

Mapping for *Wheat dwarf virus* (WDV) resistance 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 WDV infection in wheat include chlorosis, dwarfing and streaking, and high yield losses. The economic importance of insect-borne viruses will increase in the coming years with climate change and the associated greater global vector activity. Control of leafhoppers with insecticides is limited. Legal regulations and measures for environmentally and consumer friendly crop production further limit their use. However, little is known about the sources of WDV resistance.

A previous project screened wheat accessions for WDV resistance/tolerance and used genome-wide association studies (GWAS) to identify quantitative trait loci (QTL) involved in the expression of WDV tolerance. The aim of the present project was to make these sources of tolerance useful for wheat breeding. For this purpose, breeding partners produced biparental populations by crossing the tolerant accession 'Fisht' with susceptible cultivars. This material was phenotyped for WDV tolerance in field and greenhouse trials and genotyped with a 25k Illumina Infinium chip. Based on these data, QTL for WDV resistance were mapped.

The identified QTL for WDV resistance will enable the development of molecular markers essential to replace the tedious and time-consuming resistance testing with WDV-bearing locusts. This will facilitate the integration of breeding for WDV resistance/tolerance into applied wheat breeding.