



Data in Brief

The genome sequence of *Acinetobacter baumannii* isolated from a septicemic patient in a local hospital in Malaysia



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ABSTRACT

Acinetobacter baumannii is a Gram negative, strictly aerobic clinical pathogen causing mostly nosocomial infections globally. The DNA of an isolate from the blood of a local septicemic patient was sequenced using the Illumina GA IIx. The draft genome generated is 4,178,008 bp with a G + C content of 42%. From the annotation results, 47 resistance determinants including 16 multidrug resistance (MDR) genes were identified. The data may be accessed via the GenBank WGS master accession number APWV00000000.

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Specifications	
Organism/cell line/tissue	<i>Acinetobacter baumannii</i>
Sex	n/a
Sequencer or array type	GA IIx
Data format	Analyzed
Experimental factors	Genome sequencing of an antimicrobial susceptible strain
Experimental features	The whole genome sequence of a locally acquired clinical strain of <i>A. baumannii</i> was acquired and annotated to reveal several multidrug resistant elements.
Consent	n/a
Sample source location	Puncak Alam, Malaysia

meningitis [3,4,9]. The identification of *A. baumannii* has thus far been a problem due to their phenotypic ubiquity. This, coupled with its rapid acquisition of antimicrobial resistance, and ability to survive in desiccated surfaces makes it a threat in both hospital and community environments [6,8,12].

The bacterial sample was isolated from the blood of a male septicemic patient in a local hospital in Malaysia. The sample was cultured in Mueller Hinton Broth (MHB) and Mueller Hinton Agar (MHA). DNA extraction was performed using a 24-hour culture in MHB following the protocol provided by the Wizard® Genomic DNA Purification Kit (Promega, USA). The sequencing was done via the Genome Analyzer IIx (Illumina, CA, USA) at the Pharmacogenomics Centre (PROMISE), UiTM Puncak Alam, yielding a total of 6,878,406 reads with a read length of 36 bp, and 62× coverage. The GC content of the reads was determined to be 42%.

The quality of the sequencing data was analyzed using SolexaQA and FastQC. De novo assembly was performed using SOAPdenovo v1.05, producing a total of 1486 contigs, which was used to construct 679 scaffolds. Ordering and orienting of the scaffolds were done using OSLAY against four reference strains: ACICU, AYE, SDF, and ATCC 17978. The optimal synteny was obtained when aligned against strain AYE, and the subsequent analyses were done using that output. Annotation of the scaffolds via BASys yielded a 4,178,008 bp genome with 5845 genes identified, where 5838 of them were successfully annotated [13]. The output of the annotation was compared against the RAST online annotation service, as well as a combination of the PRODIGAL gene finder and BLAST2GO annotation software [1,5,7].

Analysis of the genes identified revealed 30 efflux genes, six of which are RND and one macrolide-specific. A total of 56 mobile elements were

1. Direct link to deposited data

<http://www.ncbi.nlm.nih.gov/nucore/APWV00000000.1>

2. Experimental design, materials and methods

The clinical pathogen, *Acinetobacter baumannii* is a Gram negative, strictly aerobic, oxidase negative coccobacillus that is ubiquitous within the hospital environment [2,3,10,11]. Depending on the strain, this pathogen is capable of causing a multitude of infections ranging from skin infections and bacteremia, to necrotizing fasciitis and secondary

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identified which include 19 insertion genes, 27 transposons and 10 integrase-associated elements. Pili-associated determinants were identified to include seven type-IV assembly genes, two twitching mobility proteins (*pilT*), one type-4 fimbrial expression regulatory protein (*pilR*), and two pilin-like competence factors (*ppD*). More than 60 regulator elements were found, comprising 13 repressor genes, seven *tetR* transcriptional regulators and one arsenical resistance operon repressor. The annotation results also revealed the presence of 47 resistance genes composed of 16 MDR genes, eight copper resistance genes, three acriflavine genes, and singular *bla*_{OXA-10}, tellurite, tetracycline, fosmidomycin, albicidin, arsenite resistance genes. Two resistance regulatory elements were identified as well.

This Whole Genome Shotgun project has been deposited at GenBank under the accession APWV00000000. The version described in the paper is the first version APWV00000000 [12].

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