

Draft Genome Sequence of the Antifungal-Producing Plant-Benefiting Bacterium *Burkholderia pyrrocinia* CH-67

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***Burkholderia pyrrocinia* CH-67 was isolated from forest soil as a biocontrol agent to be utilized in agriculture. Here, we report the 8.05-Mb draft genome sequence of this bacterium. Its genome contains genes involved in biosynthesis of secondary metabolites and plant growth promotion, which may contribute to probiotic effects on plants.**

B*urkholderia* species are widely distributed in diverse environmental niches. Several members of the genus are found in close association with plants, such as endophytic colonization, plant growth promotion, and suppression of plant pathogens (7, 11). *Burkholderia pyrrocinia*, which belongs to the *Burkholderia cepacia* complex genomovar IX, has been isolated from soil and the rhizosphere (1, 5) and is known to produce the fungicide pyrrolnitrin (10). *B. pyrrocinia* CH-67 was isolated from forest soil in Seung Hak Mountain, Busan, South Korea, by using a chitin-baiting method (8). With its antifungal activity, the strain has been assessed to be useful as a biocontrol agent because it effectively suppresses tomato leaf mold and the damping off of crisphead lettuce caused by *Fulvia fulva* and *Rhizoctonia solani*, respectively (8). Here, we analyzed the genome sequence of CH-67 to provide the genetic information and to explore useful traits that may contribute to plant health.

The whole-genome shotgun sequencing was carried out using Illumina platforms and the GS FLX+ system at NICEM and Macrogen in Korea. A 400-bp paired-end library and 2-kb, 6-kb mate-pair libraries were constructed for Illumina sequencing, and a GS FLX shotgun library was used for 454 pyrosequencing. A total of 12.7 Gb from the paired-end library, 2.8 Gb from the mate-pair libraries, and 108 Mb from the GS FLX shotgun library were used to assemble the genome sequence. The sequence reads were trimmed and assembled using CLC Genomics Workbench 4.8. The SSPACE v1.1 (3), IMAGE v2.1 (12), and GapFiller v1.9 (4) programs and perl scripts developed in-house were used to improve the assembly and to close gaps. Annotation was performed by using the RAST server (2). BLAST and HMMER searches were used for further analysis of genes, with comparisons against the GenBank nonredundant, Uniref90, Pfam, and KEGG databases.

The draft genome sequence of CH-67 consists of 8,049,701 bp with a 67.37% GC content in 131 contigs. A total of 8,121 open reading frames were predicted, and 5,305 (65.3%) were functionally assigned. The genome information displays several genetic factors beneficial for plants. For example, there exists in the genome the gene encoding 1-aminocyclopropane-1-carboxylate deaminase (*accD*). *AccD* can modulate the ethylene level in plants (9). The presence of genes for biosynthesis of secondary metabolites and ribosomally synthesized antimicrobial peptides indicates its ability to inhibit the growth of microbial competitors in the environment. Gene clusters for pyrrolnitrin (10), polyketides

(PK), nonribosomal peptides (NRP), and PK-NRP hybrids and genes for colicin V production were detected in the genome sequence. The genome has genes encoding enzymes for aromatic compound degradation. A multitude of the genes related to motility and chemotaxis indicate that CH-67 may have an advantage for approaching environmental nutrients, such as plant exudates or aromatic compounds. The genome sequence will be useful in exploiting the bacterium for biocontrol or bioremediation and for comparisons with other genomes of the *Burkholderia cepacia* complex group.

Nucleotide sequence accession number. The assembled whole-genome shotgun sequence of *B. pyrrocinia* CH-67 has been deposited in GenBank under the accession number ALWI00000000. The sequence and annotation are also available from the Genome Encyclopedia of Microbes (GEM; <https://www.gem.re.kr>) (6).

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