The endosphere mycobiome of common wheat (*Triticum aestivum* L.) and its characteristics in terms of the mode of transmission of endophytic fungi and their impact on wheat immune responses.

Microorganisms, including fungi, play an important role in the proper development and functioning of plants. Although these interactions may seem asymptomatic, the presence of microorganisms improves the adaptability of the plant to the environment in which it lives. Fungi play an important role in natural ecosystems. Endophytes occur in the internal tissues of plants without causing disease symptoms. Interactions between endophytic fungi and host plants are extremely complex and their effects vary. Unambiguous determination of the function (commensal, pathogenic, symbiotic) of endophytes in a plant is difficult because the same species of fungi, depending on environmental conditions, can change their lifestyle and go from pathogen to commensal or vice versa. Endophytic fungi were observed in wheat tissues. Their presence reduces susceptibility to biotic and abiotic stresses and positively influences the growth and development of plants. Current knowledge about endophytic fungi in wheat is based on research conducted under a narrow range of experimental conditions, including wheat genotypes, plant organs, plant development stage, and environmental conditions. This doctoral thesis aimed to learn the structure and factors determining the species composition of fungi inhabiting the endosphere of common wheat (*Triticum aestivum* L.) and to investigate the impact of changes in the mycobiome of the wheat endosphere on the expression of selected plant genes.

Ten Polish cultivars of common wheat (*Triticum aestivum* L.) were tested in the presented paper: five spring forms: Arabella, Bombona, Kandela, Rospuda, and Rusałka, and five winter forms: Arkadia, Bamberka, Euforia, Legenda and Ostroga. Four closely related experiments were performed. As a result of this research, 879 fungal isolates were isolated from the endosphere of Polish common wheat cultivars, of which 828 were identified molecularly and 521 were identified at the species level. The aim of Experiment No. 1 was to determine the diversity and changes in the composition of fungal communities isolated from the plant endosphere conditioned by wheat variety, plant organs, and growth conditions. 28 species or genera of endophytic fungi isolated from plants grown under greenhouse conditions, 35 species or genera of endophytes isolated from plants growing in the field and cultivated in an ecological system, and 52 species or genera endophytic fungi isolated from plants grown in a traditional

system were identified. Experiment no. 2 consisted in performing antagonistic tests in bicultures, using the following fungal strains: *T. viride* E80, *T. koningii* E191, *T. hamatum* E81, *P. olsonii* E69_1, *P. expansum* E193, *P. crustosum* E106, *S. spinificis* E11, *S. strictum* E22, *F. proliferatum* E202, *P. album* E35, *C. candelabrum* E83, *N. golenkoana* E208. The percentage of growth inhibition was calculated for all test strains on day five of co-incubation. The analysis of the results showed the influence of the tested strains on each other. Experiment No. 3 consisted of the analysis of the composition of the fungal community in two generations of G1 and G2 plants grown under greenhouse conditions, as well as in axenic wheat seedlings treated with fungal strains selected based on the results obtained in Experiment No. 2, with a mixture of these fungi and sterile water as a control. Almost 3 times fewer isolates were isolated and identified in the G2 generation than in the G1 generation. Only 9 species/genera of endophytic fungi were common to both generations: *Fusarium sp., F. proliferatum, T. koningii, A. lecanii, Trichoderma sp., P. crustosum, T. hamatum, P. olsonii, Cladosporium sp*. Comparative analysis of the mycobiome composition of two generations of G1 and G2 wheat plants showed that *F. proliferatum* occurs in all varieties of winter wheat and both generations studied. In addition to *F. proliferatum*, the occurrence of *A. lecanii* in the cultivar Legenda and *T. koningii* in the cultivar Euforia was observed in both generations. In contrast, *Trichoderma* fungi were identified in two generations of Bombona wheat. Seven days after treating 14-day-old wheat axenic seedlings with selected endophytes, molecular identification of the re-isolated fungal strains was performed. For this purpose, a comparative analysis of the nucleotide sequences of the appropriate phylogenetic markers for the isolated fungi was performed using the nucleotide sequences obtained initially after the primary isolation of the tested endophytes from wheat tissues. Comparative sequence analysis showed that the strains of *F. proliferatum, P. olsonii, P. expansum*, and *T. hamatum* were able to repopulate the tissues of the tested wheat cultivars. Experiment no. 4 was aimed at analyzing the expression of selected wheat genes 7 days after treatment of the plants with a suspension of *F. proliferatum* E202, *P. olsonii* E69_1, *P. expansum* E193, *T. hamatum* E81, and a mixture of these fungi. The *HSP70* gene encoding heat shock protein, *PR9* gene encoding peroxidase, and *SOD* gene encoding superoxide dismutase were selected for analysis. It was observed that the expression of the studied genes (*SOD, PR9, HSP70*) depended on the genotype of the plant/variety as well as the species of fungi with which the plants were treated.