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EXPRESSIONAL ANALYSIS OF *PHYTOPHTHORA INFESTANS* INDUCED RESISTANCE RESPONSE GENES IN POTATO

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Information on the molecular genetic background of biotic stress response is accumulating rapidly. High-throughput analyzing methods, like next generation sequencing (NGS) enable the real time profiling of whole genome transcripts. In this study, we analyzed the expressional profile of biotic stress response genes which showed transcript number increase in potato after inoculation with *Phytophthora infestans*. Quantitation of the transcripts was done by qPCR. Genes for analysis were chosen from an NGS generated transcriptome (TC) dataset that was established from the potato cultivar White Lady. This cultivar has high tolerance to *P. infestans* races presently widespread in Hungary. From among the more than 38 thousand transcriptomes of the TC dataset biotic stress response genes were chosen for quantitation according to heat map analysis and according to the RPKM (reads per kilobase per million mapped reads) value, which latter indicates the pathogen inoculation induced changes in the copy number of a transcriptome. Inoculation with the H12/10 *P. infestans* isolate (containing avr1, 3, 4, 7, 10 and 11) was done on leaves of developed White Lady plants obtained from pathogen-free in vitro plants. Gene expression was tested in the following time points: just before infection (for control), then 1, 4, 17, 24, 31, 48 and 65 hours post inoculation (hpi). In total five different protease inhibitors, four genes belonging to the reactive oxygen species (ROS), three pathogenesis related protein (PR) genes, seven NBS-LRR type *P. infestans* resistance genes and one plant immune receptor gene was analyzed by qPCR. The beta-tubulin gene was applied as housekeeping gene in the analysis.
All the tested genes belong to gene families which according to the literature play important role in the pathogen induced hypersensitive response (HR). In our TC dataset different number of genes belong to these families (Fig.1) from which in this study only those with different type of homologs and high copy number increase were quantitated. The expressional profile of each gene was different in the tested time interval and results will be summarized and discussed here.

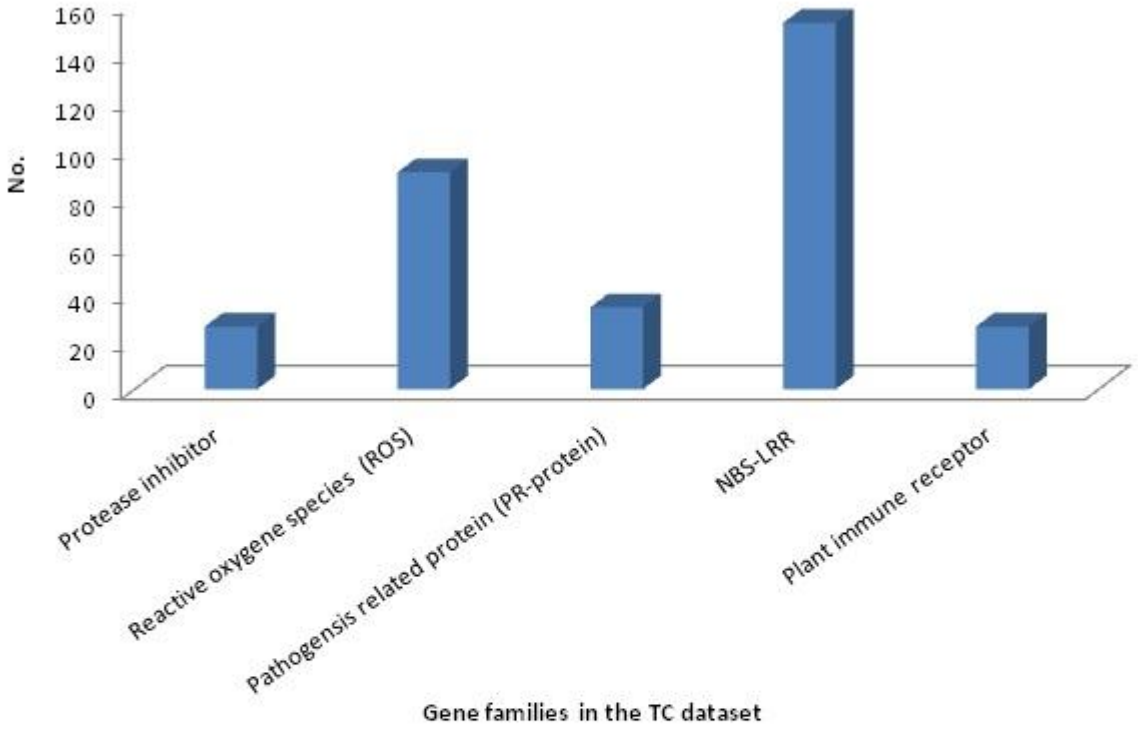

Fig.1. Number of gene homologs belonging to different gene families involved in resistance response