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Draft genome sequence of *Salmonella enterica* subsp. *enterica* serovar Typhimurium SBI_US10_MRI_BD isolated from broiler chicken in Bangladesh

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ABSTRACT *Salmonella enterica* is a rod-shaped, gram-negative bacterium classified under the *Enterobacteriaceae* family. Herein, we report the 4,918,555 bp genome (50.08% G+C) with 272.5× genome coverage of *S. enterica* SBI_US10_MRI_BD, containing a total of 4,754 CDSs, 55 tRNA, 2 rRNA, and 14 ncRNA genes.

KEYWORDS Bangladesh, broiler chicken, BV-BRC, PGAP, *Salmonella enterica*

Salmonella spp. are gram-negative bacilli (*Enterobacteriaceae*) widely found in the intestine of animals and humans (1, 2). As a significant zoonotic pathogen, transmission to humans frequently occurs via the fecal-oral route through contaminated animal-derived foods, particularly poultry and meat products (3). To understand the growing frequency of multidrug resistance (MDR), genomic surveillance of broiler-derived bacterial strains has become essential.

Salmonella enterica SBI_US10_MRI_BD was isolated in 2024 from cloacal swabs of processed broiler chickens from Uttara Sector-12 (latitude: 23.8714°N, 90.3807°E), Uttara, Bangladesh. Briefly, samples (N = 12) were collected aseptically using sterile cotton swabs and placed into 15 mL sterile tube containing 3 mL buffered peptone water (BPW) as a transport and pre-enrichment medium. Samples were then transported to the Microbiology laboratory at North South University and incubated in a shaking incubator (150 rpm) at 37°C for 18 h. After 10-fold serial dilution, single colonies were isolated on selective Salmonella-Shigella agar. Pure cultures were streaked onto nutrient agar, and 12 isolates were preserved in glycerol at −20°C.

Presumptive identification was performed using Gram staining and standard biochemical tests, including TSI, Simmons citrate, MR-VP, catalase, oxidase, MIU, and nitrate reduction assays. Antibiotic sensitivity testing was conducted using the Kirby-Bauer disk diffusion method. Among the isolates, we performed whole-genome sequencing (WGS) on the multidrug-resistant *S. enterica* strain SBI_US10_MRI_BD to determine its serovar, antimicrobial resistance, virulence profiles, and genomic features relevant to public health surveillance.

For WGS, the *S. enterica* SBI_US10_MRI_BD was cultured overnight on nutrient agar at 37°C. The isolate was submitted for WGS to the Genome Sequencing Laboratory, BCSIR, Dhaka, Bangladesh. Genomic DNA extraction and library preparation were performed as per the manufacturer's instructions using Qiagen DNeasy Blood & Tissue Kit (Cat. 69504, Hilden, Germany) and Nextera DNA Flex Library Preparation Kit (Cat. 20018705, Illumina, San Diego, USA), respectively. Sequencing was carried out on the Illumina NextSeq 550 platform, generating Illumina paired-end raw 150 bp reads, as previously described (4, 5).

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Genome quality assessment was performed using the workflows provided by the Bacterial and Viral Bioinformatics Resource Center (BV-BRC) with default parameters. For quality control, Trim Galore version 0.6.5dev (6, 7) was used to trim paired-end reads, and *de novo* assembly was conducted using Unicycler (v0.4.8) (8), implemented within the BV-BRC pipeline (v3.46.3) (9) using the default parameters except where otherwise noted. Assembly quality metrics, including coarse consistency (99.2%), fine consistency (98.7%), contamination (1.2%), and CheckM completeness (100%), indicated a high-quality genome assembly. The total raw reads of the original sample contained 4,463,482 reads (319.15 million bases) with an average read length of 35.8. The final genome size was 4,918,555 bp, with an average G+C content of 50.08% and an average sequencing coverage of 272.5×. The draft genome assembly comprises 71 contigs (>300 bp), with an N_{50} of 157,886 bp and an L_{50} of 12.

Genome annotation for *S. enterica* SBI_US10_MRI_BD was performed using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) version 6.10 with default parameters (10). The annotated genome contained a total of 4,754 CDSs, 55 tRNA genes, 2 rRNA genes, and 14 ncRNA genes.

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Software, Supervision, Writing – original draft, Writing – review and editing | Spencer Mark Mondol, Conceptualization, Formal analysis, Software, Supervision, Writing – review and editing | Md Murshed Hasan Sarkar, Data curation, Formal analysis, Software, Writing – review and editing | S. M. Bakhtiar UL Islam, Conceptualization, Formal analysis, Methodology, Software, Supervision, Writing – original draft, Writing – review and editing

DATA AVAILABILITY

The data described in this report are publicly accessible through NCBI BioProject PRJNA1313641 and BioSample SAMN50904865. The draft genome sequences have been deposited in GenBank under SRA accession number SRR35210187. This Whole Genome Shotgun project has been deposited at DDBJ/ENA/GenBank under accession JBQWDY000000000. The version described in this paper is version JBQWDY000000000.1.

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