Microbiol. Biotechnol. Lett. (2024), 52(3), 325–327
http://dx.doi.org/10.48022/mbl.2406.06004
pISSN 1598-642X eISSN 2234-7305

MBL
Microbiology and Biotechnology Letters

Genome Reports

Complete Genome Sequence of an ESBL-producing *Salmonella* Infantis Strain IJCS5-22 that Harbors $bla_{CTX\text{-}M\text{-}65}$ Isolated from Retail Chicken Meat in Korea

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Received: June 9, 2024 / Revised: July 12, 2024 / Accepted: July 15, 2024

We report the complete genome sequence of an extended-spectrum beta-lactamase-producing *Salmonella enterica* subsp. *enterica* Serovar Infantis strain IJCS5-22 that harbors $bla_{CTX\text{-}M\text{-}65}$, which was isolated from whole chicken meat purchased from a retail market in South Korea. The assembled IJCS5-22 genome comprised a 4,727,133 bp circular chromosome and a 318,349 bp plasmid that encoded several antimicrobial resistance genes, including $bla_{CTX\text{-}M\text{-}65}$, with 52.27% and 50.39% GC contents, respectively.

Keywords: ***Salmonella enterica* Infantis, $bla_{CTX\text{-}M\text{-}65}$, extended spectrum beta-lactamase, retail chicken meat**

Salmonella is a major gastroenteritis causing (e.g., salmonellosis) food-borne pathogen in humans that has a significant impact on public health [1]. *Salmonella* infections are associated with consumption of contaminated foods, particularly poultry products [2, 3]. While third-generation cephalosporins and fluoroquinolones have been used to effectively treat salmonellosis, the emergence of antibiotic-resistant *Salmonella*, including extended-spectrum beta-lactamase (ESBL)-producing *Salmonella* in recent years, has become a major concern worldwide [4, 5]. *Salmonella enterica* subsp. *enterica* serovar Infantis is one of the most common serovars causing human salmonellosis worldwide. The emergence of *S.* Infantis harboring $bla_{CTX\text{-}M\text{-}65}$ in the mega plasmid, named as plasmid of emerging *S.* Infantis (pESI), is associated with ESBL-producing phenotypes [6–8]. We report the complete genome sequence of the ESBL-producing *S.* Infantis strain IJCS5-22, which was isolated from whole chicken meat purchased from a retail market in South Korea following the Food Code isolation protocol [9]. Antimicrobial susceptibility test was performed against 16 antimicrobials using the Sentititre™ KRNV6F kit (Thermo Fisher Scientific, USA). Minimum inhibitory concentration was determined by the Clinical and Laboratory Standards Institute criteria [10]. The genomic DNA of the strain was extracted using Nucleo Spin® Microbial DNA mini kit (Macherey-Nagel, Germany). Genome sequencing of the IJCS5-22 strain was performed by Illumina NextSeq and Nanopore sequencing techniques. Library preparation was performed using the TruSeq Nano DNA Prep Kit (Illumina, USA) as per the manufacturer's instructions for NextSeq sequencing. Libraries were sequenced using NextSeq P1 600 cycles in a NextSeq2000 system using 2x 300bp pair-ends, and individual sequence reads were analyzed using FastQC (v.0.11.8). A library was constructed using a ligation sequencing kit (Oxford Nanopore Technologies, UK), and sequencing data were

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Table 1. Genomic features of *S.* Infantis strain IJCS5-22.

Genome features	Value
Number of contigs	2
Chromosome size (bp)	4,727,133 (Chromosome), 318,349 (Plasmid)
GC contents (%)	52.27 (Chromosome), 50.39 (Plasmid)
Coding genes (CDSs)	4,403 (Chromosome), 322 (Plasmid)
Transfer RNAs (tRNAs)	86 (Chromosome)
Ribosomal RNAs (rRNAs)	22 (Chromosome)
MLST[a]	ST32[b]
Antimicrobial resistance phenotypes[c]	AMP-CHL-CTX-FIS-GEN-NAL-STR-SXT-TET
Antimicrobial resistance genes	*mdsB*, *mdsA*, *gyrA*_D87Y, *aadA1*, *sul1*, *tet(A)*, *blaCTX-M-65*, *floR*, *aph(4)-Ia*, *aac(3)-Iva*, *dfrA14*, *aph(3')-Ia*

[a]MLST, multilocus sequence typing.
[b]ST, sequence type.
[c]AMP, ampicillin; CHL, chloramphenicol; CTX, cefotaxime; FIS, sulfisoxazole; GEN, gentamicin; NAL, nalidixic acid; STR, streptomycin; SXT, trimethoprim/sulfamethoxazole; TET, tetracycline.

based on the guppy (v.4.2.2) for nanopore sequencing. All sequencing data were processed for *de novo* genome assembly using Unicycler (v.0.5.0) and annotated with Prokka (v.1.14.6). The serotype and sequence type (ST) of IJCS5-22 were confirmed using MLST (v.2.23.0) and Seqsero2 (v.1.2.1). Virulence factor Database (VFDB, http://www.mgc.ac.cn/cgi-bin/VFs/v5/main.cgi) was used for the detection of virulence genes. Antimicrobial resistance genes (ARGs) were identified using NCBI AMRFinderPlus (v.3.11.26). The complete genome of the IJCS5-22 strain was found to comprise one circular chromosome (4,727,133 bp, 52.27% guanine-cytosine [GC] content) and one plasmid, designated as pIJCS5-22 (318,349 bp, 50.39% GC content) (Table 1). The complete genome of the strain IJCS5-22 encoded 4,725 protein-coding sequences (CDSs) and 108 non-coding genes (22 rRNA and 86 tRNA genes). Further, the IJCS5-22 strain was identified as ST32, and the predicted serotype was *S.* Infantis (antigenic formula: 7:r:1,5). Comparative genomic analysis of publicly available sequences of *S.* Infantis was conducted using FastANI (v.1.3.3). The average nucleotide identity (ANI) value of the chromosome of IJCS5-22 in comparisons with the sequence data of *S.* Infantis strain Z1323CSL0002 (GenBank accession No. CP148836.1) was calculated to be 99.99%. A total of 158 virulence genes were detected in IJCS5-22 (Supplementary material). Most of the virulence genes were located in the chromosome, whereas 12 yersiniabactin genes (*irp1*, *irp2*, *fyuA*/*psn*, *fyuA*, *ybtA*, *ybtE*, *ybtP*, *ybtQ*, *ybtS*, *ybtT*, *ybtU*, *ybtX*) were present in the plasmid pIJCS5-22. Several ARGs related to aminoglycoside (*aadA1*, *aph(4)-Ia*, *aac(3)-Iva*, *aph(3')-Ia*), beta-lactams (*blaCTX-M-65*), sulfonamide (*sul1*), tetracycline (*tet(A)*), phenicol (*floR*), trimethoprim (*dfrA14*) and the point *gyrA* mutation (D87Y) were identified in IJCS5-22, and these genotypes were corresponding to the observed resistance phenotype (Table 1) [8]. While most ARGs were present in plasmids, *mdsB*, *mdsA*, and *gyrA* point mutations were detected in the IJCS5-22 chromosome. The complete genome sequence of *S.* Infantis strain IJCS5-22 was deposited in the NCBI GenBank sequence database under the accession numbers, CP157394.1 (chromosome) and CP157395.1 (plasmid).

Acknowledgments

This study was supported by a grant from the Ministry of Food and Drug Safety (22192MFDS021) of the Republic of Korea.

Conflict of Interest

The authors have no financial conflicts of interest to declare.

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