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GENOME SEQUENCES

Complete Genome Sequence of *Staphylococcus aureus* CI/BAC/25/13/W, Isolated from Contaminated Platelet Concentrates in England

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ABSTRACT We present the genome sequence of *Staphylococcus aureus* CI/BAC/25/13/W, which was isolated in 2013 as a contaminant of a platelet concentrate with abnormal clotting at the National Health Service Blood and Transplant. Assessment of the genome sequence showed the presence of one chromosome (2,719,347 bp) and one plasmid (1,533 bp).

Staphylococcus aureus is naturally present in the mucosa of healthy humans, and it is responsible for community- and health care-associated infections (1, 2). A major platelet concentrate (PC) contaminant (3), it is introduced into donated blood during venipuncture and is predominant in PCs due to the growth-promoting storage conditions for this blood product (4). *S. aureus* often escapes detection during routine PC screening with culture methods, sometimes causing septic transfusion reactions (3, 5).

Here, we announce the whole-genome sequence of *S. aureus* strain CI/BAC/25/13/W, part of hemovigilance studies in the United Kingdom. PC samples isolated by the National Health Service Blood and Transplant (NHSBT) from a 5-day-old contaminated split apheresis PC unit were cultured in the BacT/Alert system and yielded positive results within 3 h (6). For DNA isolation, *S. aureus* CI/BAC/25/13/W was streaked on blood agar plates from frozen stocks at −80°C, and single colonies were cultured at 35°C in 5 ml Trypticase soy broth with 0.6% yeast extract (7). Cells were collected by centrifugation and resuspended in DNA/RNA Shield tubes (Cedarlane), and DNA was extracted using the Quick-DNA high-molecular-weight (HMW) MagBead kit (Zymo Research Corp.) with lysozyme and RNAse A treatment according to the manufacturer's manual. The same DNA extraction was used for both Nanopore and Illumina libraries.

Paired-end Illumina sequencing was performed using the Nextera XT DNA library preparation kit and a MiSeq instrument (v3 chemistry, 2 × 300-bp reads; Illumina Inc.) according to the manufacturer's instructions. Nanopore sequencing libraries were constructed using the rapid barcoding sequencing kit (SQK-RBK004) and run using a FLO-MIN106 flow cell (R9.4) and a 1D MinION system (Oxford Nanopore Technologies) for 16 h according to the manufacturer's protocol. Signal processing, base calling, demultiplexing, and adapter trimming were performed using Guppy (Guppy GPU v3.3.3+fa743ab).

Illumina reads (987,908 reads) were processed using fastp v0.20.0 (8) to remove adapter and barcode sequences, to correct mismatched bases in overlaps, and to filter low-quality reads, resulting in 971,430 filtered reads. From the Nanopore data (28,406 raw reads), reads of <1 kb were removed using Filtlong v0.2.0 (https://github.com/rrwick/Filtlong), resulting in 21,886 filtered reads with an N_{50} value of 11,786 bp. Hybrid assembly using Illumina and Nanopore filtered reads was performed using Unicycler v0.4.8 (cluster, reconcile,

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TABLE 1 Provenance and NCBI accession numbers for the CI/BAC/25/13/W isolate

Parameter	Details
Isolate	CI/BAC/25/13/W
BioProject accession no.	PRJNA703973
GenBank accession no.	
Chromosome	CP071102
Plasmid	CP071103
SRA accession no.	
Illumina reads	SRR13745244
Nanopore reads	SRR13745250
Country (region)	United Kingdom (England)
Year	2013

partition, and consensus functions, with default circularization and rotation) (9) in normal mode, yielding a closed, circular genome comprising a 2,719,347-bp chromosome and a circular 1,533-bp plasmid, with a GC content of 32.88% and average coverage of 96.2× and 61.5× for Illumina and Nanopore data, respectively. Genome annotation was performed using PGAP (release 2020-09-24.build4894; best-placed reference protein set) with GeneMarkS-2+ (https://github.com/ncbi/pgap) and analyzed with QUAST v5.0.2 (https://github.com/ablab/quast) (10). Default parameters were used for computational tools except where otherwise noted.

A total of 2,699 features were identified, including 2,537 genes, 79 pseudogenes, 0 CRISPR arrays, 19 rRNAs, 60 tRNAs, and 4 noncoding RNAs. PC storage conditions facilitate *S. aureus* proliferation and virulence enhancement, posing a serious health risk. *S. aureus* CI/BAC/25/13/W was assigned to sequence type 12 (ST12) based on the PubMLST database (11).

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

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REFERENCES

1. Jenul C, Horswill AR. 2019. Regulation of *Staphylococcus aureus* virulence. Microbiol Spectr 7:GPP3-0031-2018. https://doi.org/10.1128/microbiolspec.GPP3-0031-2018.
2. Sato A, Yamaguchi T, Hamada M, Ono D, Sonoda S, Oshiro T, Nagashima M, Kato K, Okazumi S, Katoh R, Ishii Y, Tateda K. 2019. Morphological and biological characteristics of *Staphylococcus aureus* biofilm formed in the presence of plasma. Microb Drug Resist 25:668–676. https://doi.org/10.1089/mdr.2019.0068.
3. Loza-Correa M, Kou Y, Taha M, Kalab M, Ronholm J, Schlievert PM, Cahill MP, Skeate R, Cserti-Gazdewich C, Ramirez-Arcos S. 2017. Septic transfusion case caused by a platelet pool with visible clotting due to contamination with *Staphylococcus aureus*. Transfusion 57:1299–1303. https://doi.org/10.1111/trf.14049.
4. Ramirez-Arcos S, Evans S, McIntyre T, Pang C, Yi QL, DiFranco C, Goldman M. 2020. Extension of platelet shelf life with an improved bacterial testing algorithm. Transfusion 60:2918–2928. https://doi.org/10.1111/trf.16112.
5. Chen L, Tang ZY, Cui SY, Ma ZB, Deng H, Kong WL, Yang LW, Lin C, Xiong WG, Zeng ZL. 2020. Biofilm production ability, virulence and antimicrobial resistance genes in *Staphylococcus aureus* from various veterinary hospitals. Pathogens 9:264. https://doi.org/10.3390/pathogens9040264.
6. Brailsford SR, Tossell J, Morrison R, McDonald CP, Pitt TL. 2018. Failure of bacterial screening to detect *Staphylococcus aureus*: the English experience of donor follow-up. Vox Sang 113:540–546. https://doi.org/10.1111/vox.12670.
7. U.S. Food and Drug Administration. 1998. BAM media M157: Trypticase soy broth with 0.6% yeast extract (TSBYE). https://www.fda.gov/food/laboratory-methods-food/bam-media-m157-trypticase-soy-broth-06-yeast-extract-tsbye.
8. Chen S, Zhou Y, Chen Y, Gu J. 2018. fastp: an ultra-fast all-in-one FASTQ preprocessor. Bioinformatics 34:i884–i890. https://doi.org/10.1093/bioinformatics/bty560.
9. Wick RR, Judd LM, Gorrie CL, Holt KE. 2017. Unicycler: resolving bacterial genome assemblies from short and long sequencing reads. PLoS Comput Biol 13:e1005595. https://doi.org/10.1371/journal.pcbi.1005595.
10. Gurevich A, Saveliev V, Vyahhi N, Tesler G. 2013. QUAST: quality assessment tool for genome assemblies. Bioinformatics 29:1072–1075. https://doi.org/10.1093/bioinformatics/btt086.
11. Jolley KA, Bray JE, Maiden MC. 2018. Open-access bacterial population genomics: BIGSdb software, the PubMLST.org website and their applications. Wellcome Open Res 3:124. https://doi.org/10.12688/wellcomeopenres.14826.1.