

New approaches to the identification and 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.

The assessment of resistant lines is based on inoculation with virus bearing leafhoppers and subsequent phenotyping in gauze houses. Abiotic conditions, especially temperature, have a crucial influence on the success of the inoculation. In previous approaches, the inoculation of plants took place under semi-field conditions in gaze houses. Considerable fluctuations in the infection rates were observed and spontaneous infections could occur after warm winters. Furthermore, the stock of cicadas living in captivity had to be rebuilt after each infection, which delayed the screening process.

As a part of an actual project on marker-based selection for WDV tolerance in wheat, we have addressed this problem and developed an improved approach. In this methodology, plants are inoculated in small greenhouses and are subsequently planted out in the gaze houses. This gives the leafhoppers optimal environmental conditions for WDV transmission and WDV infection can develop under natural environmental conditions. In addition, the virus bearing leafhoppers can be removed from the plants after infection, so that a sustainable use of the animals is possible. The method thus allows more reliable phenotyping through a higher infection success and the testing of a larger number of genotypes in a shorter time.