

Draft Genome Sequences of Multidrug-Resistant *Acinetobacter* sp. Strains from Colombian Hospitals

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The draft genome sequences of the strains *Acinetobacter baumannii* 107m, *Acinetobacter nosocomialis* 28F, and *Acinetobacter pittii* 42F, isolated from Colombian hospitals, are reported here. These isolates are causative of nosocomial infections and are classified as multidrug resistant, as they showed resistance to four different antibiotic groups.

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A major antimicrobial resistance problem in Latin American countries is the growing prevalence of multidrug-resistant (MDR) *Acinetobacter* spp. (1, 2). Four species of *Acinetobacter* have been grouped as the *Acinetobacter calcoaceticus*-*Acinetobacter baumannii* (ACB) complex because they are genetically similar and difficult to identify with automated or routine laboratory methods (3). Three of these species (*A. baumannii*, *A. nosocomialis*, and *A. pittii*) are associated with nosocomial infections, and in spite of their similarity, they exhibit different resistance profiles (4).

In Colombia, several studies of outbreaks and molecular characterization of *Acinetobacter* spp. have been carried out from approximately 2001 to the present (5–7).

To date, there are no whole-genome sequences of *Acinetobacter* species strains isolated in Colombia available in GenBank/EMBL/DBJ. This report announces the draft genome sequences of strains *A. baumannii* 107m, *A. nosocomialis* 28F, and *A. pittii* 42F. These multidrug-resistant isolates were selected from an initial set of 139 nosocomial isolates from 20 hospitals in Bogotá collected from 2005 to 2010.

Whole-genome shotgun (WGS) sequencing was performed using the HiSeq 2000 Illumina paired-end platform and the 454 pyrosequencing mate-pair (7.5-kb insert) platform. Sequences were *de novo* assembled using Velvet 1.2.07 (8) and Newbler 2.7 (Roche Diagnostics Corporation) and were mapped using BWA 0.6.1 (9) to the reference genomes of strains *A. baumannii* ATCC 17978, *A. nosocomialis* RUH 2624, and *A. pittii* SH024. Automatic annotation was done through the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) (10) and by the NMPDR RAST 4.0 server (11). Annotations were visualized and manually curated with Artemis 14.0.0 (12).

The *A. baumannii* 107m draft genome has a total of 3,954,000 bp consisting of 56 contigs. There are 3,735 predicted genes, with an average size of 912 bp, 3,796 coding sequences (CDSs), and 57 tRNAs. A total of 2,884 CDSs were assigned to Clusters of Orthologous Groups (COGs), while the CDSs were

classified into 441 metabolic subsystems by RAST. The *A. nosocomialis* 28F draft genome has a total of 3,833,431 bp consisting of 92 contigs. There are 3,626 predicted genes, with an average size of 910 bp, 3,680 CDSs, and 54 tRNAs. A total of 2,849 CDSs were assigned to COGs, while CDSs were classified into 433 metabolic subsystems by RAST. Finally, the *A. pittii* 42F draft genome has a total of 3,782,611 bp consisting of 72 contigs. There are 3,611 predicted genes, with an average size of 910 bp, 3,665 CDSs, and 54 tRNAs. A total of 2,832 CDSs were assigned to COGs, while CDSs were classified into 423 metabolic subsystems by RAST. Genes associated with multidrug resistance were annotated and compared with other *Acinetobacter* genomes that had already been sequenced.

Nucleotide sequence accession numbers. These whole-genome sequencing projects have been deposited at DDBJ/EMBL/GenBank under the following accession no.: [CBSG000000000](https://www.ncbi.nlm.nih.gov/nuccore/CBSG000000000) (*A. baumannii* 107m), [CBSD000000000](https://www.ncbi.nlm.nih.gov/nuccore/CBSD000000000) (*A. nosocomialis* 28F), and [CBRO000000000](https://www.ncbi.nlm.nih.gov/nuccore/CBRO000000000) (*A. pittii* 42F). The versions described in this paper are CBSG01000000, CBSD01000000, and CBRO01000000.

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REFERENCES

1. Sader HS, Jones RN, Gales AC, Silva JB, Pignatari AC, the SENTRY Participants Group (Latin America). 2004. SENTRY antimicrobial surveillance program report: Latin American and Brazilian results for 1997 through 2001. *Braz. J. Infect. Dis.* 8:25–79.
2. Miranda MC, Pérez F, Zuluaga T, Olivera MR, Correa A, Reyes SL, Villegas MV, Grupo de Resistencia Bacteriana Nosocomial de Colombia. 2006. Resistencia a antimicrobianos en bacilos Gram negativos aislados en unidades de cuidado intensivo en hospitales de WHONET, Colombia 2003, 2004 y 2005. *Biomédica* 26:424–433.

3. Hernández MA, Valenzuela EM, Pulido IY, Reguero MT, Restrepo S, Gualteros S, Santofimio D, Ramirez M, Quintero LE, Mantilla JR. 2011. The genomic identification of Colombian *Acinetobacter baumannii* clinical isolates by RFLP-PCR analysis of the 16S-23S rRNA gene spacer region. *Rev. Colomb. Biotecnol.* 13:110–114.
4. Reguero MT, Medina OE, Hernández MA, Flórez DV, Valenzuela EM, Mantilla JR. 2013. Antibiotic resistance patterns of *Acinetobacter calcoaceticus*-*A. baumannii* complex species from Colombian hospitals. *Enferm. Infecc. Microbiol. Clin.* 31:142–146.
5. Leal AL, Buitrago G, Sanchez-Pedraza R, Castillo-Londoño JS, Cortes-Luna JA, Álvarez-Moreno CA, Escobar-Villalba N, GREBO. 2011. The emergence of multidrug-resistant *Acinetobacter baumannii* in Colombia: a time-series analysis, 2001–2007. *Rev. Salud Pública* 13:691–702.
6. Pinzón JA, Mantilla JR, Valenzuela EM, Fernández F, Álvarez CA, Osorio EJ. 2006. Caracterización molecular de aislamientos de *Acinetobacter baumannii* provenientes de la unidad de quemados de un hospital de tercer nivel de Bogotá. *Infectio* 10:71–78.
7. Dutta S, Sur D, Manna B, Sen B, Bhattacharya M, Bhattacharya SK, Wain J, Nair S, Clemens JD, Ochiai RL. 2008. Emergence of highly fluoroquinolone-resistant *Salmonella enterica* serovar Typhi in a community-based fever surveillance from Kolkata, India. *Int. J. Antimicrob. Agents* 31:387–389.
8. Zerbino DR, Birney E. 2008. Velvet: algorithms for *de novo* short read assembly using de Bruijn graphs. *Genome Res.* 18:821–829.
9. Li H, Durbin R. 2009. Fast and accurate short read alignment with Burrows-Wheeler transform. *Bioinformatics* 25:1754–1760.
10. Angiuoli SV, Gussman A, Klimke W, Cochrane G, Field D, Garrity G, Kodira CD, Kyrpides N, Madupu R, Markowitz V, Tatusova T, Thomson N, White O. 2008. Toward an online repository of Standard Operating Procedures (SOPs) for (meta)genomic annotation. *Omics* 12: 137–141.
11. 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. doi:10.1186/1471-2164-9-75.
12. Rutherford K, Parkhill J, Crook J, Horsnell T, Rice P, Rajandream MA, Barrell B. 2000. Artemis: sequence visualization and annotation. *Bioinformatics* 16:944–945.