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# Draft Genome Sequence of *Acinetobacter bereziniae* HPC229, a Carbapenem-Resistant Clinical Strain from Argentina Harboring $bla_{NDM-1}$

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**We report here the draft genome sequence of an NDM-1-producing *Acinetobacter bereziniae* clinical strain, HPC229. This strain harbors both plasmid and chromosomal resistance determinants toward different β-lactams and aminoglycosides as well as several types of multidrug efflux pumps, most likely representing an adaptation strategy for survival under different environments.**

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*Acinetobacter bereziniae* is isolated primarily from clinical specimens and health care-associated environments (1). Although most *A. bereziniae* isolates are susceptible to antimicrobials (2), clinical strains bearing metallo-beta-lactamase genes have just been reported (3-6). We recently described the sequence of a $bla_{NDM-1}$-harboring plasmid (pNDM229, KT072713.1) carried by a carbapenem-resistant *A. bereziniae* strain (HPC229) from Argentina (4). We report here the whole-genome sequencing (WGS) of HPC229, which constitutes the sixth *A. bereziniae* genome in databases. Genes involved in β-lactam and aminoglycoside resistance were found in the HPC229 genome. Moreover, genes involved in different efflux pump systems associated with resistance to antimicrobials and toxic compounds were identified (7, 8). These findings support the notion that *A. bereziniae* represents an environmental reservoir of resistance genes of clinical relevance.

HPC229 DNA was prepared using the Wizard genomic DNA purification kit (Promega) and subjected to 454 pyrosequencing (Roche Diagnostics Corporation) at INDEAR, Rosario. Data generated were assembled using Newbler v2.9, resulting in 134 contigs, 5 of them constituting the pNDM229 plasmid (4). The remaining 129 contigs have a length of 4,596,631 bp and a G+C content of 38.00%. Genome annotation was done using the NCBI Prokaryotic Genomes Annotation Pipeline (9), and eight contigs were left out for being shorter than 200 bp. The RAST server was employed for subsystem classification and functional annotation (10) and then the genome was manually curated. Complementary gene identification analyses were done using Mauve (11), ISFinder (12), Res-Finder 2.1 (13), and TCDB (14). A total of 4,124 protein-coding sequences, 4 rRNAs, and 62 tRNA genes were predicted by these analyses.

WGS analyses revealed genes associated with β-lactam resistance, including $bla_{NDM-1}$ (4), *ampC*, a new $bla_{OXA-229}$-like (15) variant, and 3 other putative β-lactamase genes, as well as a new *carO* allele coding for an outer membrane protein associated with imipenem uptake (16). Other resistance genes included *aphA6* (4), and a putative phosphotransferase encoding resistance to aminoglycosides. Efflux pump- and membrane-associated transporter genes of different superfamilies included (7, 8, 14, 17) ABC (MacA, MacB); BART (Acr3); IT (ArsB); MOP (NorM, AbeM); MFS (CraA, SmvA, MFS transporter, Bcr/CflA, MFS permease); DMT (AbeS, QaceΔ1-like); MER (MerT, MerC); and RND (AdeABC, AdeIJK, AdeE, CzcABC, and CusABC). The latter operon, absent in the other *A. bereziniae* genomes, exhibits 95% nucleotide identity to a portion of the GI2 genomic island in *A. baumannii* LAC-4 (8). Downstream from *cusABC*, there are regions encompassing IS*Aba2*, *acr3*, and *feoAB* genes, with *acr3* showing the highest identity to its ortholog of *A. tandoii* DSM14970, whereas *feoAB* was identified in the *A. baumannii* LAC-4 GI2 immediately downstream of its *cusABC* operon. These observations suggest a chimeric construct in HPC229 derived from gene exchange among *Acinetobacter* species. WGS analyses will provide further evidence of the ability of *A. bereziniae* to act as a reservoir of resistance genes and may help to understand the adaptability mechanisms of *Acinetobacter* in response to environmental challenges.

**Nucleotide sequence accession numbers.** This WGS project has been deposited at DDBJ/EMBL/GenBank under the accession LKDJ00000000. We describe here the version LKDJ00000000.1.

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