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Draft Genome Sequences of 20 *Salmonella enterica* subsp. *enterica* Serovar Typhimurium Strains Isolated from Swine in Santa Catarina, Brazil

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ABSTRACT Salmonellosis is a disease with a high incidence worldwide, and *Salmonella enterica* subsp. *enterica* serovar Typhimurium is one of the most clinically important serovars. We report here the draft genome sequences of 20 *S.* Typhimurium strains isolated from swine in Santa Catarina, Brazil. These draft genomes will improve our understanding of *S.* Typhimurium in Brazil.

Salmonella enterica subsp. *enterica* serovar Typhimurium has often been isolated from pigs, among which it generally does not cause severe diseases and can be asymptomatic (1). According to the Brazilian Association of Animal Protein (ABPA), pork production in Brazil was 3.73 billion tons in 2016. Furthermore, exports to Russia, Hong Kong, China, and Singapore, among other countries, reached 733 million tons in 2016, and Santa Catarina has been the largest pork producer in recent years in Brazil (http://abpa-br.com.br/storage/files/final_abpa_relatorio_anual_2017_ingles_web.pdf). In this report, we announce 20 draft genome sequences from a collection of *S.* Typhimurium strains isolated from swine between 2000 and 2012 in Santa Catarina, Brazil.

DNA from each strain was extracted according to the method used by Campioni and Falcão (2). Libraries were prepared using 1 ng of genomic DNA with the Nextera XT DNA library preparation kit (Illumina, San Diego, CA, USA), and the genomes were sequenced using the NextSeq 500 desktop sequencer with the NextSeq 500/500 high-output version 2 kit (Illumina) for 2 × 151 cycles according to the manufacturer's instructions. *De novo* assemblies were generated from all raw sequence data. The Illumina reads were assembled using CLC Genomics Workbench version 10.0.1. The contigs for each isolate (draft genomes) were annotated with NCBI's Prokaryotic Genome Annotation Pipeline (PGAP) (3).

The genomes ranged from 4.6 to 5.1 Mb in size, as described for other *Salmonella* strains (4). Sequencing generated an average G+C content of 52.03%, which is similar to that reported previously for other *Salmonella* isolates (5). The number of contigs per assembly for each isolate ranged between 63 and 152.

These data will provide support for understanding the molecular epidemiology of *S.* Typhimurium strains isolated from swine in Brazil. It will also provide phylogenetic insights into their evolution. More information about these genomic features will be detailed in future publications.

Accession number(s). The draft genome sequences of the 20 *S.* Typhimurium isolates reported here are available in GenBank under the accession numbers listed in Table 1.

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TABLE 1 Metadata of the 20 *S.* Typhimurium strains isolated from swine between 2000 and 2012 in Santa Catarina, Brazil

CFSAN[a] no.	GenBank accession no.	Genome size (Mb)	No. of contigs	Coverage (×)
CFSAN068028	PHJE00000000	4,646,120	63	189
CFSAN068029	PHJD00000000	4,973,359	139	215
CFSAN068030	PHJC00000000	5,081,769	133	205
CFSAN068031	PIJC00000000	4,762,964	96	152
CFSAN068032	PHJB00000000	4,863,147	117	156
CFSAN068033	PHJA00000000	5,011,448	101	150
CFSAN068034	PHIZ00000000	5,156,236	152	246
CFSAN068035	PHIY00000000	5,156,159	147	206
CFSAN068036	PHIX00000000	4,836,615	109	187
CFSAN068037	PHIW00000000	5,028,984	130	218
CFSAN068038	PHIV00000000	4,767,364	96	75
CFSAN068039	PHIU00000000	4,767,112	101	167
CFSAN068040	PHIT00000000	5,133,854	129	157
CFSAN068041	PHIS00000000	4,859,215	103	143
CFSAN068042	PHIR00000000	4,864,560	126	203
CFSAN068043	PHIQ00000000	4,884,181	121	211
CFSAN068044	PHIP00000000	4,973,979	150	179
CFSAN068045	PHIO00000000	4,859,028	113	194
CFSAN068046	PHIN00000000	4,772,921	129	203
CFSAN068047	PHIM00000000	4,765,254	91	163

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