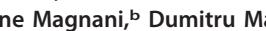# Draft Genome Sequences of 26 *Salmonella* Isolates Associated with Multiple Outbreaks in Brazil

Guojie Cao,[a] Maria Balkey,[a] Qing Jin,[a] Eric Brown,[a] Marc Allard,[a] Adma Nadja Ferreira de Melo,[b]
Daniel Farias Marinho do Monte,[c] Tereza Cristina Rocha Moreira de Oliveira,[d] Marciane Magnani,[b] Dumitru Macarisin[a]

[a]Center for Food Safety and Applied Nutrition, Office of Regulatory Science, Division of Microbiology, U.S. Food and Drug Administration, College Park, Maryland, USA
[b]Laboratory of Microbial Processes in Foods, Department of Food Engineering, Federal University of Paraíba, João Pessoa, Brazil
[c]Department of Food and Experimental Nutrition, Faculty of Pharmaceutical Sciences, Food Research Center, University of São Paulo, São Paulo, Brazil
[d]Department of Food Science, State University of Londrina, Londrina, Paraná State, Brazil

ABSTRACT *Salmonella enterica* subsp. *enterica* isolates are the leading cause of foodborne illness worldwide. Here, we report the draft genomes of 26 *Salmonella* isolates of food and clinical origin, belonging to four serovars, associated with outbreaks from 1999 to 2006 in the south of Brazil.

Nontyphoidal *Salmonella* spp. are a major cause of diarrheal illness worldwide, leading to an estimated 93 million enteric infections and around 155,000 deaths annually (1). These 26 *Salmonella enterica* subsp. *enterica* strains (from serovars Infantis, $n = 7$; London, $n = 6$; Typhimurium, $n = 7$; or Johannesburg, $n = 6$) were isolated from a variety of sources, including chicken meat, turkey sausage, humans, etc., related to multiple outbreaks in the south of Brazil between 1999 and 2006 (Table 1). *S.* Infantis has been resistant to a variety of antibiotics and identified as an etiological agent of severe gastroenteritis, leading to hospitalized children in Brazil since 1994 (2). *S.* London has been reported to be resistant to colistin in strains isolated from swine in Brazil (3). *S.* Johannesburg, isolated in Brazil and carrying the genes *qnrA1* and *qnrB19*, showed plasmid-mediated resistance to nalidixic acid, a first-generation quinolone (4). *S.* Typhimurium has been one of the top serovars causing gastroenteritis worldwide (5). Sequence type 19 (ST19) has been reported as the most prevalent ST, followed by the more invasive ST313 (5). As of 6 February 2020, without counting our submission, the Pathogen Detection isolates browser (https://www.ncbi.nlm.nih.gov/pathogens/) contained 54 *S.* Infantis, 1 *S.* London, 223 *S.* Typhimurium, and 0 *S.* Johannesburg isolates from Brazil. Besides offering genomic diversity information for isolates implicated in these outbreaks 2 decades ago, our data are also valuable for ongoing outbreak investigations and evolutionary history for these four serovars' isolates.

The 26 *Salmonella* isolates were from the Central Laboratory of Parana State and the State University of Londrina, Brazil (6–8). A DNeasy blood and tissue kit (Qiagen, Inc., Valencia, CA) was used to extract genomic DNA from the culture after a 16-h incubation period at 37°C in tryptic soy broth (TSB) (Becton, Dickinson, Franklin Lakes, NJ). A Qubit 3.0 fluorometer (Life Technologies, MD) was used to measure DNA concentrations. Library preparation was conducted following Nextera XT protocols, and paired-end reads were sequenced on the NextSeq 500 system (Illumina, San Diego, CA) using a NextSeq 500/550 high output kit v2 (300 cycles). We selected data based on the following criteria: cluster density (between 170,000 and 220,000/mm²) and percentage of clusters passing filters (greater than 80%). Trimmomatic (9) was used to trim the raw reads, and SPAdes v3.8.2 (10) was used to assemble the data using default parameters. The NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v4.10 (11)

TABLE 1 Strain and genome information for the current study

Name	Source[a]	Yr	Size (bp)	GC (%)	No. of genes	No. of RNA genes	No. of reads	Coverage (×)	N_{50} (bp)	No. of contigs	SRA accession no.	GenBank accession no.
CFSAN077726[b]	Smoked turkey sausage	2001	4,604,173	52.25	4,445	102	12,387,058	369	208,947	45	SRS5956604	AANBIU000000000
CFSAN077739[b]	Food	2005	4,605,454	52.25	4,445	104	9,563,052	292	202,265	42	SRS5955826	AANBII000000000
CFSAN077748[b]	Food	2005	4,603,927	52.15	4,430	78	1,133,076	35	160,857	57	SRS5956596	AANBIP000000000
CFSAN077750[b]	Food	2005	4,605,811	52.15	4,432	99	7,399,642	232	202,248	42	SRS5956599	AANBIN000000000
CFSAN077779[b]	Clinical	2004	4,606,135	52.25	4,437	99	3,100,564	96	196,847	45	SRS5955850	AANBIQ000000000
CFSAN077742[b]	Food	2005	4,577,295	52.23	4,408	100	7,277,648	227	201,873	43	SRS5955824	AANBIL000000000
CFSAN077781[b]	Clinical	2005	4,576,346	52.23	4,410	99	8,990,252	285	202,133	42	SRS5955721	AANBIC000000000
CFSAN077751[c]	Food	2005	4,626,211	52.27	4,532	89	7,050,846	217	434,659	33	SRS5956607	AANBIV000000000
CFSAN077753[c]	Chicken meat	2002	4,625,978	52.27	4,530	92	6,396,868	198	340,103	32	SRS5955820	AANBIE000000000
CFSAN077778[c]	Clinical	2004	4,626,171	52.27	4,511	90	2,708,156	83	191,397	44	SRS5955822	AANBID000000000
CFSAN077786[c]	Clinical	2006	4,626,949	52.27	4,513	91	4,631,292	145	208,128	39	SRS5955828	AANBIT000000000
CFSAN077789[c]	Clinical	2006	4,626,970	52.27	4,512	92	3,295,404	103	208,100	38	SRS5955720	AANBIB000000000
CFSAN077790[c]	Clinical	2006	4,625,073	52.27	4,517	90	2,609,344	81	213,324	38	SRS5955827	AANBIG000000000
CFSAN077707[d]	Chicken meat with sauce	2000	4,580,419	52.25	4,402	93	7,708,866	245	229,086	44	SRS5955829	AANBIJ000000000
CFSAN077736[d]	Food	2004	4,580,327	52.26	4,398	90	8,954,394	280	237,179	38	SRS5964586	AANBIW000000000
CFSAN077743[d]	Food	2005	4,579,849	52.25	4,403	92	8,001,610	249	221,794	44	SRS5955848	AANBIO000000000
CFSAN077745[d]	Food	2005	4,669,736	52.22	4,502	91	9,316,388	283	237,179	41	SRS5955819	AANBIF000000000
CFSAN077746[d]	Food	2005	4,552,171	52.25	4,384	91	8,304,902	257	237,179	43	SRS5955821	AANBIH000000000
CFSAN077747[d]	Food	2005	4,578,138	52.25	4,400	90	2,612,096	81	226,309	42	SRS5956598	AANBIR000000000
CFSAN077701[e]	Morcela beef salami	1999	4,763,160	52.13	4,637	101	10,051,244	293	176,749	55	SRS5956603	AANBIX000000000
CFSAN077715[e]	Food	2001	4,997,643	51.78	4,904	97	6,144,112	177	171,826	67	SRS5955823	AANBIK000000000
CFSAN077727[e]	Roast chicken meat	2001	4,880,727	52.17	4,781	91	9,441,774	271	175,545	60	SRS5637490	AANBIA000000000
CFSAN077758[e]	Chicken meat	2006	4,914,580	52.14	4,829	72	991,930	29	172,267	71	SRS5964585	AANBIZ000000000
CFSAN077780[e]	Clinical	2005	4,877,842	52.18	4,778	88	1,231,090	36	145,178	71	SRS5956601	AANBIY000000000
CFSAN077783[e]	Clinical	2005	4,878,625	52.18	4,782	96	3,088,720	90	208,949	66	SRS5956600	AANBIM000000000
CFSAN077785[e]	Clinical	2006	4,881,092	52.18	4,782	99	9,172,298	268	246,869	61	SRS5956602	AANBIS000000000

[a] All strains were isolated from states in the south of Brazil.
[b] *S*. Infantis.
[c] *S*. Johannesburg.
[d] *S*. London.
[e] *S*. Typhimurium.

was used to conduct annotation of the assemblies, which were subsequently deposited in GenBank.

Data availability. The genome sequences of these 26 *Salmonella* isolates were deposited in GenBank, and the SRA and whole-genome sequence (WGS) accession numbers are available in Table 1.

REFERENCES

1. Panzenhagen PHN, Paul NC, Conte Junior CA, Costa RG, Rodrigues DP, Shah DH. 2018. Draft genome sequences of 11 Salmonella enterica serovar Typhimurium strains isolated from human systemic and nonsystemic sites in Brazil. Genome Announc 6:e01223-17. https://doi.org/10.1128/genomeA.01223-17.

2. Fonseca EL, Mykytczuk OL, Asensi MD, Reis EMF, Ferraz LR, Paula FL, Ng LK, Rodrigues DP. 2006. Clonality and antimicrobial resistance gene profiles of multidrug-resistant Salmonella enterica serovar Infantis isolates from four public hospitals in Rio de Janeiro, Brazil. J Clin Microbiol 44:2767–2772. https://doi.org/10.1128/JCM.01916-05.

3. Morales AS, Fragoso de Araújo J, de Moura Gomes VT, Reis Costa AT, dos Prazeres Rodrigues D, Porfida Ferreira TS, de Lima Filsner PH, Felizardo MR, Micke Moreno A. 2012. Colistin resistance in Escherichia coli and Salmonella enterica strains isolated from swine in Brazil. ScientificWorld-Journal 2012:109795. https://doi.org/10.1100/2012/109795.

4. Ferrari R, Galiana A, Cremades R, Rodriguez JC, Magnani M, Tognim MCB, Oliveira TCRM, Royo G. 2011. Plasmid-mediated quinolone resistance by genes qnrA1 and qnrB19 in Salmonella strains isolated in Brazil. J Infect Dev Ctries 5:496–498. https://doi.org/10.3855/jidc.1735.

5. Almeida F, Seribelli AA, da Silva P, Medeiros MIC, Dos Prazeres Rodrigues D, Moreira CG, Allard MW, Falcão JP. 2017. Multilocus sequence typing of Salmonella Typhimurium reveals the presence of the highly invasive ST313 in Brazil. Infect Genet Evol 51:41–44. https://doi.org/10.1016/j.meegid.2017.03.009.

6. Ferrari R, Galiana A, Cremades R, Rodríguez JC, Magnani M, Tognim MCB, Oliveira TCRM, Royo G. 2013. Plasmid-mediated quinolone resistance (PMQR) and mutations in the topoisomerase genes of Salmonella enterica strains from Brazil. Braz J Microbiol 44:651–656. https://doi.org/10.1590/S1517-83822013000200046.

7. Ferrari RG, Galiana A, Cremades R, Rodríguez JC, Magnani M, Tognim MC,

Oliveira TC, Royo G. 2013. Expression of the marA, soxS, acrB and ramA genes related to the AcrAB/TolC efflux pump in Salmonella enterica strains with and without quinolone resistance-determining regions gyrA gene mutations. Braz J Infect Dis 17:125–130. https://doi.org/10.1016/j.bjid.2012.09.011.

8. Kottwitz LBM, Scheffer MC, Dalla-Costa LM, Farah SMDSS, Moscalewski WSB, Magnani M, de Oliveira TCRM. 2011. Molecular characterization and resistance profile of Salmonella Enteritidis PT4 and PT9 strains isolated in Brazil. J Med Microbiol 60:1026–1031. https://doi.org/10.1099/jmm.0.028597-0.

9. Bolger AM, Lohse M, Usadel B. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. Bioinformatics 30:2114–2120. https://doi.org/10.1093/bioinformatics/btu170.

10. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol 19:455–477. https://doi.org/10.1089/cmb.2012.0021.

11. Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, Ostell J. 2016. NCBI Prokaryotic Genome Annotation Pipeline. Nucleic Acids Res 44:6614–6624. https://doi.org/10.1093/nar/gkw569.