Salmonella enterica causes health problem worldwide. The relationships among strains that are from the same serotype but different hosts, countries, and continents remain elusive. Few genome sequences are available from S. enterica isolates from South America. Therefore, we sequenced the genomes of 33 strains from diverse sources isolated in Chile and determined that they were of different serotypes. These genomes will improve phylogenetic analysis of Salmonella strains from Chile and the rest of South America.

Salmonella enterica is a major pathogen in the world, and it causes >1,000,000 cases of foodborne disease in the United States every year (1). In Chile, Salmonella is the most frequently involved foodborne pathogen in outbreaks in recent years (2). More than 2,500 Salmonella serovars are described (3), and they associate with a wide range of hosts. The pathogen causes infection not only in humans and domestic animals, but it also can infect wildlife; recent studies demonstrated the presence of Salmonella in pinnipeds, penguins, and waterfowl (4–6). Currently, only one genome sequence from Salmonella isolated in Chile is available (7). Here, we announce 33 draft genome sequences from a collection of S. enterica strains isolated in Chile from 2010 to 2012 and from different hosts and geographical locations, including 12 human clinical samples and wildlife samples.

DNA from each strain was isolated from overnight cultures with the DNeasy blood and tissue kit (Qiagen, Valencia, CA). Libraries were prepared using 1 ng of genomic DNA with the Nextera XT kit (Illumina, San Diego, CA), and the genomes were sequenced using MiSeq Illumina with the V2 kit (2 × 250 bp), according to the manufacturer’s instructions, at 40 to 190× coverage. The genomic sequence contigs for each strain were de novo assembled using CLC Genomics Workbench version 7.6.1 (CLC bio, Germantown, MD, USA). Ridom Seqsphere+ was used for in silico multilocus sequence type (MLST) analysis, and the sequences were annotated using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) (http://www.ncbi.nlm.nih.gov/genome/annotation_prok).

The average G+C mol% of these strains was 52.1%, similar to the reported G+C content for other Salmonella strains (8). The genome length was also within the range described for Salmonella (4.6 Mb to almost 5.1 Mb) (9). The number of contigs per assembly for each isolate ranged from 32 to 92 (Table 1). While the samples were isolated from different hosts and geographic locations, in silico analysis determined that they belong to only 11 sequence types (ST), most of which were already reported in the S. enterica MLST database (http://mlst.warwick.ac.uk/mlst/dbs/Senterica) (Table 1). S. enterica strain serotype Havana presented different STs (ST588 and ST1524); the remaining 9 serotypes displayed a single ST each (Table 1). Those STs agreed with the serotyping results reported for the same strains in previous studies (4, 5, 10). Moreover, we found a new ST for S. enterica serovar Paratyphi B, with a hemD gene differing from previously described allele 24 by one new substitution at position 270 (T instead of C). Additionally, a preliminary analysis for detecting the presence of plasmids indicated that 13 of these isolates carry plasmids (Table 1) (11). We used two approaches, PlasmidFinder and pMLST (https://cge.cbs.dtu.dk/services); the first detects plasmid replication origins, and the second determines incompatibility types, both allowing mining for contigs with those characteristics.

The data provided will help in understanding the differences between Salmonella strains isolated from different countries and continents, improving traceback investigations for foodborne-related outbreak events. Moreover, these new draft genome sequences will contribute to the analysis of host-associated differences among Salmonella strains and provide phylogenetic insights into their evolution on different continents. A detailed report of these genomic features will be addressed in a future publication.

Nucleotide sequence accession numbers. The draft genome sequences for these 33 Salmonella isolates are available in GenBank and are listed in Table 1.

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The findings and conclusions in this report are those of the authors and do not necessarily represent the official position of the U.S. Food and Drug Administration.
### TABLE 1 Metadata for *S. enterica* subsp. *enterica* strains isolated in Chile from different hosts

| CFSAN no. | Isolate name | WGS accession no. | Source | Serotype | No. of contigs | ST | PlasmidFinder/pMLST*  |
|-----------|--------------|-------------------|--------|----------|---------------|----|-----------------------|
| CFSAN024756 | SAG1 | JWQW0000000000 | Penguin | Agona | 55 | 13 | –/– |
| CFSAN024757 | SAG2 | JWQV0000000000 | Kelp gull | Agona | 55 | 13 | –/– |
| CFSAN024758 | SAG3 | JWQU0000000000 | Penguin | Agona | 64 | 13 | –/– |
| CFSAN024759 | SAG4 | JWQT0000000000 | Clinical | Agona | 60 | 13 | –/– |
| CFSAN024760 | SAG5 | JWQS0000000000 | Clinical | Agona | 48 | 13 | –/– |
| CFSAN024761 | SAG6 | JWQR0000000000 | Penguin | Agona | 52 | 13 | –/– |
| CFSAN024763 | SAN3 | JWQP0000000000 | Clinical | Anatum | 32 | 64 | –/– |
| CFSAN024764 | SAN4 | JWQQ0000000000 | Clinical | Anatum | 60 | 64 | –/– |
| CFSAN024765 | SBR1 | JWQN0000000000 | Sea lion | Brandenburg | 38 | 65 | –/– |
| CFSAN024767 | SDU1 | JWQM0000000000 | Kelp gull | Dublin | 47 | 10 | +/+ |
| CFSAN024768 | SDU2 | JWQL0000000000 | Clinical | Dublin | 37 | 10 | +/+ |
| CFSAN024769 | SDU3 | JWKK0000000000 | Clinical | Dublin | 35 | 10 | +/+ |
| CFSAN024770 | SHA1 | JWKO0000000000 | Sea lion | Havana | 49 | 1524 | +/+ |
| CFSAN024771 | SHA2 | JWKO0000000000 | Gray gull | Havana | 41 | 588 | +/– |
| CFSAN024773 | SHE2 | JWQG0000000000 | Kelp gull | Heidelberg | 35 | 15 | +/– |
| CFSAN024774 | SHE3 | JWQF0000000000 | Kelp gull | Heidelberg | 44 | 15 | +/– |
| CFSAN024776 | SHE5 | JWQE0000000000 | Clinical | Heidelberg | 38 | 15 | +/– |
| CFSAN024777 | SHE6 | JWQD0000000000 | Clinical | Heidelberg | 39 | 15 | +/– |
| CFSAN024778 | SIN1 | JWQC0000000000 | Kelp gull | Infantis | 41 | 32 | –/– |
| CFSAN024779 | SIN2 | JWQB0000000000 | Kelp gull | Infantis | 47 | 32 | –/– |
| CFSAN024780 | SIN3 | JWQA0000000000 | Kelp gull | Infantis | 42 | 32 | –/– |
| CFSAN024781 | SIN6 | JWPZ0000000000 | Clinical | Infantis | 44 | 32 | –/– |
| CFSAN024715 | SIN7 | JWRI0000000000 | Clinical | Infantis | 39 | 32 | –/– |
| CFSAN024716 | SL1 | JWRG0000000000 | Sea lion | Livingstone | 32 | 457 | –/– |
| CFSAN024717 | SL2 | JWRF0000000000 | Sea lion | Livingstone | 41 | 457 | –/– |
| CFSAN024718 | SSK1 | JWRX0000000000 | Kelp gull | Senftenberg | 32 | 14 | –/– |
| CFSAN024719 | SSK2 | JWRD0000000000 | Kelp gull | Senftenberg | 43 | 14 | –/– |
| CFSAN024720 | SSK3 | JWRW0000000000 | Kelp gull | Senftenberg | 56 | 14 | –/– |
| CFSAN024721 | SSK4 | JWRJ0000000000 | Clinical | Senftenberg | 52 | 14 | +/– |
| CFSAN024722 | SSE5 | JWRK0000000000 | Clinical | Senftenberg | 45 | 14 | +/– |
| CFSAN024723 | SSE6 | JWRJ0000000000 | Clinical | Senftenberg | 72 | 14 | –/– |
| CFSAN024724 | SSE7 | JWRJ0000000000 | Kelp gull | Senftenberg | 92 | 14 | –/– |
| CFSAN024725 | SGB1 | JWQX0000000000 | Kelp gull | Paratyphi B | 58 | New | –/– |

*WGS, whole-genome shotgun.
PlasmidFinder/pMLST, presence of plasmids. +, positive; –, negative.

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