

Identification of targets genes for miRNAs of the pathogenic fungus *Fusarium oxysporum* in a *de novo* transcriptome assembly of the Siberian larch (*Larix sibirica* Ledeb.)

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Motivation and Aim: MicroRNAs (miRNAs) play important regulatory roles in animals and plants and can regulate metabolic pathways related to ontogenesis, cell differentiation and response to environmental factors, such as stress [1]. In addition, there is evidence that miRNAs play a particular role in cross-species communication due to miRNA transmission [2]. We studied whether miRNAs of a pathogenic fungus *Fusarium oxysporum* could potentially regulate host's (Siberian larch) biotic stress response pathways through targets genes in the host genome.

Methods and Algorithms: We used the Siberian larch (*Larix sibirica*) transcriptome that was originally *de novo* sequenced and assembled in the Laboratory of Forest Genomics at Siberian Federal University. The sequence data of *L. sibirica* was obtained using the Illumina HiSeq 2000 sequencer. *De novo* assembly was done using the Trinity assembler. To predict potential targets in the Siberian larch transcriptome for previously published miRNAs of *F. oxysporum* a specially developed plant small RNA target analysis server (psRNATarget) was used [3, 4].

Results: 576 target sequences were detected in total transcriptome of Siberian larch. Annotation of the targets showed that the most matches are associated with leucine-rich and pentatricopeptide repeat domains. Targets with glutathione S-transferase, RNA-recognition and ribonuclease H activities were also found.

Conclusion: Based on our own and published data we suggest that the detected targets can be involved in complex plant defense responses to pathogens. Thereby, miRNAs produced by fungi can weaken the defense mechanisms of the host tree. These results may be also of particular interest in further fungi pathogenicity studies.

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