



Draft Genome Sequences of 81 *Salmonella enterica* Strains from Informal Markets in Cambodia

Carla L. Schwan,^a Valentina Trinetta,^a Maria Balkey,^b  Peter W. Cook,^c Randall K. Phebus,^a Sara Gragg,^a Justin Kastner,^d Jessie L. Vipham,^a  Sara Lomonaco^b

^aDepartment of Animal Sciences and Industry, Food Science Institute, Kansas State University, Manhattan, Kansas, USA

^bCenter for Food Safety and Applied Nutrition, U.S. Food and Drug Administration, College Park, Maryland, USA

^cCenters for Disease Control and Prevention, Atlanta, Georgia, USA

^dDepartment of Diagnostic Medicine/Pathobiology, Kansas State University, Manhattan, Kansas, USA

ABSTRACT *Salmonella enterica* is an important global pathogen due to its contribution to human morbidity and death. The presence of *S. enterica* in Southeast Asian informal markets is amplified by cross-contamination between market surfaces and food products. Here, we describe the draft genome sequences of 81 *Salmonella enterica* isolates from informal markets in Cambodia.

Nontyphoidal *Salmonella enterica* causes the most cases of diarrheal disease worldwide and is a pathogen of global importance, particularly in low-income countries (LICs) (1). Major data gaps in LICs stem from inadequate national monitoring and surveillance programs. Whole-genome sequencing (WGS) can provide accurate information on foodborne pathogens (2). The availability of molecular data is crucial for improving food safety outcomes in LICs and understanding foodborne outbreaks and transmission pathways.

Herein, we describe the draft genome sequences of 81 *S. enterica* isolates collected from two Cambodian informal markets (i.e., those escaping food safety oversight). Sixty-four vendors classified by market location (inside versus outside) were sampled during the rainy (June 2018) and dry (January 2019) seasons. For each vendor, samples from three food contact surfaces (FCSs) and three non-food contact surfaces (NFCs) were collected, totaling 384 samples. Screening and isolation of *S. enterica* strains were conducted according to the U.S. Department of Agriculture Food Safety and Inspection Service guidelines (3). Samples were enriched with buffered peptone water, followed by selective enrichments of tetrathionate bile broth and Rappaport-Vassiliadis broth (HiMedia). Selective enrichments were streaked onto xylose-lysine-Tergitol 4 and brilliant green sulfa agar (HiMedia). Typical colonies were tested using the *Salmonella* latex agglutination kit (Oxoid, Basingstoke, UK), and presumptive isolates were confirmed by PCR (4). Genomic DNA was obtained using the DNeasy blood and tissue kit (Qiagen, Hilden, Germany), following the manufacturer's instructions. Libraries were prepared from genomic DNA with the Nextera XT DNA library preparation kit, and WGS was conducted on either a MiSeq or NextSeq sequencer, using a MiSeq reagent kit v2 (500 cycles) or a NextSeq 500/550 high-output kit v2 (300 cycles), respectively (Illumina, San Diego, CA). Minimum sequence quality was represented by average coverage of >30× and Q scores for reads 1 and 2 of >30 (5). Absence of contamination was affirmed with Kraken (6). Default parameters were used for all software unless otherwise specified. *De novo* assemblies were generated with SKESA v2.2 either by NCBI Pathogen Detection or in-house using GalaxyTrakr with standard settings (7, 8). Antibiotic resistance (AMR), stress, and virulence genotypes

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TABLE 1 Metadata for the 81 *Salmonella enterica* strains isolated from informal markets in Cambodia

Sample no. ^a	NCBI BioSample no.	SRA accession no.	GenBank accession no.	No. of contigs	Total length (bp)	N ₅₀ (bp)	GC content (%)	Coverage (x)	Avg quality scores (read 1, read 2)	No. of reads	Serotype	SPI(s)	AMR gene(s)
Isolates collected in June 2018													
CFSAN094565 (inside)	SAMN12663190	SRR10050324	JABGCS0000000000	69	4,873,866	219,252	52.4	70	36, 34	1,418,030	Typhimurium	1, 3, 4, 5, 13, 14, C63PI	None
CFSAN094567 (inside)	SAMN12668245	SRR10051127	AAKBCQ0000000000	57	4,955,643	172,452	52.5	44	36, 33	897,000	I 4,[5],12:i:-	1, 3, 5, 13, 14, C63PI	<i>aph(3'')-lb</i> , <i>aph(6)-ld</i> , <i>bla</i> _{TEM-1} , <i>sul2</i> , <i>tet(B)</i>
CFSAN094568 (inside)	SAMN12668243	SRR10051124	AAKBCK0000000000	55	5,198,930	373,560	51.9	55	36, 34	1,108,382	Derby	1, 3, C63PI	<i>aac(3)-IId</i> , <i>bla</i> _{CTX-M-3} , <i>φ</i> , <i>floR</i> , <i>fosA7</i> , <i>qnrS1</i> , <i>sul2</i> , <i>tet(A)</i> , <i>tet(M)</i>
CFSAN094569 (inside)	SAMN12668230	SRR10051109	AAKBBW0000000000	26	4,701,855	499,670	52.5	70	36, 34	1,421,354	Hvittingfoss	1, 3, 4, 5, 13, 14, C63PI	None
CFSAN094571 (inside)	SAMN12662740	SRR10049763	AAKAXV0000000000	69	5,184,225	226,413	52.2	50	31, 33	995,476	Derby	3, C63PI	<i>aac(3)-IId</i> , <i>bla</i> _{CTX-M-3} , <i>φ</i> , <i>floR</i> , <i>fosA7</i> , <i>qnrS1</i> , <i>sul2</i> , <i>tet(A)</i> , <i>tet(M)</i>
CFSAN094572 (inside)	SAMN12663184	SRR10050161	AAKBBL0000000000	32	4,680,319	331,356	52.6	55	32, 33	1,111,732	Altona	9, C63PI	None
CFSAN094573 (inside)	SAMN12663133	SRR10050104	AAKBAJ0000000000	29	4,680,915	513,284	52.7	62	32, 33	1,250,594	Altona	1, 3, C63PI	None
CFSAN094574 (outside)	SAMN12667774	SRR10051051	AAKBS0000000000	47	4,925,460	283,403	52.5	100	32, 34	2,006,780	Rissen	C63PI	<i>aph(3'')-lb</i> , <i>aph(6)-ld</i> , <i>bla</i> _{TEM-1} , <i>tet(A)</i>
CFSAN094575 (outside)	SAMN12663163	SRR10050134	AAKBAN0000000000	27	4,677,013	410,252	52.5	48	32, 33	969,076	Javiana	13, 14, C63PI	None
CFSAN094577 (outside)	SAMN12667725	SRR10050996	AAKBBO0000000000	29	4,679,187	328,974	52.7	41	31, 32	824,578	Altona	C63PI	None
CFSAN094584 (outside)	SAMN13293250	SRR10452822	AAPREJ0000000000	47	4,889,561	256,881	52.2	52	33, ^b 32 ^b	1,702,736	Typhimurium	5, 13, 14, C63PI	<i>aadA1</i> , <i>aadA2</i> , <i>bla</i> _{TEM-1} , <i>cmiA1</i> , <i>dfrA12</i> , <i>qacEA1</i> , <i>qacL</i> , <i>sul1</i> , <i>sul3</i> , <i>tet(A)</i> , <i>aph(3'')-lb</i> , <i>aph(6)-ld</i> , <i>bla</i> _{TEM-1} , <i>tet(A)</i>
CFSAN094585 (outside)	SAMN13293256	SRR10452813	AAQIHK0000000000	55	4,916,559	278,635	52.3	73	33, ^b 32 ^b	2,348,336	Rissen	C63PI	None
CFSAN094586 (outside)	SAMN13293254	SRR10452812	AAPDIY0000000000	33	4,735,977	237,700	52.5	43	33, ^b 32 ^b	1,410,512	Uganda	13, 14	None
CFSAN094587 (outside)	SAMN13293452	SRR10454469	AAPDKA0000000000	47	5,006,945	303,350	52.4	68	33, ^b 32 ^b	2,229,632	Rissen	C63PI	<i>aadA1</i> , <i>aadA2</i> , <i>bla</i> _{TEM-1} , <i>cmiA1</i> , <i>dfrA12</i> , <i>qacEA1</i> , <i>qacL</i> , <i>sul1</i> , <i>sul3</i> , <i>tet(A)</i>
CFSAN094588 (outside)	SAMN13293455	SRR10454468	AAQJIL0000000000	23	4,738,724	454,824	52.7	98	33, ^b 32 ^b	3,189,200	Uganda	13, 14, C63PI	None
CFSAN094590 (outside)	SAMN13293118	SRR10452790	AAPCHN0000000000	59	4,918,011	213,300	52.6	94	33, ^b 32 ^b	3,046,128	Rissen	C63PI	<i>aph(3'')-lb</i> , <i>aph(6)-ld</i> , <i>bla</i> _{TEM-1} , <i>tet(A)</i>
CFSAN094591 (inside)	SAMN13293114	SRR10452791	AAQOJH0000000000	49	4,918,530	223,933	52.5	93	33, ^b 32 ^b	3,015,232	Rissen	None	<i>aph(3'')-lb</i> , <i>aph(6)-ld</i> , <i>bla</i> _{TEM-1} , <i>tet(A)</i>
CFSAN094592 (inside)	SAMN13293095	SRR10452788	AAPCJA0000000000	29	4,679,294	397,032	52.8	102	33, ^b 32 ^b	3,329,360	Altona	C63PI	None
CFSAN094593 (inside)	SAMN13293094	SRR10452789	AAQNRR0000000000	67	4,960,359	271,790	52.6	99	33, ^b 32 ^b	3,194,896	Krefeld	1, 3, C63PI	<i>aph(3'')-lb</i> , <i>aph(6)-ld</i> , <i>bla</i> _{TEM-1} , <i>sul2</i> , <i>tet(A)</i> , <i>tet(B)</i>
CFSAN094595 (outside)	SAMN13293187	SRR10452793	AAPCIY0000000000	201	4,824,904	172,092	51.8	48	33, ^b 32 ^b	1,598,464	Altona	None	None
CFSAN094597 (outside)	SAMN13293518	SRR10454708	AAPMUB0000000000	68	4,687,319	151,326	52	41	33, ^b 32 ^b	1,373,328	Altona	None	None
CFSAN094599 (outside)	SAMN13293252	SRR10452811	AAPCIC0000000000	468	5,167,830	84,530	51.2	30	33, ^b 32 ^b	998,032	Rissen	None	<i>aph(3'')-lb</i> , <i>aph(6)-ld</i> , <i>bla</i> _{TEM-1} , <i>tet(A)</i>

(Continued on next page)

TABLE 1 (Continued)

Sample no. ^a	NCBI BioSample no.	SRA accession no.	GenBank accession no.	No. of contigs	Total length (bp)	N ₅₀ (bp)	GC content (%)	Coverage (x)	Avg quality scores (read 1, read 2)	No. of reads	Serotype	SPI(s)	AMR gene(s)
Isolates collected in January 2019													
<u>CFSAN096602</u> (inside)	SAMN13293236	SRR10452800	AAPUPR0000000000	53	4,846,101	252,467	52.3	70	33, ^b 32 ^b	2,278,400	Anatum	3, 13, 14, C63PI	<i>aadA1</i> , <i>bla_{LAP-2}</i> , <i>bla_{TEM-1*}</i> , <i>cmiA1</i> , <i>qacL</i> , <i>qnrS1</i> , <i>sul3</i> , <i>tet(A)</i>
<u>CFSAN096603</u> (inside)	SAMN13321513	SRR10483448	AAPLYZ0000000000	72	4,997,549	222,935	52.4	74	33, ^b 32 ^b	2,417,008	Rissen	None	<i>aadA1</i> , <i>aadA2</i> , <i>bla_{TEM-1*}</i> , <i>cmiA1</i> , <i>dfrA12</i> , <i>floR</i> , <i>qacL</i> , <i>qnrS1</i> , <i>sul2</i> , <i>sul3</i> , <i>tet(A)</i> , <i>tet(M)</i>
<u>CFSAN096604</u> (inside)	SAMN13321512	SRR10483450	AAPMWO0000000000	56	4,914,011	238,068	52.3	56	33, ^b 32 ^b	1,833,712	Rissen	None	<i>aph(3'')-Ib</i> , <i>aph(6)-Id</i> , <i>bla_{TEM-1*}</i> , <i>tet(A)</i>
<u>CFSAN096606</u> (inside)	SAMN13321510	SRR10483455	AAOZWR0000000000	84	4,609,585	110,513	52.4	30	33, ^b 32 ^b	1,011,424	Javiana	13	None
<u>CFSAN096608</u> (inside)	SAMN13321506	SRR10483451	AAPBBZ0000000000	125	4,983,354	99,781	52.5	35	33, ^b 32 ^b	1,265,040	Rissen	None	<i>aadA1</i> , <i>aadA2</i> , <i>bla_{TEM*}</i> , <i>bla_{TEM-1*}</i> , <i>cmiA1</i> , <i>dfrA12</i> , <i>floR</i> , <i>qacL</i> , <i>qnrS1</i> , <i>sul2</i> , <i>sul3</i> , <i>tet(A)</i> , <i>tet(M)</i>
<u>CFSAN096609</u> (inside)	SAMN13321503	SRR10483453	AAPCYP0000000000	102	4,993,067	148,483	52.3	37	33, ^b 32 ^b	1,255,248	Rissen	None	<i>aadA1</i> , <i>aadA2</i> , <i>bla_{TEM*}</i> , <i>bla_{TEM-1*}</i> , <i>cmiA1</i> , <i>dfrA12</i> , <i>floR</i> , <i>qacL</i> , <i>qnrS1</i> , <i>sul2</i> , <i>sul3</i> , <i>tet(A)</i> , <i>tet(M)</i>
<u>CFSAN096610</u> (inside)	SAMN13322387	SRR10484095	AAQJUG0000000000	104	4,979,073	139,864	52.5	36	33, ^b 32 ^b	1,211,136	Rissen	None	<i>aadA1</i> , <i>aadA2</i> , <i>bla_{TEM-1*}</i> , <i>cmiA1</i> , <i>dfrA12</i> , <i>floR</i> , <i>qacL</i> , <i>qnrS1</i> , <i>sul2</i> , <i>sul3</i> , <i>tet(A)</i> , <i>tet(M)</i>
<u>CFSAN096611</u> (inside)	SAMN13321502	SRR10483452	AAQKJ0000000000	94	4,994,667	133,140	52.5	51	33, ^b 32 ^b	1,698,016	Rissen	None	<i>aadA1</i> , <i>aadA2</i> , <i>bla_{TEM-1*}</i> , <i>cmiA1</i> , <i>dfrA12</i> , <i>floR</i> , <i>qacL</i> , <i>qnrS1</i> , <i>sul2</i> , <i>sul3</i> , <i>tet(A)</i> , <i>tet(M)</i>
<u>CFSAN096612</u> (outside)	SAMN13321624	SRR10483525	AAOYHR0000000000	91	4,994,881	170,117	52.5	48	33, ^b 32 ^b	1,603,888	Rissen	None	<i>aadA1</i> , <i>aadA2</i> , <i>bla_{TEM-1*}</i> , <i>cmiA1</i> , <i>dfrA12</i> , <i>floR</i> , <i>qacL</i> , <i>qnrS1</i> , <i>sul2</i> , <i>sul3</i> , <i>tet(A)</i> , <i>tet(M)</i>
<u>CFSAN096613</u> (outside)	SAMN13321528	SRR10483478	AAPUSA0000000000	86	4,994,170	186,856	52.4	45	33, ^b 32 ^b	1,488,848	Rissen	None	<i>aadA1</i> , <i>aadA2</i> , <i>bla_{TEM-1*}</i> , <i>cmiA1</i> , <i>dfrA12</i> , <i>floR</i> , <i>qacL</i> , <i>qnrS1</i> , <i>sul2</i> , <i>sul3</i> , <i>tet(A)</i> , <i>tet(M)</i>
<u>CFSAN096614</u> (outside)	SAMN13322384	SRR10484096	AAOZZM0000000000	50	4,937,735	231,881	52.4	41	33, ^b 32 ^b	1,361,888	Mbandaka	None	<i>aadA1</i> , <i>aadA2</i> , <i>bla_{TEM-1*}</i> , <i>cmiA1</i> , <i>dfrA12</i> , <i>floR</i> , <i>qacL</i> , <i>qnrS1</i> , <i>sul2</i> , <i>sul3</i> , <i>tet(A)</i> , <i>tet(M)</i>
<u>CFSAN096615</u> (outside)	SAMN13322378	SRR10484097	AAPMWP0000000000	97	4,994,949	130,669	52.3	36	33, ^b 32 ^b	1,196,224	Rissen	None	<i>aadA1</i> , <i>aadA2</i> , <i>bla_{TEM-1*}</i> , <i>cmiA1</i> , <i>dfrA12</i> , <i>floR</i> , <i>qacL</i> , <i>qnrS1</i> , <i>sul2</i> , <i>sul3</i> , <i>tet(A)</i> , <i>tet(M)</i>
<u>CFSAN096616</u> (outside)	SAMN13322423	SRR10484100	AAOVVC0000000000	91	4,755,022	101,724	52.5	31	33, ^b 32 ^b	1,037,840	Corvallis	None	<i>aadA1</i> , <i>aadA2</i> , <i>bla_{TEM-1*}</i> , <i>cmiA1</i> , <i>dfrA12</i> , <i>floR</i> , <i>qacL</i> , <i>qnrS1</i> , <i>sul2</i> , <i>sul3</i> , <i>tet(A)</i> , <i>tet(M)</i>
<u>CFSAN096617</u> (outside)	SAMN13322444	SRR10484327	AAPRFQ0000000000	46	4,763,876	292,857	52.5	51	33, ^b 32 ^b	1,696,144	Corvallis	None	<i>qnrS1</i>
<u>CFSAN096618</u> (outside)	SAMN13322169	SRR10483546	AAPBYN0000000000	41	4,763,794	260,239	52.5	59	33, ^b 32 ^b	1,959,120	Corvallis	3	<i>qnrS1</i>
<u>CFSAN096619</u> (outside)	SAMN13321508	SRR10483454	AAQKQE0000000000	36	4,772,637	292,860	52.6	81	33, ^b 32 ^b	2,662,560	Corvallis	3, C63PI	<i>qnrS1</i>
<u>CFSAN096620</u> (outside)	SAMN13321532	SRR10483477	AAOXFD0000000000	97	5,023,926	107,850	52.7	83	33, ^b 32 ^b	2,727,728	Weltevreden	13, 14, C63PI	None

(Continued on next page)

TABLE 1 (Continued)

Sample no. ^a	NCBI BioSample no.	SRA accession no.	GenBank accession no.	No. of contigs	Total length (bp)	N ₅₀ (bp)	GC content (%)	Coverage (x)	Avg quality scores (read 1, read 2)	No. of reads	Serotype	SPI(s)	AMR gene(s)
CFSAN096622 (outside)	SAMN13321595	SRR10483508	AAOXHT0000000000	127	4,992,049	86,615	52.4	32	33, ^b 32 ^b	1,060,272	Weltevreden	None	None
CFSAN096623 (outside)	SAMN13321591	SRR10483504	AAOWPT0000000000	54	4,884,751	162,476	52.3	44	33, ^b 32 ^b	1,426,064	Hvittingfoss	13, 14	None
CFSAN096624 (outside)	SAMN13321587	SRR10483507	AAQMOL0000000000	111	5,011,432	104,441	52.6	51	33, ^b 32 ^b	1,674,544	Weltevreden	13, 14	None
CFSAN096625 (outside)	SAMN13321619	SRR10483514	AAOYAQ0000000000	103	5,015,404	104,982	52.6	52	33, ^b 32 ^b	1,694,784	Weltevreden	13, 14	None
CFSAN096626 (outside)	SAMN13321607	SRR10483502	AAPAQG0000000000	121	4,988,881	99,968	52.3	32	33, ^b 32 ^b	1,070,256	Weltevreden	None	None
CFSAN096627 (outside)	SAMN13321604	SRR10483509	AAPUXJ0000000000	46	4,886,976	225,268	52.3	41	33, ^b 32 ^b	1,347,840	Hvittingfoss	13, 14	None
CFSAN096628 (outside)	SAMN13321600	SRR10483506	AAOXYW0000000000	117	4,997,196	94,034	52.4	38	33, ^b 32 ^b	1,269,280	Weltevreden	13, 14	None
CFSAN096629 (outside)	SAMN13321598	SRR10483510	AAOXFL0000000000	40	4,763,596	256,627	52.3	38	33, ^b 32 ^b	1,262,464	Corvallis	None	<i>qnrS1</i>
CFSAN096630 (outside)	SAMN13322150	SRR10483543	AAPRFR0000000000	64	4,885,698	149,476	52.7	50	33, ^b 32 ^b	1,625,728	Hvittingfoss	13	None
CFSAN096631 (outside)	SAMN13321593	SRR10483511	AAQIBY0000000000	69	4,880,849	136,339	52.5	33	33, ^b 32 ^b	1,087,728	Hvittingfoss	13, 14, C63PI	None
CFSAN096632 (outside)	SAMN13321589	SRR10483512	AAQFWT0000000000	76	4,882,637	112,271	52.6	39	33, ^b 32 ^b	1,274,576	Hvittingfoss	13, 14	None
CFSAN096633 (outside)	SAMN13322151	SRR10483544	AAPBIM0000000000	48	4,888,754	163,819	52.5	41	33, ^b 32 ^b	1,339,280	Hvittingfoss	13, 14	None
CFSAN096634 (outside)	SAMN13293471	SRR10454525	AAPDHS0000000000	45	4,886,448	297,538	52.5	46	33, ^b 32 ^b	1,568,144	Hvittingfoss	3, 13, 14	None
CFSAN096635 (outside)	SAMN13293474	SRR10454524	AAPCTJ0000000000	47	4,888,472	163,860	52.6	65	33, ^b 32 ^b	2,130,128	Hvittingfoss	5, 9, 13, 14, C63PI	None
CFSAN096636 (outside)	SAMN13293495	SRR10454571	AAOVNP0000000000	38	4,941,926	231,887	52.4	61	33, ^b 32 ^b	1,975,648	Mbandaka	None	<i>tet(A)</i>
CFSAN096637 (outside)	SAMN13293478	SRR10454554	AAOZSX0000000000	34	4,986,876	336,928	52.1	102	33, ^b 32 ^b	3,260,192	Mbandaka	C63PI	<i>tet(A)</i>
CFSAN096638 (inside)	SAMN13293513	SRR10454709	AAPURY0000000000	39	4,941,739	234,898	52.3	79	33, ^b 32 ^b	2,583,600	Mbandaka	None	<i>tet(A)</i>
CFSAN096639 (inside)	SAMN13293559	SRR10454722	AAPREC0000000000	36	4,890,402	263,956	52.3	60	33, ^b 32 ^b	1,972,576	Hvittingfoss	5, 12, 13, 14, C63PI	None
CFSAN096640 (inside)	SAMN13293548	SRR10454720	AAPUPU0000000000	37	4,891,877	225,246	52.4	69	33, ^b 32 ^b	2,235,248	Hvittingfoss	5, 13, 14, C63PI	None
CFSAN096641 (inside)	SAMN13293552	SRR10454721	AAPBFP0000000000	35	4,892,034	237,120	52.2	88	33, ^b 32 ^b	2,925,152	Hvittingfoss	5, 12, 13, 14, C63PI	None
CFSAN096642 (inside)	SAMN13293550	SRR10454719	AAQJIM0000000000	46	4,756,930	279,551	52.4	84	33, ^b 32 ^b	2,787,552	Virchow	12, 13, 14	None
CFSAN096643 (inside)	SAMN13293560	SRR10454725	AAPBTO0000000000	38	4,983,844	199,234	52.5	139	33, ^b 32 ^b	4,528,976	Mbandaka	C63PI	<i>tet(A)</i>
CFSAN096644 (inside)	SAMN13293554	SRR10454718	AAOGLD0000000000	39	4,891,900	236,887	52.6	116	33, ^b 32 ^b	3,775,040	Hvittingfoss	5, 13, 14, C63PI	None
CFSAN096645 (inside)	SAMN13293468	SRR10454522	AAOWKQ0000000000	50	4,957,603	240,177	52.1	141	33, ^b 32 ^b	4,515,936	Corvallis	C63PI	None
CFSAN096646 (inside)	SAMN13293464	SRR10454477	AAQFPZ0000000000	41	4,959,060	266,854	52.3	129	33, ^b 32 ^b	4,143,408	Corvallis	1, 3, 8, C63PI	None
CFSAN096647 (inside)	SAMN13293481	SRR10454526	AAQMBA0000000000	52	4,963,011	260,889	52.1	152	33, ^b 32 ^b	4,875,888	Lexington	C63PI	None

(Continued on next page)

TABLE 1 (Continued)

Sample no. ^a	NCBI BioSample no.	SRA accession no.	GenBank accession no.	No. of contigs	Total length (bp)	N ₅₀ (bp)	GC content (%)	Coverage (x)	Avg quality scores (read 1, read 2)	No. of reads	Serotype	SPI(s)	AMR gene(s)
<u>CFSAN096648</u> (inside)	SAMN13293179	SRR10452792	AAQJFP000000000	50	4,884,485	278,698	52.3	142	33. ^b 32. ^b	4,544,784	Typhimurium	1, 5, 9, 13, 14, C63PI	None
<u>CFSAN096649</u> (inside)	SAMN13293237	SRR10452801	AAQJIF000000000	55	4,886,407	271,030	52.3	193	33. ^b 32. ^b	6,212,320	Rissen	None	None
<u>CFSAN096650</u> (inside)	SAMN13293340	SRR10453836	AAQLUZ000000000	59	4,925,157	233,820	52.2	219	33. ^b 32. ^b	7,025,728	Krefeld	13, 14, C63PI	<i>aph(3'')-lb</i> , <i>aph(3')-la</i> , <i>aph(6)-ld</i> , <i>bla_{TEM-1}</i> , <i>sul2</i> , <i>tet(B)</i>
<u>CFSAN096651</u> (inside)	SAMN13293437	SRR10453845	AAOVOL000000000	57	4,914,721	233,820	52.2	186	33. ^b 32. ^b	5,968,960	Krefeld	1, 3, 8, C63PI	<i>aph(3'')-lb</i> , <i>aph(3')-la</i> , <i>aph(6)-ld</i> , <i>bla_{TEM-1}</i> , <i>sul2</i> , <i>tet(B)</i>
<u>CFSAN096652</u> (inside)	SAMN13293509	SRR10454712	AAQLVG000000000	59	4,926,743	233,820	52.2	156	33. ^b 32. ^b	4,990,512	Krefeld	1, 3, 8, C63PI	<i>aph(3'')-lb</i> , <i>aph(3')-la</i> , <i>aph(6)-ld</i> , <i>bla_{TEM-1}</i> , <i>sul2</i> , <i>tet(B)</i>
<u>CFSAN096653</u> (outside)	SAMN13293549	SRR10454716	AAOYDR000000000	57	4,920,767	277,388	52.2	84	33. ^b 32. ^b	2,692,272	Krefeld	3, C63PI	<i>aph(3'')-lb</i> , <i>aph(3')-la</i> , <i>aph(6)-ld</i> , <i>bla_{TEM-1}</i> , <i>sul2</i> , <i>tet(B)</i>
<u>CFSAN096654</u> (outside)	SAMN13293562	SRR10454724	AAQJMM000000000	62	4,927,585	233,696	52.3	182	33. ^b 32. ^b	5,832,112	Krefeld	C63PI	<i>aph(3'')-lb</i> , <i>aph(3')-la</i> , <i>aph(6)-ld</i> , <i>bla_{TEM-1}</i> , <i>sul2</i> , <i>tet(B)</i>
<u>CFSAN096655</u> (outside)	SAMN13293551	SRR10454714	AAQJIL000000000	59	4,924,859	276,634	52.2	122	33. ^b 32. ^b	3,896,496	Krefeld	3, 8, C63PI	<i>aph(3'')-lb</i> , <i>aph(3')-la</i> , <i>aph(6)-ld</i> , <i>bla_{TEM-1}</i> , <i>sul2</i> , <i>tet(B)</i>
<u>CFSAN096656</u> (outside)	SAMN13293561	SRR10454723	AAPMVH000000000	50	4,961,397	365,146	52.3	181	33. ^b 32. ^b	5,840,736	Krefeld	1, 3, 8, C63PI	None
<u>CFSAN096657</u> (outside)	SAMN13293555	SRR10454717	AAQKV700000000	37	4,971,264	382,215	52.2	125	33. ^b 32. ^b	4,059,616	Corvallis	3, 8, C63PI	<i>aph(3'')-lb</i> , <i>aph(6)-ld</i> , <i>qnrS1</i> , <i>sul2</i> , <i>tet(A)</i>
<u>CFSAN096658</u> (outside)	SAMN13293462	SRR10454521	AAOV0G000000000	35	4,970,109	464,760	52.1	123	33. ^b 32. ^b	3,959,344	Corvallis	3, 8, C63PI	<i>aph(3'')-lb</i> , <i>aph(6)-ld</i> , <i>qnrS1</i> , <i>sul2</i> , <i>tet(A)</i>
<u>CFSAN096659</u> (outside)	SAMN13293326	SRR10452834	AAQLZF000000000	39	4,737,400	337,520	52.4	126	33. ^b 32. ^b	4,068,208	Braenderup	13, 14, C63PI	None
<u>CFSAN096660</u> (outside)	SAMN13293349	SRR10452835	AAPDJJ000000000	79	5,000,081	222,935	52.3	145	33. ^b 32. ^b	4,664,640	Rissen	8, C63PI	<i>aadA1</i> , <i>aadA2</i> , <i>bla_{TEM-1}</i> , <i>cmiA1</i> , <i>dfrA12</i> , <i>flor</i> , <i>qacL</i> , <i>qnrS1</i> , <i>sul2</i> , <i>sul3</i> , <i>tet(A)</i> , <i>tet(M)</i>
<u>CFSAN096661</u> (outside)	SAMN13293344	SRR10453838	AAQJFK000000000	80	5,004,186	222,935	52.1	148	33. ^b 32. ^b	4,735,072	Rissen	8, 9, C63PI	<i>aadA1</i> , <i>aadA2</i> , <i>bla_{TEM-1}</i> , <i>cmiA1</i> , <i>dfrA12</i> , <i>flor</i> , <i>qacL</i> , <i>qnrS1</i> , <i>sul2</i> , <i>sul3</i> , <i>tet(A)</i> , <i>tet(M)</i>
<u>CFSAN096662</u> (outside)	SAMN13293463	SRR10454475	AAQJNH000000000	79	5,002,383	222,935	52.3	169	33. ^b 32. ^b	5,406,656	Rissen	8, C63PI	<i>aadA1</i> , <i>aadA2</i> , <i>bla_{TEM-1}</i> , <i>cmiA1</i> , <i>dfrA12</i> , <i>flor</i> , <i>qacL</i> , <i>qnrS1</i> , <i>sul2</i> , <i>sul3</i> , <i>tet(A)</i> , <i>tet(M)</i>
<u>CFSAN096663</u> (outside)	SAMN13293461	SRR10454463	AAPLYY000000000	32	4,969,793	502,099	52	128	33. ^b 32. ^b	4,091,808	Corvallis	C63PI	<i>aph(3'')-lb</i> , <i>aph(6)-ld</i> , <i>qnrS1</i> , <i>sul2</i> , <i>tet(A)</i>

^aSamples collected from food contact surfaces (FCSs) are underlined, while the rest were collected from non-food contact surfaces (NFCSS); the location of the vendor is indicated as inside or outside. All isolates belong to BioProject number PRJNA628951.

^bNextSeq run with an average of four lanes.

were available at NCBI Pathogen Detection (9). *Salmonella* pathogenicity islands (SPIs) were identified with SPIFinder (<https://cge.cbs.dtu.dk/services/SPIFinder>) (Center for Genomic Epidemiology). Draft genomes were annotated using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (10). The serotype of each isolate was determined *in silico* using SeqSero v1.0 on draft genomes (11). Draft genomes ranged between 4,609,585 and 5,198,930 bp in size, with an average GC content of 52.4%. The number of contigs for each isolate ranged from 23 to 468. A total of 16 *S. enterica* serotypes were identified, including Rissen ($n = 19$); Hvittingfoss ($n = 13$); Corvallis ($n = 10$); Krefeld ($n = 8$); Weltevreden ($n = 6$); Altona ($n = 6$); Mbandaka ($n = 5$); Typhimurium ($n = 3$); Javiana, Uganda, and Derby ($n = 2$ each); and Anatum, Braenderup, Lexington, Virchow, and the potential monophasic variant of *S. enterica* serotype Typhimurium (I 4,[5],12:i:–) ($n = 1$ each). AMR genes, including those encoding for tetracycline, β -lactam, sulfonamide, quinolone, aminoglycoside, phenicol, trimethoprim, and fosfomycin resistance, were identified in 43 of 81 strains. A total of 10 SPIs were detected in 59 genomes (Table 1) (12, 13). The draft genome sequences described will be valuable for understanding the dynamics of *S. enterica* diversity and persistence in informal markets in Cambodia, as well as supporting global epidemiological investigations of outbreaks.

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

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