Genome Resource for Barley Leaf Stripe Pathogen *Pyrenophora graminea*

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Abstract

Pyrenophora graminea is the causative agent of barley leaf stripe disease. In this study, the strong pathogenic isolate QWC was used to generate DNA for Illumina sequencing. After assembly, its genome size was 42.5 Mb, consisting of 264 scaffolds, and a total of 10,376 genes was predicted. This is the first genome resource available for *P. graminea*. The genome sequences of *P. graminea* will accelerate the understanding interaction of *P. graminea* and barley.

Barley leaf stripe is a seedborne disease caused by the fungus *Pyrenophora graminea* S. Ito & Kurib. (anamorph *Drechslera graminea* (Rabenh. ex. Schltdl.) S. Ito). When the seed germinates, the mycelium of the fungus survives in the pericarp, hull, and seed coat but not in the embryo; the fungus then penetrates the coleorhiza and colonizes the plant systemically, beginning with the root tip (Platenkamp 1976). Due to the cool and humid weather conditions required for infection during germination, this disease can occur in Europe and Northern America as well as in northern Africa, Russia, India, and China. Barley leaf stripe is responsible for substantial reductions in barley yields in different cultivation areas (Zad et al. 2002). When the seed infection percentage is high, this disease results in severe yield reduction (Porta-Puglia et al. 1986). Thus far, research has been conducted regarding the genetic diversity of the pathogen (Bayraktar and Akan 2012; Si et al. 2019; Zein et al. 2010), pathogenicity differentiation (Bayraktar and Akan 2012; Si et al. 2019), resistance evaluation (Mueller et al. 2003; Tekauz 1983), resistance gene mapping (Arru et al. 2002, 2003; Biselli et al. 2010; Pecchioni et al. 1996; Tacconi et al. 2001; Thomsen et al. 1997), and candidate gene screening involved in the host–pathogen interactions (Ghannam et al. 2016); yet, little is known about the genome of *P. graminea*. In genus *Pyrenophora*, only three species, including *P. teres* (Ellwood et al. 2010), *P. tritici-repentis* (Moolhuijzen et al. 2018), and *P. seminiperda* (Solai et al. 2014), have genomic information currently available. Further knowledge of the genome could be useful for understanding of the molecular basis of this disease.

The QWC isolate, collected from Yongdeng, Gansu Province in 2009, was collected for sequencing given its extensive pathogenicity compared with other isolates (Si et al. 2017). Mycelia tissue of *P. graminea* QWC isolated from barley in China was used for genomic DNA extraction with the cetyltrimethylammonium bromide method (Bayraktar and Akan 2012; Si et al. 2019). The genome size was estimated, using K-mer statistics, to be 43.9 Mb. Three genomic DNA libraries, including a 170-, 500-, and 6,000-bp library, were constructed and sequenced using an Illumina HiSeq 2000 platform. In total, 4,146 Mb of clean data were obtained by removing low-quality data, including adapters, duplications, and those reads

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Keywords

barley leaf stripe, genome resource, *Pyrenophora graminea*

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Table 1. Summary statistics of the draft genome assembly of *Pyrenophora graminea*

Features	Numbers
Herbarium number	ACCC 39601
Genome size (Mb)	43.9
Total length (Mb)	42.5
Number of scaffolds	264
Max. scaffold length (kb)	3,520.8
Scaffold N ₅₀ (kb) ^a	1,056.1
Scaffold average length (kb)	160.9
GC content (%)	47.4
Number of predicted genes	10,367

^a N₅₀ = scaffold length at which 50% of the total assembly length is covered.

containing N more than 10%. A de novo genome assembly was performed with the software SOAPdenovo (Li et al. 2008, 2010).

The size of the *P. graminea* QWC genome assembly was 42.47 Mb, which is larger than that of *P. teres* (Ellwood et al. 2010). The *P. graminea* QWC genome consists of 264 scaffolds, with the scaffold length at which 50% of the total assembly length is covered of 1,056.1 kb. The GC content is 47.4%. Many of the 10,367 genes were predicted with four software programs, including GeneWise (Birney et al. 2004), SNAP (Johnson et al. 2008), Augustus (Keller et al. 2011), and Genemarkes (Ter-Hovhannisyan et al. 2008). Of the 10,367 predicted genes, 6,156 could be categorized by BLAST (Tatusov et al. 1997, 2003) to a clusters of orthologous groups (COG) category and 5,860 genes could be categorized by BLAST (Kanehisa 1997; Kanehisa et al. 2004, 2006) to a Kyoto Encyclopedia of Genes and Genomes (KEGG) category. Based on the Carbohydrate-Active Enzymes (CAZy) database (Cantarel et al. 2009), the genome contains 178 genes encoding carbohydrate esterases, 680 genes encoding glycoside hydrolases, 386 genes encoding glycosyl transferases, 15 genes encoding polysaccharide lyases, and 295 genes categorized as carbohydrate-binding modules. There were 133 secreted proteins predicted based on standards (Emanuelsson et al. 2007), of which 27 were classified as potential effectors by EffectorP 2.0 (Sperschneider et al. 2018). The summary statistics of the genome assembly are shown in Table1.

The Whole-Genome project described in this article can be accessed from NCBI SRA Bioproject ID PRJNA 544435 (<https://dataview.ncbi.nlm.nih.gov/object/PRJNA544435?reviewer=3b9sgmh1cj3gs4ujgspaiagsd>). Specimens of the isolate QWC are available at the Agricultural Culture Collection of China (Table 1).

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