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GENOME SEQUENCES

Draft Genome Sequence of *Salmonella enterica* Serovar Enteritidis from Jos, Plateau State, Nigeria

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ABSTRACT *Salmonella enterica* serovar Enteritidis causes the highest incidence of human salmonellosis infections. Here, we describe the whole-genome sequence and annotation of *Salmonella enterica* serovar Enteritidis strain 1145s, isolated in Nigeria. The strain has a genome of 4.57 Mb with a GC content of 52% and contains one plasmid.

Salmonella enterica serovar Enteritidis causes the highest incidence of human salmonellosis infections (1). It is considered an emerging pathogen, with changing epidemiology over the last 20 years (2). *Salmonella Enteritidis* is a zoonotic disease associated with poultry (3). In this study, the genome of *Salmonella enterica* serovar Enteritidis strain 1145s, recovered from a poultry farm in Jos (Plateau State, Nigeria), was sequenced and annotated.

Strain 1145s was isolated from chicken organs (liver, heart, spleen, and kidney) from a chicken with salmonellosis. Samples of these organs were streaked onto 5% blood agar and MacConkey agar plates, which were incubated aerobically at 37°C for 24 h. Tiny colonies growing on MacConkey agar contained cells that were Gram negative when stained. Biochemical tests such as starch hydrolysis, oxidase, catalase, indole, and sugar fermentation tests (4) were performed, identifying the strain as *Salmonella*.

For sequencing, DNA extraction was performed using a DNeasy blood and tissue kit (Qiagen), following the manufacturer's instructions. A sequencing library was prepared using the Nextera XT DNA sample preparation kit (Illumina), following the manufacturer's protocol. Whole-genome sequencing was performed at the Antimicrobial Resistance Laboratory, Microbial Genomics Reference Laboratory, CIDMLS, ICPMR, Westmead Hospital (Australia), using the Illumina NextSeq 500 platform. A total of 650 Mbp of 2 × 150-bp paired-end reads were generated, with a coverage of 152× for the genome. The raw data were trimmed using fastp (5) and assembled using SPAdes v3.13.0 (6). The genome completeness was determined using QUAST v5.0.2 (7) and BUSCO (8). Genome annotation was performed using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v5.2 (9). *Salmonella* serotyping was predicted using the SeqSero v2.0 software tool (6). *Salmonella* pathogenicity islands (SPIs) were identified

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using the SPIFinder v1.0 online tool (https://cge.cbs.dtu.dk/services/SPIFinder). Default parameters were used for the tools.

PlasmidFinder v2.1 (https://cge.cbs.dtu.dk/services/PlasmidFinder/) was used to determine the presence of plasmids (10). The presence of antimicrobial resistance (AMR) genes was investigated using ResFinder v3.1 with default settings (https://cge.cbs.dtu.dk/services/ResFinder/). The results were correlated with the phenotypic observations obtained using antimicrobial susceptibility testing (AST). *S. Enteritidis* 1145s has a total of 36 contigs in a genome of 4.57 Mb, with an average GC content of 52% and an N_{50} value of 304,938 bp. The strain contains one plasmid identical to pSPCV (*Salmonella enterica* subsp. *enterica* serovar Paratyphi C; GenBank accession number CP000858) (11). Strain 1145s is 98.8% complete based on the benchmarking universal single-copy ortholog (BUSCO) values (containing 122 of the 124 total BUSCO genes).

Data availability. The complete genome sequences of the strain have been deposited at the NCBI GenBank database under the accession number JAGDDT000000000, the BioProject accession number PRJNA713960, and the BioSample accession number SAMN18275554.

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REFERENCES

1. Hendriksen RS, Vieira AR, Karlsmose S, Lo Fo Wong DM, Jensen AB, Wegener HC, Aarestrup FM. 2011. Global monitoring of Salmonella serovar distribution from the World Health Organization Global Foodborne Infections Network Country Data Bank: results of quality assured laboratories from 2001 to 2007. Foodborne Pathog Dis 8:887–900. https://doi.org/10.1089/fpd.2010.0787.
2. Retamal P, Fresno M, Dougnac C, Gutierrez S, Gornall V, Vidal R, Vernal R, Pujol M, Barreto M, González-Acuña D, Abalos P. 2015. Genetic and phenotypic evidence of the Salmonella enterica serotype Enteritidis human-animal interface in Chile. Front Microbiol 6:464. https://doi.org/10.3389/fmicb.2015.00464.
3. Jackson BR, Griffin PM, Cole D, Walsh KA, Chai SJ. 2013. Outbreak-associated Salmonella enterica serotypes and food commodities, United States, 1998–2008. Emerg Infect Dis 19:1239–1244. https://doi.org/10.3201/eid1908.121511.
4. Olutiola PO, Famurewa O, Sonntag HG. 1991. Biochemical reactions of microorganisms. *In* An introduction to general microbiology—a practical approach, p 157–178. Heidelberger Verlagsanstalt und Druckerei GmbH, Heidelberg, Germany.
5. Chen S, Zhou Y, Chen Y, Gu J. 2018. fastp: an ultra-fast all-in-one FASTQ preprocessor. Bioinformatics 34:i884–i890. https://doi.org/10.1093/bioinformatics/bty560.
6. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol 19:455–477. https://doi.org/10.1089/cmb.2012.0021.
7. Gurevich A, Saveliev V, Vyahhi N, Tesler G. 2013. QUAST: quality assessment tool for genome assemblies. Bioinformatics 29:1072–1075. https://doi.org/10.1093/bioinformatics/btt086.
8. Seppey M, Manni M, Zdobnov EM. 2019. BUSCO: assessing genome assembly and annotation completeness, p 227–245. *In* Gene prediction. Springer Nature, Basingstoke, UK.
9. Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, Ostell J. 2016. NCBI Prokaryotic Genome Annotation Pipeline. Nucleic Acids Res 44:6614–6624. https://doi.org/10.1093/nar/gkw569.
10. Arndt D, Grant JR, Marcu A, Sajed T, Pon A, Liang Y, Wishart DS. 2016. PHASTER: a better, faster version of the PHAST phage search tool. Nucleic Acids Res 44:W16–W21. https://doi.org/10.1093/nar/gkw387.
11. Liu W-Q, Feng Y, Wang Y, Zou Q-H, Chen F, Guo J-T, Peng Y-H, Jin Y, Li Y-G, Hu S-N, Johnston RN, Liu G-R, Liu S-L. 2009. Salmonella paratyphi C: genetic divergence from Salmonella choleraesuis and pathogenic convergence with Salmonella typhi. PLoS One 4:e4510. https://doi.org/10.1371/journal.pone.0004510.