

Marker-assisted selection for *Wheat dwarf virus* (WDV) tolerance in wheat (*Triticum aestivum*)

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Wheat dwarf virus (WDV) is an important pathogen in wheat and other cereals. In many European countries, e.g. Hungary, Spain and Germany, WDV causes high yield losses. WDV is transmitted by the leafhopper *Psammotettix alienus*. Symptoms of a WDV infection on wheat include chlorosis, dwarfing and streaking along with high yield loss. Due to climate change, the incidence of insect-transmitted viruses will become more important worldwide due to the extended survival time of the vector. The absence of insecticides efficient against *P. alienus* renders growing of WDV resistant/tolerant varieties the only effective way to control WDV.

However, little is known about WDV resistance/tolerance sources. Based upon a previous project- in which wheat accessions were screened for WDV resistance/tolerance and quantitative trait loci (QTL) were identified by genome-

wide association studies (GWAS), this project aims to use this tolerance in breeding. For this purpose, breeding partners produced single seed descent (SSD) and doubled haploid (DH) populations by crossing tolerant genotypes with susceptible varieties.

This material will be phenotyped for WDV tolerance and agronomical traits and will be genotyped using the 20K Illumina Infinium Chip. Based on the obtained data the WDV tolerance will be mapped and molecular markers (KASP/CAPS) will be developed. The identification of QTL for WDV resistance and the development of molecular markers are essential to replace the laborious and time-consuming resistance tests with WDV bearing leafhoppers. This will facilitate the integration of breeding for WDV resistance/tolerance into applied wheat breeding.