



# Whole-Genome Sequence of *Acinetobacter baumannii* Strain NUBRI-A, Isolated from a Hospitalized Patient in Khartoum, Sudan

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**ABSTRACT** *Acinetobacter baumannii* has emerged as an important pathogen leading to multiple nosocomial outbreaks. Here, we describe the genomic sequence of a multidrug-resistant *Acinetobacter baumannii* sequence type 164 (ST164) isolate from a hospital patient in Sudan. To our knowledge, this is the first reported draft genome of an *A. baumannii* strain isolated from Sudan.

*Acinetobacter baumannii* is an aerobic Gram-negative bacillus frequently linked to health care-associated infections. *A. baumannii* causes a wide spectrum of infections that includes pneumonia, bacteremia, meningitis, and urinary tract infection (1, 2). Its ability to persist for extended periods, in combination with increasing antibiotic resistance, makes it a frequent cause of nosocomial outbreaks. Here, we report the draft genome sequence of an *A. baumannii* strain (NUBRI-A) isolated from a patient admitted to a private hospital in Khartoum, Sudan.

A sputum sample was collected from a 35-year-old male admitted to the Royal Care International Hospital in Khartoum, Sudan, with a pneumonia infection. The specimen was directly inoculated on MacConkey agar and then incubated overnight under aerobic conditions at 37°C. The colony was identified using Gram staining and biochemical tests that included oxidase, catalase, Kligler's iron agar, sulfide indole motility, citrate agar, and urea tests. The analytical profile index was used to confirm the species (3). Genomic DNA was extracted using the QIAamp DNA minikit (Qiagen, Germany), and paired-end libraries were prepared using the Nextera DNA Flex library kit, followed by 2 × 300-bp sequencing on a MiSeq platform (Illumina, Inc., USA). The sequenced reads were trimmed using Sickle version 1.33 (with the parameters -q 20 -l 75) (<https://github.com/najoshi/sickle>) and *de novo* assembled using SPAdes version 3.11 (with the parameters -careful and -cov-cutoff auto) (4). All resultant contiguous sequences were then submitted to the NCBI Prokaryotic Genome Annotation Pipeline (5). Multilocus sequence typing (MLST) was determined using mlst (<https://github.com/tseemann/mlst>). This study was approved by the Research Ethics Committee at the National University in Sudan.

A total of 1,777,192 paired-end reads were obtained from the whole-genome sequencing of NUBRI-A. Quality-controlled reads (1,768,578 reads; average length, 211 bp) with a Phred score of ≥20 were assembled. The assembled genome was composed of 33 contigs (all were longer than 200 bp), and the longest contig size was 1,777,326 bp, covering 3,743,802 bp. The GC content and  $N_{50}$  value were 38.9% and 390,599 bp, respectively. The genome assembly metric was calculated with QUAST version 5.0.2 using default parameters. The total number of genes is 3,576; of those, 3,444 are protein-coding genes, 70 are RNA genes, and 62 are pseudogenes. MLST (Oxford scheme) on this strain revealed that it belongs to sequence type 164 (ST164).

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According to the *A. baumannii* PubMLST database (<https://pubmlst.org/abaumannii/>), four isolates from Brazil and Turkey sharing this ST have been reported.

The whole-genome sequence of *A. baumannii* strain NUBRI-A will provide a starting point for studying the genomic diversity of this opportunistic bacterial pathogen in Sudan.

**Data availability.** This whole-genome sequence project has been deposited at DDBJ/ENA/GenBank under the accession number [SOYV00000000](https://www.ncbi.nlm.nih.gov/nuccore/SOYV00000000). The version described in this paper is the first version, SOYV01000000. The sequencing reads have been deposited under the SRA accession number [SRP195526](https://www.ncbi.nlm.nih.gov/sra/SRP195526).

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