




Genome Sequence of Clinical *Acinetobacter baumannii* Strain V15

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ABSTRACT *Acinetobacter baumannii* is recognized as a critical human pathogen by the World Health Organization, and therefore there is increasing interest in studying its biology and pathophysiology. Among other strains, *A. baumannii* V15 has been extensively used for these purposes. Here, the genome sequence of *A. baumannii* V15 is presented.

In the last 50 years, the world has experienced the emergence and rapid spread of a new plague: microbes resistant to multiple antibiotics, preventing the treatment of many diseases (1–3). Of these microbes, *A. baumannii* has been recognized by the World Health Organization (WHO) as a critical pathogen (4).

A. baumannii strain V15 presents differential characteristics with respect to domesticated strains ATCC 17978 and ATCC 19606. V15 forms robust biofilms, produces a capsule, and generates large amounts of extracellular compounds (5). Moreover, it responds to light at both environmental temperatures and those of warm-blooded hosts (6). Furthermore, V15 is sensitive to multiple antibiotics and genetically manipulable.

Here, we present the draft genome sequence of *A. baumannii* V15, which was isolated in 2010 from a patient in the Toxicology Unit of the Vilnius University Emergency Hospital, Lithuania (7). Initial identification was performed using the Phoenix system (BD, USA) and amplified rDNA gene restriction analysis (7). For sequencing, a single colony of V15 was inoculated into 3 mL LB broth medium and grown at 37°C for 18 h. The cells were then pelleted and used for DNA extraction using a commercial kit (Macherey-Nagel, Allentown, USA) (8).

The genome of V15 was sequenced using the Illumina NovaSeq 6000 platform at Novogene Co. Briefly, genomic DNA was randomly sheared into short fragments, which were then end-repaired, A-tailed, and further ligated with Illumina adapters. The fragments with adapters were PCR amplified, size selected, and purified. The library was checked using Qubit and real-time PCR for quantification and Bioanalyzer for size distribution detection. The quantified libraries were pooled and sequenced on Illumina platforms, with quality parameters (Q scores) between Q20 and Q30. The sequence quality distribution was ascertained by a Phred score higher than 35, and the error distribution was normal for Illumina sequences. Read quality control, adapter trimming, and sequence filtering were performed using fastp v0.23.3 software with default parameters (8).

Sequencing yielded 7,884,616 paired-end reads of 150 bp, which were assembled into 44 contigs using the Read Assembly and Annotation Pipeline Tool (RAPT) v0.5.4 (rap-41589182; SKESA v2.5.0; PGAPX v2022-10-03.build6384; <https://www.ncbi.nlm.nih.gov/rapt/>). Contigs 1 and 2 corresponded to two complete plasmids named pV15_1 and pV15_2, respectively. The resulting assembly yielded N_{50} and L_{50} values of 194,502 bp and 8, respectively.

The complete genome size of *A. baumannii* V15 is 3,863,035 bp, including the chromosome and plasmids. V15 has one chromosome of 3,786,160 bp, encoding 3,610 predicted

Editor David Rasko, University of Maryland School of Medicine

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The authors declare no conflict of interest.

Received 16 March 2023

Accepted 11 June 2023

Published 26 June 2023

coding sequences (CDSs), with a GC content of 38.5%. Plasmid pV15_1 contains 68,113 bp, with a GC content of 33%, while pV15_2 has 8,762 bp, with a GC content of 38%. The plasmids encode 87 and 12 predicted CDSs, respectively.

Average nucleotide identity (ANI) values were obtained between V15 and type strains ATCC 17978, ATCC 19606, and UPAB1 using the ANI Calculator platform (OrthoANLu v1.2) (9). The ANI values were found to be 97.92%, 97.98%, and 97.80%, respectively.

The sequences and contigs were assembled using SKESA (10) (within the RAPT pipeline). Open reading frames (ORFs) were predicted using the Prokaryotic Genome Annotation Pipeline (PGAP) (11) (within the RAPT pipeline). Default parameters were used for all software unless otherwise specified.

Data availability. This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under accession number [JAQSVAA000000000](https://doi.org/10.1093/bioinformatics/btad000). The version described in this paper is version [JAQSVAA010000000](https://doi.org/10.1093/bioinformatics/btad000). The raw reads were submitted to the NCBI SRA under accession number [SRR23455319](https://doi.org/10.1093/bioinformatics/btad000), BioProject accession number [PRJNA931904](https://doi.org/10.1093/bioinformatics/btad000), and BioSample accession number [SAMN33101523](https://doi.org/10.1093/bioinformatics/btad000). The GenBank accession numbers for pV15_1 and pV15_2 are [JAQSVAA010000035](https://doi.org/10.1093/bioinformatics/btad000) and [JAQSVAA010000036](https://doi.org/10.1093/bioinformatics/btad000), respectively. The GenBank accession numbers of the type strain genome sequences used for comparison are [GCF_029459615.1](https://doi.org/10.1093/bioinformatics/btad000), [GCF_009035845.1](https://doi.org/10.1093/bioinformatics/btad000), and [GCF_006843645.1](https://doi.org/10.1093/bioinformatics/btad000) for ATCC 17978, ATCC 19606, and UPAB1, respectively.

ACKNOWLEDGMENTS

This work was supported by grants from the Agencia Nacional de Promoción Científica y Tecnológica (PICT 2018-0793) to M.A.M. M.A.M. is a career investigator at CONICET, while B.P.M., R.G., N.A., and V.P. are fellows at the same institution. M.T.N. is CONICET support staff.

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