

# Draft Genome Sequence of *Pantoea ananatis* B1-9, a Nonpathogenic Plant Growth-Promoting Bacterium

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***Pantoea ananatis* B1-9 is an endophytic Gram-negative rhizobacterium that was isolated for its ability to promote plant growth and improve crop yield in the field. Here we report the draft genome sequence of *P. ananatis* B1-9. Comparison of this sequence to the sequenced genome of a plant-pathogenic *P. ananatis* strain, LMG20103, indicated that the pathogenesis-related genes were absent, but a subset of gene functions that may be related to its plant growth promotion were present.**

*Pantoea ananatis* is one of a number of well-known bacterial species that cause diverse symptoms, depending on their hosts, and are biocontrol agents possessing antifungal and antibacterial properties (2). A nonpathogenic *P. ananatis* strain, B1-9, was isolated from rhizosphere of green onion in Korea and was capable of promoting plant growth. This strain has phosphate solubilization activity, engages in nitrogen fixation and siderophore production, and produces high levels of indole (5). Root drenching with *P. ananatis* B1-9 enhanced red pepper crop yield in a field about 3 times (4). Previously, the genome sequence of a pathogenic *P. ananatis* strain was determined (3), but the genome sequence of a biocontrol agent of *P. ananatis* has not been available.

The genomic DNA of *P. ananatis* B1-9 was isolated, and a library was prepared from a sheared-DNA fraction of ~300 bp using Illumina paired-end sample preparation kits according to the manufacturer's instructions. This library was sequenced on an Illumina genome analyzer II (Illumina, San Diego, CA) for 76 cycles, generating over 6 million good-quality paired-end reads amounting to over 400 million nucleotides (nt). The short-read sequences were assembled using Velvet version 0.7.55 (7, 8) into a sequence with an empirically determined optimal hash length of 39 nt and a minimum contig length of 150 nt. The assemblies were uploaded to the automated annotation platform RAST (Rapid Annotation using Subsystems Technology) server maintained by the National Microbial Pathogen Data Resource (1) and visualized with the SEED viewer (6).

This shotgun genome sequence of *P. ananatis* B1-9 has a total of 5,105,557 nt. The annotation indicates that 169 contigs harbor a total of 4,988 protein-encoding genes (PEGs). Sequence coverage was 62-fold or greater for 99% of the annotated genes. Additionally, 81.7% of the annotated PEGs were greater than 300 nt in length. The assembly did not adequately reconstruct the rRNA genes, but 65 tRNA sequences were identified. Preliminary annotation of the draft genome sequence of *P. ananatis* B1-9 did not show any homologues to genes involved in pathogenesis, but several type IV secretion system homologues were identified. Potential homologues to genes involved in plant growth promotion and yield improvement were identified in the B1-9 genome sequence. The genome sequences of *P. ananatis* B1-9 will provide useful

information and insights into plant growth promotion and improvement in crop yield.

**Nucleotide sequence accession numbers.** The assembled shotgun genome sequence and annotations of *P. ananatis* B1-9 have been deposited in the European Nucleotide Archive (<http://www.ebi.ac.uk/genomes/wgs.html>) under accession no. CAEI01000001 to CAEI01000169.

## ACKNOWLEDGMENTS

We are grateful to Tea Meulia and Asela Wijeratne and the whole MCIC sequencing and bioinformatics team at The Ohio State University, OARDC, for technical assistance.

This work was supported by the World Class University project of the National Research Foundation of Korea (grant no. R32-2009-000-20047-0).

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Received 7 November 2011 Accepted 11 November 2011

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doi:10.1128/JB.06484-11