



# Draft Genome Sequences of 11 *Salmonella enterica* Serovar Typhimurium Strains Isolated from Human Systemic and Nonsystemic Sites in Brazil

Pedro Henrique N. Panzenhagen,<sup>a,b</sup> Narayan C. Paul,<sup>a</sup> Carlos A. Conte Junior,<sup>b,d,e</sup> Renata G. Costa,<sup>c</sup> Dália P. Rodrigues,<sup>c</sup> Devendra H. Shah<sup>a</sup>

<sup>a</sup>Department of Veterinary Microbiology and Pathology, Washington State University, Pullman, Washington, USA

<sup>b</sup>Food Science Program, Chemistry Institute, University Federal of Rio de Janeiro, Rio de Janeiro, Brazil

<sup>c</sup>National Reference Laboratory for Diagnosis of Enteric Bacteria, Oswaldo Cruz Institute, Rio de Janeiro, Brazil

<sup>d</sup>National Institute of Quality Control in Health, Oswaldo Cruz Foundation, Rio de Janeiro, Brazil

<sup>e</sup>Department of Food Technology, Faculty of Veterinary Medicine, Federal Fluminense University (UFF), Niterói, Brazil

**ABSTRACT** *Salmonella enterica* serovar Typhimurium strains isolated from systemic sites outside sub-Saharan Africa have been rarely sequenced. Here, we report the draft genome sequences of *S. Typhimurium* sequence type 19 (ST19) ( $n = 9$ ), ST1649 ( $n = 1$ ), and ST313 ( $n = 1$ ) strains isolated from human systemic (e.g., blood) and nonsystemic (e.g., stool and wounds) sites in Brazil.

Nontyphoidal *Salmonella* (NTS) is one of the major causes of diarrheal disease worldwide, with an estimated 93 million enteric infections and 155,000 deaths annually (1). However, these estimates do not include the infections caused by invasive nontyphoidal *Salmonella* (iNTS) *enterica* serovar Typhimurium sequence type 313 (ST313), which is often associated with systemic infection. *S. Typhimurium* ST313 strains account for >50% of the systemic infections in sub-Saharan Africa (2, 3). Two genetic lineages of *S. Typhimurium* ST313 have been linked with the emergence of iNTS across sub-Saharan Africa (4). In Brazil, *S. Typhimurium* is frequently isolated from systemic sites, such as blood and cerebrospinal fluid (CSF), from human patients (5, 6); however, the genetic underpinning of *S. Typhimurium* isolates recovered from systemic sites in Brazil remains unknown. We sequenced 11 *S. Typhimurium* strains isolated from blood ( $n = 4$ ), stool ( $n = 4$ ), and extraintestinal ( $n = 3$ ) sites between 2010 and 2014 from different geographic regions of Brazil (Table 1).

Paired-end sequencing libraries ( $2 \times 250$  bp) were prepared using the Nextera XT kit (Illumina, San Diego, CA) following the protocol described in the DNA library reference guide (7), size selected to be in the range of 600 to 1,000 bp (average peaks, ~800 bp), and sequenced using the MiSeq Illumina version 2 kit, according to the manufacturer's instructions. The number of paired reads per sample ranged from 941,320 to 1,389,798. The average G+C content was 52.5% (8). *De novo* assembly was performed using Velvet 1.2.10 set at default for all parameters (9). Contigs were organized by aligning to the genome sequence of the reference strain *S. Typhimurium* LT2 (accession no. NC\_003197) using Mauve multiple alignments (10). Whole-genome multilocus sequence typing was performed using Enterobase (<https://enterobase.warwick.ac.uk/>). A total of three sequence types, ST19 ( $n = 9$ ), ST1695 ( $n = 1$ ), and ST313 ( $n = 1$ ), were identified. Detailed comparative genomics analysis of these strains is currently ongoing and will be published independently. These genome sequences will provide better insights into the molecular epidemiology of invasive *S. Typhimurium* strains in Brazil.

Received 28 September 2017 Accepted 19 December 2017 Published 1 February 2018

**Citation** 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>.

**Copyright** © 2018 Panzenhagen et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Devendra H. Shah, [dshah@vetmed.wsu.edu](mailto:dshah@vetmed.wsu.edu).

**TABLE 1** GenBank accession numbers of *Salmonella* Typhimurium strains isolated from human clinical samples in Brazil

Strain	SRA accession no.	WGS accession no. <sup>a</sup>	No. of contigs	N <sub>50</sub> (bp)	Length (bp)	Source <sup>b</sup>	Yr	State
PP_BR007	SAMN05505504	<a href="#">NPJP00000000</a>	156	57,229	4,632,574	Blood	2014	Rio de Janeiro
PP_BR026	SAMN05505503	<a href="#">NPJQ00000000</a>	149	62,099	4,777,031	Blood	2012	Rio Grande do Sul
PP_BR027	SAMN05505502	<a href="#">NPJR00000000</a>	175	44,398	4,626,743	WS	2012	Rio Grande do Sul
PP_BR031	SAMN05505501	<a href="#">NPJS00000000</a>	190	46,721	4,594,320	WS	2012	Rio Grande do Sul
PP_BR032	SAMN05505500	<a href="#">NPJT00000000</a>	122	99,313	4,650,556	ABS	2012	Rio Grande do Sul
PP_BR045	SAMN05505499	<a href="#">NPJU00000000</a>	147	76,702	4,827,606	RS	2011	Santa Catarina
PP_BR057	SAMN05505498	<a href="#">NRDL00000000</a>	131	103,073	4,787,663	Blood	2011	Amapá
PP_BR060	SAMN05505496	<a href="#">NPMT00000000</a>	123	96,334	4,776,943	Feces	2011	Minas Gerais
PP_BR062	SAMN05505495	<a href="#">NRDM00000000</a>	118	142,310	4,958,705	Feces	2010	Santa Catarina
PP_BR063	SAMN05505494	<a href="#">NRDN00000000</a>	161	50,016	4,365,189	Blood	2010	Rio Grande do Sul
PP_BR076	SAMN05505493	<a href="#">NSDQ00000000</a>	125	120,490	5,065,902	Feces	2010	Rio Grande do Sul

<sup>a</sup>WGS, whole-genome sequencing.

<sup>b</sup>WS, wound secretion; ABS, abdominal abscess; RS, rectal swab.

**Accession number(s).** The draft genome sequences are available in GenBank under the accession numbers listed in Table 1.

## ACKNOWLEDGMENTS

We thank Li Zhen at the Washington Department of Health (WADOH) and Mark Allard at the FDA Center for Food Safety and Applied Nutrition (CFSAN) for sequencing the strains used in this study.

This research was funded by the Safe Food Initiative and Agricultural Animal Health Program at the Washington State University, Pullman, WA. Pedro Henrique N. Panzenhagen received scholarship support by the Doctoral Sandwich Abroad Program CAPES/PDSE at the Federal University of Rio de Janeiro.

We declare no conflicts of interest.

## REFERENCES

1. WHO. 2016. *Salmonella* (non-typhoidal). World Health Organization, Geneva, Switzerland. <http://www.who.int/mediacentre/factsheets/fs139/en/>.
2. Ao TT, Feasey NA, Gordon MA, Keddy KH, Angulo FJ, Crump JA. 2015. Global burden of invasive nontyphoidal salmonella disease, 2010. *Emerg Infect Dis* 21:941–949. <https://doi.org/10.3201/eid2106.140999>
3. Reddy EA, Shaw AV, Crump JA. 2010. Community-acquired bloodstream infections in Africa: a systematic review and meta-analysis. *Lancet Infect Dis* 10:417–432. [https://doi.org/10.1016/S1473-3099\(10\)70072-4](https://doi.org/10.1016/S1473-3099(10)70072-4).
4. Okoro CK, Barquist L, Connor TR, Harris SR, Clare S, Stevens MP, Arends MJ, Hale C, Kane L, Pickard DJ, Hill J, Harcourt K, Parkhill J, Dougan G, Kingsley RA. 2015. Signatures of adaptation in human invasive *Salmonella* Typhimurium ST313 populations from sub-Saharan Africa. *PLoS Negl Trop Dis* 9:e0003611. <https://doi.org/10.1371/journal.pntd.0003611>.
5. Fernandes SA, Tavechio AT, Ghilardi AC, Dias AM, Almeida IA, Melo LC. 2006. *Salmonella* serovars isolated from humans in São Paulo State, Brazil, 1996–2003. *Rev Inst Med Trop Sao Paulo* 48:179–184. <https://doi.org/10.1590/S0036-46652006000400001>
6. de Castro FA, dos Santos VR, Martins CHG, Fernandes SA, Zaia JE, Martinez R. 2002. Prevalence and antimicrobial susceptibility of *Salmonella* serotypes in patients from Ribeirão Preto, São Paulo, Brazil, between 1985 and 1999. *Braz J Infect Dis* 6:244–251. <https://doi.org/10.1590/S1413-86702002000500005>.
7. Illumina. 2016. Nextera XT DNA library prep kit. Reference guide (15031942 v01). Illumina, San Diego, CA.
8. McClelland M, Sanderson KE, Spieth J, Clifton SW, Latreille P, Courtney L, Porwollik S, Ali J, Dante M, Du F, Hou S, Layman D, Leonard S, Nguyen C, Scott K, Holmes A, Grewal N, Mulvaney E, Ryan E, Sun H, Florea L, Miller W, Stoneking T, Nhan M, Waterston R, Wilson RK. 2001. Complete genome sequence of *Salmonella enterica* serovar Typhimurium LT2. *Nature* 413:852–856. <https://doi.org/10.1038/35101614>.
9. Zerbino DR, Birney E. 2008. Velvet: algorithms for *de novo* short read assembly using de Bruijn graphs. *Genome Res* 18:821–829. <https://doi.org/10.1101/gr.074492.107>.
10. Darling ACE, Mau B, Blattner FR, Perna NT. 2004. Mauve: multiple alignment of conserved genomic sequence with rearrangements. *Genome Res* 14:1394–1403. <https://doi.org/10.1101/gr.2289704>.