

Plants are often exposed to diverse environmental stresses and have acquired specific mechanisms to combat these conditions. Over the past decade, the molecular mechanisms underlying biotic and abiotic stress tolerance have been intensely studied with much emphasis on tolerance mechanisms pertaining to individual stresses. The main contributors to the growing complexity in this type of research are the rapid changes in plant development. In many plant–pathogen interactions, the expression of resistance depends on the developmental stage at which the plant is infected. Plant development is an important factor in revealing the nature of plant resistance to stress, but often has been neglected. Thus, the influence of plant development on disease resistance is a crucial element for our understanding of plant–pathogen interactions. All plants produce wax that helps their leaves repel water and shield the plant from insects and other pathogen like fungus. The cuticle is the plant's barrier against abiotic and biotic stresses, and the deposition of epicuticular wax crystals results in the scattering of light, an effect termed glaucousness. The epidermis structure and its role in plant biology are regarded as an important factors contributing to the stress resistance due to the fact the structures are markers for rapid changes in plant immunity.

We decided to focus on interaction between abiotic (drought) and biotic (fungal infection) stresses in relation to the structure of the epidermal layer (cuticle and trichomes) as well as changes in the genes transcriptional level and chemical content of wax compositions of the studied plant at different stages of plant development. In the proposed research, both chemical and physical structures of cuticle and trichomes as well as their role in fungal infection and drought will be considered. The goal of the proposed research is to investigate the role of cuticle and trichomes, which are regarded as sophisticated defense structures, in drought and fungal infection response in relation to (i) transcriptome analysis, (ii) wax content, (iii) microstructure analysis, and (iv) real-time phenotypic evaluation of plants in terms of both phenology and wax content.

Our proposal is based on the hypothesis that plant resistance is not a solid trait but rather the effect of given conditions in particular duration of the plant life. Moreover, we assumed that acquired immunity can deteriorate (or boost) during vegetation due to the occurrence of additional factors and may be linked to the rapid changes in the anatomy, morphology, genetics, and biochemistry of plants. To validate this hypothesis, we will use methods that affect wax mutant development and tailored tools to assess the epidermis structure. The project will achieve its biological aim by conducting complementary experiments with selected barley genotypes - the lines of crosses combinations derived from glaucous or nonglaucous mutants and early/ late heading barley genotypes. The project focuses on the dynamic changes in structure of plant epidermis in relation to multiple stresses resistance. The planned experiments will elucidate the underlying mechanisms contributing to multiple-stress combinations response in cereal crops at different scales: genes, epigenetic mechanisms, metabolom analysis and the detailed histological and morphological observations.

The proposed project will provide a new insight into the underlying mechanisms contributing to tolerance to combination of multiple stresses in cereal crops at different scales and will considerably extend the knowledge on the relationship between the epidermis structure and resistance to multiple stresses in relation to changes in plant phenology. Our integrative approach will verify the roles of cuticle and trichomes in response to drought combined with fungal infection. The project will provide significant knowledge on the still enigmatic phenomenon – the changeability in plant resistance, which is also referred to as adult seedling resistance or flowering-induced resistance. The outcome of our project will have a profound impact in this area of barley genome research. This knowledge can be potentially used in studies on other monocot plant species as barley is regarded as a model plant.