Genome Resource of *Podosphaera xanthii*, the Host-Specific Fungal Pathogen That Causes Cucurbit Powdery Mildew

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Abstract

Approximately 33 types of commonly consumed fruits and vegetables are members of the family Cucurbitaceae, making it an important crop family worldwide. However, pathogen resistance to pesticides and fungicides has become a growing problem in cultivation practices. The identification of the effector proteins in each unique fungus–host pair would help toward the development of strategies for preventing the infection of important crops. In this study, we characterized the genome of *Podosphaera xanthii*, the fungal pathogen that causes powdery mildew disease in cucurbitaceous plants. A first-draft genome of 209.08 MB was assembled and compared with those of 25 other fungal pathogens, particularly for identifying candidate secreted effector proteins. This draft genome can serve as a valuable resource for future genomic and proteomic studies of *P. xanthii* and its host-specific pathogenesis.

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Keywords

Cucurbitaceae, Erysiphaceae, fungus–plant interactions, genome, genomics, metabolomics, pathogen, *Podosphaera xanthii*, proteomics

Genome Announcement

Powdery mildew disease (PMD) is a plant disease that is caused by members of the fungal family Erysiphaceae (Cook, 2012), of which there are currently 724 known species across 27 genera (NCBI Taxonomy Database; accessed April 2020). These obligate parasites exist mainly on the plant leaves, where they attach to the surfaces via their haustoria and in the form of conidiophores (Polonio et al. 2019b). They are airborne and highly resistant to cold and drought environments (De Miccolis Angelini et al. 2019). Since 300 BCE, PMD has been recorded as a major disease of a large number of plants (Wu et al. 2018). Although many PMD-causing pathogens have identical morphological characteristics, the measures adopted for their control (e.g., spraying of biocontrollers and fungicides) are not unique and are, in fact, mostly ineffective. A proposed alternative approach is to identify the effector proteins from each fungus–host pair, which would help toward the development of targeted biocontrollers or

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*The *e-Xtra* logo stands for “electronic extra” and indicates that a supplementary file, supplementary figures, and supplementary tables are published online.

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Table 1. Summary of genome assemblies and gene annotations

Assemblies and annotations		Statistics
Assembly		
Contigs		1,112
Total bases		209,067,775
Average length		188,010.59
Minimum length		19,987
Maximum length		2,325,138
N ₅₀		581,650
N (%)		0.00
GC (%)		44.25
Gene		
Genes		12,834
Average gene length		2,418.79
Average exon length		425.23
Repeat elements		132,699,478 (63.41%)
Gene coverage		14.83%
BUSCO		98.3%; C:745 [S:367, D:378], F:0, M:13, n:758
Annotations		
Blast-hits		10,461 (81.51%)
Kyoto Encyclopedia of Genes and Genomes (KEGG)		7,375 (57.46%)
Gene Ontology (GO)		8,529 (66.46%)
No-hits		2,373 (18.49%)
Candidate secrete effector proteins (CSEP)		455
Secreted proteins (SP)		690
Nonclassical secreted proteins (NCSP)		169
Cytochrome (CYP)		37
Carbohydrate-active enzymes (CAZY)		519

fungicides (Martínez-Cruz et al. 2018; Polonio et al. 2019a). To accelerate this approach, elucidation of the pathogenesis of PMD at the molecular level would be the primary goal, of which the minimum requirement is the reference genomes of both the hosts and the pathogens. Although the genomes of a few PMD-causing fungi have been sequenced and used to aid the identification and annotation of some candidate secreted effector proteins (CSEPs) through functional assays (Martínez-Cruz et al. 2018), most of the pathogens that cause this disease have not been genomically characterized (Bindschedler et al. 2016). In this study, we sequenced the genome of *Podosphaera xanthii*, a highly infectious PMD-causing pathogen. Several studies have generated genetic resources for this fungal species before, such as features of the transcriptome from epiphytic fungal material (Vela-Corcía et al. 2016), the haustorium (Polonio et al. 2019b), the progenies of sexual mating (De Miccolis Angelini et al. 2019), the genetic diversity among *P. xanthii* races assessed by genotype-based sequencing (Hong et al. 2018; Xiang et al. 2020), and the mitochondrial genome (Kim et al. 2019). However, most of these studies gained partial knowledge only owing to the lack of a full reference genome. To the best of our knowledge, the genome assembled in this study has better contiguity N₅₀ score compared with the first available draft genome of *P. xanthii* (Polonio et al. in press).

Preliminary Genome Report

Our dataset includes both long- and short-read sequences from the DNA and mRNA molecules of *P. xanthii* (Supplementary Table S1). The detailed methods used to assemble and annotate the genome are presented as a workflow in Supplementary Figure S1. To ensure that the sequenced molecules were from *P. xanthii*, three contamination checks were conducted: host contamination (*Cucumis sativus*), bacterial contaminations, and other fungal cocontaminations. The genome of *P. xanthii* was estimated to be 253.13 MB in size, as determined with the *k*-mer major peak method using the contamination- and mitochondria-free short reads (Supplementary Fig. S2A). Of the assembled genome, 209.07 MB was obtained from error-corrected long-read sequences (38.9 GB) using the haplotype-aware assembler FALCON-Unzip v0.30 (Table 1). The assembled contigs were checked for contamination using the candidate selected from the short-read contamination removal process (Supplementary Table S2 and S3). In this assembly, 133 MB (63.41%) of the full

genome was predicted to be repeats, most of which were long terminal repeats. The genome carried 12,834 genes in total, according to the predictions of three modules: an evidence-based gene modeler (EvidenceModeler), an ab initio gene modeler, and a consensus gene modeler (Table 1). Among those genes, 10,461 (81.51%) were homologous with genes of other genomes in the GenBank NR nucleotide database (Table 1). The assembled genome was assessed for two different quality metrics: N₅₀ (5.8 MB) for contiguity and BUSCO (98.3% for the Fungi dataset) for gene completeness (Supplementary Fig. S3 for other BUSCO datasets). Finally, genomes were assessed for identity with the internal transcribed spacer (ITS) from the assembled genome, because the in vitro culture of *P. xanthii* is difficult without the host (Martínez-Cruz et al. 2018). The complete ITS fragments present in the genome (Supplementary Table S4) were identical to MT242593.1, a GenBank reference of the *P. xanthii* ribosomal RNA gene. Additionally, the BLAST score (E-value = 0.0) also confirmed the genome identity as *P. xanthii*. Finally, the *P. xanthii* proteome was compared with those of 25 other fungal pathogens that cause various diseases in different crops (Supplementary Table S5). This comparative genome analysis provided an overview of the CSEPs and other multifamily proteins (e.g., cytochromes and carbohydrate-active enzymes) in this fungus through the perspective of gene gain-of-function and loss-of-function analyses (Table 1; Supplementary Fig. S2C), along with its evolutionary relationships. Furthermore, the genome size and proteome revealed that the *P. xanthii* genome is the second largest of the PMD-causative pathogens (Supplementary Fig. S2B). In addition, the transcriptome libraries from this study and entries in the Sequence Read Archive (SRA) database were mapped to this draft genome (Supplementary Table S6).

Dataset Information to the User

The complete sequences generated in this study were deposited in the SRA repository under the accession PRJNA590048. The assembled contigs and the annotation files (coding sequences, gff, repeats, and proteins) are available in the figshare repository with all the annotations details in the Readme file. The contig assembly of this draft genome was submitted to the NCBI-Assembly under the accession JAAAXZ000000000. The materials and methods are given in Supplementary File S1.

Author-Recommended Internet Resources

Figshare repository: https://figshare.com/articles/dataset/P_xanthii_genome_project/12292841

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