Genome sequencing of differently pathogenic Fusarium oxysporum f. sp. lini strains

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Fusarium oxysporum f. sp. *lini* causes flax wilt which is one of the most devastating diseases of flax grown for the production of numerous consumer and industrial goods. At the same time, *Fusarium oxysporum* demonstrates considerable diversity. For instance, representatives of the species may vary in the number of chromosomes and the presence and homology of the *SIX* genes associated with virulence, whereas strains can be hardly classified by morphology and differ in severity of caused wilt symptoms within the same forma specialis. Consequently, whole-genome sequencing is needed to establish the differences between genome structures of the flax pathogen. This work aimed at sequencing the genomes of 5 strains of *F. oxysporum* f. sp. *lini* of high (strain #483), medium (#476, #525), and low (#456, #482) virulence. The DNA was extracted according to the developed protocol and sequenced on the Oxford Nanopore Technologies and Illumina platforms (300+300 bp), and the collected Nanopore data were used to assemble draft genomes of the strains. In addition, we reassembled the genome of the highly pathogenic isolate #39 using our previously obtained data. Illumina reads of the sequenced strains were mapped against the resulting assemblies and the genome of the endophyte Fo47 (GenBank, GCA_013085055.1). Nearly 99% of the isolate #39 genome were covered by its Illumina reads, whereas the Illumina reads of other strains mapped against a larger fraction of the isolate #39 assembly in comparison with the Fo47 genome, but the percentages were similar for all but strain #482. The received data will be useful for further investigation of *F. oxysporum* virulence mechanisms and the structure of its population for the development of methods to prevent the disease and economic losses. This work was funded by RFBR according to the research project 19-34-90055.

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