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Complete genome sequence of *Salmonella enterica* strain K_SA184, multidrug resistance bacterium isolated from lamb (*Ovis aries*)

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Abstract

Salmonella enterica is a representative foodborne pathogen in the world. The *S. enterica* strain K_SA184 was isolated from the lamb (*Ovis aries*), which was collected from a local traditional market in South Korea. In this study, the *S. enterica* strain K_SA184 was sequenced using PacBio RS II and Illumina NextSeq 500 platforms. The final complete genome of the *S. enterica* strain K_SA184 consist of one circular chromosome (4,725,087 bp) with 52.3% of guanine + cytosine (G + C) content, 4,363 of coding sequence (CDS), 85 of tRNA, and 22 of rRNA genes. The *S. enterica* strain K_SA184 genome includes encoding virulence genes, such as Type III secretion systems and multidrug resistance related genes.

Keywords: *Salmonella enterica* K_SA184, Lamb (*Ovis aries*), Whole genome sequencing, Antimicrobial resistance, Type III secretion systems

INTRODUCTION

Salmonella is a representative foodborne pathogen which is the most commonly identified in poultry, eggs and dairy products. The most common symptom of *salmonella* infection is gastroenteritis, follow by bacteremia and enteric fever. Most forms of poultry meat, pork, and beef are the main sources responsible for salmonella infection [1] because the contamination of the organ and carcass with *salmonella* easily occurs during the slaughtering process of the food animals at abattoirs [2].

The *Salmonella enterica* strain K_SA184 was isolated from a lamb (*Ovis aries*) purchased from the local traditional market in Suwon, Gyeonggi-do, Korea. The *S. enterica* strain K_SA184 was streaked to xylose lysine tergitol 4 (XLT4) agar and incubated at 37℃ for 24 h. The suspected colony in XLT4 agar was inoculated into Luria-Bertani (LB) broth and incubated at 37℃ for 24 h. To analyze the complete genome, the *S. enterica* strain K_SA184 was sequenced by PacBio RS II (Pacific Biosciences, Menlo

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Competing interests
No potential conflict of interest relevant to this article was reported.

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Availability of data and material
The complete genome sequences of *Salmonella enterica* K_SA184 were deposited in GeneBank under the accession numbers CP061159.1. The BioSample accession number is SAMN15891899, and BioProject accession number is PRJNA658857.

Authors' contributions
Conceptualization: Cho Jin Ho, Song M, Kim HB, Lee JH.
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Writing - original draft: Kim H, Cho Jin Ho, Song M, Kim HB, Lee JH.
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Ethics approval and consent to participate
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Park, CA, USA) at Insilicogen (Yong-in, Korea) and Illumina NextSeq 500 (Illumina, San Diego, CA, USA) platform at LabGenomics (Seongnam, Korea) [3]. The genomic DNA of *S. enterica* K_SA184 for PacBio and Illumina sequencing were extracted using the MagAttract HMW DNA Kit (QIAGEN), and NucleoSpin® Microbial DNA kit (TAKARA) according to the manufacturer's instructions. Library preparation was conducted using SMRTbell™ Template Prep Kit 1.0 for Pacbio (Pacific Biosciences) and TruSeq DNA Sample Preparation Kit for Illumina (Illumina) according to the manufacturer's instructions. PacBio sequencing yielded 1,474,738,487 base pairs and 190,304 long reads after filtering, and 5,513,948 paired-end reads with 832,606,148 bp was obtained with Illumina sequencing. *De novo* assemble was conducted using the hierarchical genome assembly process (HGAP v2.3.0) workflow and polished using Quiver. Subsequently, Illumina NextSeq reads were aligned to the PacBio RSII assembly using Burrows-Wheeler Aligner (BWA)-MEM v0.7.17-r1188, and the errors were corrected by using Pilon version 1.23 [4,5]. The quality of genome assembly and the validation of the final genome were assessed by using Quality Assessment Tool for Genome Assemblies (QUAST) v5.0.2 and Benchmarking Universal Single-Copy Orthologs (BUSCO) v3.0.2 [6,7].

Open reading frames (ORFs) and RNA genes of *S. enterica* strain K_SA184 were predicted and functionally annotated by rapid prokaryotic genome annotation (PROKKA) v1.14.5 and Rapid Annotation using Subsystem Technology (RAST) v2.0. The functional categorization and classification of all predicted ORFs were conducted using the RAST server-based SEED viewer and Clusters of Orthologous Groups (COG) – based EggNOG. The putative virulence factors and Antimicrobial resistance were described using BLAST according to the Virulence Factor Database (VFDB) and antibiotic resistome surveillance with the comprehensive antibiotic resistance (CARD) [8,9]. The whole genome of *S. enterica* strain K_SA184 is composed of one circular chromosome (4,725,087 bp) with 52.3% of guanine + cytosine (G + C) content, 4,363 of coding sequence (CDS), 85 of tRNA, and 22 of rRNA genes.

The complete genome of the *S. enterica* strain K_SA184 contains the virulence genes encoding *Salmonella* pathogenicity island 1 & 2 Type III secretion systems which serve several pathogenic functions in killing of macrophages and in interference with immune responses as reported by others [10]. Furthermore, the *S. enterica* strain K_SA184 also possesses multidrug resistance coding genes which are associated with a variety of drugs resistance Efflux Pumps (mdtk) and Resistance

Table 1. Genome features of *Salmonlla enterica* strain K_SA184

Property	Term
Libraries used	PacBio SMRTbell™ library TruSeq DNA Sample Preparation Kit
Sequencing platforms	PacBio RS II sequencer Illumina NextSeq 500
Assemblers	PacBio SMRT analysis v2.3.0 HGAP.3
Annotation method	PROKKA v1.14.5 and RAST v2.0
Average genome coverage	159×
Chromosome length (bp)	4,725,087 bp
No. of contigs	1
guanine + cytosine (G + C) content (%)	52.3
Protein-coding genes (CDSs)	4,363
rRNA genes	22
tRNA genes	85
Plasmids	0
Genbank accession No.	CP061159.1

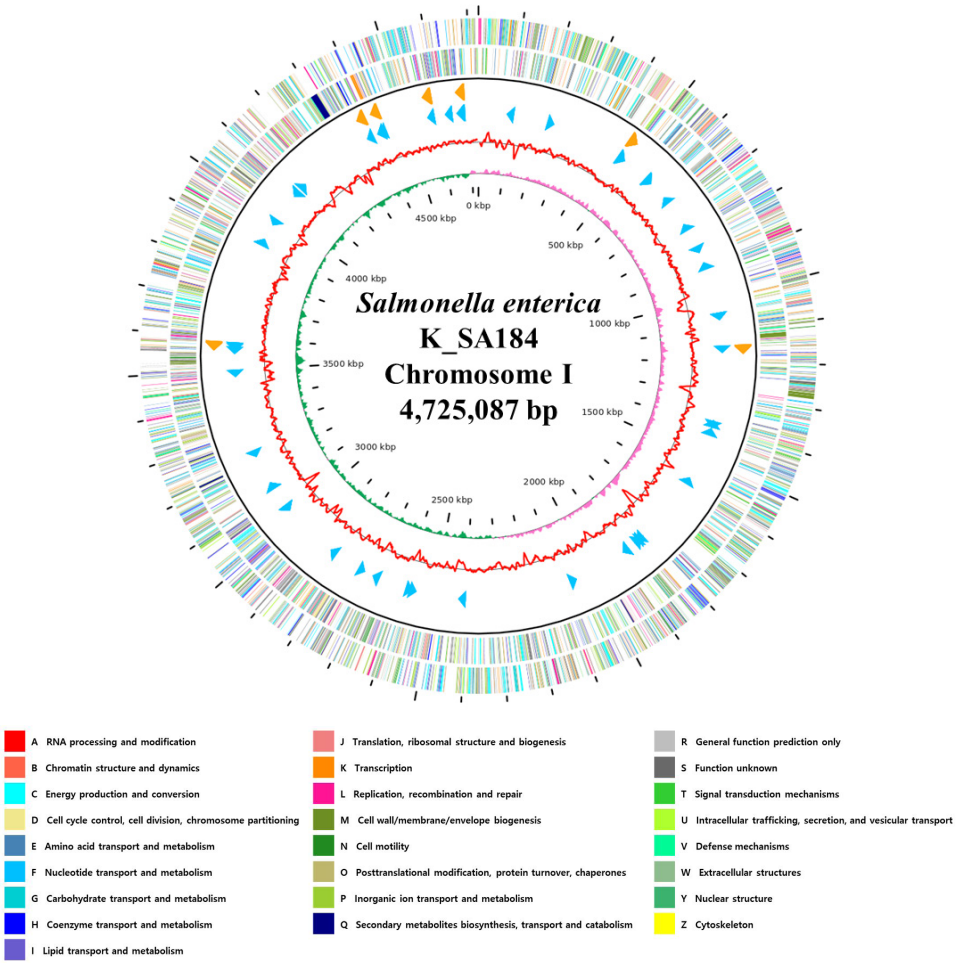

Fig. 1. Genome map of *Salmonella enterica* strain K_SA184. The outer circle denotes the locations of all annotated open reading frames (ORFs), and the inner circle with the red denotes guanine + cytosine (GC) content. Pink, and green peaks denote GC skew. The orange arrows denote rRNAs, and the sky blue arrows denote the tRNA operons. All annotated ORFs are colored differently based on the Clusters of Orthologous Groups (COG) assignments.

to fluoroquinolones, such as, cephalosporins (AmpC), and fluoroquinolones (Par, Gyr). We summarized the general properties of the *S. enterica* strain K_SA184's complete genome in Fig. 1 and Table 1. The further in-vivo studies using *S. enterica* strain K_SA184 will help us to decipher the potential roles of the virulence genes in the pathogenesis.

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