Genome Resource for Peanut Web Blotch Causal Agent *Peyronellaea arachidicola* Strain YY187

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Abstract

Peyronellaea arachidicola is the causal agent of peanut (*Arachis hypogaea* L.) web blotch. Here, we report an assembled draft genome sequence of *P. arachidicola* strain YY187 obtained from the symptomatic leaf of peanut in China. The genome size is 47.3 Mb, consisting of 26 contigs ($N_{50} = 2.2$ Mb) with G+C content of 56.37%. This genome will provide a valuable foundation for further research on genetics and comparative genomics of *P. arachidicola*.

Genome Announcement

Peanut web blotch, caused by *Peyronellaea arachidicola* (also known as *Didymella arachidicola* or *Phoma arachidicola*) (Aveskamp et al. 2010; Chen et al. 2015; Marasas et al. 1974; Tomilin 1979), is one of the most important foliar fungal diseases of peanut in China (Cui et al. 2016; Li et al. 2018). Peanut web blotch was first reported in Texas, U.S.A., in 1972 (Pettit et al. 1986) and then found in Liaoning, Shandong, Shaanxi, and Henan provinces of China during the 1980s to 1990s (Fu et al. 2013). Web blotch lesions are characterized as having a net-like webbing pattern, brown to tan in color, which typically grow together to cover the entire leaf in the later stage. This disease occurs at all growth stages of peanut and results in significant yield losses of up to 30% (Xu et al. 1995). Past studies focused on the epidemic dynamics and management practices of peanut web blotch (Cui et al. 2016; Fu et al. 2013; Lancaster et al. 2005; Taber et al. 1984; Van Wyk et al. 1987), while little is known about the biology of the causal agent *P. arachidicola* on the genomic level. In this study, we report the first draft genome sequence of *P. arachidicola* strain YY187, providing a valuable resource for understanding the genetic diversity and further comparative genomics of the fungal pathogen.

YY187 was isolated from symptomatic leaves of peanut (*Arachis hypogaea* L.) collected from Yuanyang, Henan Province, China, in September 2015. Genomic DNA was extracted from mycelia by using the DNeasy plant mini kit (QIAGEN). Genomic DNA was quantified by a NanoDrop spectrophotometer 2000c and Qubit Fluorometer (Thermo Fisher Scientific Inc.). SMRT bell libraries were constructed and sequenced on the PacBio Sequel platform (Pacific Biosciences) using SMRT cells.

A total of 7.86 Gb filtered subreads with average length of 8.09 kb were generated from PacBio Sequel sequencing. PacBio polymerase reads were processed by SMRT analysis package version 2.3.0 to filter out reads with quality less than 0.8, to remove adapters and to

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Keywords

Peyronellaea arachidicola, peanut web blotch, genome

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Table 1. Summary statistics of the draft genome assembly of *Peyronella arachidicola*

Features	Numbers
Genome size (Mb)	47.3
Number of contigs	26
Max. contig length (kb)	6,557.3
Contig N ₅₀ (Mb)	2.2
Contig N ₉₀ (Mb)	1.4
G+C content (%)	56.4
Number of predicted genes	17,447

extract subreads with length of at least 1,000 bp. The de novo genome assembly was generated by merging a Canu 1.5 (Koren et al. 2017) assembly with a Wtdbg 2.2 (Ruan and Li 2020) assembly using Quickmerge 0.2 (Chakraborty et al. 2016). The Arrow correction was performed by using SMRT Link 5.0 (Pacific Biosciences). Genome completeness (complete BUSCOs = 98.6%) and assembly quality were assessed using BUSCO 2.0 (Simão et al. 2015; Waterhouse et al. 2017). The size of the *P. arachidicola* genome was 47.3 Mb, consisting of 26 contigs with N₅₀ of 2.2 Mb with a G+C content of 56.4% (Table 1). The functional genes were predicted by Genscan 1.0 (Burge and Karlin 1997), Augustus 2.4 (Stanke and Waack 2003), GlimmerHMM 3.0.4 (Majoros et al. 2004), GeneID 1.4 (Blanco et al. 2007), and SNAP (2006-07-28) (Korf 2004) using the genome of *Ascochyta rabiei* strain ArDII as a reference (GenBank accession no. GCA_001630375.1). A total of 17,447 genes (average length 1,590.28 bp), 38,508 coding sequences (CDSs, average length 657.21 bp), and 38,508 exons (average length 657.21 bp) were predicted by integrating all the above gene sets to a nonredundant gene set using EVM 1.1.1 (Haas et al. 2008).

The draft genome sequence has been deposited under BioProject PRJNA562378 and Biosample SAMN12638752. This Whole Genome Shotgun project has been deposited at DDBJ/ENA/GenBank under the accession WOCF00000000. The version described in this paper is version WOCF01000000. Data has also been deposited in the Sequence Read Archive (SRA) database, under SRA accession SRR10589210.

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