Genome Sequence Data of Six Isolates of *Phytophthora capsici* from Mexico

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Keywords

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Abstract

Phytophthora capsici is an oomycete plant pathogen with a wide host range. Worldwide, *P. capsici* is known for causing the principal disease of chili pepper crops. Our goal was to expand the available genome resources for this diverse pathogen by generating whole-genome sequences for six isolates of *P. capsici* from Mexico.

Genome Announcement

Phytophthora capsici is an important oomycete plant pathogen on vegetable crops. It is the causal agent of the principal disease of *Capsicum annuum* worldwide, and can infect many other economically important vegetables in the Solanaceae and Cucurbitaceae families (Reis et al. 2018). Disease can be on all portions of the host plants, including root rot, stem necrosis, foliar blight, and fruit rot (Candole et al. 2012). The main virulence factors of this pathogen are secreted RXLR and Crinkler (CRN) effector proteins that counteract the plant defense response and facilitate infection (Kong et al. 2017; Stam et al. 2013). *P. capsici* has shown great adaptability to fungicides and new hosts. Analysis of the reference genome suggested that the loss of heterozygosity could be involved in fixing alleles and facilitating adaptation to its environment (Lamour et al. 2012). To expand upon the available sequenced genomes, we assembled six genomes of isolates of *P. capsici* from four hosts in Michoacan, Mexico. These isolates are from hosts that are not represented in previous studies of *P. capsici* (Hu et al. 2018).

P. capsici isolates were obtained from *Cucurbita pepo* (CPV-262 and CPV-267, from the same field), *Capsicum annuum* (CPV-270 and CPV-277), *C. chinense* (CPV-302), and *C. pubescens* (CPV-219) in Michoacan, Mexico. The isolates were cultivated in V8 agar. Genomic DNA was extracted following the method described by Saghai-Marooof et al. (1984). For sequencing, 2× 150-bp paired-end PCR-free Illumina libraries with an average insert size of 250 bp were constructed using the KAPA hyperprep kit according to the manufacturer's directions. Sequencing was performed on a HiSeq X device at Admera Health according to current Illumina protocols. The sequences obtained had the following

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Table 1. General metrics of the genome assemblies of *Phytophthora capsici*

Isolate	Total length (Mb)	Number of contigs	N50	L50	Total predicted proteins	RXLR content	CRN content	NPP1
CPV-219	58.88	7,580	14,052	1,184	25,102	379	230	83
CPV-262	40.77	11,754	4,558	2,492	19,275	263	121	64
CPV-267	52.19	11,832	6,599	2,287	23,579	341	183	79
CPV-270	58.29	8,363	11,645	1,422	25,004	371	213	75
CPV-277	53.43	9,341	9,423	1,599	23,404	350	181	82
CPV-302	56.90	9,277	9,970	1,652	24,322	353	187	85

read depth per genome: CPV-219 = 111×, CPV-262 = 62×, CPV-267 = 74×, CPV-270 = 80×, CPV-277 = 77×, and CPV-302 = 98×. The raw sequences were quality filtered and adapter trimmed with Trim-Galore (Babraham Bioinformatics). Platanus-allee version 2.0.1 was used for the de novo genome assembly (Kajitani et al. 2014). To remove alternative heterozygous contigs and to obtain less fragmented assemblies, the Redundans pipeline was applied to each genome (Pryszcz and Gabaldón 2016). Contigs shorter than 1 kb were filtered out of the final assembly. General statistics of the genome assemblies were assessed with QUAST (Gurevich et al. 2013). The GC content ranged between 49.85 and 49.96% among genomes. The genome sizes, number of contigs assembled, and N50 and L50 values are shown in Table 1.

GeneMark-ES was used for the *ab initio* prediction of genes and to obtain protein sequences (Lomsadze et al. 2005). The assembly completeness was calculated with BUSCO v3 (Simão et al. 2015), based on the alveolata_stramenophiles_ensembl data set. The BUSCO analysis produced the following percentage of complete or partially complete gene groups: CPV-219 = 91.5%, CPV-262 = 72.6%, CPV-267 = 82.9%, CPV-270 = 89.8%, CPV-277 = 91.0%, and CPV-302 = 93.2%.

A core of 11,248 orthologs from the seven genomes was obtained using OrthoMCL (Li et al. 2003). Two phylogenetic trees were obtained using 6,555 single-copy orthologous genes from our six genomes and the reference genome using MRBAYES with the evolution model GTR + G (Huelsenbeck and Ronquist 2001) and PhyML (maximum likelihood) (Guindon et al. 2010). Both trees showed an identical topology and indications of different relationships across core genes based on posterior probability and bootstrap support values. The majority of core genes did not cluster isolates by host or collection location.

Protein predictions were annotated by comparing our sequences against the Pfam database 32.0 (El-Gebali et al. 2019). Among the predicted proteins, we found an average of 78 genes belonging to an NPP1 *Phytophthora* toxins family. The total number of predicted proteins by genome were in the range of 19,275 to 25,102. We retrieved high-quality RXLR and CRN protein sequences from the GenBank to create a protein model for each effector family. Protein models were created with hmm-build tool from HMMER v3.2.1. The proteome of each sequenced strain was scanned with the protein effector models, using hmm-search from HMMER v3.2.1. We found an average of 345.8 RXLR and 185.8 CRN proteins, of which 1,756 RXLR and 430 CRN are not in the reference genome. The effector sequences were deposited in the Database of Virulence Factors in Fungal Pathogens from the University of Nebraska-Lincoln (Lu et al. 2012). These data may reveal conserved and host-specific RXLR and CRN effectors, for which one could determine specific functions and mechanisms of action during the development of the disease in plants.

Data availability. This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accessions numbers RQEI00000000 (CPV-302), RQEI00000000 (CPV-277), RQEK00000000 (CPV-270), RQEL00000000 (CPV-267), RQEM00000000 (CPV-262), and RQEN00000000 (CPV-219). The versions described in this article are the first versions. The reads for all isolates were deposited at NCBI/SRA under the accession number PRJNA505815.

Author-Recommended Internet Resources

alveolata_stramenophiles_ensembl data set: <https://busco.ezlab.org/>
HMMER v3.2.1: <http://hmmer.org/>

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