



Draft Genome Sequences of 30 *Salmonella enterica* Serovar Enteritidis Isolates Associated with Multiple Outbreaks in Brazil

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ABSTRACT *Salmonella enterica* subsp. *enterica* serovar Enteritidis has been the prevalent serovar isolated from gastroenteritis cases in Brazil since the 1990s. Here, we report the draft genomes of 30 *S. Enteritidis* isolates originating from a variety of patients and implicated foods during outbreaks between 1999 and 2006 in Brazil.

Salmonella enterica subsp. *enterica* serovar Enteritidis is a major and long-standing public health concern worldwide and one of the top serovars causing human salmonellosis (1). In South America, *S. Enteritidis* has been associated with epidemic human illnesses since the 1990s (2). In particular, in Brazil, prior to the 1990s, $\leq 1\%$ of *Salmonella* samples isolated from both human and nonhuman sources were *S. Enteritidis* (2, 3). It became the most prevalent serovar in both human and nonhuman sources in 1994, accounting for 65% of all *Salmonella* isolates in Brazil (2, 3). The 30 selected outbreak-associated *S. Enteritidis* isolates discussed here originated from a variety of foods and patients involved in multiple outbreaks in Brazil during 1999 to 2006 (Table 1). As of 29 November 2019, there were 365 *S. Enteritidis* isolates from Brazil in the Pathogen Detection Isolates Browser (<https://www.ncbi.nlm.nih.gov/pathogens/>), classified as 22 defined single nucleotide polymorphism (SNP) clusters, including the genomes reported here. The isolates sequenced in the current study will provide genomic information for implicated outbreaks and will contribute to a better understanding of the genomic diversity of *S. Enteritidis* in Brazil.

The 30 *S. Enteritidis* isolates were from the reference collections of epidemic *Salmonella* strains of the Central Laboratory of Paraná State, Brazil, and the State University of Londrina, Paraná State, Brazil (4–6). The genomic DNA was extracted after incubation of the cultures for 16 h at 37°C in Trypticase soy broth (Becton, Dickinson, Franklin Lakes, NJ) using the DNeasy blood and tissue kit (Qiagen, Inc., Valencia, CA). Concentrations of DNA were measured using a Qubit 3.0 fluorometer (Life Technologies, MD). The libraries were prepared according to Nextera XT protocols and sequenced on the NextSeq 500 platform (Illumina, San Diego, CA) using a NextSeq 500/550 high-output kit v2 (300 cycles). The run quality was assessed using the following parameters: cluster density, 170 to 220 k/mm²; and clusters passing filters, >80%. The raw reads were trimmed using Trimmomatic (7) and assembled *de novo* using SPAdes software v3.8.2 (8) with default settings. Contigs less than 500 bp long were filtered out. Annotations of assemblies were processed using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (9) and subsequently deposited at DDBJ/EMBL/GenBank.

Data availability. The genome sequences of the 30 *S. Enteritidis* isolates were deposited in DDBJ/EMBL/GenBank. Detailed information is listed in Table 1.

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