

Fusarium head blight is one of the most serious and most dangerous diseases of cereals caused by fungi of the genus *Fusarium*. *F. avenaceum*, *F. graminearum* and *F. culmorum* are particularly dangerous in temperate climates. These fungi can strike up to 90% plants at the infected field and significantly reduce the quantity and quality of crops. The main problem associated with the disease is the production of mycotoxins that accumulate in grains. These toxic compounds when ingested by an animal or human lead to numerous diseases and even to death. The creation of cultivars of crops that are resistant to Fusarium head blight is becoming increasingly important aim of plant breeding, especially that in Poland there are few such cereal cultivars. Breeding progress in cereals, towards increasing resistance to Fusarium head blight largely takes place through knowledge of the basic mechanisms of plant response to the pathogen attack. The search for sensitive metabolomic and proteomic markers of plant resistance to Fusarium head blight is necessary for the development of sustainable agriculture.

Therefore, the primary objective of the study is to understand the molecular mechanisms of plant defense against Fusarium head blight and determine which of them are common to a wider group of plants and which are species-specific. These studies will be carried out by comparing the response to infection by *F. culmorum* between three species from grass family: the two most important cereals: wheat and barley and a model plant, purple false brome, that is well characterized in terms of genetics. The study has been divided into seven research tasks: (1) Phenotypic evaluation of degree of infestation by *F. culmorum* of ears of the test plants which will be carried out by analyzing the content of mycotoxins in the grain and quantitative measurement of DNA of the fungus, (2) Analysis of secondary metabolites induced in plants during fungal infection, especially phenolic compounds and flavonoids known for its antioxidant and antifungal properties. These compounds are also involved in mechanical defense against fungi through participation in the cell walls thickening in the infected areas, (3) Analysis of proteins induced in plants during fungal infection related to the production of secondary metabolites and other defense elements, (4) Analysis of expression of selected genes involved in the induction of secondary metabolites and proteins, in plants affected by fungal infection. This will give the opportunity to examine the speed of response of plants to infection. (5) Assessment of antioxidant capacity of secondary metabolome in plants during fungal infection for overall picture of the importance of antioxidant compounds in the plant response to fungal infection, (6) Pre-processing of metabolomic, proteomic and transcriptomic data and (7) Statistical analysis and integration of biochemical, physiological, proteomic, transcriptomic and metabolomic results will be the basis to detect differences between the tested samples and will allow visualization of the obtained results.

The analytical methods used in this study include largely the most modern technologies with extraordinary sensitivity and precision and they will enable fully automated study of dozens of samples simultaneously. High throughput metabolomic and proteomic research methods based on mass spectrometry combined with chromatographic separation of complex plant extracts will provide a comprehensive picture of the relationships between plant and pathogen. Gene expression will be analyzed by extremely accurate device for polymerase chain reaction in real time (RT-PCR). Advanced mathematical and statistical tools will enable the creation of a correlation network and visualization according to investigated relationships.

Study of plant-fungal pathogen interaction is undoubtedly one of the most interdisciplinary projects of plant biology. Combining data from chemistry, physiology, mycology, metabolomics, transcriptomics, mathematics and statistics will allow us to explain and illustrate metabolic changes in plants during infection by *F. culmorum*. To our knowledge, such detailed and comprehensive studies in this field have not yet been realized.