Genome Sequence Resource of *Magnaporthe oryzae* Laboratory Strain 2539

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Abstract

Magnaporthe oryzae causes blast disease on more than 50 species of monocot plants, including important crops such as rice, millet, and most recently wheat. Additionally, it is an important model system for studying host-pathogen interaction. Here, we report a high-quality genome assembly and annotation of a laboratory strain 2539 of *M. oryzae*, which is a widely used progeny of a rice-infecting isolate and a grass-infecting isolate. The genome sequence of strain 2539 will be useful for studying the evolution, host adaption, and pathogenicity of *M. oryzae*, which will be beneficial for a better understanding of the mechanisms of host-pathogen interaction.

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Keywords

genome plasticity, host adaption, host-pathogen interaction, *Magnaporthe oryzae* laboratory strain 2539, monocots

Genome Announcement

Rice is one of the most important staple foods in the world. However, rice blast disease caused by *Magnaporthe oryzae* results in substantial economic loss to rice producers (Dean et al. 2012). Because of its high genome plasticity and host adaption, *M. oryzae* can infect more than 50 species of plants, such as wheat, oat, finger millet, and some graminaceous weeds that grow near the cultivated crops (Ou 1985). In addition, *M. oryzae* is an important model system for studying host-pathogen interaction (Ebbel 2007). Presently, genome sequence data for numerous *M. oryzae* strains are available that greatly enhanced our understanding of essential traits, including host specificity, host adaption, and global epidemiology.

M. oryzae 2539 is a laboratory strain widely used for telomere analysis, avirulence (AVR) gene cloning, identification of transposon elements, and plant immunity micro-RNA research (Kachroo et al. 1995; Starnes et al. 2012; Wang et al. 2018; Zhang et al. 2018; Zheng et al. 2011). Strain 2539 was a single spore isolated from a single lesion on rice inoculated with an ascus culture from cross CH40-1 × 4162 (Leung et al. 1988). CH40-1 is a *M. grisea* strain that is highly virulent on nine rice cultivars (Kolmer and Ellingboe 1988). Previous studies found that 736 of 765 tested rice lines could not be infected by strain 2539, suggesting strain 2539 likely carries some predominant AVR genes (Smith and Leong 1994). Additional studies also showed that *AVR1-CO39* was one of the predominant AVR genes controlling the broad avirulence of strain 2539 against rice (Zheng et al. 2011). However, the genome sequence of this strain is still not available.

In this study, the genomic DNA of strain 2539 was extracted and purified from mycelium and was sequenced with the paired-end Illumina HiSeq2500 platform. We obtained 6.796

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Table 1. Genome features of *Magnaporthe oryzae* 2539

Variables	Statistics
Mating type	Mat1-1
Sequence coverage	34x
Genome size (Mb)	38.08
Contigs (count)	1,391
Contig N ₅₀ size (bp)	107,099
Max contig size (bp)	503,659
Average contig size (bp)	27,378
GC content (%)	51.1
Number of predicted genes	12,116
Secreted proteins	1,051
BUSCO completeness (%)	98.5
Genome accession	VCMT00000000

million 100-bp reads with 500-bp insert length, which represents 34-fold genome coverage. A 38.08 Mb genome assembly was obtained with CLC genomic workbench (v12.0.1; Qiagen). This is closer to the genome size predicted with Kmergenie (38.13 Mb) and similar to the published genome sequences of *M. oryzae* strains sequenced with short-read sequencing while smaller than strains sequenced with long-read sequencing (Bao et al. 2017; Chikhi and Medvedev 2014; Gómez Luciano et al. 2019; Zhong et al. 2016, 2018). GC content of strain 2539 is 51.1%, which is also close to isolates of the *M. oryzae* species (Zhong et al. 2016). The draft genome sequence of strain 2539 includes 1,391 contigs (N₅₀ 107 Kb) and an average contig size of 27 Kb (Table 1). The completeness of strain 2539 assembly was evaluated with BUSCO (v3.0.2) with 'Ascomycota odb9' as a reference, based on a dataset of near-universal single-copy orthologous genes of 1,315 common Ascomycota genes (Waterhouse et al. 2017). This analysis indicates strain 2539 is a genome with high completeness (98.5% complete).

Protein-coding genes were predicted by conducting through a combination of evidence-based prediction by Exonerate (v2.2.0) with *M. oryzae* 70-15 genes as reference and *ab initio* prediction with Fgenesh with *Magnaporthe* as training organism (Dean et al. 2005). Our prediction identified a total of 12,116 protein-coding genes. Secreted proteins, as used in this study, refer to proteins containing a N-terminal signal peptide cleavage site (predicted with SignalP 4.0) and with no transmembrane domain after the region signal peptide cleavage site (predicted with TMHMM 2.0) (Krogh et al. 2001; Petersen et al. 2011). With this method, we identified 1,051 secreted proteins in strain 2539. Gene functions were annotated with HMMER (v 3.1) (Finn et al. 2011). Genome-wide gene comparison between strain 2539 and strain 70-15 revealed a total of 748 genes are present in the 2539 genome but may be absent in the 70-15 genome. Putative carbohydrate-active enzymes (CAZymes) were predicted using dbCAN (Yin et al. 2012). We identified a total of 738 CAZymes, including 105 auxiliary activity family proteins, 274 glycoside hydrolases, 103 glycosyltransferases, five polysaccharide lyases, 129 carbohydrate esterases, and 122 noncatalytic carbohydrate-binding modules. With GPCRHMM, we also recorded 51 G protein-coupled receptors (GPCRs) in the genome of strain 2539 compared with 56 recorded for the 70-15 genome (Wistrand et al. 2006). Additionally, we annotated AVR genes in the strain 2539 genome and found that the 2539 genome contains *Avr-Pi54*, *Avr1-CO39*, *AvrPi9*, *AvrPib*, *AvrPiz-t*, and *ACE1*, while *Avr-Pik*, *AvrPia*, *AvrPii*, *AvrPita*, *PWL1*, and *PWL2* are absent in the genome.

Assembled contigs are available at the National Center for Biotechnology Information under BioProject ID PRJNA544882, BioSample ID SAMN11866126. The genome version described in this paper is VCMT00000000. The genome annotation file and lists of secreted proteins, unique genes, CAZymes, GPCRs, and AVRs are available in Figshare (Chen et al. 2020).

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