genomeA
Journals.ASM.org

Genome Sequence of an Extremely Drug-Resistant Clinical Isolate of *Acinetobacter baumannii* Strain AB030

Peter C. Loewen,[a] Yasser Alsaadi,[a] Dinesh Fernando,[a] Ayush Kumar[a,b]

Departments of Microbiology[a] and Medical Microbiology,[b] University of Manitoba, Winnipeg, Canada

We report the 4.3-Mbp genome sequence of a blood isolate of *Acinetobacter baumannii* strain AB030.

Received 3 September 2014 **Accepted** 8 September 2014 **Published** 16 October 2014

Citation Loewen PC, Alsaadi Y, Fernando D, Kumar A. 2014. Genome sequence of an extremely drug-resistant clinical isolate of *Acinetobacter baumannii* strain AB030. Genome Announc. 2(5):e01035-14. doi:10.1128/genomeA.01035-14.

Address correspondence to Ayush Kumar, ayush.kumar@umanitoba.ca.

Acinetobacter baumannii is notorious for causing infections that are very difficult to treat because of its high resistance to all classes of antibiotics (1, 2). Multidrug-resistant (MDR), extremely drug-resistant (XDR), and pandrug-resistant (PDR) isolates have been reported from around the globe (3–7). Here, we report the complete genome sequence of *A. baumannii* strain AB030, an XDR isolate from a bloodstream infection in a 29-year-old female (8). *A. baumannii* strain AB030 is resistant to aminoglycosides (amikacin, gentamicin); carbapenems (imipenem, meropenem); fluoroquinolones (ciprofloxacin, levofloxacin, moxifloxacin); penicillin and β-lactamase inhibitors (tazobactam-piperacillin); first-generation (cefzolin) and extended-spectrum (cefepime, ceftriaxone) cephalosporins; tigecycline; and trimethoprim-sulfamethoxazole (8). It is susceptible only to colistin (8). Therefore, we classified this isolate as XDR following the recommendations made by Magiorakos et al. (9).

DNA was isolated using the Ultra-Clean Microbial DNA isolation kit (MoBio Laboratories, Carlsbad, CA, USA) following the manufacturer's instructions. Genome sequencing was performed using the PacBio platform at the Genome Quebec facility (Montreal, QC, Canada) using three SMRT cells. Assembly was carried out using the PacBio SMRT analysis pipeline version 2.2.0, with 93.3× coverage to give a single contiguous genome sequence. The sequence was annotated by the National Center for Biotechnology Information (NCBI) Prokaryotic Genomes Annotation Pipeline.

The genome consists of 4,335,793 bases with a G+C content of 39%. There are a total of 4,258 putative genes, which include 4,132 protein-, 18 rRNA-, and 73 tRNA-coding sequences.

Nucleotide sequence accession number. The genome sequence of *A. baumannii* AB030 was deposited in NCBI GenBank under the accession number CP009257.

ACKNOWLEDGMENTS

This work is supported by funding from the Discovery Grants program of the Natural Science and Engineering Council of Canada (A.K. and P.C.L.), the Canada Research Chair program (P.C.L.), and the University of Manitoba Research Grant Program (A.K.). Y.A. is funded by a graduate scholarship from the Royal Government of Saudi Arabia.

REFERENCES

1. **Abbo A, Navon-Venezia S, Hammer-Muntz O, Krichali T, Siegman-Igra Y, Carmeli Y.** 2005. Multidrug-resistant *Acinetobacter baumannii*. Emerg. Infect. Dis. **11:**22–29. http://dx.doi.org/10.3201/eid1101.040001.
2. **Peleg AY, Seifert H, Paterson DL.** 2008. *Acinetobacter baumannii*: emergence of a successful pathogen. Clin. Microbiol. Rev. **21:**538–582. http://dx.doi.org/10.1128/CMR.00058-07.
3. **Apisarnthanarak A, Mundy LM.** 2009. Mortality associated with pandrug-resistant *Acinetobacter baumannii* infections in Thailand. Am. J. Infect. Control **37:**519–520. http://dx.doi.org/10.1016/j.ajic.2008.10.024.
4. **Bou G, Cerveró G, Domínguez MA, Quereda C, Martínez-Beltrán J.** 2000. Characterization of a nosocomial outbreak caused by a multiresistant *Acinetobacter baumannii* strain with a carbapenem-hydrolyzing enzyme: high-level carbapenem resistance in *A. baumannii* is not due solely to the presence of β-lactamases. J. Clin. Microbiol. **38:**3299–3305.
5. **CDC.** 2004. *Acinetobacter baumannii* infections among patients at military medical facilities treating injured U.S. service members, 2002–2004. MMWR Morb. Mortal. Wkly. Rep. **53:**1063–1066.
6. **Cristina ML, Spagnolo AM, Ottria G, Sartini M, Orlando P, Perdelli F, Galliera Hospital Group.** 2011. Spread of multidrug carbapenem-resistant *Acinetobacter baumannii* in different wards of an Italian Hospital. Am. J. Infect. Control **39:**790–794. http://dx.doi.org/10.1016/j.ajic.2011.01.016.
7. **Huys G, Cnockaert M, Vaneechoutte M, Woodford N, Nemec A, Dijkshoorn L, Swings J.** 2005. Distribution of tetracycline resistance genes in genotypically related and unrelated multiresistant *Acinetobacter baumannii* strains from different European hospitals. Res. Microbiol. **156:**348–355. http://dx.doi.org/10.1016/j.resmic.2004.10.008.
8. **Fernando D, Zhanel G, Kumar A.** 2013. Antibiotic resistance and expression of resistance-nodulation-division pump- and outer membrane porin-encoding genes in *Acinetobacter* species isolated from Canadian hospitals. Can. J. Infect. Dis. Med. Microbiol. **24:**17–21.
9. **Magiorakos AP, Srinivasan A, Carey RB, Carmeli Y, Falagas ME, Giske CG, Harbarth S, Hindler JF, Kahlmeter G, Olsson-Liljequist B, Paterson DL, Rice LB, Stelling J, Struelens MJ, Vatopoulos A, Weber JT, Monnet DL.** 2012. Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: an international expert proposal for interim standard definitions for acquired resistance. Clin. Microbiol. Infect. **18:**268–281. http://dx.doi.org/10.1111/j.1469-0691.2011.03570.x.