

Transcriptomic changes in potato after inoculation with Potato spindle tuber viroid propagated in tomato plants

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Motivation and Aim: Potato (*Solanum tuberosum* L.) is one of the most important crops worldwide. A number of pathogens can negatively affect its yield. Among such pathogens is potato spindle tuber viroid (PSTVd), a member of Pospiviroid genus. Tomato strains of PSTVd are highly pathogenic to potato cultivars [1]. However, after three cycles of propagation in tomato, PSTVd causes only mild symptoms in potato.

Methods and Algorithms: Transcriptome of potato leaves at three time points (prior to inoculation, 14 dpi and 30 dpi) was sequenced using Illumina NextSeq 550 platform. RNA-seq analysis was performed, with reads being mapped to the *S. tuberosum* reference genome with Dart software, and differential expression assessed with EdgeR package for R language. Gene Ontology and pathway involvement analysis of differentially expressed genes was undertaken.

Results: RNA-seq analysis allowed to observe significant changes of gene expression at 14 dpi and 30 dpi. Genes with decreased expression at 30 dpi are associated with DNA replication, regulation of cell cycle and cell wall-associated and microtubule-based processes, indicating suppression of growth and cell division. Additionally, decrease in general metabolism and metabolism-related functions was observed.

Conclusion: Amount of genes with significant differential expression between 0 dpi and 30 dpi points to a considerable transcriptomic and metabolomic reprogramming of potato plants in response to PSTVd inoculation. Potato plants demonstrated general response to abiotic stresses and initiation of dormancy and transient growth delay [2].

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