



Draft Genome Sequence of *Streptococcus suis* Strain SsRC-1, a Human Isolate from a Fatal Case of Toxic Shock Syndrome

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ABSTRACT *Streptococcus suis* is an economically important pathogen in the pig industry and is also an emerging zoonotic agent responsible for severe infections in humans. Here, we report the genome sequence of *S. suis* strain SsRC-1. Specifically, this strain was a serotype 2 and was isolated from a human fatal case of toxic shock syndrome (TSS) in Italy.

Streptococcus suis is a swine pathogen important in the pig industry economy. This microorganism is also an emerging human pathogen that affects people who are exposed to infected pigs or who handle raw pork. *S. suis* infection is typically an occupational disease, but several predisposing factors, such as splenectomy or malignancy, may favor the infection (1, 2). Of the 35 identified serotypes, only a few are accountable for human infection, which are usually assigned to serotype 2, sequence type 1 (ST1) (1).

Here, we report the draft genome sequence of the *S. suis* SsRC-1 strain, isolated from a 55-year-old man who lived and worked on a farm in South Italy (3). The patient, with a previous splenectomy for a Hodgkin's lymphoma, presented with severe sepsis, multiple organ failure, and disseminated intravascular coagulopathy. The patient died 28 days after hospital admission. The strain was isolated from blood culture, and the bacterium identification was conducted by microbiological and molecular methods. Specifically, this strain was serotype 2, belonged to sequence type 1, and exhibited the following virulence and antimicrobial resistance gene profiles: *mrp*⁺/*epf*⁺/*sly*⁺/*arcA*⁺/*ofstyp^e1*/*cps2*, *erm*(B), *tet*(O/W/32/O), and *tet*(40) (3).

For genome sequencing, the microorganism was grown in LB liquid culture, and whole DNA was extracted using a MasterPure Gram-positive purification kit (Lucigen Co., WI). The library was prepared using a Nextera XT DNA sample preparation kit v3 (Illumina, San Diego, CA), and a 2 × 300-nucleotide (nt) paired-end sequencing run was performed on an Illumina MiSeq platform. The reads were trimmed and *de novo* assembled using the SPAdes genome assembler (4). The assembly of reads generated 58 contigs of >500 nt, with a 213× coverage. The estimated genome size is 2,093,539 bp, with a G+C content of 42.0%, and there are 2,100 coding sequences (CDSs) that account for 97.44% of the genome (2,155 genes), 45 tRNAs, 6 rRNAs, 4 noncoding rRNAs, and 73 pseudogenes. The genome of the *S. suis* SsRC-1 strain shows some candidate virulence genes, such as *pgdA*, *dltA*, *ccpA*, *endoD*, *gtfA*, *purA*, *scrB*, *cdd*, and *neuC* (5). The *S. suis* SsRC-1 strain was similar to three Italian strains, namely, two clinical isolates, SsCA-1 and SsUD, and *S. suis* strain 32457, which was isolated from a pig (6–8). This draft genome sequence will offer insight about the genetics of *S. suis* and will be helpful for comparing strains from different geographic sites.

Accession number(s). This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under the accession number [PYUF00000000](https://www.ncbi.nlm.nih.gov/nuccore/PYUF00000000). The version described in this paper is version PYUF01000000.

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