pISSN 1229-1153 / eISSN 2465-9223 *J. Food Hyg. Saf.*
Vol. 40, No. 5, pp. 400~402 (2025)
https://doi.org/10.13103/JFHS.2025.40.5.400

**Journal of Food Hygiene and Safety**
Available online at http://www.foodhygiene.or.kr

Research note

# Complete Genome Sequence of *Salmonella enterica* subsp. *enterica* serovar Enteritidis Strain IJCS4-13 Isolated from Retail Chicken Meat in Korea

Yeona Kim[1], Eunji Choi[2], Kun Taek Park[1,2]*

[1]*Department of Digital Anti-aging and Healthcare, Inje University, Gimhae, Korea*
[2]*Department of Biological Sciences, Inje University, Gimhae, Korea*

(Received September 19, 2025/Revised October 12, 2025/Accepted October 12, 2025)

**ABSTRACT -** *Salmonella* spp. are a leading cause of gastrointestinal diseases. Here, we report the complete genome sequence of *Salmonella enterica* subsp. *enterica* serovar Enteritidis strain IJCS4-13, which was isolated from retail chicken meat in Korea. The complete genome sequence of IJCS4-13 comprised a 4,678,812 bp circular chromosome with a G+C content of 52.17%, and a 59,372 bp plasmid with a G+C content of 51.96%. In addition, genomic analysis revealed 147 virulence-associated genes, including chromosomal and plasmid-borne determinants, highlighting the pathogenic potential of this strain.

**Key words:** *S.* Enteritidis, Whole-genome sequence, Chicken meat

*Salmonella* is a major etiological agent of diarrheal disease and continues to pose a significant global health threat, with an estimated 93 million instances of gastroenteritis reported annually[1]. The pathogenesis of *Salmonella* is multifactorial and largely determined by its capacity to adhere to and invade host cells, as well as to survive and replicate within epithelial cells and macrophages. These processes are mediated by a wide range of virulence determinants often plasmid-encoded[2]. Notably, a substantial number of virulence genes are organized within horizontally acquired genomic regions termed *Salmonella* pathogenicity islands (SPIs)[3,4]. Given its importance as a major foodborne pathogen, genomic characterization is essential to better understand its pathogenic potential and epidemiological impact. Among its numerous serovars, *Salmonella enterica* subsp. *enterica* serovar Enteritidis (*S.* Enteritidis) is one of the most prevalent worldwide and is frequently associated with poultry products, which are the primary sources of human infection[5]. Although various draft genome sequences of *S.* Enteritidis strains isolated from retail chicken meat have been reported, hybrid assembly–based complete genome sequences have rarely been described in Korea, as most previous studies relied on short-read assemblies. Therefore, in this study, we report the complete genome sequence of *S.* Enteritidis strain IJCS4-13, which was isolated from whole chicken meat purchased from a retail market in Korea in 2023.

The isolate was obtained using the Food Code isolation protocol documented by the Ministry of Food and Drug Administration[6]. The genomic DNA of the strain was extracted using NucleoSpin® Microbial DNA mini kit (Macherey-Nagel, Düren, Germany). Whole genome sequencing (WGS) of the IJCS4-13 strain was performed by Illumina NextSeq and Oxford Nanopore sequencing techniques. For Illumina sequencing, library preparation was performed using the TruSeq Nano DNA Prep Kit (Illumina, San Diego, CA, USA) according to the manufacturer's instructions. Libraries were sequenced on a NextSeq 2000 system with 2×150 bp pair-ends using the NexSeq P1 600 cycles. Subsequently, the individual sequence reads were analyzed using FastQC (v.0.11.8). For Nanopore sequencing, a library was constructed using a ligation sequencing kit (Oxford Nanopore Technologies, Oxford, UK). The sequencing data were based on Guppy (v.4.2.2). All sequencing data were processed and *de novo* assembled using Unicycler (v.0.5.0) and the genome was annotated using Prokka (v.1.14.6). The sequence type (ST) and serotype of IJCS4-13 were confirmed using MLST (v.2.23.0) and Seqsero2 (v.1.2.1). Antimicrobial resistance genes and virulence-associated genes were identified using AMRFinder Plus (v.4.0.22) and Virulence factor Database (VFDB, http://www.mgc.ac.cn/cgi-bin/VFs/v5/main.cgi), respectively.

*Correspondence to: Kun Taek Park, Department of Biological Sciences, Inje University, Gimhae 50834, Korea
Tel: +82-55-320-3213, Fax: +82-55-336-7706
E-mail: ktpark@inje.ac.kr

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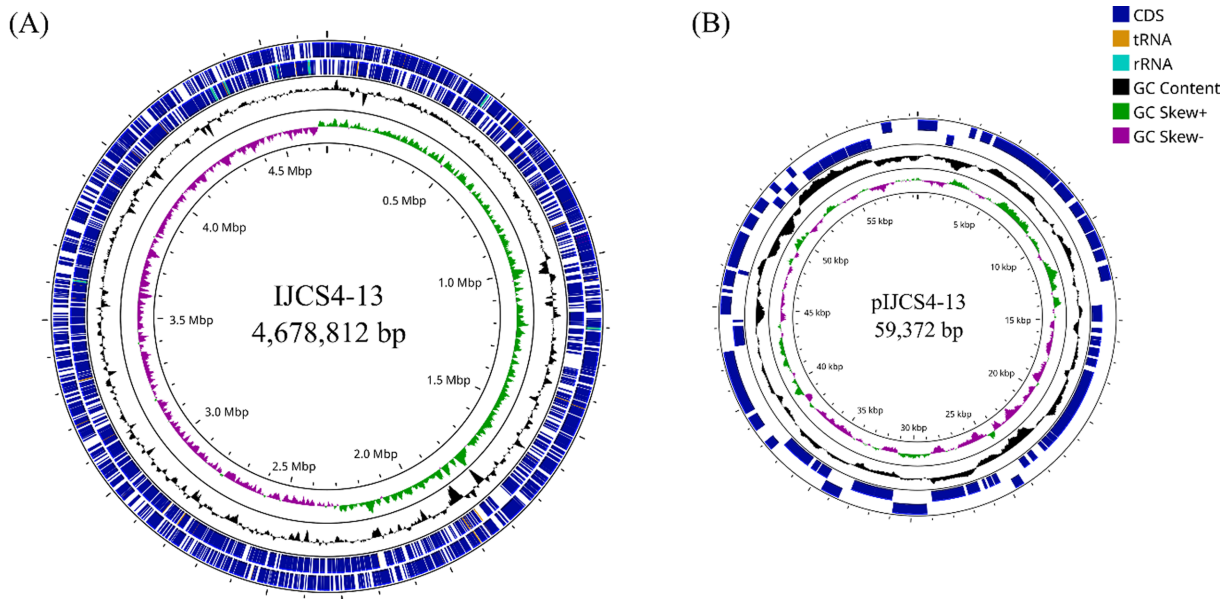


**Fig. 1.** Complete genome map of *S.* Enteritidis strain IJCS4-13.
Circular maps of chromosome (A) and plasmid (B). Marked characteristics are shown from outer to the center; coding sequences (CDS) on forward stand, CDS on reverse stand, tRNA, rRNA, G+C content, and GC skew.

**Table 1.** Genomic features of *S.* Enteritidis strain IJCS4-13

| Genome features | Characteristics | |
|---|---|---|
| | Chromosome | Plasmid |
| Genome size (bp) | 4,678,812 | 59,372 |
| G+C contents (%) | 52.17 | 51.96 |
| No. of CDS | 4,343 | 75 |
| No. of rRNA | 22 | - |
| No. of tRNA | 86 | - |
| Sequence type | ST11 | - |
| No. of virulence genes | 138 | 9 |

Pathogenicity islands of the *S.* Enteritidis strain were predicted using the SPIFinder v.2.0, available at the Center for Genomic Epidemiology website (https://www.genomicepidemiology.org/).

The genome of the *S.* Enteritidis strain IJCS4-13 consists of a single circular chromosome (4,678,812 bp, 52.17% G+C content), and a plasmid (59,372 bp, with 51.96% G+C content) (Table 1 and Fig. 1). The complete genome of the strain IJCS4-13 encoded 4,418 protein coding sequences (CDSs) in total (chromosome, 4,343; plasmid, 75) and 108 non-coding genes (22 rRNA and 86 tRNA genes). Further, the sequence type of the IJCS4-13 strain was identified as ST11, and the predicted serotype was *S.* Enteritidis (antigenic formula: 9:g,m:-). Only one antimicrobial resistance gene with a point mutation in *gyrA* (D87Y) was identified, which confers resistance to quinolones[7]. Of note, a total of 147 virulence genes (138 on the chromosome and 9 on the plasmid) were identified. These virulence genes encoded by the chromosome and plasmid were categorized into 11 virulence factor classes encompassing adherence determinants, macrophage inducible genes, magnesium uptake system, stress adaption, immune evasion, secretion system and others. SPIFinder analysis identified several SPIs in the genome of the isolate, with SPI-1 and SPI-2 being completely detected. In the genome of *S.* Enteritidis strain IJCS4-13, a total of 32 Type III secretion system (T3SS)-associated genes (*hilACD*, *iacP*, *iagB*, *invABCEFGHIJ*, *orgABC*, *prgHIJK*, *sicAP*, *sipBCD*, *spaOPQRS*, *sprB*) were located on SPI-1, and 32 T3SS genes (*spiC*, *ssaCDEGHIJKLMNOPQRSTUVX*, *sscAB*, *sseABCDEFG*, *ssrAB*) were located on SPI-2. These SPIs are critical for epithelial cell invasion, intracellular survival, and systemic dissemination[3]. Moreover, partial detection of additional SPIs was also observed, including SPI-4, 5, 9, 10, 12, 13, 14. Several plasmid-borne virulence genes were also detected. Among the nine plasmid-encoded virulence factors identified, the fimbrial operon *pefABCD*, which mediates adhesion to the intestinal epithelium, and the *rck* gene, which confers resistance to complement-mediated killing, were included[8,9]. The plasmid also harbored *mig-5*, a macrophage-inducible gene involved in intracellular survival, as well as the *spvBCD* operon, which plays a major role in systemic infection[8,10]. Together, these chromosomal and plasmid-borne virulence determinants highlight the considerable pathogenic potential of this isolate. The complete genomic information of *S.* Enteritidis IJCS4-13

offers a valuable foundation for elucidating its virulence mechanisms and contributes to the broader understanding of this important foodborne pathogen.

## Acknowledgements

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

## 국문요약

*Salmonella*는 전 세계적으로 위장관 질환을 일으키는 주요 식중독 원인균 중 하나이다. 본 연구에서는 국내 유통 닭고기에서 분리된 *Salmonella enterica* subsp. *enterica* serovar Enteritidis (*S.* Enteritidis) IJCS4-13 균주에 대해 WGS를 이용한 유전체 분석을 진행하였다. 해당 균주의 유전체는 4,678,812 bp 크기의 원형 염색체 (G+C 함량 52.17%)와 59,372 bp 크기의 플라스미드 (G+C 함량 51.96%)로 구성되어 있었다. 유전체 분석 결과, 총 147개의 병원성 관련 유전자를 확인하였다. 이들 유전자는 부착, 침입, 대식세포 내 생존, 스트레스 적응 등 다양한 병원성 기전에 관여하는 것으로 알려져있다. 따라서 본 균주는 다수의 병원성 인자를 보유하고 있어 높은 독력 잠재력을 지니고 있음을 시사한다. 본 연구에서 보고한 유전체 정보는 *S.* Enteritidis의 병원성 메커니즘 규명 및 식품 매개 감염병 관리에 중요한 기초 자료를 제공할 것이다.

## Conflict of interests

The authors declare no potential conflict of interest.

## ORCID

Yeona Kim https://orcid.org/0000-0002-3231-6232
Eunji Choi https://orcid.org/0009-0004-8626-2972
Kun Taek Park https://orcid.org/0000-0001-6177-0373

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