

Exploiting the natural variability to identify the key genes for building the broad and durable resistance to mite pests.

The massive increase in sequence information on genomes and transcriptomes creates new possibilities of using these data to solve real and urgent problems of agriculture. Specifically, we see great potential in the use of translational genomics which involves the discovery and analysis of defense mechanisms against pests in the model plant and strengthening them in economically important crop species.

The aim of this project is the identification of quantitative trait loci (QTLs) significantly contributing to the susceptibility/resistance to the two-spotted spider mite (TSSM; *Tetranychus urticae*) in *Arabidopsis thaliana* and verification of their role in tomato and maize. This goal will be achieved using genome-wide association mapping (GWAS) based on existing polymorphism among known genomic sequences of more than a thousand *A. thaliana* accessions and directed mutagenesis of orthologous genes in cultivated species by the CRISPR/Cas9 method.

Despite the fact that many components of the plant-pest interaction show a high specificity (pest race/plant variety), in the case of generalists (pests with a broad range of hosts), the search for more general defense mechanisms gives a chance for wider use. Building the TSSM resistance in plants seems to require such strategy – attacks over a thousand species of plants. The host range includes the model *A. thaliana*, as well as economically important tomato and maize. Moreover, the actual integrated approach to control mites faces some problems that this project will help to solve: TSSM easily develops the pesticide resistance and there is a lack of well-characterized plant resistance genes useful for breeding.

We will accomplish the goal of this project by verification the following hypotheses: (1) the variability in the TSSM susceptibility and the existing polymorphism among *A. thaliana* accessions are sufficient to map a new and important resistance QTLs, (2) precise phenotyping based on TSSM performance and leaf damages on *A. thaliana* accessions is sufficient to reliably evaluate the susceptibility of the accessions studied, (3) selected genes represent a conserved mechanism working in dicots and monocots, (4) the expression of selected genes following mite infestation correlates with plant species tested susceptibility to the TSSM, (5) CRISPR/Cas9 mutagenesis of selected genes allows the generation of TSSM susceptibility variation in tomato and maize sufficient for further breeding.

In this project, we propose an innovative strategy to search for evolutionarily selected gene variants and to verify their constitutive or herbivore-regulated role. In the planned work packages we will apply the latest methodology to conduct basic research on the molecular aspects of plant-mite interaction. However, the selection of the species to study may allow in the future for direct use of our results in crop improvement. The targeted mutagenesis using the genome editing tools is currently the most rapidly developing biotechnology technique, and the resulting plants are in many countries excluded from GMO regulations, whereas in others, there is a realistic chance that this will happen.