ABSTRACT OF THESIS

Genetic analysis of PVY resistance in potato

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PVY is a major potato crop threat, causing huge yearly yield losses. To better understand the underlying mechanism of resistance against PVY, samples of the resistance breeding line 89.451 and the sensitive cultivar Somogyi kifli were transcriptome sequenced. The resistant cultivar showed 9000 upregulated transcripts not expressed in S. kifli. The PVY-NTN-H isolate was used for infection. The uninfected control and the 24th, 48th, and 72nd-hour samples were transcriptome sequenced. The reads were matched to the White Lady haplotype reference transcriptome. The study identified 16,000 transcripts, from which 9,000 were upregulated, that were absent from the sensitive cultivar Somogyi kifli but present in the PVY-resistant breeding line, 89.451. Using the NCBI Blast tool, the top 100 upregulated transcripts were annotated. The whole transcriptome datasets were checked for similarity with 609 resistance genes of the Solanum genus which are registered in the NCBI. Out of these 26 were found to be unique hits for the resistant variety, and two of them were virus-resistant genes. The dissertation contends that 89.451 is a suitable genotype for the study of the genetic background of PVY resistance, but further annotation research is needed, and a final *in vivo* determination of any assumed gene function is necessary. The study's findings offer insightful information about gene expression patterns in potato plants infected with PVY, with the aim of developing potato cultivars that are PVY-resistant.