



# Draft Genome Sequence of *Streptococcus parasuis* 4253, the First Available for the Species

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**ABSTRACT** Here, we report the draft genome sequence of *Streptococcus parasuis* strain 4253. This is the first publicly available genome sequence of a *S. parasuis* strain.

*Streptococcus parasuis* is a species that consists of members that formerly belonged to *Streptococcus suis* serotypes 20, 22, and 26 (1). It is closely related to *S. suis* but can be distinguished from it based on genetic content and biochemical features, such as the absence of both  $\beta$ -galactosidase activity and arginine hydrolyses (1, 2). Strains can easily be classified as *S. parasuis* based on a positive PCR targeting a 679-bp fragment near the *recN* gene (2).

*S. parasuis* has been isolated almost exclusively from saliva of both healthy and diseased pigs. Until now it was unclear whether *S. parasuis* is a pathogen, like its close relative *S. suis*, or whether it is a member of the commensal microbiota of pigs (2).

*S. parasuis* 4253 was isolated from a tube of a teat sealer which was applied to a dried-up cow suffering from subsequently lethal mastitis. The teat sealer (1 g) was enriched at 37°C for 24 h under aerobic conditions in brain heart infusion broth (Thermo Fisher Diagnostics AG, Pratteln, Switzerland) and thereafter streaked on Columbia blood sheep agar (Thermo Fisher Diagnostics AG) and incubated for 48 h at 37°C under aerobic conditions.

Genomic DNA was isolated with the DNA blood and tissue kit (Qiagen, Hombrechtikon, Switzerland). The DNA was sequenced with a Nextera DNA Flex sample preparation kit (Illumina, San Diego, CA, USA) and a MiniSeq sequencer (Illumina). The sequencing output was 1,018,561 150-bp paired-end reads. Reads were checked for quality with the software package FastQC 0.11.7 (Babraham Bioinformatics, Cambridge, UK) and were assembled with SPAdes 3.12 and Shovill 1.0.4, a tool that accelerates SPAdes (3, 4), with default settings. The assembly was filtered, retaining contigs larger than 500 bp and with coverage more than 25-fold. The draft genome sequence of *S. parasuis* 4253 consists of 1,881,656 bp divided over 106 contigs with an  $N_{50}$  length of 25,681 bp and a largest contig size of 125 kbp. The GC content of the genome is 39.9 mol%, very close to the 39.8 mol% recorded for the type strain SUT-286<sup>T</sup> (1). The genome encodes 1,867 protein-coding genes and 39 tRNAs. The number of rRNA operons was estimated to be four.

An *in silico* PCR tool (5) using our genome as the template and *S. parasuis*-specific primers resulted in an expected 679-bp fragment, thereby confirming the species identification of strain 4253 as *S. parasuis*.

The genome sequence of *S. parasuis* 4253 might provide information about the spread of this bacterium in different hosts and environments. This is the first available genome sequence of a strain identified as *S. parasuis*.

**Data availability.** This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number [SHGT00000000](https://www.ncbi.nlm.nih.gov/nuccore/SHGT00000000). The version described in this paper is version number SHGT01000000. Reads were deposited in the Sequence Read Archive under accession number [SRX5381921](https://www.ncbi.nlm.nih.gov/sra/PRX5381921).

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