High-Quality Genome Sequence Resource of the Taro Pathogen *Phytophthora colocasiae*

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Phytophthora colocasiae is an oomycete phytopathogen causing leaf blight and corm rot on taro (*Colocasia esculenta*), and its damage is a serious problem worldwide. Although the disease had not been reported in Japan for approximately 100 years, it began to spread in 2015.

Taro (*C. esculenta*) is a staple crop grown in the humid tropics of Asia, Africa, the Pacific, and the Caribbean (Kreike et al. 2004). In these regions, leaf blight and corm rot caused by *P. colocasiae* are the most limiting factor in taro production (Singh et al. 2012). *P. colocasiae* was first reported in Java by Raciborski (1900), moved from Java to Taiwan (Butler and Kulkarni 1913), and was thought to have spread to Japan and Hawaii in 1920 (Trujillo 1967). Even though Japan had been free of the epidemic for nearly 100 years afterward, severe damage caused by *P. colocasiae* was confirmed in 2015, and the disease has continued to spread throughout the country, reducing yields by approximately 20% (Anonymous 2020). The cause of the current epidemic is not known. To understand what pathways caused the spread of the disease and whether the diversification of the pathogenicity is occurring, it is essential to collect genomic information on *P. colocasiae* in various regions. The genome of *P. colocasiae* 7290 from Vietnam was first sequenced by Vetukuri et al. (2018) using Illumina HiSeq2000. The short-read assemblies were fragmented and do not provide long-range haplotype and gene information. In this study, we report the genome of a new strain, EPC201509, isolated in Ehime Prefecture, Japan in 2015, sequenced using PacBio Sequel. The genomic DNA was extracted from mycelia cultured in liquid potato dextrose agar using the NucleoBond HMW DNA kit (Macherey-Nagel, Düren, Germany). The DNA concentration was measured using Nanodrop and Qubit (Thermo Fisher Scientific, Waltham, MA, U.S.A.).

The genomic DNA was sequenced by the long-read sequencer PacBio sequel. A DNA library was constructed with SMRTbell Express Template Prep Kit v 2.0 according to the manufacturer's protocol (Pacific Biosciences, Menlo Park, CA, U.S.A.) and was cut off at 20 kbp using the Blue Pippin size selection system (Sage Science, Beverly, MA, U.S.A.). A total of 11.5 Gbp was generated on a cell and assembled using SMRTLink v 8.0 (Pacific Biosciences) with minimum mapped length 1,000 bp. Finally, 428 contigs were generated with 143 Mbp of the estimated genome size and 51 kbp of N₅₀ contig length (Table 1). The possibility that strain EPC201509, like strain 7290, is triploid has not yet been investigated

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Table 1. Assembly results of EPC201509

Parameters ^a	Numbers
Total length (bp)	143,214,017
Number of the total contigs	428
N ₅₀ contig (bp)	509,258
Largest contig (bp)	2,045,440
GC contents (%)	50.9
BUSCOs (eukaryota_odb10)	94.9%, with 484 complete, 2 fragmented, and 11 missing
BUSCOs (stramenopiles_odb10)	100%, with 100 complete
Total interspersed repeats (bp)	71,765,842
Intact LTR-RTs (bp)	17,399,166
Number of intact LTR-RT elements	2,146 (1,508 is gypsy and 463 copia-like elements)
Number of predicted genes	29,886
RXLR genes	289
Crinkler genes	416
NPP1 genes	105
Elicitin genes	74

^a BUSCO = benchmarking universal single-copy orthologs and LTR-RTs = long-terminal repeat retrotransposons.

(Shrestha et al. 2017), and highly accurate long-read sequencing analysis would be required to determine whether this may have influenced the assembly. The draft genome of strain EPC201509 was evaluated by benchmarking universal single-copy orthologs (BUSCO v4) (Seppey et al. 2019) and showed 100% completeness using stramenopiles_odb10. Because of the diversity in repetitive DNA content among *Phytophthora* spp. (Judelson 2012), the repeated sequences were searched using RepeatModeler v 2.0.1 (Flynn et al. 2020) and long-terminal repeat (LTR) retriever v2.9.0 (Ou and Jiang 2018). Finally, we detected 72 Mbp of total interspersed repeats and 17 Mbp of intact LTR retrotransposons (LTR-RTs) on the genome. The gene prediction was done using AUGUSTUS with the coding sequence data-sets of *P. capsici* strain LT1534-B (GCA_016618375.1_Pcap_4.1_cds_from_genomic.fna), which belongs to the same clade 2 as *P. colocasiae* (Yang et al. 2017), as a training model (Hoff and Stanke 2013), resulting in 29,886 predicted genes with untranslated regions. The prediction of proteins involved in the pathogenicity using HMMER v3.3.2 with the corresponding profile HMMs resulted in 289 RXLR, 416 Crinkler, 105 NPP1, and 74 elicitin candidates (Table 1). Recently, the genome sequencing of a Chinese strain of *P. colocasiae* was reported using Oxford Nanopore Technologies PromethION (Wang et al. 2021).

This high-quality genome sequence resource will provide fundamental information for investigations of geographic origins, transmission routes, and virulence diversity. Further sequencing and comparative analysis of the genomes of strains from a variety of different regions will shed light on geographic origins, transmission routes, and virulence diversity. This Whole-Genome Shotgun project has been deposited at GenBank under the accession JAHQCX000000000. The version described in this article is version JAHQCX010000000.

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