



HAL
open science

Complete Genome Sequence of the Multiresistant Acinetobacter baumannii Strain AbH12O-A2, Isolated during a Large Outbreak in Spain

María Merino, Laura Alvarez-Fraga, M J Gómez, Ana M Aransay, J L Lavín, F.
Chaves, Germán Bou, Margarita Poza

► **To cite this version:**

María Merino, Laura Alvarez-Fraga, M J Gómez, Ana M Aransay, J L Lavín, et al.. Complete Genome Sequence of the Multiresistant *Acinetobacter baumannii* Strain AbH12O-A2, Isolated during a Large Outbreak in Spain. *Genome Announcements*, 2014, 2 (6), <10.1128/genomea.01182-14>. <hal-04939861>

HAL Id: hal-04939861

<https://hal.science/hal-04939861v1>

Submitted on 11 Feb 2025

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons CC BY 4.0 - Attribution - International License

Complete Genome Sequence of the Multiresistant *Acinetobacter baumannii* Strain AbH12O-A2, Isolated during a Large Outbreak in Spain

M. Merino,^a L. Alvarez-Fraga,^a M. J. Gómez,^b A. M. Aransay,^c J. L. Lavín,^c F. Chaves,^d G. Bou,^a M. Poza^a

Servicio de Microbiología, Instituto de Investigación Biomédica (INIBIC), Complejo Hospitalario Universitario (CHUAC), Sergas, A Coruña, Spain^a; Departamento de Microbiología Clínica, Hospital Universitario 12 de Octubre, Madrid, Spain^b; Departamento de Evolución Molecular, Centro de Astrobiología INTA-CSIC, Madrid, Spain^c; Plataforma de Análisis Genómico CIC bioGUNE & CIBERehd, Derio, Spain^d

We report the complete genome sequence of *Acinetobacter baumannii* strain AbH12O-A2, isolated during a large outbreak in Spain. The genome has 3,875,775 bp and 3,526 coding sequences, with 39.4% G+C content. The availability of this genome will facilitate the study of the pathogenicity of the *Acinetobacter* species.

Received 3 October 2014 Accepted 6 October 2014 Published 13 November 2014

Citation Merino M, Alvarez-Fraga L, Gómez MJ, Aransay AM, Lavín JL, Chaves F, Bou G, Poza M. 2014. Complete genome sequence of the multiresistant *Acinetobacter baumannii* strain AbH12O-A2, isolated during a large outbreak in Spain. *Genome Announc.* 2(6):e01182-14. doi:10.1128/genomeA.01182-14.

Copyright © 2014 Merino et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](http://creativecommons.org/licenses/by/4.0/).

Address correspondence to G. Bou, german.bou.arevalo@sergas.es, or M. Poza, margarita.poza.dominguez@sergas.es.

Acinetobacter baumannii is a major cause of hospital-acquired infections. Its success in the hospital environment lies in its genetic versatility and its ability to persist in extreme conditions. During 2006–2008, 377 patients were colonized/infected with multiresistant *A. baumannii* strains in a hospital in Madrid, Spain. This was one of the most important nosocomial outbreak produced by *A. baumannii* known to date (1, 2). The clones isolated during the outbreak harbored different plasmids, all containing a *bla*_{OXA-24} gene mobilized through a Xer recombination mechanism. Two mutations found to modify the gene expression of virulence factors provided an advantage to strain AbH12O-A2, whose genome sequence is described here. Previous studies have described the molecular mechanisms involved in the spread and epidemiology of this strain (1–6).

The total genomic DNA isolated from strain AbH12O-A2 was sheared into smaller fragments with the Covaris S/E210 system. Specific adapters were ligated to DNA fragments, and libraries containing inserts of 500 bp were purified and selectively enriched by PCR. After quality and quantity controls, 90 nucleotide fragments were paired-end sequenced in an HiSeq2000 system, with the TruSeq PE cluster kit version 3, cBot-HS, and TruSeq SBS kit-HS version 3 (Illumina Inc.). Once the gaps were identified, pairs of primers were designed and specific regions were amplified. Products were sequenced by BigDye Terminator version 3.1 chemistry in an ABI Seq Instrument (Applied Biosystems). After quality control of the raw data, clean data were aligned to *Acinetobacter baumannii* ATCC 17978, as a reference sequence. Assembly of the short reads into the genome sequence was performed using the SOAPdenovo version 1.05 program (<http://soap.genomics.org.cn/soapdenovo.html>). Key parameter K setting at 47 is determined by optimal assembly according to the paired-end and overlap relationship via mapping reads to contigs.

The *A. baumannii* AbH12O-A2 complete genome consists of 3,875,775 bp with a G+C content of 39.4% and contains 3,526 coding sequences, 72 tRNA genes, and 6 rRNA clusters. *A. bau-*

mannii ACICU (score 518), *A. baumannii* AB900 (score 500), and *A. baumannii* AYE (score 483) were the closest neighbors to strain AbH12O-A2. Moreover, 56 genes associated with resistance to antibiotics and toxic compounds were found. The ResFinder bioinformatic application (7) was used to identify genes coding for antibiotic resistance. The following resistance genes were detected in the genome: *aac(3)-IIa*, *strA*, and *strB* conferring resistance to aminoglycosides; *bla*_{OXA-65}, *bla*_{ADC-25}, and *bla*_{TEM-1B} conferring resistance to β -lactams; and *sul2* conferring resistance to sulfonamides. Comparison of the AbH12O-A2 genome with other completed genomes of *A. baumannii* by use of Mauve version 2.3.1 (8) revealed a resistance island (3,612,846–3,637,461 bp) flanked by two sequences of *ISAbal* in opposite directions. PHAST (9) analysis revealed four putative intact phages integrated in the genome, two of which are similar to *Acinetobacter* phage *Bphi*-B1251 and another two that have not previously been identified in *A. baumannii*: one is similar to Enterobacteria phage *mEp235* and the other is similar to *Haemophilus* phage SuMu.

Nucleotide sequence accession number. This whole-genome shotgun project has been deposited in GenBank under accession number CP009534.

ACKNOWLEDGMENTS

This work was supported by grants from the Instituto de Salud Carlos III—Ministerio Economía y Competitividad Unión Europea—Fondo Europeo de Desarrollo Regional (FEDER) PI11/01034, awarded to M.P., and from the Spanish Network for the Research in Infectious Diseases (REIPI) RD12/0015 awarded to G.B.), the Departamento de Desarrollo Económico y Competitividad del Gobierno Vasco (GV)—Etorrek Research Programs 2011–2013 (EI11-300 and IE13-370), and the Diputación Foral de Bizkaia (DFB)—Departamento de Promoción Económica awarded to A.M.A. and J.L.L.

REFERENCES

- Acosta J, Merino M, Viedma E, Poza M, Sanz F, Otero JR, Chaves F, Bou G. 2011. Multidrug-resistant *Acinetobacter baumannii* harboring OXA-24

- carbapenemase, Spain. *Emerg. Infect. Dis.* 17:1064–1067. <http://dx.doi.org/10.3201/eid1706.091866>.
2. Merino M, Acosta J, Poza M, Sanz F, Beceiro A, Chaves F, Bou G. 2010. OXA-24 carbapenemase gene flanked by XerC/XerD-like recombination sites in different plasmids from different *Acinetobacter* species isolated during a nosocomial outbreak. *Antimicrob. Agents Chemother.* 54:2724–2727. <http://dx.doi.org/10.1128/AAC.01674-09>.
 3. Rumbo C, Fernández-Moreira E, Merino M, Poza M, Mendez JA, Soares NC, Mosquera A, Chaves F, Bou G. 2011. Horizontal transfer of the OXA-24 carbapenemase gene via outer membrane vesicles: a new mechanism of dissemination of carbapenem resistance genes in *Acinetobacter baumannii*. *Antimicrob. Agents Chemother.* 55:3084–3090. <http://dx.doi.org/10.1128/AAC.00929-10>.
 4. Gayoso CM, Mateos J, Méndez JA, Fernández-Puente P, Rumbo C, Tomás M, Martínez de Ilarduya O, Bou G. 2014. Molecular mechanisms involved in the response to desiccation stress and persistence in *Acinetobacter baumannii*. *J. Proteome Res.* 13:460–476. <http://dx.doi.org/10.1021/pr400603f>.
 5. Mendez JA, Soares NC, Mateos J, Gayoso C, Rumbo C, Aranda J, Tomas M, Bou G. 2012. Extracellular proteome of a highly invasive multidrug-resistant clinical strain of *Acinetobacter baumannii*. *J. Proteome Res.* 11:5678–5694. <http://dx.doi.org/10.1021/pr300496c>.
 6. Soares NC, Spat P, Mendez JA, Nakedi K, Aranda J, Bou G. 2014. Ser/Thr/Tyr phosphoproteome characterization of *Acinetobacter baumannii*: comparison between a reference strain and a highly invasive multidrug-resistant clinical isolate. *J. Proteomics.* 102:113–124. <http://dx.doi.org/10.1016/j.jprot.2014.03.009>.
 7. Zankari E, Hasman H, Cosentino S, Vestergaard M, Rasmussen S, Lund O, Aarestrup FM, Larsen MV. 2012. Identification of acquired antimicrobial resistance genes. *J. Antimicrob. Chemother.* 67:2640–2644. <http://dx.doi.org/10.1093/jac/dks261>.
 8. Darling AC, Mau B, Blattner FR, Perna NT. 2004. Mauve: multiple alignment of conserved genomic sequence with rearrangements. *Genome Res.* 14:1394–1403. <http://dx.doi.org/10.1101/gr.2289704>.
 9. Zhou Y, Liang Y, Lynch KH, Dennis JJ, Wishart DS. 2011. PHAST: a fast phage search tool. *Nucleic Acids Res.* 39:W347–W352. <http://dx.doi.org/10.1093/nar/gkr485>.