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Draft Genome Sequences of Three *Salmonella enterica* Serovar 4,[5],12:i:− Strains and One *S. enterica* Serovar Typhimurium Strain, Isolated in Brazil

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ABSTRACT Draft genomes of three *Salmonella enterica* 4,[5],12:i:− (STi) strains isolated from human infections were obtained using Illumina sequencing. They were negative for the *fljBA* operon but positive for *hin*, and k-mer analyses revealed their identity as *S. enterica* 4,[5],12:i:− 08-1736 and *S.* Typhimurium. A draft *S.* Typhimurium sequence is described for comparison.

Salmonella enterica, an important human and animal pathogen (1, 2), is often associated with antibiotic resistance (3). This species is classified into different serotypes according to its somatic, flagellar, and, when expressed, capsular antigens (4). It is classified as either typhoid *Salmonella* (TS) or nontyphoid *Salmonella* (NTS) based on the serovar and host specificity. *S. enterica* subsp. *enterica* serovar Typhimurium (antigenic formula *S. enterica* I 4,[5],12:i:1,2) is among the most frequently identified NTS serovars isolated from human infections (2). Characteristics of this serovar include the nonconcomitant expression of two flagellar antigens (flagellar phases I and II), encoded by the *fliC* and *fljB* genes, respectively (5). Expression of *fliC* is negatively regulated by the *fljA* gene product, which forms an operon with *fljB* (6–8). The promoter of the *fljBA* operon extends into the *hin* sequence, a DNA fragment that is able to invert its orientation. Therefore, the type of flagellar antigen expressed is governed by the orientation of *hin* (5). Since the last century, *S.* Typhimurium variants unable to express flagellar phase II antigen have been isolated at an increased rate, becoming emergent an *S. enterica* serotype (9). *S. enterica* 4,[5],12:i:− originated from *S.* Typhimurium through the deletion of the *fljBA* operon. Different clones are distinguished based on the molecular events responsible for the *fljBA* deletion (9). Here, we describe the draft genome of three strains of *S. enterica* 4,[5],12:i:− (607STi, 633STi, and 691STi) and one of *S.* Typhimurium (662ST), all isolated in Brazil from human infections. Genomic DNA was prepared using the Wizard R genomic DNA purification kit (Promega, USA) according to manufacturer's instructions. Genomic DNA integrity was assessed by electrophoresis on 1% agarose gel. Library preparation was performed using the Nextera paired-end sample preparation kit and TruSeq DNA PCR-free LT sample prep kit and processed in a HiSeq 2500 system (Illumina, San Diego, CA). Genome assembly was performed with Velvet (10) and annotation with RAST (11).

The number of contigs was 30 or 36, and the mean scaffold length was 134,767 to 163,767 bp. The GC content of all strains was 52.2%. Bacterial typing was performed

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with MLST 1.7, a platform for multilocus sequence typing (MLST) from assembled genomes (12). All strains were typed as sequence type 19 (ST-19), although the *S.* Typhimurium strain did not match perfectly for the *thrA* locus due to a 1-base substitution. The ST-19 type is common for *S.* Typhimurium.

The prediction of prokaryotic species by k-mer genomic comparisons using KmerFinder 2.0 (13) indicated high scores for *S. enterica* 4,[5],12:i:− strain 08-1736, a 4,[5],12:i:− strain, and other *S.* Typhimurium strains. Scores for other *S. enterica* serovars were lower. BLAST analyses indicated an absence of the *fljBA* operon in the *S. enterica* 4,[5],12:i:− strains, though the *hin* sequence was present. The *S.* Typhimurium strain was positive for both sequences.

In conclusion, the three sequenced 4,[5],12:i:− strains presented high identity to *S. enterica* 4,[5],12:i:− strain 08-1736 and *S.* Typhimurium. Further analyses are under way to characterize this *S.* Typhimurium variant serovar in Brazil.

Accession number(s). This whole-genome shotgun project has been deposited in GenBank under the accession no. QAWG00000000, QAWH00000000, QAWI00000000, and QAWJ00000000. The versions described in this paper are the first versions, QAWG01000000, QAWH01000000, QAWI01000000, and QAWJ01000000.

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