A newly isolated bacterium, *Pseudomonas geniculata* N1, can efficiently degrade nicotine. Here we present a 4.51-Mb assembly of its genome, which is the first sequence of the *P. geniculata* group. The sequence contains the genes related to nicotine catabolism and may provide insights into its molecular mechanism for N-heterocyclic degradation.

Large quantities of nonrecyclable tobacco powdery waste, containing a high content of nicotine, accumulate during tobacco manufacture (4). Nicotine-degrading bacteria would be beneficial for the biological treatment of tobacco waste. A novel nicotine-degrading bacterium, named N1, was isolated and identified as *Pseudomonas geniculata*, based on the morphological, physiological, and biochemical features as well as the 16S rRNA gene sequence. Strain N1 was deposited at the China Center for Type Culture Collection (CCTCC M2011183). It efficiently degraded nicotine, using nicotine as the sole carbon and nitrogen source, with the formation of a golden yellow pigment on the plate (data not shown). To date, none of the genome of *P. geniculata* has been sequenced to investigate its genetic variability. The genome sequencing of this species will provide insights into its molecular mechanism for the biodegradation of nicotine.

Here, we present the draft genome sequence of *P. geniculata* N1, which was obtained using Illumina High-Seq 2000 paired-end sequencing (100 bp for each read; ∼88-fold coverage) and assembled into 46 large contigs (>500 bp) using the Velvet software version 1.2.03 (N50 length, 163,564 bp) (12). The annotation was performed using the RAST server (2) and the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (8). The contigs were searched against the KEGG and Clusters of Orthologous Groups (COG) databases to analyze the gene functions and metabolic pathways (6). The draft genome sequence of strain N1 comprises 4,511,336 bp with a GC content of 66.5%. It contains 4,012 predicted coding sequences (CDSs; 989-bp average length; 87.9% identity) and 61 tRNA genes. There are 447 subsystems represented in the genome sequence (1,837 CDSs in total), and the metabolic network of N1 (as determined using the RAST server) was reconstructed (2).

Different from other *Pseudomonas* strains, less than 20 aromatic compound degradation-related genes were predicted by KEGG analysis and genome annotation of the *P. geniculata* N1 sequence. The nicotine degradation-related genes, including nicA, hspa, and hspb in *Pseudomonas putida* S16 (9–11), as well as ndh, 6hno, kdh, and dhph in *Arthrobacter oxidans* (3), were not found in the genome sequence of strain N1. Therefore, the findings imply that there may be novel nicotine-degrading genes and a new nicotine catabolic pathway(s) in strain N1. Additionally, according to the genomic analysis, strain N1 may have a powerful membrane transport capacity, and 9.3% of the proteins in the subsystems of the genome may be membrane transport-related proteins (2). The genome carries 28 multidrug resistance efflux pump genes, including smeABC and smeDEF, that fall into the drug resistance type based on sequence homology (1, 7). Besides these genes, 23 genes for proteins related to pilus/fimbria production, such as the Smf-1 fimbrial operon, were found in the N1 genome sequence; these are likely associated with biofilm formation and drug resistance (5). The announced genome information for strain N1 will allow further studies on the isolation of nicotine-degrading genes and other genes related to *P. geniculata* genetic variability.

**Nucleotide sequence accession numbers.** The results of this whole-genome shotgun project have been deposited at DDBJ/EMBL/GenBank under accession number AJLO0000000. The version described in this paper is the first version, AJLO01000000.

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