# Genetic Analysis of *Phytophthora infestans* Resistance in Potato

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Late blight caused by the oomycete fungus, *Phytophthora infestans* (Pi), is the most devastating disease affecting potato (*Solanum tuberosum*) production in the world. This disease is hard to control because the Pi races possess high evolutionary potential, and can overcome known resistance genes. Recently, farmers have controlled late blight primarily with chemicals, but the chemical sprays are expensive and result in environmental pollution. The general purpose of this research project is to explore the genetic background of resistance against *P. infestans*. In the gene bank of the Potato Research Centre at Keszthely, there are different genotypes that convey resistance against the late blight-causing *P. infestans*. The final result of this project should be the development of molecular tools, which can be effectively used in resistance breeding of potatoes. For this goal, we use high-throughput molecular technologies with the following approaches: 1. Highly saturated maps of the potato genome were constructed based on 31,190 SNP markers which are identified by microarray analysis. 2. The haplotype-resolved whole genome sequence of the tetraploid cultivar, White Lady, was reconstructed from short (150 bp) Illumina reads and long (8,000 bp) PacBio HiFi reads. 3. For each genotype, transcriptome datasets of samples taken before and after the infections were generated. The present study analyzed the resistance response to *P. infestans* inoculation of the variety, White Lady, as a part of the project. This variety contains the R1, R2, R3a, R4, R5, R6, R7, R8, R10, and R11 genes that convey strain-specific resistance against *P. infestans*. The result of this study showed that the White Lady potato cultivar exhibited time-point-specific induction/repression of the late blight response genes. These results provide valuable information for understanding potato's late blight resistance mechanism. However, there is a need to validate the results of RNA-seq data by analyzing the expression levels of the DEGs through qRT-PCR. Comparing the transcription profiling data from the RNA-seq analysis and qRT-PCR will help us determine/validate the reliability of our result.