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Whole-Genome Sequence of a Multidrug-Resistant Clinical Isolate of *Acinetobacter lwoffii*▽

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***Acinetobacter lwoffii* has been considered an opportunistic pathogen that can cause nosocomial infections in humans. Here, we present the genome sequence of *A. lwoffii* WJ10621, a multidrug-resistant clinical isolate that carries a plasmid with the NDM-1 resistance gene.**

Acinetobacter lwoffii, formerly known as *Mima polymorpha* or *Acinetobacter calcoaceticus* var. *lwoffii*, is a nonfermentative aerobic Gram-negative bacillus. Being a ubiquitous bacterium in nature, it is seen as a member of the normal flora that inhabits the oropharynx, human skin, and the perineum in approximately 20 to 25% of the healthy individuals (11). When patients have their immune system impaired or compromised, the bacteria turn into opportunistic pathogens that can cause nosocomial infections (3, 12, 14). Moreover, studies have indicated that new clinical isolates of *A. lwoffii* showed increased resistance to irradiation in comparison with isolates from the 1970s, which raises concerns about the persistence of *A. lwoffii* on medical devices that are sterilized by irradiation, especially in intensive care units (ICU) (11).

According to the Genomes OnLine Databse (GOLD) (6), there is only one draft sequence (76 scaffolds) available for *A. lwoffii*, strain SH145 (unpublished). Here we present the whole-genome sequence of *A. lwoffii* WJ10621, a multidrug-resistant clinical isolate from a urine specimen from a 62-year-old woman who suffered from a urinary tract infection after chemotherapy for pancreatic cancer. This strain displayed high resistance to ampicillin, cefazolin, cefotaxime, ceftazidime, cefpirome, ceftriaxone, imipenem, and meropenem.

The genomic DNA was sequenced using a whole-genome shotgun strategy with an Illumina genome analyzer (totaling ~350.18 Mb with ~100-fold coverage of the genome). The paired-end reads were assembled by SOAPdenovo (5), and a final assembly with only one scaffold was obtained.

The annotation was done by using MetaGeneAnnotator (10), tRNAscan-SE 1.21 (8), RNAmmer 1.2 (4), and Tandem Repeats Finder 4.04 (2). In addition, the predicted coding sequences (CDSs) were searched against Pfam (1), COGs (13), SEED subsystems (9), ARDB (7), and the NCBI NR protein databases for annotation.

The genome of *A. lwoffii* WJ10621 includes 3,419,011 bases and contains 3,394 predicted CDSs, with a G+C content of 41.57%. The genome contains 83 tandem repeat regions, 6 copies of the 5S rRNA gene, 7 copies of the 23S rRNA gene, and 6 copies of the 16S rRNA gene, as well as 91 predicted tRNA genes. The CDSs were classified into 23 clusters of orthologous groups (COGs), and 1,589 COGs and 392 and 300 CDSs were affiliated with the R (general function prediction only) and S (function unknown) categories, respectively.

In this genome, 62 genes were assigned to the "resistance to antibiotics and toxic compounds" subsystem according to MG-RAST, and 56 gene products showed at least 50% protein similarity with antibiotic resistance genes in ARDB. A total of 26 genes coding for cobalt-zinc-cadmium resistance and 14 coding for multidrug resistance efflux pumps were predicted. Furthermore, this strain harbors abundant genes involved in amino acids and derivatives (309 genes) and carbohydrate (243 genes) metabolism. In addition, we found 84 predicted transposase genes distributed in the genome, which suggests the existence of frequent horizontal gene transfer events. Further analysis of this genome will facilitate a deep comprehensive understanding of the resistance, virulence and evolution of *A. lwoffii*.

Nucleotide sequence accession number. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under accession no. AFQY00000000. The version described in this paper is the first version, AFQY01000000.

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