

# Complete Genome Sequence of the Clinical Strain *Acinetobacter baumannii* R2090 Carrying the Chromosomally Encoded Metallo- $\beta$ -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- $\beta$ -lactamase gene *bla*<sub>NDM-1</sub> in its chromosome within the transposon Tn125.**

Received 23 July 2015 Accepted 25 July 2015 Published 10 September 2015

**Citation** Krahn T, Wibberg D, Maus I, Winkler A, Nordmann P, Pühler A, Poirel L, Schlüter A. 2015. Complete genome sequence of the clinical strain *Acinetobacter baumannii* R2090 carrying the chromosomally encoded metallo- $\beta$ -lactamase gene *bla*<sub>NDM-1</sub>. *Genome Announc* 3(5):e01008-15. doi:10.1128/genomeA.01008-15.

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*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 3,108,361 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 *rrn* 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 267. Calculation of the average nucleotide identity (ANI calculator [<http://enve-omics.ce.gatech.edu/ani/>]) confirmed close relatedness of both strains with an ANI value of 99.92%.

Comparative analyses of strains R2090 and D1279779 revealed differences in putative virulence determinants. In strain

D1279779, genes encoding a type VI secretion system are missing (11). In contrast, strain R2090 carries at least 13 of 17 genes of the type VI secretion system cluster. Moreover, strain D1279779 harbors three type I pili systems putatively involved in adherence and biofilm formation (12), whereas two of these clusters featured insertions of transposable elements in strain R2090.

An ARG-ANNOT analysis (13) indicated presence of the metallo- $\beta$ -lactamase (MBL) gene *bla*<sub>NDM-1</sub> exclusively in the R2090 chromosome in addition to other putative resistance determinants present in both genomes. The gene *bla*<sub>NDM-1</sub> encodes a broad-spectrum carbapenemase with the capability to inactivate all  $\beta$ -lactam antibiotics except aztreonam (14). As previously described, this gene is located on the transposon Tn125 (15, 16). Occurrence of *bla*<sub>NDM-1</sub> in strain R2090 is important with regards to the dissemination of this serious antibiotic resistance determinant among *A. baumannii* strains (11, 17).

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](https://www.ncbi.nlm.nih.gov/nuccore/LN868200).

## ACKNOWLEDGMENTS

The bioinformatics support of the BMBF-funded project “Bielefeld-Gießen Center for Microbial Bioinformatics”—BiGi (grant 031A533) within the German Network for Bioinformatics Infrastructure (de. NBI) is gratefully acknowledged. I.M. and D.W. acknowledge the receipt of a scholarship from the CLIB Graduate Cluster “Industrial Biotechnology,” cofinanced by the Ministry of Innovation of North Rhine-Westphalia.

## REFERENCES

- Gootz TD, Marra A. 2008. *Acinetobacter baumannii*: an emerging multidrug-resistant threat. *Expert Rev Anti Infect Ther* 6:309–325. <http://dx.doi.org/10.1586/14787210.6.3.309>.

2. Bergogne-Bérézin E, Towner KJ. 1996. *Acinetobacter* spp. as nosocomial pathogens: microbiological, clinical, and epidemiological features. *Clin Microbiol Rev* 9:148–165.
3. Falagas ME, Karveli EA, Kelesidis I, Kelesidis T. 2007. Community-acquired *Acinetobacter* infections. *Eur J Clin Microbiol Infect Dis* 26: 857–868. <http://dx.doi.org/10.1007/s10096-007-0365-6>.
4. Davenport KW, Daligault HE, Minogue TD, Bruce DC, Chain PS, Coyne SR, Jaissle JG, Koroleva GI, Ladner JT, Li PE, Palacios GF, Scholz MB, Teshima H, Johnson SL. 2014. Draft genome assembly of *Acinetobacter baumannii* ATCC 19606. *Genome Announc* 2(4):e00832-14. <http://dx.doi.org/10.1128/genomeA.00832-14>.
5. Wibberg D, Blom J, Rückert C, Winkler A, Albersmeier A, Pühler A, Schlüter A, Scharf BE. 2013. Draft genome sequence of *Sinorhizobium meliloti* RU11/001, a model organism for flagellum structure, motility and chemotaxis. *J Biotechnol* 168:731–733. <http://dx.doi.org/10.1016/j.jbiotec.2013.10.015>.
6. Maus I, Wibberg D, Stantscheff R, Eikmeyer FG, Seffner A, Boelter J, Szczepanowski R, Blom J, Jaenicke S, König H, Pühler A, Schlüter A. 2012. Complete genome sequence of the hydrogenotrophic, methanogenic archaeon *Methanococcus bourgensis* strain MS2<sup>T</sup>, isolated from a sewage sludge digester. *J Bacteriol* 194:5487–5488. <http://dx.doi.org/10.1128/JB.01292-12>.
7. Wibberg D, Blom J, Jaenicke S, Kollin F, Rupp O, Scharf B, Schneiker-Bekel S, Szczepanowski R, Goesmann A, Setubal JC, Schmitt R, Pühler A, Schlüter A. 2011. Complete genome sequencing of *Agrobacterium* sp. H13-3, the former *Rhizobium lupini* H13-3, reveals a tripartite genome consisting of a circular and a linear chromosome and an accessory plasmid but lacking a tumor-inducing Ti-plasmid. *J Biotechnol* 155:50–62. <http://dx.doi.org/10.1016/j.jbiotec.2011.01.010>.
8. Tomazetto G, Hahnke S, Maus I, Wibberg D, Pühler A, Schlüter A, Klocke M. 2014. Complete genome sequence of *Peptoniphilus* sp. strain ing2-D1G isolated from a mesophilic lab-scale completely stirred tank reactor utilizing maize silage in co-digestion with pig and cattle manure for biomethanation. *J Biotechnol* 192:59–61. <http://dx.doi.org/10.1016/j.jbiotec.2014.09.011>.
9. Krahn T, Wibberg D, Maus I, Winkler A, Poirel L, Pühler A, Schlüter A. 2015. Complete genome sequence of *Acinetobacter baumannii* CIP 70.10, a susceptible reference strain for comparative genome analyses. *Genome Announc* 3(4):e00850-15. <http://dx.doi.org/10.1128/genomeA.00850-15>.
10. Meyer F, Goesmann A, McHardy AC, Bartels D, Bekel T, Clausen J, Kalinowski J, Linke B, Rupp O, Giegerich R, Pühler A. 2003. GenDB—an open source genome annotation system for prokaryote genomes. *Nucleic Acids Res* 31:2187–2195. <http://dx.doi.org/10.1093/nar/gkg312>.
11. Farrugia DN, Elbourne LD, Hassan KA, Eijkelkamp BA, Tetu SG, Brown MH, Shah BS, Peleg AY, Mabbutt BC, Paulsen IT. 2013. The complete genome and phenome of a community-acquired *Acinetobacter baumannii*. *PLoS One* 8:e58628. <http://dx.doi.org/10.1371/journal.pone.0058628>.
12. Eijkelkamp BA, Stroehrer UH, Hassan KA, Paulsen IT, Brown MH. 2014. Comparative analysis of surface-exposed virulence factors of *Acinetobacter baumannii*. *BMC Genomics* 15:1020. <http://dx.doi.org/10.1186/1471-2164-15-1020>.
13. Gupta SK, Padmanabhan BR, Diene SM, Lopez-Rojas R, Kempf M, Landraud L, Rolain JM. 2014. ARG-ANNOT, a new bioinformatic tool to discover antibiotic resistance genes in bacterial genomes. *Antimicrob Agents Chemother* 58:212–220. <http://dx.doi.org/10.1128/AAC.01310-13>.
14. Shakil S, Azhar EI, Tabrez S, Kamal MA, Jabir NR, Abuzenadah AM, Damanhouri GA, Alam Q. 2011. New Delhi metallo- $\beta$ -lactamase (NDM-1): an update. *J Chemother* 23:263–265. <http://dx.doi.org/10.1179/joc.2011.23.5.263>.
15. Pfeifer Y, Wilharm G, Zander E, Wichelhaus TA, Göttig S, Hunfeld KP, Seifert H, Witte W, Higgins PG. 2011. Molecular characterization of *bla*<sub>NDM-1</sub> in an *Acinetobacter baumannii* strain isolated in Germany in 2007. *J Antimicrob Chemother* 66:1998–2011. <http://dx.doi.org/10.1093/jac/dkr256>.
16. Bonnin RA, Poirel L, Naas T, Pirs M, Seme K, Schrenzel J, Nordmann P. 2012. Dissemination of New Delhi metallo- $\beta$ -lactamase-1-producing *Acinetobacter baumannii* in Europe. *Clin Microbiol Infect* 18:E362–E365. <http://dx.doi.org/10.1111/j.1469-0691.2012.03928.x>.
17. Zeana C, Larson E, Sahni J, Bayuga SJ, Wu F, Della-Latta P. 2003. The epidemiology of multidrug-resistant *Acinetobacter baumannii*: does the community represent a reservoir? *Infect Control Hosp Epidemiol* 24: 275–279. <http://dx.doi.org/10.1086/502209>.