Genome Sequence Resource for the Oomycete Taro Pathogen *Phytophthora colocasiae*

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Abstract

Phytophthora colocasiae is a phytopathogenic oomycete that causes leaf blight and corm rot on taro (*Colocasia esculenta*), an important staple crop in the tropics. The impact of *P. colocasiae* is a serious concern for food security in Asian and Oceanic regions. Vietnamese strain 7290 of *P. colocasiae* was sequenced (Illumina) to assemble a draft genome of 56.6 Mb, comprised of 19,853 scaffolds and 19,984 predicted protein-coding genes. As in other *Phytophthora* species, *P. colocasiae* possesses numerous pathogenicity-related genes, such as the RxLR class of effectors. This draft genome sequence of *P. colocasiae* provides a resource to underpin the first steps in determining the molecular mechanisms of disease development in this pathosystem.

Genome Announcement

The impact of taro leaf blight and corm root rot (caused by the oomycete *Phytophthora colocasiae*) is a major food security concern in the tropics (Lamour 2013). Taro (*Colocasia esculenta*), the fifth most important root crop in the world, is a major staple food in Oceanic, Southern Asian, and African cultures. As well as corms, the leaves are an important dietary supplement in these tropical regions, and the pathogen is able to significantly damage both corms and leaves. Severe infection can lead to up to 50% loss of the crop (Singh et al. 2012) and cause a dramatic calorific decrease in the diets of the populations that rely on taro as their primary source of nutrition (Lamour 2013). As taro is cultivated over a 6- to 13-month crop cycle under tropical environmental conditions, there is a continuous supply of host plants for *P. colocasiae*, leading to a constant disease threat (Lamour 2013). *P. colocasiae* is a heterothallic species related to the broad host-range vegetable pathogen *Phytophthora capsici* (Lamour et al. 2012) in clade 2 of the *Phytophthora* genus (Yang et al. 2017). Despite the importance of taro and the destructive nature of this disease, *P. colocasiae* has been little studied to date and little is known of the molecular and genetic mechanisms governing disease development.

P. colocasiae 7290 was isolated from a diseased taro plant in Phú Lương, Vietnam in 2010. Culturing conditions and DNA extraction were as described (Löbmann et al. 2016). Libraries of 180- and 680-bp fragments (total of 143.58 M reads, 150-bp pair-end reads) were paired-end sequenced using the Illumina HiSeq2000 sequencing platform at SciLifeLab, Alnarp, Sweden. FastQC Trimmomatic tools were used for raw data assessment (Bolger et al.

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Table 1. Core metrics of *Phytophthora colocasiae* genome

Contents ^a	Numbers
Sequenced reads	143,580,000
Genome size	56.6 Mb
Scaffolds	19,853
N50	11,257 bp
L50	1,234 bp
Longest contig	136,767
Contigs >25 Kb	353
BUSCOs	70.86% (816 complete and 203 fragmented)
Number of predicted genes	19,984
Number of identified domains	11,200
Number of CAZy enzymes	382
RxLR	337
Crinklers	203

^a BUSCOs = benchmark universal single-copy orthologs, CAZy = carbohydrate active.

2014). SPAdes 3.5.0, a de-Bruijn graph-based assembler, was used for de novo genome assembly (Bankevich et al. 2012). A total of 56.6 Mb was assembled into 19,853 scaffolds (mean coverage, 380×), which is similar to the genome assembly sizes of other clade 2 *Phytophthora* species, e.g., *P. capsici* (64 Mb) and *P. multivora* (40 Mb) (Lamour et al. 2012; McGowan and Fitzpatrick 2017; Studholme et al. 2016). QUAST was used to assess assembly quality of contigs greater than 300 bp (N50: 11,257 bp; N75: 3,168 bp; L50: 1,234; L75: 3,564; longest contig: 136,767 bp; number of contigs >25 kb: 353; number of contigs >50 kb: 55) (Gurevich et al. 2013). Previous work had suggested that this sequenced *P. colocasiae* strain was triploid (Shrestha et al. 2014, 2017), and this likely influenced the sequence assembly process. The draft genome of *P. colocasiae* was evaluated by BUSCO for completeness, based on a set of 1,438 common fungal genes as benchmark universal single-copy orthologs (BUSCOs) (Simão et al. 2015). A total of 816 complete genes and 203 fragmented and 419 missing BUSCOs were found in the draft assembled-genome sequence for this strain. The gene predictor AUGUSTUS predicted 19,984 genes, using the previously sequenced plant pathogenic relative *P. capsici* as a training model. Primary annotation of the *P. colocasiae* genome predicted 11,200 sequences having PFAM domains. The genomes of filamentous plant pathogens encode many proteins potentially associated with a role in pathogenicity (Lu et al. 2012; McGowan and Fitzpatrick 2017). The predicted proteome of *P. colocasiae* encodes 382 predicted carbohydrate active enzymes, similar to that found in other sequenced *Phytophthora* species (Ospina-Giraldo et al. 2010). Using prediction methods used previously for *P. infestans* (Haas et al. 2009), 337 RxLR and 203 Crinkler candidate effector proteins were predicted from the *P. colocasiae* genome assembly.

The genome sequence of *P. colocasiae* presented here represents a first step toward understanding pathogenicity determinants in this pathogen and to design specific management strategies to control the disease. The genome sequence has been deposited at DDBJ/ENA/GenBank under the accession NSDL00000000. The version described in this paper is version NSDL01000000 (Table 1).

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