Acinetobacter baumannii isolate A1 was recovered in the United Kingdom in 1982 and belongs to global clone 1 (GC1). Here, we present its complete 3.91-Mbp genome sequence, generated via a combination of short-read sequencing (Illumina), long-read sequencing (PacBio), and manual finishing.

A. baumannii isolate A1 was isolated in 1982 at the Nottingham University Hospital in the United Kingdom (1) and is one of the earliest multiple-antibiotic-resistant isolates available in current collections. It has been recorded as being resistant to several of the antibiotics used therapeutically at the time, namely, sulfonamides, tetracycline, and gentamicin (2). A1 is also resistant to streptomycin and spectinomycin.

Whole-genomic DNA was sequenced on Illumina HiSeq at the Wellcome Trust Sanger Institute, generating 3,120,038 paired-end reads that were 100 bp in length, with a mean insert size of 275 bp. The reads were assembled de novo using Velvet version 1.2.10 (3) and VelvetOptimiser version 2.2.5 (http://bioinformatics.net.au/software.velvetoptimiser.shtml). The contigs were joined with the sequences of amplicons from polymerase chain reactions and assembled using Sequencher (Gene Codes Corporation, USA), producing an 8,731-bp plasmid sequence and a finished chromosomal sequence, except for the gene encoding the large repetitive protein known as the biofilm-associated protein. In order to resolve this complex repeat region, DNA was subjected to sequencing (PacBio), and manual finishing.

The genome sequence confirms that A1 is a member of global clone 1 (GC1; sequence type 1 [ST1] in the Institut Pasteur multilocus sequence type [MLST] scheme [6] and ST109 in the Oxford scheme [7]), one of the resistant clones found on all inhabited continents. It carries the K1 capsule locus and the OCL1 outer core locus (8). Its antibiotic resistance is due to the presence of the sul1, tetA(A), and aacC1 genes, together with the aadA1 gene in AbaR24, a genomic resistance island derived from AbaR0 (9) via an IS26-mediated deletion of a 10,876-bp segment that included the aphA1b and blaTEM Genes. There are no copies of the insertion sequence ISAba1. The plasmid pA1 is cryptic. The genome sequence of A1 will underpin studies of the evolution of the AbaR-carrying branch of the GC1.

Nucleotide sequence accession numbers. The complete genome sequence has been deposited in DDBJ/ENA/GenBank under the accession numbers CP010781 (chromosome) and CP010782 (plasmid). The versions described in this paper are the first versions, CP010781.1 and CP010782.2, respectively.

ACKNOWLEDGMENTS
This work was supported by the NHMRC of Australia (project grant 1026189 to R.M.H., and fellowship 1061409 to K.E.H.), the Welcome Trust (grant 098051 to WTSI), and the Victorian Life Sciences Computation Initiative (VLSCI) (no. VR0082).

We thank Kevin Towner for supplying the A1 isolate.

REFERENCES


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Title:
Genome Sequence of Acinetobacter baumannii Strain A1, an Early Example of Antibiotic-Resistant Global Clone 1

Date:
2015-03-01

Citation:

Persistent Link:
http://hdl.handle.net/11343/260103

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