

**EFFICIENCY OF THE MOLECULAR MARKERS LINKED TO THE STB
RESISTANCE LOCI IN WHEAT**

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Septoria tritici blotch (STB) is one of the most devastating foliar diseases of wheat, that accounts for approximately 70% of the annual usage of cereal fungicides in Europe. Nevertheless, the policy on the use of chemical plant protection products has been tightening recently and therefore much greater attention has to be put on finding fast and effective methods of identification of resistance genes and their introduction into breeding materials. One of the available solutions is Marker Assisted Backcrossing (MAB) method which essentially involves two steps: selecting individuals that carry the target allele (referred as foreground selection, FS) and next selecting individuals that carry the highest number of the recipient parent alleles outside the target gene (referred as background selection, BS).

In our study, we conducted the haploblock-based GWAS on a panel of wheat, comprising of lines/cultivars demonstrating diverse resistance to STB. The analysis led to choosing two highly resistant genotypes (Mandub and M3 Synthetic) for crossing with two susceptible cultivars (Arkadia and Patras). To investigate the presence of introduced loci and genetic background within offspring generations the DArTseq genotyping as well as SSR and AS-PCR markers assays were performed. The presentation will show the efficiency of various genotyping systems in foreground and background selection.

Keywords: association and linkage mapping, DArTseq markers, Septoria tritici blotch, SSR, *Zymoseptoria tritici*