Genome Sequence Resource for the Plant Pathogen *Sclerotinia sclerotiorum* WH6 Isolated in China

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Abstract

Sclerotinia sclerotiorum is a notorious fungal pathogen that causes sclerotinia stem rot (SSR) on many important crops in China and worldwide. Here, we present a high-quality genome assembly of *S. sclerotiorum* strain WH6 using the PacBio SMRT cell platform. The assembled genome has a total size of 38.96 Mbp, with a contig N50 length of 1.90 Mbp, and encodes 10,512 predicted coding genes, including 685 secreted proteins and 65 effector candidates. This is the first report of a *S. sclerotiorum* genome sequence from China. The WH6 genome sequence provides a valuable resource for facilitating our understanding of *S. sclerotiorum*-host interactions and SSR control in China and the world.

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Keywords

fungi, disease management, oilseeds and legumes

Genome Announcement

Sclerotinia sclerotiorum is a remarkable plant pathogenic fungus for its broad host range and destructive diseases. *S. sclerotiorum* can infect over 400 different hosts, including many economically important crops such as oilseed rape, soybean, pea, sunflower, and others (Bolton et al. 2006). Sclerotinia stem rot (SSR), caused by *S. sclerotium*, is one of the most serious diseases on oilseed rape and soybean crops in China (Wang et al. 2014) and the U.S. (Bolton et al. 2006). *S. sclerotiorum* can cause up to 80% yield loss in individual oilseed rape fields during serious outbreaks (Li et al. 2006). Until now, complete genome sequence has been available only for *S. sclerotiorum* 1980 UF-70 from the U.S. (Amselem et al. 2011; Derbyshire et al. 2017). The genome sequences of *S. sclerotiorum* strains from China remain to be determined and the genomic difference between Chinese strains and other strains are still unclear.

In this study, we sequenced the genome of *S. sclerotiorum* WH6, which was isolated from a diseased rapeseed plant in our experimental field station of Hubei Province, China. The genomic DNA of the strain was extracted and sequenced using long-read PacBio platforms with single-molecule real-time (SMRT) technology (Beijing Grandomics Biosciences Co., Ltd.) with an average insert size of 20 kb. In total, 774,934 long reads, representing 166× coverage of the *S. sclerotiorum* genome, were generated after sequencing. Sequence filtering and de novo assembling were performed on full PacBio long reads using Canu v1.7.1 (Koren et al. 2017). The final genome assembly comprised 38.96 Mbp containing 28 contigs, with an N50 length of 1.90 Mbp and a GC content of 41.57%. The longest contig consisted of 3.95 Mbp. The genome of *S. sclerotiorum* WH6 was similar to the genome of *S. sclerotiorum* 1980 UF-70 (Derbyshire et al. 2017), which was 38.91 Mbp long with 41.56% GC content. These and other genome annotation statistics of 980 UF-70 were shown in Table 1. Completeness of the WH6 assembly was assessed using BUSCO v4.1.4 with the lineage-specific dataset helotiales_odb10 (Seppey et al. 2019). This analysis indicated that the genome assembly displayed a high overall completeness of 97.89%, only 0.33% of BUSCOs were present as

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Table 1. Summary of *Sclerotinia sclerotiorum* WH6 genome assembly and comparison with strain 1980 UF-70

Genomic features	WH6	1980 UF-70
Sequencing platform	PacBio RSII	PacBio
Coverage (x)	166	36
Assembly size (bp)	38,957,821	38,906,497
Number of contigs	28	17
GC content (%)	41.57	41.56
N50 length (Mbp)	1,900,497	2,387,400
BUSCO completeness (%)	97.89	97.78 ^a
Repeat rate (%)	11.99	12.96
Predicated protein-coding genes	10,597	11,130
Annotated proteins with the nonredundant database	10,512	10,802 ^a
Annotated proteins with Swiss-prot	6,375	6,401 ^a
Secreted proteins	685	711 ^b
Candidate effectors	65	70 ^b
Reference	This study	Derbyshire et al. 2017

^a These data were not described in the original study and identified by the same pipeline (this study).

^b These data were described in the original study and reanalyzed by the same pipeline (this study) to ensure a fair comparison.

fragments, and 1.78% were missing. Repeat sequences of the genome were carried out by RepeatMasker v4.0.7 (<http://www.repeatmasker.org>) using a de novo repeats library generated by Repeat Modeler pipeline v1.0.7 (Saha et al. 2008). As a result, approximately 11.99% of sequences were identified as repeat sequences.

After repeat-masking, exonerate v2.2.0 (Slater and Birney 2005) and BLAST v2.2.28 (Camacho et al. 2009) were run within Maker for evidence-based alignments and Augustus v3.2.2 (Keller et al. 2011) and SNAP v2006-07-28 (Korf 2004) for ab initio gene prediction. Overall, 10,597 protein-coding genes were identified, with an average length of 1,400 bp, constituting 38.07% of the total genome. Among the predicated genes, 10,512 were mapped to the National Center for Biotechnology Information nonredundant protein database, 6,375 were mapped to the Swiss-Prot database, 5,487 were assigned GO terms, and 3,100 were mapped to the KEGG database, respectively. After analysis with SignalP v4.1 (Petersen et al. 2011) and THMM v2.0 (Krogh et al. 2001), a total of 685 secreted proteins were identified. Among the secreted proteins predicted, 65 proteins were identified as effector candidates by EffectorP v2.0 (Sperschneider et al. 2018). In addition, 603 putative carbohydrate-active enzymes, 2,218 transporters, 115 kinases, and 3,487 pathogen-host interaction proteins were predicted using the CAZy (Cantarel et al. 2009), TCDB (Saier et al. 2006), Kinomer (Martin et al. 2009), and PHI databases (Urban et al. 2020) (*E* values were all <1e−5), respectively.

In summary, we reported a high-quality genome assembly of *S. sclerotiorum* strain WH6. Our data provides a new resource to understand the diversity of the *S. sclerotiorum* populations worldwide and the underlying mechanisms of potential pathogenicity differentiation among different *S. sclerotiorum* strains and contributes to SSR control in China and the world. The genome assembly and associated raw data have been deposited into CNGB Sequence Archive (CNSA) of the China National GeneBank Database (CNGBdb) (Chen et al. 2020) with accession number CNP0001567 (<https://db.cngb.org/cnsa/project/CNP0001567/reviewlink/>).

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