Acinetobacter baumannii strain Ab5 was isolated in the year 2007 in Chile, being one of the first multidrug-resistant (MDR) cases reported in the country. Here, we present the very first draft genome sequence of an MDR Chilean strain, which shows the presence of diverse resistance and acquired virulence genes.

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Acinetobacter baumannii is a nosocomial pathogen normally classified as multidrug resistant (MDR). Alarmingly, the number of MDR A. baumannii isolates has increased in the last few years, making it a difficult microorganism to treat (1, 2), as infections caused by it are associated with high rates of mortality and long periods of hospitalization (3). The rates of Acinetobacter species MDR isolates in Latin America have increased lately, as resistance to imipenem in Chile increased from 0.0% during 1997 to 1999, to 47.4% in the 2008 to 2010 period (4), and 65.8% in 2014 (Antibiotic Resistant Group from Chilean Society for Infectious Diseases, personal communication).

In this work, we studied the genetic features of the A. baumannii MDR strain Ab5 through whole-genome sequencing (WGS), as this was one of the first sentinel cases of MDR isolates in Chile. To date, there are no whole-genome sequences of A. baumannii strains from Chile available in GenBank. The Ab5 strain was isolated at the Hospital of the Catholic University of Santiago in 2007 from a patient who developed a wound infection. Diverse antibiotics were tested by the disk diffusion method and by the agar dilution test, according to the Clinical and Standards Institute (CLSI) guidelines (5). Ab5 was found to be resistant to ceftazidime, imipenem, meropenem, gentamicin, cefotaxime, ciprofloxacin, cefepime, and piperacillin-tazobactam. The MICs to carbapenems were 8 μg/ml to meropenem and 16 μg/ml to imipenem.

WGS was performed utilizing the Illumina HiSeq 2000 platform. The data generated were assembled using the Velvet assembly pipeline (6), with contigs >200 bp, resulting in 107 contigs, a total length of 3,937,075 bp, and an N50 contig size of 173,003 bp; meanwhile, the average G + C content was 38.9%, coinciding with the data associated with the Acinetobacter genus.

Genome annotation was performed utilizing the Rapid Annotations using Subsystems Technology (RAST) (7), and the IGS Annotation Engine was used for structural and functional annotation (8). Manatee was used to view annotations (http://manatee.sourceforge.net/), while ResFinder (9), PathogenFinder (10), and mlst (11) were utilized for complementary analyzes. We identified 3,657 coding sequences (CDSs), 57 pseudogenes, 7 rRNAs, and 57 tRNAs. Additionally, Ab5 belonged to sequence type 162 (ST-162), which was previously detected in Brazil. We identified the blaOXA-58, blaOXA-51, aph(3’)-Via, and the DNA topoisomerase type II genes that might explain its MDR phenotype. Interestingly, we found genes associated with iron acquisition, such as the pitADC, pitABC, and pituABC operons, which have been identified in Streptococcus pneumoniae. We also identified 25 pathogenesis-associated operons derived from Mycobacterium spp., whereas one detected operon, involved in internalin-like proteins synthesis, may have been imported from Listeria.

This first approach reflects the ability of A. baumannii to capture a wide range of genes derived from different species, making it a troublesome pathogen to treat in the nosocomial environment.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. LANH0000000. The version described in this paper is version LANH0100000.

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