

## Summary

Crops are exposed to many stress factors, abiotic and biotic, among which the stress caused by the pressure of pathogens is one of the main reasons that reduce the productivity of plants. One of the most important diseases of small-grain cereals, especially wheat and barley, of global economic importance, caused by fungi of the genus *Fusarium* spp. is Fusarium Head Blight (FHB). This pathogen infects the spikes, causing the embryos damage, which leads to a lack of grains or reduction in the weight of the grain and a weakening of their germination. Spike infection occurs during flowering and immediately after flowering, causing a reduction in yield not only in terms of quantity, but also quality, because the mycotoxins accumulated in the infected grain are harmful to both humans and animals.

In the presented doctoral dissertation, the characteristics of the variability of agronomic traits and resistance to FHB of the population of spring barley recombination lines, obtained from hybrids of the European variety Maresi and the Syrian line Cam/B1/CI08887/CI05761, were carried out based on the results of field experiments using spore inoculation *Fusarium culmorum* (W.G.Sm.) Sacc. The plant material obtained from hybrids with different earliness and height, and also adaptation to drought, was used to know more about the genetic determinants of the observed traits, as well as to identify the regions of the barley genome (quantitative trait loci) determining these traits, along with their functional annotation.

The studies included the phenotypic characteristics of 100 recombinant inbred lines (RIL) in the field, in a randomized block design, in triplicate, two variants (control - K and inoculation - I) and three locations (Antoniny, NAGRADOWICE, Tulce). The technique of inoculation by spraying during the flowering phase was applied, and then spraying was repeated twice at three-day intervals. Eight traits were observed: plant height (cm), spike length (cm), number of spikelets per spike, number of grains per spike, grain weight per spike (g), 1000 grain weight (g), grain yield per plot (g) and heading date (number of days). After the onset of disease symptoms, the severity of FHB was assessed on the basis of the proportion of infected spikelets per spike and the proportion of affected spikes in the plot. From these values, the FHB index (%) was calculated. On the other hand, the share of kernels damaged by *F. culmorum* was visually determined by dividing the sample into healthy kernels (HLK, Healthy Looking Kernels) and kernels with symptoms of infection (FDK, Fusarium Damaged Kernels), and the content of deoxynivalenol (DON) in grain was also assessed. Phenotypic data was analyzed in the context of a genetic map obtained from single nucleotide polymorphism (SNP) genotyping

using the Illumina 9k Infinium iSelect platform. The QTL identification for the analyzed traits was carried out according to the method described by Malosetti et al. (2013), using the Genstat 18 program (VSN Int. 2015). The functional interpretation of QTL was carried out on the basis of the available genomic resources, and their annotation using the BARLEYMAP (<http://floresta.eead.csic.es/barleymap>). Gene Ontology enrichment (GO) term overrepresentation analysis was performed using the GeneOntology database and tools (<http://geneontology.org>).

Transgression effects were observed for most of the analyzed traits for MCam population both in the natural conditions and after inoculation. The influence of biotic stress was less visible in Maresi, and the level of changes did not exceed approx. 6% of the value of the trait measured under control conditions, and the yield per plot was reduced only by 1.1%. Under the inoculation conditions, the least negative impact of FHB was observed for spike length and number of spikelets per spike both in MCam population as well as in parental genotypes. The infection was found to have a greater effect on most traits of CamB1 compared to Maresi. Only the values for the number and weight of damaged kernels under inoculated conditions were much higher in Maresi, for which there was an over 60-fold increase, while in CamB1 the increase was only 10–12 times higher than in the control.

Generally, positive phenotypic correlations were found between yield-forming traits, regardless of the environment. The exception was the FHB index, the correlation coefficients of which were negative in all examined cases. It was also found that the increase in the degree of grain infection in the spike did not always result in an increased content of DON in the grain. Moreover, lines with non-infected spikes in the plot were identified, while their grains showed the presence of DON. Despite significant differences in the content of DON, both under control and inoculated conditions, no significant correlation was found between the content of DON in the grain and other analyzed traits.

The QTL analysis carried out as part of the dissertation, including eight traits related to the yield potential and five traits related to FHB, as well as the DON content in the grain, allowed to identify 40 loci scattered throughout the genome. In the study, 29 QTLs for yield-forming traits and 11 related to FHB were identified. Additionally, four genomic regions containing more than two closely adjacent loci were distinguished, i.e. clustered within a 6 cM-long interval ( $\pm 3$  cM from the central QTL).

Six lines (MCam1, MCam10, MCam26, MCam49, MCam56, MCam129) were selected, characterized by a low degree of spike infection (IFK) in all environmental conditions with a low DON content. By integrating the results for the FHB-related QTL with the yield-forming

trait loci from previous MCam population studies (on the assessment of the relative drought effect – RDE, using the MCam spring barley population for linkage analysis in water stress conditions), they were limited to four (MCam10, MCam26, MCam56, MCam129). These lines may be a source of favorable alleles determining both better yielding in drought conditions and resistance to FHB.

In the doctoral dissertation, the use of plant material obtained from hybrids with different earliness and height, as well as different adaptation to drought, made it possible to identify two regions of the barley genome within chromosome 2H and 3H involved in the plant's response both to FHB and water deficit. Thus, such research provided new knowledge about the adaptation of plants to stressful conditions, becoming particularly useful in breeding programs, supporting biological progress.