

Draft Genome Sequence of the Biocontrol Bacterium *Pseudomonas putida* B001, an Oligotrophic Bacterium That Induces Systemic Resistance to Plant Diseases

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***Pseudomonas putida* B001 is a rhizobacterium that was isolated on the basis of its abilities to grow under low-nutrient conditions and induce systemic resistance against bacterial, fungal, and viral diseases of plants. Here we report the draft genome sequence and automatic annotation of strain B001. Comparison of this sequence to the sequenced genome of *P. putida* KT2440 points to a subset of gene functions that may be related to the defense-inducing functions of B001.**

Pseudomonas putida strains have been used in many applications of applied microbiology, including bioremediation and enzyme production and as biocontrol agents in crop protection (6). A nonpathogenic *P. putida* B001 isolate was collected from the sandy shore soil of Yellow Sea in Korea and studied for its abilities to suppress plant diseases (4). The strain was found to be oligotrophic and to be able to induce systemic resistance activities in tobacco against gray mold caused by *Botrytis cinerea* and soft rot caused by *Pectobacterium carotovorum* SCC1 and tobacco mosaic virus. Subsequent work indicated that it could be used in conjunction with other biocontrol bacteria to reduce powdery mildew of cucumber and rice blast (4, 5).

The genomic sequence of the *P. putida* B001 isolate was obtained using a whole-genome shotgun method (2) and Roche 454 GS (FLX Titanium) pyrosequencing at the Genome Resource Center, Korean Research Institute of Bioscience and Biotechnology (KRIBB). Over 544,271 good-quality paired-end reads, amounting to over 600 million nucleotides, were generated by the pyrosequencing and were processed by the use of Roche's software according to the manufacturer's instructions. The short-read sequences were assembled using a Newbler 2.3 assembler (454 Life Science), which generated 311 contigs with a minimum contig length of 100 nucleotides (nt). The assemblies were uploaded to the automated annotation platform on the Rapid Annotation using Subsystems Technology (RAST) server maintained by the National Microbial Pathogen Data Resource (1) and visualized with a SEED viewer (8).

The shotgun genome sequence of *P. putida* B001 has a total of 5,740,939 nt. The annotation indicates that 245 of the 262

RAST scaffolds harbor a total of 5,506 protein-encoding genes (PEGs). The assembly did not adequately reconstruct the rRNA genes, but 48 tRNA sequences were identified, as were portions of the 5S, 16S, and 23S ribosomal RNAs. In order to identify contigs containing genes that might be involved in the induction of plant host resistance, comparisons were made between this genome and complete genomes of *P. putida* strains KT2440 (a soil isolate) (7), WB619 (an endophyte of poplar) (9), and GB-1 (a freshwater isolate) (unpublished results and reference 3). Interestingly, we observed a high degree of relatedness of strain B001 to other *P. putida* strains isolated from diverse environments. Of the annotated PEGs in strain B001, 4,868 (88.4%), 4,797 (87.1%), and 4,945 (89.8%) were mapped to the complete genomes of strains KT2440, W618, and GB-1, respectively. The median DNA sequence identities of the shared genes were 95.7%, 91.8%, and 96.4%, respectively. Of the 561 to 709 PEGs predicted to be unique to strain B001 on the basis of single comparisons, 192 to 251 (34.2 to 35.8%) had predicted functions; of these, only 97 were absent in KT2440, W618, and GB-1. Those 97 PEGs included genes associated with pathogenicity, particularly on contigs 109 and 159, possibly indicating that the defense-inducing phenotype of B001 was derived from pathogenicity factors and/or subclinical infection of plants by the strain.

Nucleotide sequence accession numbers. The assembled shotgun genome sequence and annotations of *Pseudomonas putida* B001 were deposited in the European Nucleotide Archive (<http://www.ebi.ac.uk/genomes/wgs.html>) under accession numbers CAED01000001 to CAEE01000262.

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