



Data in Brief

Draft whole-genome sequence of the *Diaporthe helianthi* 7/96 strain, causal agent of sunflower stem canker



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ABSTRACT

Diaporthe helianthi is a fungus pathogenic to sunflower. Virulent strains of this fungus cause stem canker with important yield losses and reduction of oil content. Here we present the first draft whole-genome sequence of the highly virulent isolate *D. helianthi* strain 7/96, thus providing a useful platform for future research on stem canker of sunflower and fungal genomics. The genome sequence of the *D. helianthi* isolate 7/96 was deposited at DDBJ/ENA/GenBank under the accession number MAVT000000000 (BioProject PRJNA327798).

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Specifications [standardized info for the reader]

Organism/cell line/tissue	<i>Diaporthe helianthi</i> strain 7/96
Sex	N/A
Sequencer or array type	Illumina HiSeq 2000
Data format	Assembled
Experimental factors	Fungal strain pathogen on sunflower
Experimental features	De novo genome sequencing followed by assembly and annotation
Consent	N/A
Sample source location	<i>D. helianthi</i> 7/96 was isolated from diseased sunflowers in France

1. Direct link to deposited data

<https://www.ncbi.nlm.nih.gov/bioproject/327798>

2. Experimental design, materials and methods

Diaporthe helianthi Munt.-Cvet [1], anamorph *Phomopsis helianthi*, is one of the causal agent of stem canker of sunflower (*Helianthus*

annuus). The fungus belongs to division Ascomycota, subdivision Pezizomycotina, class Sordariomycetes, order Diaporthales, family Diaporthaceae. Disease develops on leaves by causing brown necrotic lesions at the edge of the leaf blade and then spreads through the veins to the petiole. The leaf dries and remains attached to the stem. From the junction of the leaf the pathogen gradually infects the stem causing diffuse necrosis. The main loss is the shriveling of capitula and lodging of stem, which breaks at different levels. The fungus overwinters as mycelium and perithecia on stem debris left on the soil. Ascospores are released as a yellowish jelly soluble in rainwater. The first contamination of the leaves by ascospores can occur in early spring.

D. helianthi 7/96 was isolated from diseased sunflowers in France. This isolate belongs to a group of highly virulent isolates characterized by the presence of a gene fragment having homologies with *Aspergillus terreus* lovastatin nonaketide polyketide synthase gene (*lovB*) [2].

The genome of *D. helianthi* strain 7/96 was sequenced using Illumina mate-paired sequencing technology by BGI HONG KONG CO (BGI-HONGKONG CO., Limited, 16 Dai Fu Street, Tai Po Industrial Estate, Tai Po, New Territories, Hong Kong). Mate-paired reads of 90 bp (1.80 Gbp; average coverage 38.80×) were assembled using Velvet V 1.2.10 [3]. The genome of *D. helianthi* consists of 13,383 sequence scaffolds with a total assembly length 46.50 Mbp (N50 = 6347 and N90 = 1502), 51.10% GC-content, and a maximum scaffold size of 54,299 bp. The completeness of the assembly was assessed using BUSCO v12 [4], which estimated the genome sequence to be 98.26%

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complete. The genome was annotated using the MAKER2 pipeline [5]. Overall, 14,220 protein-coding gene models were predicted. Analysis with SignalP 4.1 [6] revealed that 1433 predicted proteins (9.92% of the proteome) contain a secretion signal peptide. Among those 45 are species-specific as they do not have any sequence similarity to proteins in public databases, based on BLAST searches (e-value threshold of $1e^{-5}$). Such features are characteristic of fungal effectors, which are proteins that have key roles in restricting the host defense [7]. A first comparative analysis within Diaporthales [8] and model organisms with publically available genomes [*Fusarium* [9], *Neurospora* [10], *Colletotrichum* [11], *Magnaporthe* [12]] evidenced that *D. helianthi* 7/96 genome contains a remarkable number (at least 40) of putative polyketide synthases (PKSs). Analysis of PKS gene family in strain 7/96 could be an intriguing starting point to unravel *D. helianthi* sunflower interactions.

2.1. Nucleotide sequence accession numbers

This Whole-Genome Shotgun project has been deposited in GenBank under the accession N^o: MAVT00000000 (BioProject PRJNA327798). The version described in this paper is: MAVT00000000.1.

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