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Complete Genome Sequence of the Plant Growth-Promoting Endophyte *Burkholderia phytofirmans* Strain PsJN▽

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***Burkholderia phytofirmans* PsJN^T is able to efficiently colonize the rhizosphere, root, and above-ground plant tissues of a wide variety of genetically unrelated plants, such as potatoes, canola, maize, and grapevines. Strain PsJN shows strong plant growth-promoting effects and was reported to enhance plant vigor and resistance to biotic and abiotic stresses. Here, we report the genome sequence of this strain, which indicates the presence of multiple traits relevant for endophytic colonization and plant growth promotion.**

Bacterial endophytes are interesting candidates for application for biocontrol, plant fortification, and phytoremediation (3, 6). *Burkholderia phytofirmans* PsJN^T is a prominent and efficient plant growth-promoting endophyte (2, 5, 9), which was isolated from *Glomus vesiculiferum*-infected onion roots (4, 7).

Sequencing of the PsJN genome was performed at the Department of Energy (DOE) Joint Genome Institute via Sanger sequencing to a depth of ~11-fold coverage. All gaps in the draft assembly were scaffolded using mate pair PCR information and closed by primer walking off clones or PCR products. All nucleotide and repeat ambiguities were resolved by reseqeuncing from additional clones or PCR products, and thus the genome is completed at the "finished" level (1). The genome was loaded into IMG/M-ER for gene prediction and annotation, as described elsewhere (http://img.jgi.doe.gov/er/doc/about_index.html). The 8.2-Mb genome of strain PsJN consists of two chromosomes and one plasmid and contains a total of 7,405 genes. The gene coding density is 86.7%, and the G+C content is 62.3%. In total, 5,515 genes (73.7%) are assigned to predicted functions. Chromosome 1 contains a higher number of coding sequences (CDSs) involved in core functions like cell division, central metabolism, and other housekeeping functions, whereas chromosome 2 carries genes coding for accessory functions, such as genes for protective response, heavy metal resistance, and niche-habitat-specific properties. Interestingly, 71% of the plasmid CDSs (49/128) have no known function. Three rRNA gene operons were found, which are located on the two chromosomes. Sixty-three tRNA genes encoding all amino acids are located mainly on chromosome 1. At the genomic level, strain PsJN is most closely related to *Burkholderia xenovorans* LB400. More than 3,371 PsJN genes show more than 90% sequence similarity to strain LB400, and a Pearson coefficient of 0.94% indicates high genome synteny.

1-Aminocyclopropane-1-carboxylate (ACC) deaminase activity and the production of indole-3-acetic acid (IAA) contribute to the plant growth-promoting activity of strain PsJN (8). Besides the presence of an *acdS-acdR* operon, the genome sequence of PsJN indicates the presence of two independent IAA synthesis pathways, the indole-3-acetamide pathway and the tryptophan side chain oxidase pathway. No nitrogen fixation-encoding genes were found, and the genome does not indicate the production of antibiotics. PsJN carries two N-acyl homoserine lactone (AHL) and one 3-hydroxypalmitic-acid-methyl-ester-type quorum-sensing operons. The presence of genes encoding plant cell wall-degrading enzymes such as cellulases and endoglucanases as well as flagellar proteins explains the systemic internal plant colonization by this strain. The PsJN genome shows a range of detoxification mechanisms, including degradation of organic substances, heavy metal efflux systems, and various enzymes necessary to cope with oxidative stress. These features in combination with numerous (ABC-type) transporters and carbon source utilization pathways are likely to enable strain PsJN to successfully colonize a wide variety of plant habitats.

Nucleotide sequence accession numbers. The sequence data have been deposited in NCBI GenBank under project accession no. CP001052, CP001053, and CP001054.

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