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GENOME SEQUENCES

Genome Sequence of *Staphylococcus aureus* Strain CBS2016-05, Isolated from Contaminated Platelet Concentrates in Canada

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ABSTRACT We present the genome sequence of *Staphylococcus aureus* strain CBS2016-05, which was isolated from contaminated platelet concentrates by Canadian Blood Services in 2016. This strain caused a septic reaction in an acute leukemia patient. Genome sequence analysis revealed the presence of one chromosome (2,766,936 bp) and one plasmid (36,441 bp).

Staphylococcus aureus is an opportunistic pathogen that occurs ubiquitously in the upper respiratory tract and can colonize human skin (1). *S. aureus* is a recurrently reported bacterial contaminant of platelet concentrates (PCs), a therapeutic blood component that is used to treat patients with deficient platelet counts. *S. aureus* has emerged as a safety threat to transfusion patients in recent years because it occasionally escapes detection during PC screening with the automated BACT/ALERT culture system (2). Here, we present the genome of *S. aureus* strain CBS2016-05, which was isolated from contaminated PCs and implicated in a septic transfusion reaction in an acute myeloid leukemia patient (3) as part of a hemovigilance investigation of bacterial contamination in PCs in Canada.

S. aureus CBS2016-05 was isolated from patient samples and residual PCs obtained after the transfusion event. Upon isolation and identification, bacterial suspensions were prepared in brain heart infusion medium supplemented with 15% glycerol and stored frozen at −80°C. For DNA isolation, CBS2016-05 was streaked onto blood agar plates, and single colonies were cultured at 35°C overnight in 5 ml Trypticase soy broth with 0.6% yeast extract (4). Cells were collected by centrifugation and resuspended in DNA/RNA Shield reagent (Cedarlane). DNA extraction was performed with the Zymo Quick-DNA HMW MagBead kit (Cedarlane) with lysozyme and RNase A treatment according to the manufacturer's instructions (Zymo Research Corp.).

Illumina paired-end (2 × 300-bp) whole-genome shotgun (WGS) data were generated using Nextera XT libraries run on a MiSeq instrument (v3 chemistry) according to the manufacturer's protocol (Illumina). Illumina reads (n = 1,826,796 reads) were processed using fastp v0.20.0 (5) to remove adapter and barcode sequences, to correct mismatched bases in overlaps, and to filter low-quality reads. Nanopore WGS data (n = 29,813 reads) were obtained using the rapid barcoding sequencing kit (SQK-RBK004) and 1D MinION chemistry (R9.4 FLO-MIN106 flow cell) according to the manufacturer's protocol (Oxford Nanopore Technologies) (6). Long-read processing was performed using Guppy GPU v3.3.3+fa743ab, and reads of <1 kb were removed using Filtlong v0.2.0 (https://github.com/rrwick/Filtlong). A *de novo* assembly (Unicycler v0.4.8, normal mode, default circularization and rotation) (7) was generated using filtered Illumina (1,816,530 reads, with 162× coverage) and Nanopore (23,007 reads [N_{50} value of 15,180 bp], with 78.4× coverage) reads. Annotation was performed using Prokaryotic Genome Annotation Pipeline (PGAP) v2020-09-24.build4894 (best-placed reference protein set, GeneMarkS-2+) (https://github.com/ncbi/pgap), and metrices were

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TABLE 1 Provenance, sequencing, and assembly of the CBS2016-05 isolate

Parameter	Finding
Isolate name	CBS2016-05
BioProject accession no.	PRJNA703931
GenBank accession no.	
Chromosome	CP070991
Plasmid	CP070992
SRA accession no.	
Illumina reads	SRR13745245
Nanopore reads	SRR13745251
Location of isolation	Toronto, Canada
Year of isolation	2016

analyzed with QUAST v5.0.2 (https://github.com/ablab/quast) (8). For all computational tools, default parameters were used except where otherwise noted.

The closed *S. aureus* CBS2016-05 genome (GC content of 32.8%) comprises a 2,766,936-bp chromosome and a 36,441-bp plasmid. A total of 2,603 genes, 128 pseudogenes, 0 CRISPR loci, 19 rRNAs, 59 tRNAs, and 4 noncoding RNAs were identified. *S. aureus* CBS2016-05 was assigned to sequence type 182 (ST182) based on the PubMLST database (9).

Data availability. This WGS project is available in GenBank and the Sequence Read Archive (SRA) under the accession numbers listed in Table 1.

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