



Draft Genome Sequences of 64 *Salmonella enterica* Serotype Enteritidis Isolates Obtained from Wild Mice

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ABSTRACT *Salmonella enterica* serotype Enteritidis is a foodborne pathogen of global concern, because it is frequently isolated from foods and patients. Draft genome sequences are reported here for 64 *S. Enteritidis* strains isolated from the intestines and spleens of mice caught live on chicken farms in the U.S. Northeast. The availability of these genomes provides baseline information on the genomic diversity of *S. Enteritidis* during the 1990s, when foodborne outbreaks traced to internal contamination of eggs were prevalent.

Salmonella enterica serotype Enteritidis is an important foodborne pathogen causing salmonellosis worldwide (1). *S. Enteritidis* has been isolated from a wide range of foods, including poultry, shell eggs, egg products, and the farm environment (1, 2).

Whole-genome sequencing (WGS) has become an essential tool for investigating the evolution, diversity, and possible outbreak source of foodborne bacterial pathogens (2–9). In this report, we announce 64 draft genome sequences from a collection of *S. Enteritidis* strains isolated from mice caught live on chicken farms in the Northeast United States in the 1990s. Samples were isolated from spleens and intestines of mice.

Genomic DNA from each strain was extracted from overnight cultures using the DNeasy blood and tissue kit (Qiagen, Inc., Valencia, CA). Libraries were prepared using 1 ng of genomic DNA with the Nextera XT DNA library preparation kit (Illumina, San Diego, CA), and their genomes were sequenced using a NextSeq 500/550 high-output kit version 2 (300 cycles) on a NextSeq 500 instrument (Illumina, San Diego, CA), according to the manufacturer's instruction. Genomic data were assembled using SPAdes software version 3.8.2 (10). Annotations of assemblies were processed using the NCBI's Prokaryotic Genome Annotation Pipeline (PGAP) (11). The genome sizes range from 4.69 Mbp to 4.80 Mbp, and the number of contigs ranges from 25 to 99. Other WGS assembly data are listed in Table 1.

Accession number(s). This whole-genome project has been deposited at GenBank under the accession numbers listed in Table 1.

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TABLE 1 Draft genome sequencing quality parameters for 64 genomes

Strain	Size (Mb)	Coverage (×)	No. of genes	No. of contigs	N_{50} (bp)	Accession no.
CFSAN051823	4.69	137	4,544	25	491,477	MTV000000000
CFSAN051824	4.70	170	4,555	27	491,805	MTVN000000000
CFSAN051825	4.70	147	4,551	25	491,687	MTVM000000000
CFSAN051826	4.73	131	4,585	28	491,667	MTVL000000000
CFSAN051827	4.73	158	4,595	28	491,667	MTVK000000000
CFSAN051828	4.73	171	4,591	26	491,667	MTVJ000000000
CFSAN051829	4.73	172	4,586	28	441,751	MTVI000000000
CFSAN051830	4.73	194	4,592	27	491,667	MTVH000000000
CFSAN051831	4.73	206	4,586	26	491,667	MTVG000000000
CFSAN051832	4.73	260	4,598	27	491,670	MTVF000000000
CFSAN051833	4.73	180	4,598	30	491,670	MTVE000000000
CFSAN051834	4.70	194	4,555	30	491,711	MTVD000000000
CFSAN051835	4.70	127	4,553	27	491,829	MTVC000000000
CFSAN051836	4.70	142	4,550	28	491,838	MTVB000000000
CFSAN051837	4.70	130	4,539	26	491,720	MTVA000000000
CFSAN051838	4.70	136	4,549	28	491,720	MTUZ000000000
CFSAN051839	4.70	190	4,550	28	491,565	MTUY000000000
CFSAN051840	4.70	181	4,554	28	491,838	MTUX000000000
CFSAN051841	4.70	174	4,552	27	491,720	MTUW000000000
CFSAN051842	4.70	201	4,556	28	491,720	MTUV000000000
CFSAN051843	4.74	153	4,608	29	491,720	MTUU000000000
CFSAN051844	4.75	156	4,613	32	491,720	MTUT000000000
CFSAN051845	4.74	93	4,601	32	406,207	MTUS000000000
CFSAN051846	4.75	149	4,607	29	491,720	MTUR000000000
CFSAN051847	4.74	130	4,610	28	490,320	MTUQ000000000
CFSAN051848	4.71	173	4,570	51	491,829	MTUP000000000
CFSAN051849	4.74	159	4,605	30	491,711	MTUO000000000
CFSAN051851	4.74	96	4,610	31	681,714	MTUN000000000
CFSAN051852	4.74	113	4,613	36	355,825	MTUM000000000
CFSAN051853	4.74	77	4,602	35	490,326	MTUL000000000
CFSAN051854	4.76	126	4,641	64	406,173	MTUK000000000
CFSAN051855	4.74	176	4,611	31	400,963	MTUJ000000000
CFSAN051856	4.70	289	4,548	27	491,711	MTUI000000000
CFSAN051858	4.74	144	4,609	28	491,714	MTUH000000000
CFSAN051859	4.74	102	4,605	36	355,923	MTUG000000000
CFSAN051860	4.74	85	4,608	32	421,895	MTUF000000000
CFSAN051861	4.74	103	4,602	31	406,140	MTUE000000000
CFSAN051862	4.70	97	4,542	30	464,279	MTUD000000000
CFSAN051864	4.70	160	4,542	27	491,711	MTUC000000000
CFSAN051865	4.70	246	4,550	27	491,711	MTUB000000000
CFSAN051866	4.74	213	4,597	30	441,632	MTUA000000000
CFSAN051867	4.74	211	4,603	29	491,710	MTTZ000000000
CFSAN051868	4.74	152	4,610	28	491,828	MTTY000000000
CFSAN051870	4.74	154	4,610	28	491,711	MTTX000000000
CFSAN051871	4.70	160	4,561	32	491,821	MTTW000000000
CFSAN051872	4.73	132	4,605	89	463,567	MTTV000000000
CFSAN051873	4.70	229	4,556	26	491,808	MTTU000000000
CFSAN051874	4.70	244	4,555	28	491,808	MTTT000000000
CFSAN051875	4.70	238	4,555	28	491,690	MTTS000000000
CFSAN051876	4.70	214	4,553	27	491,690	MTTR000000000
CFSAN051877	4.70	110	4,548	28	491,690	MTTQ000000000
CFSAN051878	4.78	134	4,679	99	491,690	MTTP000000000
CFSAN051880	4.70	138	4,548	28	450,154	MTTO000000000
CFSAN051881	4.75	162	4,595	32	478,968	MTTN000000000
CFSAN051882	4.75	210	4,595	30	491,710	MTTM000000000
CFSAN051883	4.80	189	4,667	37	491,386	MTTL000000000
CFSAN051884	4.75	176	4,596	31	491,710	MTTK000000000
CFSAN051885	4.75	152	4,598	30	475,028	MTTJ000000000
CFSAN051886	4.75	62	4,599	37	406,065	MTTI000000000
CFSAN051887	4.74	100	4,594	30	441,353	MTTH000000000
CFSAN051888	4.75	116	4,603	35	400,975	MTTG000000000
CFSAN051889	4.75	222	4,615	39	491,387	MTTF000000000
CFSAN051890	4.75	274	4,604	27	491,387	MTTE000000000
CFSAN051891	4.75	267	4,599	28	491,387	MTTD000000000

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