

Draft Genome Sequence of *Pedobacter agri* PB92^T, Which Belongs to the Family *Sphingobacteriaceae*

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Strain PB92^T of *Pedobacter agri*, which belongs to the family *Sphingobacteriaceae*, was isolated from soil in the Republic of Korea. The draft genome of strain PB92^T contains 5,141,552 bp, with a G+C content of 38.0%. This is the third genome sequencing project of the type strains among the *Pedobacter* species.

The genus *Pedobacter*, proposed by Steyn et al. (11), belongs to the family *Sphingobacteriaceae* in the phylum *Bacteroidetes*. Members of the genus *Pedobacter* are characterized as aerobic, Gram-negative, and rod-shaped bacteria having menaquinone 7 (MK-7) as a major isoprenoid quinone (12). The *Pedobacter* species were isolated from various environments, such as water (2), soil (3), glacier (10), and compost (6). The strain *Pedobacter agri* PB92^T, isolated from soil in the Republic of Korea by Roh et al. (9), has 97.6% and 97.5% 16S rRNA gene sequence similarity with *Pedobacter borealis* G-1^T and *Pedobacter alluvionis* NWER-III1^T, respectively. The genus *Pedobacter* currently consists of 35 validly published species, and the genome sequences of only two type strains in the *Pedobacter* species were analyzed previously (4, 7).

Genomic DNA of *Pedobacter agri* PB92^T was extracted using a G-spin genomic DNA extraction kit (iNtRON Biotechnology, Republic of Korea). The draft genome sequence of *P. agri* PB92^T was analyzed using Roche 454 GS (FLX Titanium) pyrosequencing. A total of 383,656 reads spanning 98 Mb were generated and assembled using 454 Newbler assembler (454 Life Science) according to the manufacturer's instructions. The 379 contigs were generated to give 19.1-fold coverage. The draft genome of PB92^T contains 5,141,552 bp, with a G+C content of 38.0%. Gene annotation and prediction were analyzed using RNAmmer 1.2 (5), tRNAscan-SE 1.23 (8) software, and the RAST (Rapid Annotation using Subsystem Technology) pipeline (1). A total of 1 5S rRNA gene, 1 16S rRNA gene, 1 23S rRNA gene, and 49 tRNA genes were identified. Based on the RAST results, 5,006 coding sequences (CDSs) and 346 subsystems are predicted. More detailed genomic analyses and comparative studies with other *Pedobacter* genomes will give further information and insight into the metabolism of *Pedobacter* species.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [AJLG000000000](http://ajlg000000000). The version described in this paper is the first version, [AJLG010000000](http://ajlg010000000).

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