

High-Quality Draft Genome Sequence of *Arthrobacter* sp. OY3WO11, a Strain That Inhibits the Growth of *Phytophthora infestans*

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***Arthrobacter* sp. strain OY3WO11 inhibits the growth of the potato pathogen *Phytophthora infestans* in *in vivo* growth challenge assays. We determined the draft genome sequence of this strain, assembling it into 3 scaffolds of 4.2 Mbp total length. OY3WO11 may represent a novel species of *Arthrobacter*.**

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Arthrobacter sp. strain OY3WO11 is a Gram-positive bacterium isolated from the rhizosphere of wild oat in Oyen, Alberta, Canada. This organism is a potential biocontrol agent for potato late blight based on its phenotype of disease suppression in *Phytophthora infestans*-challenged plants. To examine the possible mechanisms by which OY3WO11 exhibits this phenotype, we determined its genomic sequence.

Arthrobacter sp. OY3WO11 was grown at 22°C in a rotary shaker for 24 to 48 h in yeast extract glucose medium (2.0 g/liter yeast extract, 2.5 g/liter glucose, 0.4 mM MgSO₄·7H₂O, 0.09 mM MnSO₄·H₂O, 0.85 mM NaCl, 0.017 mM FeSO₄·7H₂O, 1.84 mM KH₂PO₄, and 1.43 mM K₂HPO₄). Genomic DNA was purified from 1 ml of overnight culture using the Wizard genomic DNA (gDNA) extraction kit (Promega, Madison, WI, USA) and sequenced on the GS Junior using Titanium Plus chemistry (Roche Diagnostics, Laval, Quebec, Canada). A total of 142,372 shotgun reads of 644-bp average length was generated. In addition, an 8-kb-insert paired-end sequencing run was performed based on the paired-end rapid library preparation protocol for Titanium chemistry (Roche, March 2012), with modifications as described previously (1). A total of 170,435 paired-end reads was generated, with an estimated pair distance of 6,383 ± 1,595 bp. Assembly of all sequencing runs together produced an improved high-quality draft (2) sequence, with 35× genome coverage. The data were assembled using Newbler version 3.0 (454 Life Sciences), generating 3 scaffolds of 4,253,657 bp (containing 18 contigs), 258,581 bp (1 contig), and 4,841 bp (1 contig). The sequence data were annotated using the Prokaryotic Genome Annotation Pipeline version 3.1 (NCBI).

Arthrobacter sp. OY3WO11 had a total genome size of 4,517,079 bp, with a G+C content of 65.29%. Genome annotation revealed 4,225 genes and 4,163 protein-coding genes. The genome featured 1 gene encoding 5S rRNA, 2 genes encoding 16S rRNA, 1 gene encoding 23S rRNA, and 50 tRNA-encoding genes.

The genome of *Arthrobacter* sp. OY3WO11 contained genes that have been associated with biocontrol phenotypes, including phenazine carboxylic acid synthesis (3) and cell wall-degradative

enzymes. Two genes encoding putative beta-lactamases were observed. The sequences of taxonomic markers, including the 16S rRNA-encoding gene and *rpoB* (4), shared 97 to 99% identity with the corresponding genes found in *A. phenanthrenivorans* Spe3. Similarly, two copies of the bacterial barcode marker *cpn60* (5) were identified, each of which clustered with corresponding copies from *A. phenanthrenivorans* Spe3 by phylogenetic analysis and had sequence identities of 93 to 96%. Comparison of the genome sequence of *Arthrobacter* sp. OY3WO11 to 85 genomic sequences from *Arthrobacter* spp. annotated at the Integrated Microbial Genomes portal (<https://img.jgi.doe.gov/cgi-bin/mer/main.cgi>) revealed that the average nucleotide identity (ANI) of the genome of OY3WO11 was below the specified cutoff (6) for inclusion in any of the species included in the analysis (the closest ANI was *A. phenanthrenivorans* Spe3, at 85.25%). In addition, *SpeI* (7) could not assign OY3WO11 to a species cluster; the closest match was *A. phenanthrenivorans* Spe3, with an average ANI of 93.9% over 40 Clusters of Orthologous Groups (COGs). Taken together, these observations suggest that OY3WO11 may represent a previously uncharacterized or unsequenced strain of *Arthrobacter*.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession no. [LWLP00000000](https://www.ncbi.nlm.nih.gov/nuclink/LWLP00000000). The version described in this paper is version LWLP01000000.

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