

# Draft Genome Sequence of the Host-Restricted *Salmonella enterica* Serovar Abortusovis Strain SS44

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***Salmonella enterica* serovar Abortusovis is a pathogen strictly adapted to ovines, in which it causes abortion. To enhance our understanding of this pathogen, we assembled the first draft sequence of an *S. Abortusovis* genome (strain SS44). The obtained genomic data might facilitate the study of *S. enterica* evolution and host adaptation.**

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The ovine pathogen *Salmonella enterica* serovar Abortusovis is endemic in several European and Asian countries, where it causes significant economic losses due to the high rates of abortion in infected flocks. The introduction of *S. Abortusovis* epidemic strains in new areas is difficult to control due to the asymptomatic behaviors in infected adult lambs, rams, and nonpregnant ewes (1). Strain SS44 is a clinical isolate (2) that has been widely used to study *S. Abortusovis* virulence features by means of *in vitro* assays and animal experimental models (1, 3, 4). The genome sequence was obtained by a whole-genome shotgun strategy using the Roche 454 Life Sciences GS-20 sequencer and GS-FLX sequencer (478,585 reads totaling 51,883,128 bp). Reads from 3 pyrosequencing runs were assembled using the GS *de novo* Assembler software and GS Reference Mapper software (with published *Salmonella* genomes). Gaps were closed manually, reaching an assembly of 213 contigs ( $N_{50}$  length, 54,599 bp) corresponding to a total of 4,508,347 bp. The draft genome of SS44 has an estimated size of 4.6 Mb, with a G+C content of 52.1%. Contig annotation performed using the Prodigal version 1.20 analysis server (5) predicted 4,924 coding genes. Of these, 2,884 have a full-length homolog in other genomes of *S. enterica* strains (BLASTp protein identity,  $\geq 80\%$  for  $\geq 80\%$  protein length; *E* value,  $< 10^{-8}$ ). Six contigs (42,800 bp in total) have a high similarity ( $> 90\%$ ) with other *S. enterica* serovar virulence plasmids (GenBank accession no. AE006471, EU219534, AY517905, HE663166, and JN885080).

SS44 carries IS1414, a 1,344-bp insertion sequence (IS) that has been detected in several pathotypes of *Escherichia coli* infecting both humans and domesticated animals (3, 6). Read alignment with IS1414-borne *tnpA* gene sequence showed a coverage of  $\sim 100\times$ , confirming a high copy number, as was previously suggested (3). As expected, the high number of IS1414 copies affected the ability to automatically assemble the pyrosequencing reads and hampered the labor of gap closures through directed PCR and primer walking approaches. IS1414 might have been recently transferred from *E. coli* into *S. Abortusovis*, since strains isolated in Asia do not carry this IS element (3). The adaptation of *S.*

Abortusovis to sheep might also be recent, since high copy numbers of IS elements have been observed in the genomes of bacteria adapted only recently to a host-restricted pathogenic lifestyle (4, 7–10). Six *Salmonella* pathogenicity islands (SPI-1 to SPI-6) were reported to be present in SS44, with major degradation in SPI-3 and SPI-6 (of about 4 kbp and 20 kbp, respectively). Host-adapted and host-restricted serovars of *S. enterica* have been reported to depend on their environment for amino acids and essential nutrients (10). The SS44 draft genome shows that *S. Abortusovis* auxotrophy for cysteine and nicotinic acid is due to mutations in the *cysI*, *nadB*, and *nadC* genes. Further analysis of the SS44 genome will help to understand the *S. Abortusovis* evolution toward an ovine-restricted pathogenicity.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [AUYQ00000000](https://www.ncbi.nlm.nih.gov/nuccore/AUYQ00000000). The version described in this paper is version AUYQ02000000.

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