

Genome Reports

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

Yeon A Kim¹ and Kun Taek Park^{1,2*}

¹Department of Digital Anti-aging and Healthcare, Inje University, Gimhae 50834, Republic of Korea

²Department of Biological Sciences, Inje University, Gimhae 50834, Republic of Korea

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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-M-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-M-65} with 52.27% and 50.39% GC contents, respectively.

Keywords: *Salmonella enterica* Infantis, *bla*_{CTX-M-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-M-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™ KRVN6F 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

***Corresponding author**

Phone: +82-55-320-3213, Fax: +82-55-336-7706

E-mail: ktpark@inje.ac.kr

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	<i>mdsB</i> , <i>mdsA</i> , <i>gyrA</i> _D87Y, <i>aadA1</i> , <i>sul1</i> , <i>tet(A)</i> , <i>blaCTX-M-65</i> , <i>floR</i> , <i>aph(4)-Ia</i> , <i>aac(3)-Iva</i> , <i>dfrA14</i> , <i>aph(3')-Ia</i>

^aMLST, multilocus sequence typing.^bST, sequence type.^cAMP, 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).

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Conflict of Interest

The authors have no financial conflicts of interest to declare.

References

- Lamichhane B, Mawad AM, Saleh M, Kelley WG, Harrington PJ, Lovestad CW, et al. 2024. Salmonellosis: An overview of epidemiology, pathogenesis, and innovative approaches to mitigate the antimicrobial resistant infections. *Antibiotics* **13**: 76.
- Hyeon J-Y, Chon J-W, Hwang I-G, Kwak H-S, Kim M-S, Kim S-K, et al. 2011. Prevalence, antibiotic resistance, and molecular characterization of *Salmonella* Serovars in retail meat products. *J. Food Prot.* **74**: 161-166.
- Im MC, Jeong SJ, Kwon Y-K, Jeong O-M, Kang M-S, Lee YJ. 2015. Prevalence and characteristics of *Salmonella* spp. isolated from commercial layer farms in Korea. *Poultry Sci.* **94**: 1691-1698.
- Chon J-W, Jung H-I, Kuk M, Kim Y-J, Seo K-H, Kim S-K. 2015. High occurrence of extended-spectrum β -lactamase-producing *Salmonella* in broiler carcasses from poultry slaughterhouses in South Korea. *Foodborne Pathog. Dis.* **12**: 190-196.
- Franco A, Leekitcharoenphon P, Feltrin F, Alba P, Cordaro G, Iurescia M, et al. 2015. Emergence of a clonal lineage of multidrug-resistant ESBL-producing *Salmonella infantis* transmitted from broil-

- ers and broiler meat to humans in Italy between 2011 and 2014. *PLoS One* **10**: e0144802.
6. Alvarez DM, Barrón-Montenegro R, Conejeros J, Rivera D, Undurraga EA, Moreno-Switt AI. 2023. A review of the global emergence of multidrug-resistant *Salmonella enterica* subsp. *enterica* Seroovar Infantis. *Int. J. Food Microbiol.* **403**: 110297.
 7. Mattock J, Chattaway MA, Hartman H, Dallman TJ, Smith AM, Keddy K, *et al.* 2024. A one health perspective on *Salmonella enterica* Seroovar Infantis, an emerging human multidrug-resistant pathogen. *Emerg. Infect. Dis.* **30**: 701.
 8. Tate H, Folster JP, Hsu C-H, Chen J, Hoffmann M, Li C, *et al.* 2017. Comparative analysis of extended-spectrum- β -lactamase CTX-M-65-producing *Salmonella enterica* serovar Infantis isolates from humans, food animals, and retail chickens in the United States. *Antimicrob. Agents Chemother.* **61**: 10.1128/aac.00488-00417.
 9. MFDS. 2024. Food Code. Available from <https://various.foodsafetykorea.go.kr/fsd/#/ext/Document/FC>. Accessed June 6, 2024.
 10. Institute CaLS. 2021. Performance Standards for Antimicrobial Susceptibility Testing. 31st ed. CLSI supplement M100.