

Plants are continuously exposed to attacks from a variety of pathogens including bacteria, viruses, fungi or insects, that are widespread in the environment,. In order to survive their attacks, plants developed a rich set of mechanisms aimed at blocking the infection progress, neutralizing the pathogen or protection of the non-infected plant parts. Due to the tremendous significance for agriculture and ecology, these mechanisms are intensively studied. However, the very detailed characterization of genes involved in acquiring plant resistance, especially the so-called R genes, possessing nucleotide binding domains and multiple leucine rich repeats, so far failed, even in well-described model organisms. The reason for that is extraordinary complex structure of R genes. They are often clustered in the genome, forming groups of nearby highly similar genes and present tremendous dynamics, leading to the diversity observed among closely related species but also among the lines / ecotypes of the same species. It has been shown that intraspecies duplications or deletions of specific genes (collectively named copy number variation) influence the resistance phenotype of the ecotypes that carry these alleles.

In this project we aim to combine two modern techniques for genomic DNA sequencing, that rely on short and long reads, respectively, in order to evaluate the copy number variation of genes related to biotic stress in natural *Arabidopsis thaliana* ecotypes. By applying structural analyses, copy number determination and evaluation of gene expression changes in plants exposed to pathogens, followed by linking these data to the information about plant phenotypic variation in a large population study (over 1000 ecotypes will be analyzed) we hope to identify the copy number polymorphisms that correlate with the natural diversity in stress resistance. We believe that completing this project will pave the way towards more detailed, functional analyses, focusing on individual genes and – eventually – to practical applications of our findings in the future.