Genome Sequence of a Nicotine-Degrading Strain of *Arthrobacter*

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We announce a 4.63-Mb genome assembly of an isolated bacterium that is the first sequenced nicotine-degrading *Arthrobacter* strain. Nicotine catabolism genes of the nicotine-degrading plasmid pAO1 were predicted, but plasmid function genes were not found. These results will help to better illustrate the molecular mechanism of nicotine degradation by *Arthrobacter*.

Nicotine, as a chemical in the U.S. Environmental Protection Agency's "Toxics Release Inventory" (8), exists abundantly in tobacco waste (3). Microbiological degradation of nicotine is a potential method of tobacco waste treatment. *Arthrobacter* is one of the two dominant organisms capable of nicotine degradation (2). A new nicotine-degrading strain, *Arthrobacter* sp. strain M2012083, was isolated from tobacco waste, identified, and deposited at the China Center for Type Culture Collection (CCTCC M2012083). It can efficiently degrade nicotine; use nicotine as its sole carbon, nitrogen, and energy source; and generate blue pigments during nicotine degradation (data not shown). This characteristic is similar to that of well-reported *Arthrobacter nicotinovorans* pAO1 (2). A 165-kb nicotine-degrading plasmid from *A. nicotinovorans*, pAO1, has been sequenced (5); with it, the *Arthrobacter* strain degrades nicotine through the pyridine pathway. However, none of the genomes of nicotine-degrading *Arthrobacter* species have been sequenced or announced so far.

The draft genome sequence of *Arthrobacter* sp. strain M2012083 was obtained by Illumina High-Seq 2000 paired-end sequencing (15,210,232 reads, ~329-fold coverage), and *de novo* assembly was performed by using the Velvet software, version 1.2.03 (14). The sequence has 67 large contigs (>500 bp) with an N₅₀ length of 139,956 bp. These contigs were analyzed in the Clusters of Orthologous Groups and KEGG databases to predict gene functions and metabolic networks (6). Annotation was performed by the RAST server (1) and the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (9). The 4,629,172-bp draft genome sequence has a GC content of 62.0%, containing 54 tRNA genes and 4,312 predicted coding sequences (CDSs) with a 949-bp average length and an 88.4% coding density. It also contains 387 subsystems comprising 2,576 CDSs in total.

The search revealed a 69-kb sequence with homology to plasmid pAO1 (5). The GC content is about 57.9%, much lower than that of the genome (62.0%). All of the putative nicotine catabolism-related genes of plasmid pAO1 identified were contained in the sequence (4). However, the transposase genes of IS1473, supposed to be the end of the nicotine catabolic transposon (4), were not complete, and the plasmid function genes of pAO1 were not found (4). According to the genomic annotation, both Gram-negative and -positive cell wall components are included in the subsystems (1), in agreement with the typical morphological diversity of these bacteria (7). There are 522 proteins involved in carbohydrate metabolism and 59 proteins involved in the metabolism of aromatic compounds in the subsystems (1). Additionally, the genome carries 89 genes involved in stress responses (1). All of these contribute to the survival ability and competitiveness of *Ar-*

throbacter sp. strain M2012083. However, motility genes are absent from this bacterium, which suggests that the strain's competitiveness does not require movement (1). Also, the *Pseudomonas* nicotine degradation-related genes were not found (10–13). This information about the genome of strain M2012083 will help in the study of the molecular mechanism of nicotine degradation by *Arthrobacter*.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under accession number [AKKK00000000](#). The version described in this paper is the first version, AKKK01000000.

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