Data in Brief

Draft genome sequence of *Diaporthe aspalathi* isolate MS-SSC91, a fungus causing stem canker in soybean

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A B S T R A C T

*Diaporthe aspalathi* (Syn. *Diaporthe phaseolorum var. meridionalis*) is the causal agent of the southern stem canker (SSC) disease in soybean. This disease can kill plants from the middle to the end of the growing season resulting in severe yield loss. The mechanisms of SSC disease development and pathogen invasion of soybean are not fully understood. The genome sequence of *D. aspalathi* has not been described. In this article, we report the successful assembly of the draft genome sequence of a *D. aspalathi* isolate, designated MS-SSC91, that was isolated from the stem of a field-grown soybean plant in Mississippi, USA in 2006. This study represents the first reported genome sequence of *D. aspalathi* in the *Diaporthe-Phomopsis* complex. The whole genome shotgun sequence of the MS-SSC91 isolate has been deposited at DDBJ/EMBL/GenBank under the accession LJJS00000000 and the sequences could be found at the site http://www.ncbi.nlm.nih.gov/assembly/GCA_001447215.1/. The MS-SSC91 genome sequences will provide information on the genetic basis of fungal infection of the soybean stem. It is valuable for studying soybean-fungal interactions and developing new control strategies for this pathogen.

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1. Direct link to deposited data

Deposited data can be found here: http://www.ncbi.nlm.nih.gov/nuccore/LJJS00000000.

2. Materials and methods

2.1. Pathogen isolation, identification, and pathogenicity test

*Diaporthe aspalathi* (Syn. *D. phaseolorum var. meridionalis*) is the causal agent of the southern stem canker (SSC) disease in soybean [1]. This disease can kill plants from the middle to the end of the growing season resulting in severe yield loss [1]. It is one of the most economically important soybean diseases. Although SSC commonly occurs in the southern United States, *D. aspalathi* has been found in some of the northern states [2,3]. An isolate of *D. aspalathi*, MS-SSC91 was isolated from field-grown soybean stem in Stoneville, Mississippi, USA in 2006 using a modified seed plating procedure [4]. Briefly, stem samples with lesions were collected, cut into ca. 5-mm pieces, surface-disinfested with 0.5% NaOCl solution for 3 min, rinsed three times, and placed on acidified potato dextrose agar (APDA) medium (Difco Laboratories, Detroit, MI) adjusted to pH 4.8 with 25% lactic acid after autoclaving. Stem samples were placed on each Petri dish and incubated at 24 °C for 4–7 days. Colonies of interest were hyphal tipped, and examined under microscope. *D. aspalathi* was identified using morphological characteristics. Isolate of MS-SSC91 isolate were white, lanose, and turned tan with age as the typical *D. aspalathi* previously described [1]. Further identification was confirmed by analysis of the ITS region of rDNA amplified by PCR with primers ITS1, 5′-TCCGTAGGTGAACCTGCGG-3′ and ITS4, 5′-TCCTCCGGTTATGATATGC-3′ [5].

Pathogenicity tests were performed using a cut-seeding inoculation assay [6]. Soybean seed of a susceptible cultivar, Williams 82 was used in the tests. Mycelial plugs (4-mm in diameter) from the margin of a 10-day old culture on APDA were punched out with the large ends of disposable micropipette tips (200 μL). The micropipette tip containing the fungal mycelium was subsequently placed over a 3-week old cut soybean stem that was cut at just below the first trifoliolate node. Micropipette tips containing plugs of non-infested APDA were served...
as the negative control. Two days after inoculation, micropipette tips were removed. At 7 days after inoculation, the main stem length was measured from the soil line to the top of the plant, and the lesion on the stem was measured. The MS-SSC91 isolate has been used to evaluate soybean for resistance to stem canker as part of the USDA Uniform Soybean Tests (http://www.ars.usda.gov/SP2UserFiles/Place/60661000/UniformSoybeanTests/2013SoyBook.pdf).

2.2. DNA extraction, library construction, and sequencing

Genomic DNA of D. aspalathi MS-SSC91 isolate was extracted from a 4-day-old culture using a Qiagen DNeasy Plant Mini Kit (Qiagen Inc., Valencia, CA) and used to generate paired-end libraries with the TruSeq DNA PCR-Free Sample Preparation kit (Illumina San Diego, CA) according to the manufacturer’s protocol. Libraries were sequenced in separate lanes on an Illumina HiSeq 2000 sequencer using a TruSeq SBS sequencing kit (version 3, Illumina) at the Genomics Core Facility, Purdue University, West Lafayette, IN.

2.3. Data analysis and results

A total of 131,083,049 paired-end 101 bp reads were generated. The total amount of sequence was 26,478,775,898 bp. After trimming or removing low quality reads or bases with the Trimmomatic [7] and/or fastx_clipper (http://hannonlab.cshl.edu/fastx_toolkit/) using the threshold of base Phred score greater than 20, a total of 126,051,864 paired-end reads and 4,778,811 un-paired reads were retained. The total remaining sequence was 24,801 Mb (approximately 330× coverage of the genome). The filtered sequence was assembled with ABySS de novo genome assembly software [8] at kmer = 80, and resulted in an assembly with 131,083,049 sequences within genes. Of the 25.8 Mb sequences within genes, the gene was 23 kb. Approximately 46% (25.8 Mb) of the whole genome sequence was contained in genes. Of the 25.8 Mb sequences within genes, 22.5 Mb were coding sequences. The D. aspalathi sequencing and assembly statistics were summarized in Table 1.

The draft genome of MS-SSC91 represents an important soybean fungal pathogen in the Diaporthe-Phomopsis complex.

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References

[1] J.C. Rupe, Stem Canker. in: G.L. Hartman, J.C. Rupe, E.J. Sikora, L.L. Domier, J.A. Davis, K.L. Steffey (Eds.), Compendium of Soybean Diseases and Pests, fifth ed. APS Press, Minnesota, USA 2015, pp. 85–88.
[2] C.E. Gravert, S. Li, G.L. Hartman, Occurrence of Diaporthe phaseolorum var. meridionalis on soybean in Illinois. Plant Dis. 85 (2001) 1211.
[3] S. Li, N.C. Kurtzweil, C.R. Grau, G.L. Hartman, Occurrence of stem canker (Diaporthe phaseolorum var. meridionalis) on soybean in Wisconsin. Plant Dis. 88 (2004) 576.
[4] S. Li, Phomopsis seed decay of soybean: in: A. Sudaric (Ed.), Soybean – Molecular Aspects of Breeding, Intech Publisher, Vienna, Austria 2011, pp. 277–292.
[5] A.W. Zhang, G.L. Hartman, L. Riccioni, W.L. Pedersen, G.L. Hartman, Molecular identification and phylogenetic grouping of Diaporthe phaseolorum and Phomopsis longicolla isolates from soybean. Phytopathology 88 (1998) 1306–1314.
[6] S. Li, G.L. Hartman, D. Boykin, Aggressiveness of Phomopsis longicolla and other Phomopsis spp on soybean. Plant Dis. 94 (2010) 1035–1040.
[7] A.M. Bolger, M. Lohse, B. Usadel, Trimmomatic: a flexible trimmer for Illumina sequence data. Bioinformatics (2014) (btu170).
[8] J.T. Simpson, K. Wong, S.D. Jackman, J.E. Schein, S.J. Jones, I. Birol, ABySS: a parallel assembler for short read sequence data. Genome Res. 19 (2009) 1117–1123.
[9] G. Parra, K. Bradnam, I. Korf, CEGMA: a pipeline to accurately annotate core genes in eukaryotic genomes. Bioinformatics 23 (2007) 1061–1067.
[10] K.J. Hoff, M. Stanke, WebAUGUSTUS—a web service for training AUGUSTUS and predicting genes in eukaryotes. Nucleic Acids Res. 41 (2013) W123–W128.