



Draft Genome Sequence of *Cercospora* cf. *sigesbeckiae*, a Causal Agent of Cercospora Leaf Blight on Soybean

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ABSTRACT *Cercospora* cf. *sigesbeckiae* is an ascomycete fungal pathogen that infects various plants, including important agricultural commodities, such as soybean. Here, we report the first draft genome sequence and assembly of this pathogen.

Cercospora cf. *sigesbeckiae* is a broad generalist pathogen infecting at least eight different plant families and causing Cercospora leaf blight (CLB) on soybean (1). Until recently, *Cercospora kikuchii* was thought to be the only causal agent of CLB, but phylogenetic analyses of cercosporoid fungi isolated from infected soybean revealed the presence of two other morphologically similar *Cercospora* species, including *Cercospora* cf. *sigesbeckiae* from leaves and *Cercospora* cf. *flagellaris* from seeds and leaves (1, 2). Prior to 2015, most records of *Cercospora* cf. *sigesbeckiae* came from Asia (3), but recent studies also reported this pathogen from Argentina (2) and Louisiana, USA (1).

CLB infections are characterized by leaf bronzing and typically coincide with seed set. Abaxial foliar lesions are initially observed within the canopy and later develop on lower leaves, stems, and petioles. CLB-associated yield losses have occurred more frequently in the Gulf South since 1999 (4), and losses have also been reported from other soybean-growing regions in the United States (5, 6) and South America (7, 8). Management strategies to control CLB have traditionally relied on a quinone outside inhibitor, methyl benzimidazole carbamate, and thiophanate methyl foliar fungicides. However, repeated application of these compounds has resulted in the development of resistant isolates (9, 10).

More than 650 species of *Cercospora* have been described (11), although only 4 published genomes (of *C. arachidicola*, *C. zea-maydis*, *Cercospora* aff. *canescens*, and *C. sojina*) exist, with only *C. sojina* being an important soybean pathogen. There are also no molecular barcodes available to reliably discriminate among closely related *Cercospora* species. Therefore, additional genomic data may facilitate the development of species-specific markers for accurate identification, which could, in turn, add to an integrated defense management approach for CLB through improved genetic resistance in soybean cultivars.

Cercospora cf. *sigesbeckiae* strain PP_2012_071 was isolated from foliar lesions on soybean collected in Louisiana. Genomic DNA was isolated from hyphal tissue using a modified cetyltrimethylammonium bromide (CTAB) extraction protocol developed in our laboratory and was quantified using a Qubit fluorometer (Invitrogen, Carlsbad, CA, USA). Libraries were constructed using a NEBNext Fast DNA fragmentation & library prep set for Ion Torrent (New England BioLabs, Inc., Ipswich, MA, USA), evaluated for quality and size using the Agilent 2200 TapeStation system (Agilent Technologies, Santa Clara, CA, USA), and sequenced on an Ion Personal Genome Machine system

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using an Ion 318 Chip version 2. A total of 1.63 Gbp and 6,050,000 sequence reads were obtained, with a median read length of 281 bp. A total of 5,770,664 reads were assembled *de novo* using MIRA 4.0.2 (12), resulting in 469 contigs of at least 500 bp, with a total consensus length of 34,132,478 bp, largest contig size of 1,591,857 bp, and N_{50} value of 418,495 bp. The maximum total coverage of the assembly was 2,042 \times , with an average total coverage of 43.06 \times calculated from contigs of at least 5,000 bp and 13 \times coverage, with a G+C content of 51.5%.

Accession number(s). This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession no. [NKQR000000000](https://www.ncbi.nlm.nih.gov/nuccore/NKQR000000000). The version described in this paper is version NKQR01000000.

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