

## **Specificity of the regulation of *Fusarium*-asparagus interaction by host metabolites and hormones produced during infection process**

*Fusarium* wilt and root rot caused by *Fusarium* fungi is one of the most important diseases of asparagus crop worldwide. The disease not only causes serious yield reductions, but also contaminates the plants with harmful mycotoxins, rendering it unacceptable for food. It is known that *Fusarium* species usually secrete proteins and produce a range of metabolites to facilitate the infection and colonization of their hosts. However, the mechanisms of key gene regulation and signaling pathways related to *Fusarium* infection in asparagus plants remain unknown. Therefore, the main aim of the project is to gain the insight into *Fusarium*-asparagus interaction *in vitro* and *in planta* based on molecular, proteomic and metabolomic analyses.

Plant reactions to biotic and abiotic stresses have been studied for many years but mainly using model species (e.g. *Arabidopsis thaliana*), and molecular study of asparagus remains largely unexplored. Moreover, there is a constant lack of research particularly concerning the intra-specific differences in plant reaction to fungal pathogen infection, especially on metabolomic, proteomic, and molecular levels.

Proposed project is an ambitious and original approach to fill significant knowledge gaps in understanding the specificity of plant-pathogen interactions. We will try to answer the elementary questions concerning asparagus reaction to the infection with *Fusarium* fungi.

The unique characteristics of this project is to bridge results of various research domains on *Fusarium* plant responses, thereby focusing on the largely unknown processes that take place in asparagus seedlings. Moreover, examining the changes in the expression of proteins, and establishing the roles of specific metabolites during *Fusarium* treatment of asparagus plants will be the first attempt to study the potentially host-related diversity.

The integration of data originating from fungal biology, transcriptomics, proteomics, and metabolomics will provide new holistic insight into the detailed picture of *Fusarium* diversity and the influence of these fungi on plant biology and will not only improve the scientific knowledge of the agricultural ecosystem's functions but will also be essential for sustainable control of this important plant pathogen group.