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GENOME ANNOUNCEMENT

Whole-Genome Sequence of *Staphylococcus hominis*, an Opportunistic Pathogen

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***Staphylococcus hominis* is a commensal coagulase-negative species of staphylococci. It has been considered a presumptive and opportunistic pathogen that causes nosocomial infections in humans. Here we present the draft genome sequence of *S. hominis* ZBW5, a multidrug-resistant strain isolated from a human skin sample, which provides opportunities to understand the mechanism and genetic basis of its pathogenesis.**

Staphylococcus hominis is a member of the coagulase-negative staphylococci (CoNS). Among CoNS, *S. hominis* is a common species encountered in the clinical samples, usually isolated from the axillae and glabrous skin of arms, legs and trunk of humans (3, 7). Like other CoNS, *S. hominis* does not usually cause human disease, but it is increasingly recognized as a potentially opportunistic and nosocomial pathogen and may occasionally cause infection in patients with abnormally weak immune systems (12). It has been reported to cause some potentially life-threatening infections, such as infective endocarditis (6). A case of *S. hominis* endophthalmitis associated with a capsular hypopyon has also been reported (4). The increasing relevance of *S. hominis* to human health prompted us to determine the genomic sequence of *S. hominis* ZBW5, a multidrug-resistant strain isolated from a normal human skin sample in our hospital.

The whole-genome shotgun sequencing was performed with a high-throughput Illumina Hiseq 2000 system (Illumina, Inc.) and yielded 3279 Mb of high-quality raw sequence, corresponding to more than 1,400-fold genome coverage. A total of 47 contigs (500 to 375,603 bases) were *de novo* assembled by using Velvet (14) with an N_{50} value of 211,593 bp. The assembled genome sequence was analyzed using BLAST to determine the identity of the sequence. The annotation was performed by using Glimmer version 3.02 (2), tRNA genes were identified by tRNAscan-SE (9), rRNA genes were predicted by RNAmmer (8) and Tandem Repeats Finder 4.04 (1) to find 78 tandem repeats in all contigs. In addition, contigs were searched against the KEGG (5), COG (13), and NCBI NR protein databases for annotation.

The chromosome of ZBW5 was 2,335,704 bases in length, with a G+C content of 31.4%. The genome contains 2,304 predicted protein-encoding open reading frames (ORFs) that account for 86% of the genome, with an average length of 872 bp. The genome encodes 39 tRNA genes, one rRNA locus, and four copies of 16S-23S-5S operons. Approximately 71.5% of all coding sequences (CDSs) (a total of 1,894) were assigned to clusters of orthologous groups (COGs), and 1,282 CDSs can be annotated into the 1109 KEGG orthology system by using KAAS (10).

S. hominis ZBW5 carried some predicted protein coding genes involved in antibiotic resistance (such as methicillin, erythromycin, and tetracycline) and multidrug pumps, which are likely to be capable of modulating virulence potential, consistent with other CoNS (11). A wide range of genes related to putative virulence factors, adhesion, and invasion were found, in keeping with the identity of *S. hominis* as an opportunistic pathogen. A further and deep exploration of the genome sequence of *S. hominis* is now under way, which will provide the basis to elucidate the molecular principles of host colonization and insight into the genetic background of this organism's pathogenesis.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under accession no. AKGC00000000. The version described in this paper is the first version, AKGC01000000.

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