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Identifying parasite resistance genes in *Solanum tuberosum* by RNA-seq

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Motivation and Aim: Enhancing resistance of cultivated plants, namely potato *Solanum tuberosum*, to parasitic organisms is an important but complicated task. It was revealed that nucleotide-binding site-leucine-rich repeat (NBS-LRR) genes compose the largest pathogen resistance gene family [1]. This genes family includes genes potentially responsible for resistance to golden potato cyst nematode (GPCN) *Globodera rostochiensis*. GPCN is one of the most economically important potato pathogens [2]. Thus, discovery of genes controlling potato resistance to GPCN is an important task. To achieve this goal, we performed RNA-seq analysis of two potato cultivars varying in their GPCN resistance.

Methods and Algorithms: *S. tuberosum* plants of genotype i-0144786, susceptible to GPCN, and genotype i-0144787, resistant to GPCN, were inoculated with GPCN cysts or treated with water as control group, and total RNA was extracted from plant roots on different time stages. Libraries of paired-end short reads were sequenced using Illumina HiSeq 2500 system. Libraries were filtered from low-quality, low-length reads, singletons, ambiguous reads, and adapter sequences were removed. Libraries were mapped to the reference *S. tuberosum* genome, and search for differential expression was performed. In addition, *de novo* transcriptome reconstruction was carried out, and, after excluding lowly-presented transcripts, search for differentially expressed transcripts was conducted. Additionally, transcripts were functionally annotated. To achieve this, domain structures were predicted in assembled contigs. Verification of differential expression through qRT-PCR was performed for a selected list of genes.

Results: A number of differentially expressed transcripts were detected both with library mapping analysis and transcriptome *de novo* assembly. Based on motif homology, NBS-LRR genes were predicted, including a number of *de novo* assembled transcripts presented in i-0144787 resistant genotype but not in i-0144786 susceptible genotype.

Conclusion: In this study we revealed several NBS-LRR genes associated with GPCN resistance

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References

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