



# Complete Genome Sequence of Collection Strain *Acinetobacter baumannii* ATCC BAA-1790, Used as a Model To Study the Antibiotic Resistance Reversion Induced by Iodine-Containing Complexes

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**ABSTRACT** The strain *Acinetobacter baumannii* ATCC BAA-1790 was sequenced as a model for nosocomial multidrug-resistant infections. Long-read PacBio sequencing revealed a circular chromosome of 3,963,235 bp with two horizontally transferred genomic islands and a 67,023-bp plasmid. Multiple antibiotic resistance genes and genome methylation patterns were identified.

*Acinetobacter baumannii* is a common nosocomial pathogen harboring resistance to a wide variety of antibiotics. The multidrug-resistant strain *A. baumannii* ATCC BAA-1790 was isolated from sputum in 2008 in Washington, DC. In this study, it is used as a model organism to investigate genomic and population changes under the effect of a new drug, FS-1, which induces the reversion of multidrug-resistant bacteria to their antibiotic-sensitive phenotypes (1, 2).

The strain was obtained from ATCC (<https://www.lgcstandards-atcc.org/>) and cultivated in Mueller-Hinton broth (HiMedia, India) without antibiotics at 37°C with shaking. DNA was extracted from the overnight culture using the cetyltrimethylammonium bromide (CTAB) protocol (3). Sequencing was performed at Macrogen according to the SMRTbell preparation guide for the PacBio RS II platform, resulting in the generation of 326,117 reads with an average length of 10,000 bp ( $N_{50}$ , 8,662 bp). DNA reads were quality controlled and trimmed using the UGENE v1.32.0 raw DNA-Seq processing pipeline with default parameters (4). Default parameters were used for all subsequent analyses. *De novo* assembly of the complete genome was done using the polished\_falcon\_fat pipeline, available from the SMRT Link v5.0.1 software (5). Two ungapped contigs with a coverage of 100× were obtained and corresponded to a 3,963,235-bp chromosome and a 67,023-bp plasmid with average GC contents of 39.16% and 33.38%, respectively. The RAST annotation server (6) was used to automatically generate annotations for the genome, followed by manual correction. Genomic islands present on the chromosome (Fig. 1A) contributed to the antibiotic resistance of the strain, with carbapenem-hydrolyzing class D beta-lactamase OXA-23, a Sul1 sulfonamide resistance protein, and an integrase insert comprising *aadA1* (aminoglycoside 3'-adenyltransferase) and *aadC1* (aminoglycoside *N*(3')-acetyltransferase type I), rendering the strains resistant to aminoglycosides (7). Multiple genes for drug efflux pumps and beta-lactamases of the OXA-23, OXA-82, and ADC-25 families providing resistance to cephalosporins and penams were identified using the Resistance Gene Identifier (RGI) server (8). Comparing the sequences of 2,588 orthologous proteins

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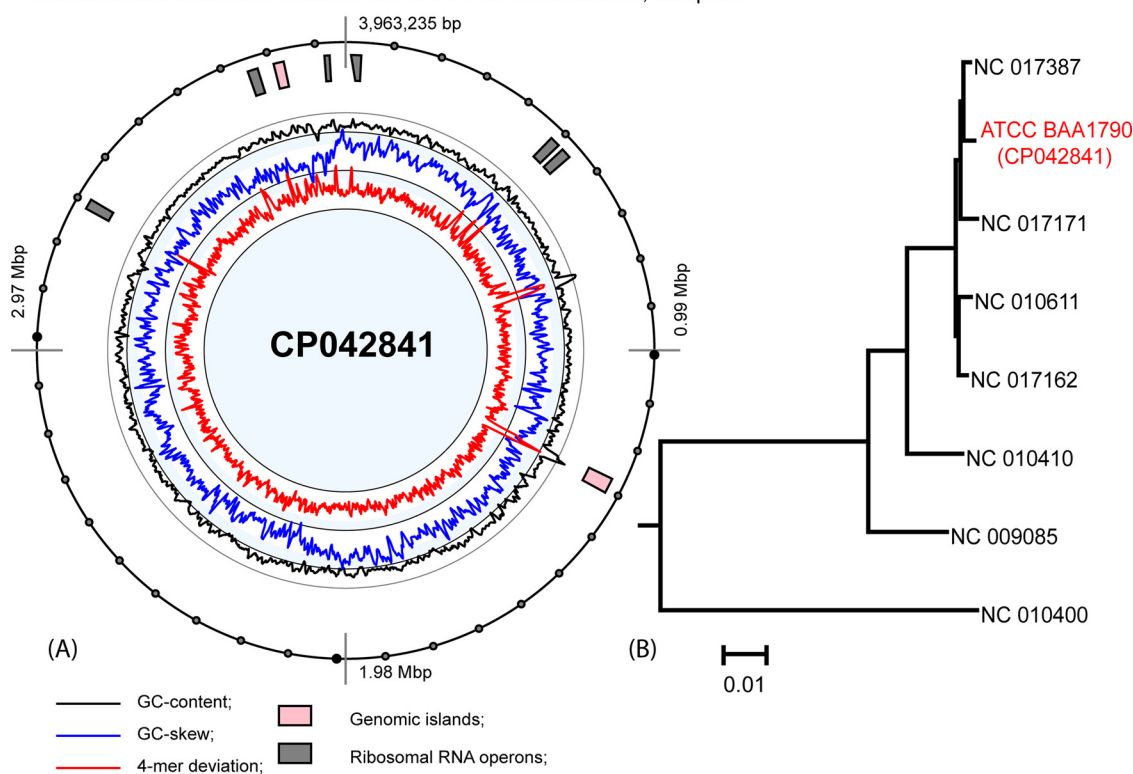
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*Acinetobacter baumannii* strain ATCC BAA-1790 chromosome, complete

**FIG 1** (A) The atlas view generated by the program SeqWord Genomic Island Sniffer (13) shows a circular map of the chromosome with predicted genomic islands, rRNA gene (*rrn*) clusters, and histograms of the GC content, GC skew, and tetranucleotide pattern deviations calculated in an 8-kbp sliding window stepping 2 kbp. (B) The neighbor-joining phylogenetic tree shows relations of the sequenced strain BAA-1790 with reference genomes of *A. baumannii*.

identified by OrthoFinder (9), which were shared by sequenced genomes of *A. baumannii*, showed that the closest phylogenetic relationship of strain BAA-1790 to *A. baumannii* TDCD-AB0715 (Fig. 1B) produced an increasing trend of carbapenem and fluoroquinolone resistance (10). The plasmid identified in strain BAA-1790 is typical for many *A. baumannii* isolates. It shows more than 99% DNA sequence identity with the plasmids pMAL-2 (KX230794) and FDAARGOS\_493 (CP033857). The plasmid contains multiple genes associated with plasmid replication and conjugation and the *telA* toxic anion resistance gene.

The SMRT Link DNA modification pipeline, *ds\_modification\_motif\_analysis*, was used for profiling of epigenetic modifications in the bacterial genome. Two major motifs, AGCNNNGCT and TGGCCA, associated with methylation of the underlined adenine and cytosine residues, were discovered. Methylation of adenine at AGCNNNGCT is caused by M.Aba7804III methyltransferase (11), and cytosine methylation at TGGCCA is associated with the activity of the Ball restriction-modification system, also common for *A. baumannii* (12).

**Data availability.** The genome is available from NCBI under the accession numbers CP042841 and CP042842 for the chromosome and plasmid sequences, respectively. The PacBio reads are available under the SRA numbers SRR10112456, SRR10112460, and SRR10112461. The BioProject accession number is PRJNA557366.

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## REFERENCES

- Ilin AI, Kulmanov ME, Korotetskiy IS, Islamov RA, Akhmetova GK, Lankina MV, Reva ON. 2017. Genomic insight into mechanisms of reversion of antibiotic resistance in multidrug resistant *Mycobacterium tuberculosis* induced by a nanomolecular iodine-containing complex FS-1. *Front Cell Infect Microbiol* 7:151. <https://doi.org/10.3389/fcimb.2017.00151>.
- Islamov R, Kerimzhanova A, Ilin A. 2019. New antituberculosis drug FS-1, p 103–116. *In* Vašková J, Vaško L (ed), *Medicinal chemistry*. IntechOpen, London, United Kingdom.
- Murray MG, Thompson WF. 1980. Rapid isolation of high molecular weight plant DNA. *Nucleic Acids Res* 8:4321–4325. <https://doi.org/10.1093/nar/8.19.4321>.
- Okonechnikov K, Golosova O, Fursov M, UGENE Team. 2012. Unipro UGENE: a unified bioinformatics toolkit. *Bioinformatics* 28:1166–1167. <https://doi.org/10.1093/bioinformatics/bts091>.
- Chin CS, Alexander DH, Marks P, Klammer AA, Drake J, Heiner C, Clum A, Copeland A, Huddleston J, Eichler EE, Turner SW, Korlach J. 2013. Non-hybrid, finished microbial genome assemblies from long-read SMRT sequencing data. *Nat Methods* 10:563–569. <https://doi.org/10.1038/nmeth.2474>.
- Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST server: Rapid Annotations using Subsystems Technology. *BMC Genomics* 9:75. <https://doi.org/10.1186/1471-2164-9-75>.
- Karah N, Dwibedi CK, Sjöström K, Edquist P, Johansson A, Wai SN, Uhlin BE. 2016. Novel aminoglycoside resistance transposons and transposon-derived circular forms detected in carbapenem-resistant *Acinetobacter baumannii* clinical isolates. *Antimicrob Agents Chemother* 60:1801–1818. <https://doi.org/10.1128/AAC.02143-15>.
- Jia B, Raphenya AR, Alcock B, Waglehner N, Guo P, Tsang KK, Lago BA, Dave BM, Pereira S, Sharma AN, Doshi S, Courtot M, Lo R, Williams LE, Frye JG, Elsayegh T, Sardar D, Westman EL, Pawlowski AC, Johnson TA, Brinkman FS, Wright GD, McArthur AG. 2017. CARD 2017: expansion and model-centric curation of the Comprehensive Antibiotic Resistance Database. *Nucleic Acids Res* 45:D566–D573. <https://doi.org/10.1093/nar/gkw1004>.
- Emms DM, Kelly S. 2015. OrthoFinder: solving fundamental biases in whole genome comparisons dramatically improves orthogroup inference accuracy. *Genome Biol* 16:157. <https://doi.org/10.1186/s13059-015-0721-2>.
- Chen CC, Lin YC, Sheng WH, Chen YC, Chang SC, Hsia KC, Liao MH, Li SY. 2011. Genome sequence of a dominant, multidrug-resistant *Acinetobacter baumannii* strain TCDC-AB0715. *J Bacteriol* 193:2361–2362. <https://doi.org/10.1128/JB.00244-11>.
- Pérez-Oseguera Á, Castro-Jaimes S, Salgado-Camargo AD, Silva-Sanchez J, Garza-González E, Castillo-Ramírez S, Cevallos MÁ. 2017. Complete genome sequence of a bla<sub>OXA-58</sub>-producing *Acinetobacter baumannii* strain isolated from a Mexican hospital. *Genome Announc* 5:e00949-17. <https://doi.org/10.1128/genomeA.00949-17>.
- Lee Y, D'Souza R, Yong D, Lee K. 2016. Prediction of putative resistance islands in a carbapenem-resistant *Acinetobacter baumannii* global clone 2 clinical isolate. *Ann Lab Med* 36:320–324. <https://doi.org/10.3343/alm.2016.36.4.320>.
- Bezuidt O, Lima-Mendez G, Reva ON. 2009. SEQWord Gene Island Sniffer: a program to study the lateral genetic exchange among bacteria. *World Acad Sci Eng Technol* 58:1169–1174.