

# Draft Genome Sequence of *Pseudomonas chlororaphis* YL-1, a Biocontrol Strain Suppressing Plant Microbial Pathogens

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***Pseudomonas chlororaphis* YL-1 was isolated from soybean root tips and showed a broad range of antagonistic activities to microbial plant pathogens. Here, we report the high-quality draft genome sequence of YL-1, which consists of a chromosome with an estimated size of 6.8 Mb with a G+C value of 63.09%.**

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Compared with chemical pesticides, biological control represents a safer, more environmentally friendly approach to managing plant pathogens (1). *Pseudomonas* species are particularly suitable to be used as agricultural biocontrol agents because they can produce large amounts of metabolites to protect plants from pathogens (2–4). Most research of *Pseudomonas chlororaphis* has focused on its antifungal activities to phytopathogens and has scarcely addressed antibacterial activities (5–10). However, *P. chlororaphis* YL-1, which was isolated from soybean root tips, can suppress both fungal pathogens and bacterial pathogens of agricultural significance *in vitro*, such as *Burkholderia glumae*, *Clavibacter michiganensis*, *Erwinia amylovora*, *Rhizoctonia solani*, *Sclerotinia sclerotiorum*, and *Fusarium oxysporum*. Here, we analyzed the genome sequence of strain YL-1 to explore its features as a potential biocontrol agent.

The genome of *P. chlororaphis* YL-1 was sequenced using the Illumina/Solexa HiSeq 2000 technology at the Shanghai Major Bio-pharm Technology Co., Ltd. (Shanghai, China), which generated 101-bp paired-end reads. We obtained approximately 12.6 million reads for assembly after the low-quality reads were filtered out. The whole genome was *de novo* assembled into 89 contigs ( $N_{50}$ , 251,854 bp) and rearranged into 82 scaffolds using SOAPdenovo (11). Comparisons between contigs and scaffolds were then made using Glimmer 3.0. Because the circular genome sequence of *P. chlororaphis* has not been completed until now, the circular genome of *P. fluorescens* Pf0-1 (NC\_007492.2) was used as a reference. Annotation was performed with the Rapid Annotations using Subsystems Technology (RAST) server version 4.0 (12), generating 6,368 candidate protein-encoding genes.

The draft genome of strain YL-1 consists of 6,801,259 bases with an average of 179-fold coverage and 63.09% G+C content. A cursory search of the genome sequence revealed the presence of gene clusters putatively involved in the synthesis of phenazine (PHZ) (13–16), pyrrolnitrin (PRN) (17, 18), and hydrogen cyanide (HCN) (19), which play important roles in biological activities. Interestingly, a putative *fit* (*ABCDEFGH*) operon that might be responsible for the synthesis of Fit insect toxin (20) was iden-

tified in the genome. Additionally, some genes which are involved in the synthesis of pyoverdine and achromobactin (21, 22) were also identified. There are multiple genes encoding antioxidative stress proteins, such as 5 catalases, 17 peroxidases, 2 superoxide dismutases, and 2 transcription factors, SoxR and OxyR (23, 24). Moreover, genes encoding pyrroloquinoline quinone (*pqqBCDEF*) were also identified in the genome (25–27). A more specific analysis of strain *P. chlororaphis* YL-1 will be carried out in future research.

**Nucleotide sequence accession number.** The draft genome sequence of *P. chlororaphis* YL-1 has been deposited at DDBJ/EMBL/GenBank under the accession number [AWVJ00000000](https://www.ncbi.nlm.nih.gov/nuccore/AWVJ00000000). The version described in this paper is the first version.

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