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GENOME ANNOUNCEMENT

Draft Genome Sequence of *Salmonella enterica* Serovar Typhimurium ST1660/06, a Multidrug-Resistant Clinical Strain Isolated from a Diarrheic Patient

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***Salmonella enterica* serovar Typhimurium is one of the most prevalent serovars of *Salmonella* that causes human gastroenteritis. Here, we report the draft genome sequence of the *S.* Typhimurium multidrug-resistant strain ST1660/06. Comparative genomic analysis unveiled three strain-specific genomic islands that potentially confer the multidrug resistance and virulence of the strain.**

Salmonella are one of the most common causative agents of food poisoning. One million cases of nontyphoidal salmonellosis are estimated to occur annually in the United States (15). Salmonellosis is seldom fatal, but it progresses occasionally to a life-threatening systemic infection, and emerging multidrug-resistant (MDR) strains are posing a serious threat to the public. Here, we report the draft genome sequence of *Salmonella enterica* serovar Typhimurium strain ST1660/06, which has acquired resistance to multiple antibiotics, including ampicillin, tetracycline, chloramphenicol, trimethoprim-sulfamethoxazole, and ciprofloxacin.

ST1660/06 was isolated from a stool specimen of a diarrheic patient admitted to a hospital in Hong Kong in 2006. Genome sequencing was performed on a 454 GS FLX Titanium platform, and the single- and paired-end reads were *de novo* assembled by using the Newbler assembler. Gaps were then resolved and filled based on the contig graph output by Newbler and ordered with reference to the commercial LT2 genome (9) and pulsed-field gel electrophoresis profiles. GeneMark.hmm (8) and Glimmer 3.02 (3) were used to predict protein-coding sequences (CDSs) across the genome. Predicted CDSs longer than 90 bp were searched against the Swiss-Prot nonredundant database to examine if there was any discordance in the two gene prediction sets (6). GenePRIMP (11) was also used to improve the gene prediction process. The tRNAs and rRNAs were identified using tRNAscan-SE 1.21 (13) and RNAmmer 1.2 (7), respectively.

The draft sequence of ST1660/06 is 4,855,057 bp in size and has a G+C content of 55.2%. It consists of seven chromosomal contigs and one plasmid contig. The genome encodes 4,837 candidate CDSs. We also identified 85 tRNAs and 7 rRNA clusters.

Comparative genomic analysis revealed 172 single-nucleotide variations (SNVs) and 74 indels in ST1660/06, compared to LT2. Three large strain-specific genomic islands (GIs) that possibly confer multidrug resistance and virulence were identified. The first GI (59,247 bp) contained the *Yersinia* high-pathogenicity island (HPI) and a complete type IV secretion system (T4SS) separated by a single transposon. The HPI encodes the yersiniabactin-mediated iron acquisition system (1) and possibly enables the strain to survive in an iron-limited environment. The T4SS could function as integrative and conjugative elements and be involved in integration and conjugation of the HPI (10). This is the first report of the coexistence of an HPI and T4SS in *Salmonella* species (5). The second GI is a 61,233-bp MDR region that is almost identical to GI-DT12 in T000240 (4), except that it lacks a 21,298-bp region that contains genes encoding the iron transporter, *sitABCD*, and the aerobactin iron acquisition siderophore system (*lutA* and *lucABC*). We speculate that ST1660/06 has adopted a new siderophore-mediated iron acquisition mechanism for better survival and infection capability (12, 14). The third GI is 3,853 bp in size and is located on a plasmid that contains the chloramphenicol resistance gene *catA2* (2). The three GIs identified in the draft genome of ST1660/06 could be used to facilitate further studies into the mechanism of drug resistance and virulence of *S.* Typhimurium.

Nucleotide sequence accession numbers. The results of this whole-genome shotgun project have been deposited with DDBJ/EMBL/GenBank under accession number AJTU00000000. The version described in this paper is the first version, AJTU01000000.

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REFERENCES

1. **Carniel E.** 1999. The *Yersinia* high-pathogenicity island. Int. Microbiol. **2**:161–167.
2. **Chen YT, et al.** 2006. Complete nucleotide sequence of pK245, a 98-kilobase plasmid conferring quinolone resistance and extended-spectrum-beta-lactamase activity in a clinical *Klebsiella pneumoniae* isolate. Antimicrob. Agents Chemother. **50**:3861–3866.
3. **Delcher AL, Bratke KA, Powers EC, Salzberg SL.** 2007. Identifying bacterial genes and endosymbiont DNA with Glimmer. Bioinformatics **23**:673–679.
4. **Izumiya H, et al.** 2011. Whole-genome analysis of *Salmonella enterica*

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serovar Typhimurium T000240 reveals the acquisition of a genomic island involved in multidrug resistance via IS*1* derivatives on the chromosome. Antimicrob. Agents Chemother. **55**:623–630.
5. **Juhas M, et al.** 2007. Novel type IV secretion system involved in propagation of genomic islands. J. Bacteriol. **189**:761–771.
6. **Kislyuk AO, et al.** 2010. A computational genomics pipeline for prokaryotic sequencing projects. Bioinformatics **26**:1819–1826.
7. **Lagesen K, et al.** 2007. RNAmmer: consistent and rapid annotation of ribosomal RNA genes. Nucleic Acids Res. **35**:3100–3108.
8. **Lukashin AV, Borodovsky M.** 1998. GeneMark.hmm: new solutions for gene finding. Nucleic Acids Res. **26**:1107–1115.
9. **McClelland M, et al.** 2001. Complete genome sequence of *Salmonella enterica* serovar Typhimurium LT2. Nature **413**:852–856.
10. **Paauw A, Leverstein-van Hall MA, Verhoef J, Fluit AC.** 2010. Evolution in quantum leaps: multiple combinatorial transfers of HPI and other genetic modules in Enterobacteriaceae. PLoS One **5**:e8662. doi:10.1371/journal.pone.0008662.
11. **Pati A, et al.** 2010. GenePRIMP: a gene prediction improvement pipeline for prokaryotic genomes. Nat. Methods **7**:455–457.
12. **Perry RD, Fetherston JD.** 2011. Yersiniabactin iron uptake: mechanisms and role in *Yersinia pestis* pathogenesis. Microbes Infect. **13**:808–817.
13. **Schattner P, Brooks AN, Lowe TM.** 2005. The tRNAscan-SE, snoscan and snoGPS web servers for the detection of tRNAs and snoRNAs. Nucleic Acids Res. **33**:W686–W689.
14. **Sebbane F, Jarrett C, Gardner D, Long D, Hinnebusch BJ.** 2010. Role of the *Yersinia pestis* yersiniabactin iron acquisition system in the incidence of flea-borne plague. PLoS One **5**:e14379. doi:10.1371/journal.pone.0014379.
15. **Voetsch AC, et al.** 2004. FoodNet estimate of the burden of illness caused by nontyphoidal *Salmonella* infections in the United States. Clin. Infect. Dis. **38**:S127–S134.