

Plants form a complex community with microbes localized within or outside plant tissues. One of the most common and diverse parts of the microbial communities associated with plant roots or above-ground plant organs are fungi. The interactions between plants and their associated fungi are complex and the consequences diverse. Fungi living in close association with plants are known to be beneficial, neutral, or pathogenic.

Due to their constant exposure to beneficial as well as pathogenic microorganisms, plants have evolved sophisticated mechanisms for the regulation of gene expression that control their response to different microbes. The essential components of this complex network of gene regulatory pathways have been found to be the endogenous, noncoding, small RNAs (sRNAs), including miRNAs and siRNAs. Previous research on the role of miRNA molecules in the interactions of plants – including wheat – with fungi focused mainly on pathogenic fungi. It has been shown that miRNA molecules are involved in the induction of defensive and immune reactions in plants as a result of infection caused by pathogenic fungi. On the other hand, little is known about the involvement and function of siRNAs in these interactions. Similarly, there is insufficient knowledge about the role of miRNAs and siRNAs in interactions between wheat plants and symbiotic fungi.

Therefore, the aim of the proposed research project is to increase knowledge about the involvement of these RNA molecules in the communication between wheat and pathogenic fungi of the genus *Fusarium* and beneficial fungi of the genus *Trichoderma*. The research will be conducted using two lines of common wheat, differentiated in terms of resistance to *Fusarium* diseases and in complex interaction systems: plant - pathogen, plant - symbiont, plant - symbiont - pathogen. In order to study the influence of the host genotype (wheat), its individual organs, fungal species and the duration of the interaction on the composition and distribution of miRNA molecules in wheat plants and to verify the participation of already selected miRNA molecules and genes in which these miRNA regulations may potentially be involved, and in order to determine the role of siRNA in the communication between wheat and fungi, high-throughput next-generation sequencing methods, high-sensitivity methods for nucleic acid detection and determination, as well as appropriate advanced statistical and bioinformatics tools and programs will be used.

The study proposed in this project may represent an important step forward in our understanding of the molecular basis of wheat-fungal interactions and the mechanisms that determine the type of these interactions. Moreover the knowledge about the involvement of small RNA in multidirectional communications between wheat and both symbiotic and pathogenic fungi could provide a novel perspective for the development of innovative strategies for wheat protection and wheat disease management.