# Draft Genome Sequence of *Staphylococcus microti* DSM 22147, Isolated from the Common Vole

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**ABSTRACT** *Staphylococcus microti* DSM 22147 was isolated from viscera of common voles (*Microtus arvalis* Pallas) with generalized *Brucella microti* infection in the Czech Republic. To the best of our knowledge, the genome sequence of the species *S. microti* has not been previously studied. The complete genome sequence of strain DSM 22147 includes a genome of 2,381,859 bp (38.0% GC content) without any plasmids.

*S*taphylococcus microti was first isolated in 2010 from internal organs of two common voles in South Moravia, Czech Republic (1). Another isolate was found on the skin of a small mammal (belonging to rodents or insectivores) living in northeast Poland (2). A case report describes the isolation of *S. microti* from milk samples collected from cows with subclinical (in most cases) and clinical mastitis (3). To date, very little is known about the occurrence and pathogenic potential of *S. microti*. It has been difficult so far to fully assess the real pathological and epidemiological significance of the microorganism. Here, we report the draft genome of *S. microti* strain DSM22147, the first genome of the species *S. microti* to be sequenced.

Strain DSM 22147 was grown aerobically on Columbia blood agar base at 37°C for 24 h. Genomic DNA was extracted using the DNeasy blood and tissue kit (Qiagen, Germany). The quantity of DNA was measured with a Qubit fluorometer. Then, 10 $\mu$g of DNA was sent to Zhejiang University.

One DNA library was generated (422-bp insert size, with the Illumina adapter at both ends), and then sequencing was performed by using an Illumina HiSeq 2000 genomic sequencer, with a 2 $\times$ 100 paired-end sequencing strategy. Clean filtered reads were assembled into scaffolds using Velvet version 1.2.07 (4), and then we used a PAGIT flow (5) to prolong the initial contigs and correct sequencing errors. Predicted genes were identified using Glimmer version 3.0 (6). tRNAscan-SE version 1.21 (7) was used to find tRNA genes, whereas ribosomal RNAs were found by using RNAmmer version 1.2 (8). To annotate predicted genes, we used HMMER version 3.0 (9). The KAAS server (10) was used to assign translated amino acids into KEGG Orthology with the single-directional best hit (SBH) method. Translated genes were aligned with the COG database using NCBI BLASTP.

The draft genome sequence of strain DSM 22147 revealed a genome size of 2,381,859 bp and a G+C content of 38.0% (186 scaffolds with an $N_{50}$ of 77,222 bp). These scaffolds contain 2,175 coding sequences (CDSs), 43 tRNAs, and 25 rRNAs. A total of 2,175 protein-coding genes were assigned as putative functional or hypothetical proteins, and 2,143 genes were categorized into cluster of orthologous groups (COG) functional groups.

To the best of our knowledge, the genome of *S. microti* has not been previously reported. The complete genome sequence will help to advance our understanding of

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the biodiversity of *Staphylococcus* phages. Also, the current study will provide valuable information for further genomic study of phages.

**Accession number(s).** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. JXWY00000000.

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