

Fungi play a major role in natural ecosystems and in modern agriculture as a result of their nutritional versatility and various interactions with plants. Fungi are important decomposers and recyclers of organic materials. They interact with plant roots in the rhizosphere or with above-ground plant components; while living in close association with plants, they are located either outside or within plant tissues.

Fungi that live inside plant tissues for all or at least part of their life cycle without causing any symptoms of disease in their host are defined as fungal endophytes.

The presence of fungal endophytes in wheat has been demonstrated by several authors. The ability to infect cultivated wheat with fungal endophytes that originated in other plant species has also been demonstrated, and various positive effects have been reported. For example, endophytes reduced wheat susceptibility to insects and, improved heat and drought tolerance and promoted plant growth. Research into the distribution and ecological role of fungal endophytes in wheat has been especially intensive in the family *Clavicipitaceae*, where the asexual genus *Neotyphodium* and closely related species of the sexual genus *Epichloë* have provided model systems. In contrast to the well-known *Epichloë* and *Neotyphodium* associations with wheat, there is a lacuna in our knowledge of the diversity, the life cycles, and accordingly the ecological role of most non-clavicipitaceous endophytic species and the effects of their presence in their wheat host. In order to gain insights into these interactions there is first the need to understand the complexity and diversity of native fungal communities associated with the wheat endosphere.

Previous studies on wheat microbiomes have largely focused on identifying microbes either in roots and rhizosphere or above-ground organs, and all of these investigations have been based on culture dependent methods. In recent years, developments in high-throughput technologies, such as next-generation sequencing, have opened new perspectives in fungal endophyte biodiversity research.

Therefore, the main goal of the research project is to broaden the understanding of the wheat endosphere mycobiome dynamics and its impact on the growth and fitness of plants.

The proposed study will be conducted to determine and compare the diversity of fungi living inside plants' tissues in winter and spring wheat cultivars grown under controlled and field conditions, to study the effects of host genotype, host organs, and plant growth conditions on the fungal species compositions and distribution in wheat plants, and, finally, to define the morphological, anatomical, physiological, and molecular wheat plants' reactions to changes in their mycobiome.

Ten bread wheat cultivars: 5 spring wheat cultivars and 5 winter wheat cultivars will be used in the proposed studies. To access taxonomic composition of cultivable and non-cultivable fungal communities across wheat cultivars, plant organs, plant growth conditions and land management strategies as well as to recognize of the transmission mode of endogenous fungi, next-generation sequencing and standard sequencing will be performed. To access the effect of endogenous fungi inoculation on the wheat morphology, anatomy, and physiological parameters of wheat plants, growth component, fluorescence, and gas exchange parameters of wheat plants will be measured as well as microscopic observations of anatomical changes in roots, stems and leaves of wheat plants will be performed. In order to get insight on the molecular interactions of wheat - endogenous fungi, the quantitatively evaluation of transcription profiles of selected genes known to be related to defence, resistance and symbiosis in wheat will be performed by using the quantitative real-time PCR (RT-qPCR). To evaluate of changes in the metabolome of wheat seedlings during interaction with endogenous fungi, high throughput and sensitive analytical methods will be used. All data will be integrated and statistically analyzed.

The knowledge about the entire phenotypic reaction of wheat plants to changes in the composition of their endosphere mycobiome could provide a novel perspective to the understanding of wheat-associated mycobiome interactions and be useful in designing new generations of biological control agents or bio-stimulators of wheat growth.