AMERICAN SOCIETY FOR MICROBIOLOGY | Microbiology Resource Announcements

| Bacteriology | Announcement

Complete genome sequence of *Staphylococcus aureus* strain MD04 isolated from the foot ulcer of a patient with diabetes in rural southwestern Uganda

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ABSTRACT We report the whole-genome sequence of *Staphylococcus aureus* strain MD04, isolated from the foot ulcer of a diabetic patient in rural southwestern Uganda. The assembled genome is 2,789,538 base pairs in length, with a GC content of 32.5%. Genome completeness is 98%, with a 2.48% contamination.

KEYWORDS wound bacteria, bacterial genomics, diabetic foot infection, WGS, Illumina sequencing, Uganda, diabetic foot ulcers

Diabetic foot ulcers (DFUs) are a major public health concern, especially in low-resource settings where access to specialized care is limited (1–3). They frequently become infected with multidrug-resistant pathogens such as *Staphylococcus aureus*, contributing to poor healing, limb amputation, and mortality (4–6). This genome announcement presents the draft genome sequence of *S. aureus* strain MD04, isolated from a chronic DFU in Uganda. It provides genomic insights into resistance and virulence genes to support genomic surveillance, antimicrobial stewardship, and pathogen evolution research.

Strain MD04 was isolated from a wound swab collected from a 58-year-old diabetic patient attending Kampala International University Teaching Hospital. The isolate was cultured on Mannitol salt agar (Himedia, India) and incubated aerobically at 37°C for 24 hours. Preliminary identification was based on Gram staining (gram-positive cocci clusters) and a positive catalase and coagulase test. Antimicrobial susceptibility testing was performed using the Kirby-Bauer disk diffusion method following CLSI guidelines (7), and it revealed resistance to multiple antibiotics, including cefoxitin, indicating methicillin resistance.

A single colony of the confirmed *Staphylococcus aureus* was grown overnight in Luria-Bertani broth (Himedia, India) in a shaking incubator at 37°C and 200 rpm, and cells were harvested by centrifugation at 12,000 × *g* for 10 min. Genomic DNA was extracted using the QIAamp DNA Mini Kit (QIAGEN, Germany), following the manufacturer's protocol. The integrity of the extracted DNA was assessed by 1%, wt/vol agarose gel electrophoresis, and DNA concentration was measured using a Qubit dsDNA High Sensitivity Assay Kit (Thermo Fisher Scientific). DNA purity was evaluated using the NanoDrop ND-1000 spectrophotometer (Thermo Fisher Scientific). The whole genome sequencing was performed using the Illumina MiSeq platform with 2 × 150 bp paired-end reads. Library preparation followed the manufacturer's instructions for the MiSeq DNA High Throughput Library Prep Kit (Illumina, USA).

Reads were quality-checked using FastQC (version 0.12.1) (8). Adapter sequences and low-quality bases were trimmed using Trimmomatic (version 0.39) (9), with a minimum read length cutoff of 36 bp. *De novo* assembly was performed with SPAdes

Editor André O. Hudson, Rochester Institute of Technology, Rochester, New York, USA

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The authors declare no conflict of interest.

Received 11 April 2025
Accepted 22 May 2025
Published 10 June 2025

TABLE 1 Data availability, genome statistics, and features of *Staphylococcus aureus* MD04

Parameter	Value
Genome size	2,789,538 bp
Number of scaffolds	29
Scaffold N_{50}	151.2 kb
Scaffold L_{50}	6
Number of contigs	50
Contig N_{50}	86.4 kb
Contig L_{50}	10
GC%	32.5
Genome coverage	32.67×
Completeness (%)	98
Contamination (%)	2.48
Total number of genes	2,756

(version 3.15.3) (10), resulting in 50 contigs. The genome was annotated using the NCBI Prokaryotic Genome Annotation Pipeline (11). The final assembled genome is 2,789,538 base pairs long, with a GC content of 32.5%, an estimated completeness of 98%, and a 2.48% contamination. It contains 2,756 genes, including 2,651 predicted protein-coding genes (Table 1). Default parameters were used for all software unless otherwise specified.

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DATA AVAILABILITY

This Whole Genome Shotgun project has been deposited in NCBI GenBank under the accession no. JBKICB000000000 (12). Raw reads are available in the NCBI SRA database under the accession number SRR31800042 (13). The annotated genome is accessible via the accession number ASM4657328v1 (14), and the associated BioSample is available under accession number SAMN45937523 (15).

ETHICS APPROVAL

The study protocol and sample collection were approved by the Research Ethics Committee of Kampala International University (KIU-2024-289) and the Ugandan National Council for Science and Technology (HS4836ES).

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