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GENOME ANNOUNCEMENT

Genome Sequence of *Staphylococcus capitis* QN1, Which Causes Infective Endocarditis

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***Staphylococcus capitis* is a subtype of coagulase-negative staphylococci (CoNS) which could emerge as a significant pathogen causing infective endocarditis, prosthetic valve endocarditis, and late-onset sepsis. We isolated *S. capitis* strain QN1 from the skin swab sample of a female. Here we prepared a genome sequence for this strain consisting of 30 contigs totaling 2,430,101 bases and a GC content of 32.76%.**

Staphylococcus capitis is a subtype of coagulase-negative staphylococci (CoNS), and it is part of the normal bacterial flora of humans and has been occasionally reported in infective endocarditis and prosthetic valve endocarditis cases (5, 10). Recent reports indicate its emergence as a significant pathogen causing late-onset sepsis in very-low-birth-weight (VLBW) infants (<1,500 g) (8). The pathogenesis of CoNS is mainly due to their ability to form biofilms on indwelling medical devices, which confers tolerance to disinfectants during surgery (12). However, there is very little information about the pathogenesis of *S. capitis*. We isolated *S. capitis* QN1 from the skin swab sample of a female in The First Affiliated Hospital of Zhejiang University at Hangzhou, China. The isolate was identified with the MicroFlex LT instrument (Bruker Daltonics) according to the manufacturer's protocols. Spectra were analyzed by using Flexcontrol 3.0 software and the Biotyper 2.0 database (Bruker Daltonics) (9). The taxonomy of this isolate also has been confirmed by 16S rRNA gene sequencing.

The sample was prepared for sequencing by growing *S. capitis* QN1 aerobically overnight at 37°C in Mueller-Hinton broth (Oxoid). Genomic DNA was extracted using the DNeasy blood and tissue kit (Qiagen) according to the manufacturer's recommended protocol. The quantity of DNA obtained was determined using a Nanodrop spectrophotometer and a Qubit fluorometer. Typically, 5 μg of DNA was then sent to the State Key Laboratory for Diagnosis and Treatment of Infectious Disease at Zhejiang University for sequencing on a Hiseq2000 (Illumina, CA) sequencer.

Here we present the whole genome sequence of *S. capitis* QN1, which was sequenced using a whole-genome shotgun strategy by Illumina Hiseq2000 (totaling ~6,481.419 Mb; ~2,667-fold coverage of the genome). The software Velvet with Illumina paired-end reads was used for assembly (13). We obtained 30 contigs (length, >500 bp), The N_{50} was 646,907 bp. The annotation was done by using Glimmer (2) to predict the open reading frame (ORF), tRNAscan-SE 1.21 (6) to find tRNA, RNAmmer 1.2 (4) to search rRNA, and Tandem Repeats Finder 4.04 (1) to find 87 tandem-repeat sequences in all contigs. After that, all contigs were searched against the KEGG (3) and COG (11) databases to annotate the genome. This genome includes 2,430,101 bases and contains 2,368 predicted coding sequences (CDSs), with a G+C content of 32.76%. There are single-copy genes predicted for 16S and 23S rRNA, 2 duplicated genes predicted for 5S rRNA, and 53 copies for tRNAs. An estimated 84.86% of nucleotides (2,062,068) are predicted to encode proteins. A total of 1,995 CDSs annotated by COGs can be classified into 63 extended COG categories, including 1,391 COGs, and 1,365 CDSs can be annotated into 1,155 KEGG Orthology categories by using KAAS (7).

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AJTG00000000. The version described in this paper is the first version, AJTG01000000.

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