

Global warming has led to the simultaneous occurrence of various abiotic and biotic stress factors in plants that trigger unique stress responses. When plants are exposed to a combination of multiple stress factors, they can elicit specific and distinct stress responses. To improve our understanding of stress tolerance, it is also advisable to integrate different information and methods from different research areas and to promote collaboration between these areas.

Water scarcity is a key factor that increases the incidence and severity of *Fusarium* diseases. In response to multiple stress factors, plants need to make tailored adaptations, as in many cases individual stress factors would normally trigger contradictory responses. Therefore, the interactions between plants and fungi need to be further explored, as climate change has a significant impact on the occurrence and severity of plant diseases. The drought escape (DE) strategy is proving to be an effective tool to combat not only water scarcity but also pathogen infections. Against this background, the activation of bioactive chemicals such as anthocyanins can be considered as one of the most efficient mechanisms to improve plant stress tolerance, as these metabolites act as potent antioxidants and have also shown antiviral, antibacterial and fungicidal activities in plant–pathogen interactions.

The main objective of the project is to decipher the multifactorial stress response of plants and its relationship to anthocyanin content and biosynthesis. This project will provide new insights into the underlying mechanisms that contribute to the tolerance of cereal plants when confronted with a combination of multiple stressors. We will explore these mechanisms at different levels: transcriptomic profiling, epigenetic mechanisms, phenolome analysis and detailed histological and micromorphological observations. In addition, innovative phenotyping technologies will be used to gain a comprehensive understanding of the dynamic changes in root and shoot morphology and architecture associated with multifactorial stress conditions.

Our proposal is based on the hypotheses that: (i) stress tolerance resulting from an early-heading habit is associated with variations in anthocyanin biosynthesis in different plant tissues or parts, and the intensity of this biosynthesis is influenced by the dynamic changes in plant development, and (ii) that anthocyanin activity allows late-heading plants that cannot accelerate their growth sufficiently to avoid stress conditions to develop the ability to minimize the negative effects of stress, distinguishing them from early-heading plants.

To test these hypotheses, we will use methods that can alter the development of anthocyanin-rich or anthocyanin-poor plants derived from cross combinations between anthocyanin mutants and early- and late-heading genotypes, respectively. The use of growth regulators will allow us to accelerate or delay the growth of early and late sprouting plants. In addition, we will use specific tools to evaluate the role of anthocyanin organization, which is considered a marker for rapid changes in plant immunity.

In the proposed study, we will perform complex assays to explore the role of anthocyanins in various stress-induced plant responses. These investigations include (i) transcriptome analysis, (ii) phenolic compound profiling, (iii) microdistribution of anthocyanin molecules, and (iv) real-time phenotypic assessment of plants differing in both phenology and anthocyanin content.

The integration of multi-omics methods is a fundamental aspect of this research, as it enables the link between genotype and phenotype, providing a comprehensive understanding of biological processes, such as the multiple stress responses in plants. The proposed project is able to significantly improve our understanding of the complex relationship between anthocyanin accumulation and resistance to various stress factors, especially in the context of changes in plant phenology. Our integrative approach will shed light on the role of anthocyanins in the response to drought in combination with fungal infections.