Complete Genome Sequence of the Clinical Strain *Acinetobacter baumannii* R2090 Carrying the Chromosomally Encoded Metallo-β-Lactamase Gene *bla*<sub>NDM-1</sub>

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*Acinetobacter baumannii* is an emerging human pathogen causing nosocomial and community-acquired infections. Here, we present the complete genome sequence of the clinical *A. baumannii* strain R2090 carrying the metallo-β-lactamase gene *bla*<sub>NDM-1</sub> in its chromosome within the transposon Tn125.

*Acinetobacter baumannii* is a widespread serious pathogen (1) causing nosocomial infections (2). Also, community-acquired infections initiated by this pathogen feature high mortality rates (3). In this study, we present the complete genome sequence of the strain R2090, representing a community-acquired *A. baumannii* sequence type.

The strain R2090 was recovered from a rectal swab from a patient hospitalized in an Egyptian hospital. It was classified as belonging to the species *A. baumannii*, since its 16S rRNA gene sequence is identical to the corresponding sequence of the *A. baumannii* type strain ATCC 19606 (4).

For the establishment of the *A. baumannii* R2090 genome sequence, purified chromosomal DNA was used to construct an 8-kb mate pair sequencing library (Nextera mate pair sample preparation kit, Illumina, Inc.). The sequencing approach on an Illumina MiSeq system yielded 1,038,361 sequence reads accounting for 699,271,346 bases sequence information. Thus, a 183-fold coverage was achieved for the 3.8-Mb *A. baumannii* genome. The obtained sequence reads were assembled using the GS De Novo Assembler software (version 2.8, Roche) (5, 6), which resulted in one scaffold composed of 57 contigs. Subsequently, an *in silico* gap closure approach followed by a PCR-based finishing strategy (7–9) was applied to complete the circular chromosome. Annotation of the 3,819,158-bp genome featuring a G+C content of 39.04% was performed within the GenDB 2.0 system (10) and resulted in the prediction of 3,601 coding sequences, 73 tRNA genes, and 6 rRNA operons.

The genome of *A. baumannii* R2090 is highly related to the community-acquired *A. baumannii* strain D1279779 that was isolated from an indigenous Australian patient who suffered from a bacteremic infection (11). Both strains belong to sequence type 5. Mutation analysis of the genome of strain R2090 revealed that the *bla*<sub>NDM-1</sub> gene is located on the transposon Tn125 (11, 12).

Comparison of the R2090 genome to the genomes of other clinical *A. baumannii* isolates is expected to provide deeper insights into the development of multiresistant derivatives of this emerging human pathogen.

**Nucleotide sequence accession number.** The *Acinetobacter baumannii* R2090 genome sequence has been deposited in the EMBL/GenBank database (EBI, NCBI) under the accession number LN868200.

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