

Identification of *Wheat dwarf virus* (WDV) resistance/tolerance in wheat

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Wheat dwarf virus (WDV) causes high yield losses in wheat and other cereals. WDV is transmitted by the leafhopper *Psammotettix alienus*. Symptoms include yellowing and dwarfing of infected plants along with heavy yield loss. Due to global warming, insect-transmitted viruses become more important. Growing WDV-resistant/tolerant varieties is the most effective and environmentally friendly way to control WDV.

Hence, the aim of our project is to identify WDV resistant/tolerant genotypes by screening gene bank accessions and breeding lines for WDV tolerance/resistance and to identify quantitative trait loci (QTL) by genome-wide association studies.

A set of 500 genotypes comprising different wheat species and wild relatives was tested by artificial infection in gauze houses and under natural infection in field trials in Žabčice, Czech Republic during the last two growing seasons.

The majority of the tested genotypes turned out to be highly susceptible. The susceptible standard cultivar 'Hybnos' revealed an average infection rate of 75% indicating a high infection pressure. Six accessions were identified with a very low infection rate (0 - 12%) in two year trials. Among these, one cultivar showed no yield reduction after virus infection during the test in 2014/15. Crosses with this cultivar were conducted by the breeding partners and SSD/DH populations will be developed. The most resistant genotypes (42) are tested repeatedly in this year. A subset of 250 genotypes was selected and will be genotyped by the 15k iSelect chip. The identification of QTL for WDV resistance and development of molecular markers are the prerequisite to replace the laborious and time consuming resistance tests with WDV-bearing leafhoppers. This will facilitate the integration of breeding for WDV tolerance/resistance into applied wheat breeding.