

Expression of *Fusarium oxysporum* genes upon infection of *Linum usitatissimum* plants

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Motivation and Aim: *Fusarium oxysporum* sp. *lini*, which leads to fusarium wilt, is one of the most harmful flax (*Linum usitatissimum* L.) pathogens. Flax cultivars are varied in their resistance to fusarium wilt [1]. Specific expression alterations were revealed for a number of genes in resistant flax genotypes compared to susceptible ones under inoculation of *F. oxysporum* [2]. However, the question of whether there is any difference in expression of the fungus genes, when the pathogen infects genotypes with diverse resistance, remains open. In the present study, we performed such investigation.

Methods and Algorithms: Seedlings of resistant (Dakota and #3896) and susceptible (AP5 and TOST) to *F. oxysporum* flax cultivars were inoculated with the pathogen isolate #39 from the collection of the All-Russian Research Institute for Flax. RNA was isolated from plant roots in duplicate for each variety. TruSeq Stranded Total RNA Sample Prep Kit (Illumina) was used for cDNA library preparation and high-throughput sequencing on NextSeq500 sequencer (Illumina) using 80-nucleotide pair-end reads was performed. The number of reads for each *F. oxysporum* transcript was assessed, and expression analysis was performed using the edgeR.

Results: Eight cDNA libraries, which were obtained from roots of inoculated with *F. oxysporum* flax cultivars with diverse resistance, were sequenced, and about 25 million pair-end reads were obtained for each cultivar. About 30–40 % of reads were mapped on genome of *F. oxysporum*. The similarity of gene expression profiles was higher within groups of varieties with similar resistance to the pathogen. *F. oxysporum* genes with the greatest differences in expression level upon inoculation of resistant and susceptible flax genotypes were identified.

Conclusion: The study of *F. oxysporum* expression changes when the fungus infects flax genotypes with diverse resistance is important for understanding of plant-pathogen interactions. Data on genes with distinct expression when pathogen infects resistant and susceptible cultivars bring new insights into mechanisms of fungal infection.

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References

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