Marker-assisted selection for WDV tolerance in wheat (Triticum aestivum)

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Wheat dwarf virus (WDV)

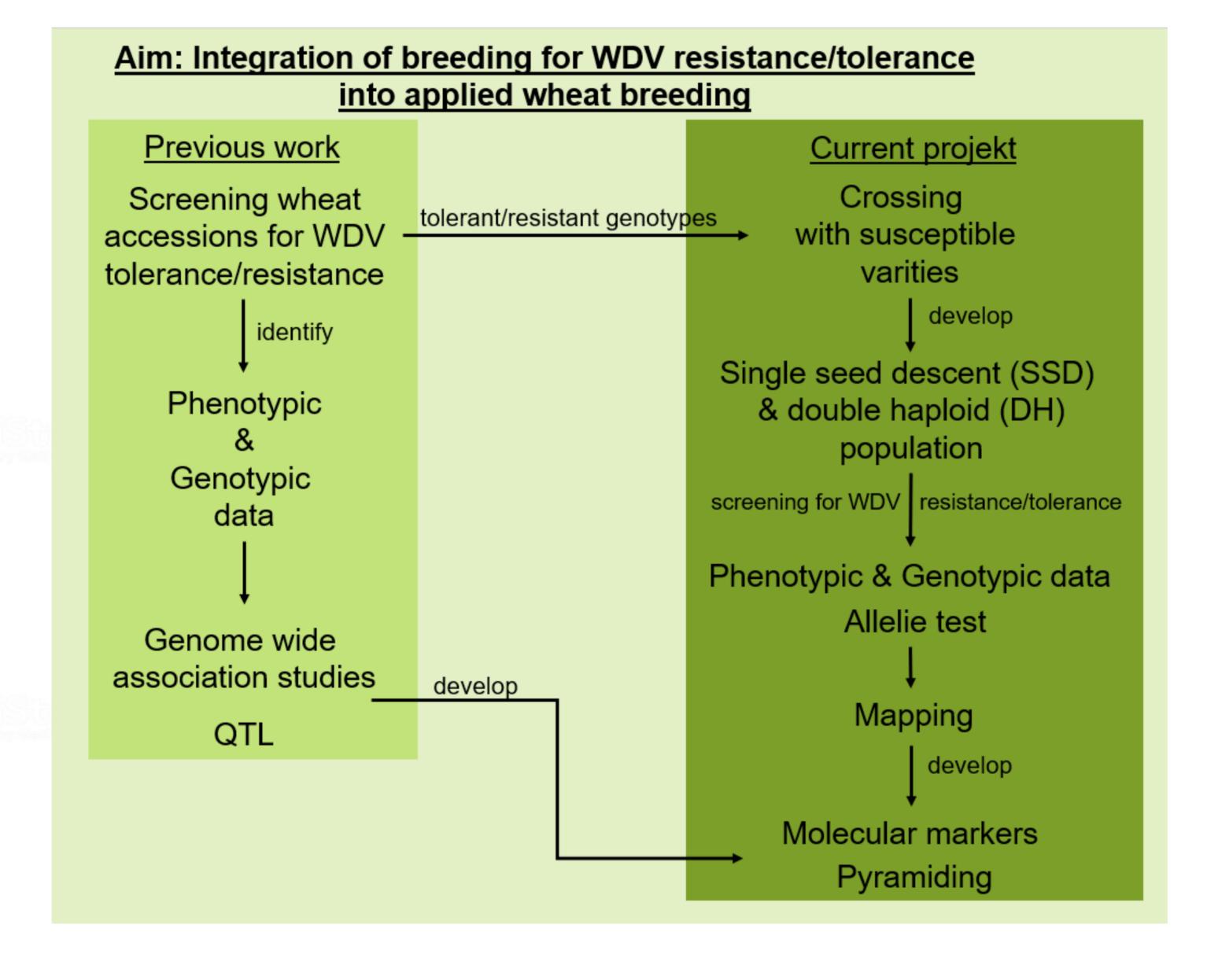
WDV is an important pathogen in many European countries and causes severe damage in plants of the family Poaceae, e.g. wheat. Due to climate change, the incidence of insecttransmitted viruses will become more important worldwide the because increased occurrence and longer activity of the transmitting vectors in autumn.



The absence of approved insecticides against alienus renders growing of WDV resistant/tolerant varieties the only effective WDV. control way However, no such varieties are available yet. Based upon a previous project, doubled haploid (DH) and single-seed descent (SSD) lines will be used to develop molecular markers based wide genome on association studies suited future marker-based selection.

Experimental concept

The SSD and DH population WDV tested tor resistance/tolerance by artificial infection viruliferous with leafhoppers and gauze greenhouses and field under conditions in (CZ).Zabcice Additionally, the promising most be genotypes tested again in the 2nd year.



The material be phenotyped for WDV by ELISA and agronomical traits like heading date, height, number of plant ears per plant, TKW yield The plant. per will genotyping be performed by using the 20K Illumina Infinium Chip (Trait genetics, Gatersleben). Based the obtained data the WDV resistance/tolerance will be molecular mapped and markers (KASP/CAPS) will be developed.

Results

So far, the evaluation of the 1st year gauze house test identified resistant/tolerant SSD and DH lines, which are retested in 2019/2020.

Perspective

Additional information on tolerant genotypes will be available after harvesting in 2020. In the next step the WDV tolerance/resistance associated SNP markers will be converted into Caps or KASPar markers and verified in the phenotyped SSD and DH population from the 1st year.

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