

Genome Sequence of the Plant Pathogen *Pseudomonas syringae* pv. *panici* LMG 2367

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***Pseudomonas syringae* pv. *panici* is a phytopathogenic bacterium causing brown stripe disease in economically important crops worldwide. Here, we announce the draft genome sequence of *Pseudomonas syringae* pv. *panici* LMG2367 to provide further valuable insights for comparison of the pathovars among species *Pseudomonas syringae*.**

Pseudomonas syringae pv. *panici*, first identified from proso millet (*Panicum miliaceum* L.), is a Gram-negative phytopathogenic bacterium which can cause diseases in a wide range of plant species, including many economically important crops, and appears to be widely distributed worldwide (4, 5, 11, 12). As previously reported, it is pathogenic to proso millet, lilac, pearl millet, and rice (13). In rice, this pathogen can cause rice bacterial brown stripe disease. The symptoms consist of water-soaked stripes on the leaves and leaf sheaths, which turn brown. The pathogen can also attack young, unfolded leaves, resulting in the stunting or death of seedlings (3, 5, 6), which is similar to the symptoms caused by *Acidovorax avenae* subsp. *avenae* (10). The disease is more severe in the years after floods. Therefore, this pathogen has been gaining increasing attention in China.

We sequenced and annotated the draft genome of *P. syringae* pv. *panici* LMG2367 collected from proso millet. Genomic DNA was isolated with a Wizard genomic DNA purification kit (Promega, Madison, WI), and sequencing was performed using a 454 sequencing system. The whole-genome sequencing approach resulted in 561,825 high-quality filtered reads with an average paired-end read length of 431 bp and 300-fold sequencing coverage on average. Quality-filtered reads were assembled *in silico* with Newbler 2.7 and the Geneious Pro 5.6 program, resulting in a total of 148 contigs. Functional annotation was done by analyzing results obtained from the RAST (Rapid Annotation using Subsystem Technology) server (2), BLAST (1), tRNAscan-SE 1.21 (8), and RNAmmer 1.2 (7).

Here we present the draft genome sequence of strain LMG2367, comprising 5,993,947 bp, with a G+C content of 59.0%. A total of 5,440 coding sequences (CDSs) were predicted using GLIMMER (9). The draft genome sequence encodes 70 RNAs, including 10 16S rRNA genes, four copies of 23S rRNA genes, and 56 tRNAs. Furthermore, 80% of the open reading frames (ORFs) have orthologs in the reference strain *Pseudomonas syringae* pv. *syringae* FF5 (BLASTP E-value, 1E−20), but 1,093 ORFs were not found in the released genomes of members of the *Pseudomonas* genus.

Pathogenicity-related genes (such as those involved in hypersensitive response and the type III secretion system-related proteins) and the type VI secretion system, which are essential for many plant-pathogenic bacteria, are found in *P. syringae* pv. *panici*. Meanwhile, several loci encoding resistance-nodulation-cell division (RND) efflux system, fimbrial biosynthesis, and adhesion-type proteins were also found. Overall, the genome sequence of *P.*

syringae pv. *panici* provides a basis for both basic and agricultural applied research. The genome sequence of *P. syringae* pv. *panici* also provides an important data resource for epidemiological studies, comparative genomics, and quarantine measures for this devastating phytopathogen.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under accession number ALAC00000000. The version described in this paper is the first version, ALAC01000000.

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