	AAOQUO000000000
CFSAN086450 ^b	Enteritidis	24	4,727,865	438,869	87	1,754,310	52.2	4,692	SRR10827559	AAAYAGU000000000
CFSAN086451 ^b	Enteritidis	22	4,727,798	478,638	110	2,193,954	51.9	4,693	SRR10827560	AAAYAGX000000000
CFSAN086452 ^b	Enteritidis	27	4,724,006	406,451	90	1,824,596	51.9	4,651	SRR10321115	AAMMBN000000000
CFSAN086453 ^b	Enteritidis	29	4,723,894	376,176	81	1,620,758	52.0	4,656	SRR10320790	AAMIRA000000000
CFSAN086454 ^b	Enteritidis	27	4,725,455	406,451	95	1,991,928	52.0	4,651	SRR10321163	AAMMBX000000000
CFSAN086455 ^b	Enteritidis	26	4,725,656	406,919	74	1,593,176	51.9	4,654	SRR10321157	AAMMBR000000000
CFSAN086456 ^b	Enteritidis	31	4,724,132	406,115	77	1,568,088	51.9	4,660	SRR10321156	AAMMBS000000000
CFSAN086457 ^b	Enteritidis	33	4,723,372	375,768	64	1,357,908	51.9	4,658	SRR10321184	AAMMCF000000000
CFSAN086458 ^b	Enteritidis	30	4,725,176	401,025	98	2,236,302	51.6	4,598	SRR10484556	AAPMEN000000000
CFSAN086459 ^b	Enteritidis	31	4,724,450	283,989	72	1,784,426	51.6	4,598	SRR10484701	AAPCAG000000000
CFSAN086460 ^b	Enteritidis	36	4,723,538	358,574	95	2,561,110	51.6	4,599	SRR10484524	AAPRFY000000000
CFSAN086461 ^b	Enteritidis	38	4,723,436	358,578	56	1,396,254	51.5	4,606	SRR10484530	AAQKJL000000000
CFSAN086462 ^b	Kentucky	74	4,838,403	128,841	71	1,796,366	51.3	4,692	SRR10484599	AAQKAY000000000
CFSAN086463 ^b	Kentucky	81	4,839,549	127,898	51	1,162,956	51.5	4,695	SRR10484597	AANCCW000000000
CFSAN086464 ^b	Liverpool	55	4,751,693	216,848	49	1,160,362	49.7	4,581	SRR10484528	AAQKAU000000000
CFSAN086465 ^b	Liverpool	51	4,762,648	287,276	55	1,414,554	49.3	4,585	SRR10484708	AAPBHR000000000
CFSAN086466 ^b	Enteritidis	33	4,721,330	376,208	59	1,489,142	51.5	4,602	SRR10484700	AAQKOF000000000
CFSAN086467 ^b	Enteritidis	38	4,721,966	268,212	58	1,378,244	51.6	4,697	SRR10824531	AAOKEH000000000
CFSAN086468 ^b	Enteritidis	38	4,722,595	313,679	57	1,284,516	51.5	4,606	SRR10484651	AAOYAC000000000
CFSAN086469 ^b	Enteritidis	42	4,722,183	268,207	63	1,503,496	51.4	4,707	SRR10824934	AAOQRK000000000
CFSAN086470 ^b	Kentucky	115	5,026,979	126,570	87	1,963,946	51.0	4,902	SRR10484643	AAQICG000000000
CFSAN086471 ^b	Kentucky	119	5,024,990	111,845	56	1,277,668	51.3	4,900	SRR10484631	AAQKLU000000000
CFSAN086472 ^b	Alachua	50	4,899,077	371,315	53	1,391,358	50.6	4,778	SRR10484652	AAPXJP000000000
CFSAN086473 ^b	Alachua	52	4,904,853	235,986	62	1,487,642	50.8	4,783	SRR10484684	AAPUXR000000000

^a Collected in 2017.^b Collected in 2018.

Montevideo ($n = 11$), Infantis and Meleagridis ($n = 8$ each), and Braenderup and Muenster ($n = 7$ each). *Salmonella* serovars Alachua, Falkensee, Liverpool, and I -z10:e,n,z15 each had two isolates. One isolate of I 4,[5],12:i:-, the monophasic variant of *S. Typhimurium*, was recovered. Finally, several isolates belonging to *S. enterica* subsp. *arizonae* were observed, namely, serovars IIIa -z4,z24:- ($n = 6$) and IIIa 4:z4,z24:- ($n = 1$).

Data availability. The genome sequences of these 278 *S. enterica* isolates have been deposited in GenBank, and the accession numbers for each SRA and whole-genome shotgun sequencing project are available in Table 1.

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REFERENCES

- Centers for Disease Control and Prevention. 2019. Surveillance for foodborne disease outbreaks—United States, 2017: annual report. Centers for Disease Control and Prevention, Atlanta, GA. <https://stacks.cdc.gov/view/cdc/82378>.
- Gould LH, Walsh KA, Vieira AR, Herman K, Williams IT, Hall AJ, Cole D, Centers for Disease Control and Prevention. 2013. Surveillance for foodborne disease outbreaks—United States, 1998–2008. *MMWR Surveill Summ* 62:1–34.
- Gould LH, Mungai EA, Johnson SD, Richardson LC, Williams IT, Griffin PM, Cole D, Hall AJ. 2013. Surveillance for foodborne disease outbreaks—United States, 2009–2010. *MMWR Morb Mortal Wkly Rep* 62:41–47.
- Dewey-Mattia D, Manikonda K, Hall AJ, Wise ME, Crowe SJ. 2018. Surveillance for foodborne disease outbreaks—United States, 2009–2015. *MMWR Surveill Summ* 67:1–11. <https://doi.org/10.15585/mmwr.ss6710a1>.
- Centers for Disease Control and Prevention. 2018. Surveillance for foodborne disease outbreaks—United States, 2016: annual report. Centers for Disease Control and Prevention, Atlanta, GA. <https://stacks.cdc.gov/view/cdc/59698>.
- Olsen SJ, MacKinnon LC, Goulding JS, Bean NH, Slutsker L. 2000. Surveillance for foodborne disease outbreaks—United States, 1993–1997. *MMWR CDC Surveill Summ* 49:1–62.
- Bean NH, Griffin PM. 1990. Foodborne disease outbreaks in the United States, 1973–1987: pathogens, vehicles, and trends. *J Food Prot* 53:804–817. <https://doi.org/10.4315/0362-028X-53.9.804>.
- Bean NH, Goulding JS, Daniels MT, Angulo FJ. 1997. Surveillance for foodborne disease outbreaks—United States, 1988–1992. *J Food Prot* 60:1265–1286. <https://doi.org/10.4315/0362-028X-60.10.1265>.
- Batz MB, Hoffmann S, Morris JG. 2012. Ranking the disease burden of 14 pathogens in food sources in the United States using attribution data from outbreak investigations and expert elicitation. *J Food Prot* 75:1278–1291. <https://doi.org/10.4315/0362-028X-JFP-11-418>.
- Scallan E, Hoekstra RM, Angulo FJ, Tauxe RV, Widdowson MA, Roy SL, Jones JL, Griffin PM. 2011. Foodborne illness acquired in the United States—major pathogens. *Emerg Infect Dis* 17:7–15. <https://doi.org/10.3201/eid1701.P11101>.
- Mead G, Lammerding AM, Cox N, Doyle MP, Humbert F, Kulikovskiy A, Panin A, Do Nascimento VP, Wierup M, Salmonella on Raw Poultry Writing Committee. 2010. Scientific and technical factors affecting the setting of *Salmonella* criteria for raw poultry: a global perspective. *J Food Prot* 73:1566–1590. <https://doi.org/10.4315/0362-028X-73.8.1566>.
- Fanelli MJ, Sadler WW, Brownell JR. 1970. Preliminary studies on persistence of salmonellae in poultry litter. *Avian Dis* 14:131–141. <https://doi.org/10.2307/1588564>.
- Snoeyenbos GH, Carlson VL, McKie BA, Smyser CF. 1967. An epidemiological study of salmonellosis of chickens. *Avian Dis* 11:653–667. <https://doi.org/10.2307/1588308>.
- Olesiuk OM, Snoeyenbos GH, Smyser CF. 1971. Inhibitory effect of used litter on *Salmonella typhimurium* transmission in the chicken. *Avian Dis* 15:118–124. <https://doi.org/10.2307/1588396>.
- Chen Z, Jiang X. 2014. Microbiological safety of chicken litter or chicken litter-based organic fertilizers: a review. *Agriculture* 4:1–29. <https://doi.org/10.3390/agriculture4010001>.
- Gutierrez A, De J, Schneider KR. 2020. Prevalence, concentration, and antimicrobial resistance profiles of *Salmonella* isolated from Florida poultry litter. *J Food Prot* 83:2179–2186. <https://doi.org/10.4315/JFP-20-215>.
- Souvorov A, Agarwala R, Lipman DJ. 2018. SKESA: strategic k-mer extension for scrupulous assemblies. *Genome Biol* 19:153. <https://doi.org/10.1186/s13059-018-1540-z>.
- Wood DE, Salzberg SL. 2014. Kraken: ultrafast metagenomic sequence classification using exact alignments. *Genome Biol* 15:R46. <https://doi.org/10.1186/gb-2014-15-3-r46>.
- Timme RE, Wolfgang WJ, Balkey M, Venkata SLG, Randolph R, Allard M, Strain E. 2020. Optimizing open data to support one health: best practices to ensure interoperability of genomic data from bacterial pathogens. *One Health Outlook* 2:20. <https://doi.org/10.1186/s42522-020-00026-3>.
- Timme R, Venkata SLG, Balkey M, Randolph R, Wolfgang W, Strain E. 2022. Quality control assessment for microbial genomes: GalaxyTrakr Micro-RunQC workflow. <https://protocols.io/view/quality-control-assessment-for-microbial-genomes-g-b5niq5ce.html>.
- Zhang S, den Bakker HC, Li S, Chen J, Dinsmore BA, Lane C, Lauer AC, Fields PI, Deng X. 2019. SeqSero2: rapid and improved *Salmonella* serotype determination using whole-genome sequencing data. *Appl Environ Microbiol* 85:e01746-19. <https://doi.org/10.1128/AEM.01746-19>.