Draft Genome Resource of *Fusarium oxysporum* f. sp. *capsici*, the Infectious Agent of Pepper *Fusarium* Wilt

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Abstract

Fusarium oxysporum f. sp. *capsici* is the specific pathogen of pepper *Fusarium* wilt and causes a significant reduction in pepper yield. Its narrow host specificity has led to the concept of formae speciales. This interesting phenomenon has great potential and needs to be analyzed at the molecular level. In this study, we obtained the draft genome sequence of *F. oxysporum* f. sp. *capsici*, using the Oxford Nanopore sequencing technology. The long read-based assembly consisted of 34 contigs, with a total length of 54,516,562 bp. The contig N₅₀ was 4,962,668 bp and the GC content was 47.6%. Our genome assembly of *F. oxysporum* f. sp. *capsici* provides a valuable resource for the study of pepper *Fusarium* wilt, and the comparative genomic study of *F. oxysporum*.

Genome Announcement

Fusarium oxysporum is a filamentous fungus that is a soilborne pathogen of plants and an opportunistic pathogen of humans. Moreover, *F. oxysporum* is considered to be a complex species with a broad host range, and its host specificity can be used for classification into various formae speciales (ff. spp.) (Ma et al. 2013). *Fusarium oxysporum* f. sp. *capsici* infects pepper plants and causes wilting, which results in heavy production losses in China.

Many *F. oxysporum* genomes have been sequenced, with most of them sequenced using the short reads of Illumina sequencing technology, resulting in a highly fragmented genome assembly (Wang et al. 2020; Ye et al. 2011). Highly fragmented genomes are not conducive to structural resolution. The third-generation platform from Oxford Nanopore Technologies (ONT) is able to generate ultra-long read lengths. Several hundred kilobases can be reached, resulting in more contiguous genomes being acquired and facilitating the analysis of genome structural variants (De Maio et al. 2019; Jain et al. 2018).

In June 2014, the *F. oxysporum* f. sp. *capsici* strain was isolated from a susceptible pepper—HaiJiao 4—in Putian City, Fujian Province, China. The pathogen was identified morphologically and through an internal transcribed sequencing analysis. The pathogenicity was confirmed by Koch's postulates. In this study, we extracted high-molecular weight genomic DNA of *F. oxysporum* f. sp. *capsici* from a pure culture, using a Qiagen genomic DNA

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Keywords

Fusarium oxysporum f. sp. *capsici*, *Fusarium* wilt, genome, pepper

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*The e-Xtra logo stands for “electronic extra” and indicates there is supplementary material published online.

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Table 1. Assembly statistics of the *Fusarium oxysporum* f. sp. *capsici*

Feature	Statistics
Genome [bp]	54,516,562
Read length N ₅₀	15,656
Mean read length[bp]	11,037.4
Maximum read length	143634
Number of contigs	34
Largest contigs [bp]	7,838,233
Contig N ₅₀ [bp]	4,962,668
GC	47.6%
Assemble completeness (FGMP)	93.5%
National Center for Biotechnology Information accession	JABCS000000000

extraction kit. The sequencing library was prepared using a ligation sequencing kit in accordance with the ONT standard protocol. For sequencing, flow cells version and pore version R10.3 were used on the PromethION device.

According to the data, we obtained 1,058,257 reads, which is about 11.68 Gb bases (approximately 200× genome coverage). Overall, the mean read length was 11,037.4 bp and the read length N₅₀ value was 15,656 bp. We assembled the genome using Canu version 1.6 (Koren et al. 2017) and polished the initial assembly based on Nanopore reads using Racon version 1.4.3, with the default parameters (Vaser et al. 2017) (Table 1). All 35 contigs were compared with the mitochondrial genome MF155191.1 (Zeng et al. 2017), and only tig00000113 had a high similarity with mitochondrial sequences. Based on gene models from *Fusarium graminearum*, we predicted repeat sequences and protein-encoding genes from the final assembly, using RepeatMasker version 4.0.7, based on the Repbase fungi data set (Chen 2004), and AUGUSTUS version 2.7 (Stanke et al. 2004), respectively. Using AUGUSTUS, the predicted number of protein-encoding genes was 16,618. The total size of the interspersed repeats was 1,875,337 bp, accounting for 3.44% of the *F. oxysporum* f. sp. *capsici* genome. Furthermore, we used FGMP version 1.0.2 (Cissé and Stajich 2019) to evaluate the assembly quality and found 93.5% completeness.

The *F. oxysporum* species complex has received substantial attention from scientists for more than a century because of its economic losses and wide host range. The narrow host specificity of pathogenic strains has led to the concept of formae speciales. This interesting phenomenon has great potential and needs to be analyzed at the molecular genetics level. Various forms of draft genome resources have a wide range of potential uses. The draft genome resource presented in this study is the first reported genome of *F. oxysporum* f. sp. *capsici* and will provide a fundamental resource for the investigation of the pathogenic mechanism of this strain. In addition, it will also be useful for the study of the comparative genome of *F. oxysporum*. This Whole Genome Shotgun project has been deposited at DDBJ/ENA/GenBank under the accession JABCS000000000. The version described in this paper is version JABCS000000000.

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