

Plant immunity genes of *Solanum tuberosum* L. cultivars associated with resistance to potato late blight

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Motivation and Aim: Tuber potato *Solanum tuberosum* L. is one of the most important agricultural crops in the world. Its yield can be affected by various factors, including pathogens and parasites. One of the most dangerous pathogens of *S. tuberosum* is *Phytophthora infestans* (Mont.), an oomycete that causes late blight in potato and tomato. Mechanisms of plant immunity involve proteins of the family of Nucleotide-Binding Site – Leucine Rich Repeat (NBS-LRR, NLR for short). Family of genes encoding NLR proteins is believed to be one of the largest gene families in plants, with more than 700 NLR-coding genes identified in *S. tuberosum* genome [1]. Once NLR protein-coding genes associated with resistance to a specific pathogen are identified, marker-assisted selection can be used to create new crop varieties bearing resistance genes.

Methods and Algorithms: Three Russian potato cultivars – Sudarynya, Siverskij and Evraziya, – cultivar Bintje originating in Netherlands, and wild potato relative *Solanum stoloniferum* L. were used in present study. Studied cultivars were examined for their resistance to late blight infection.

Samples of leaves before inoculation and 24 hours after inoculation with *P. infestans* were taken. RNA-seq analysis using Illumina Nextseq 550 platform was performed in order to study transcriptomic changes of *Solanum* samples. Potato transcriptomes were reconstructed *de novo*, and NLR-encoding transcripts were identified in the transcriptomes of potato cultivars. *De novo* reconstructed transcriptomes were aligned to the reference potato genome, and transcripts that did not align were considered novel transcripts, specific for potato cultivars, or otherwise not observed in potato genome previously. Thus, NLR-encoding potato transcripts and novel NLR-encoding potato transcripts were identified. Finally, transcripts expression levels were estimated, and differentially expressed NLR-encoding transcripts were identified.

Results: Sudarynya, Siverskij cultivars are shown to be resistant to late blight, while Evraziya and Bintje are susceptible; *S. stoloniferum* is highly resistant to late blight. Five individual *Solanum* transcriptomes contain from 334 to 504 full-length NLR-encoding transcripts. Furthermore, from 103 to 133 novel NLR-encoding transcripts are present in in *S. tuberosum* transcriptomes, and 160 such transcripts are present in *S. stoloniferum* transcriptome. These transcripts are not present in *S. tuberosum* genome.

Sequences of *R3b* and *Rpi-blb1* genes, known for association with resistance to late blight, are present in transcriptomes of Siversky and Sudarynya cultivars; sequence of *R3b* gene is also present in transcriptome of Evraziya cultivar. Expression of gene *Rpi-blb1* is induced in presence of *P. infestans*.

Conclusion: Novel transcripts observed in *Solanum* genotypes resistant to late blight represent a valuable resource for selection. These sequences can be used to create new potato cultivars highly resistant to *P. infestans* attack, using technologies such as marker-assisted selection. Regulation of NLR genes expression sheds light on mechanisms of plant immunity and reaction to pathogens as well as evolution of plant immunity genes and host-pathogen coevolution.

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References

1. Jupe F. et al. Resistance gene enrichment sequencing (RenSeq) enables reannotation of the NB-LRR gene family from sequenced plant genomes and rapid mapping of resistance loci in segregating populations. *Plant J.* 2013;76:530-544. doi: 10.1111/tpj.12307.
2. Kochetov A. V. et al. NLR Genes Related Transcript Sets in Potato Cultivars Bearing Genetic Material of Wild Mexican *Solanum* Species. *Agronomy.* 2021;11:2426. doi: 10.3390/agronomy 11122426.