

High resolution mapping of resistance genes against barley mosaic disease and *Barley yellow dwarf virus*

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Barley (*Hordeum vulgare*) is an important crop in Germany and on the world wide level. The crop is hit by many fungal and viral diseases reducing yield and production. Therefore, breeding for resistance is of prime importance. Due to the transmission by the soil-borne plasmodiophorid *Polymyxa graminis*, yield losses caused by *Barley mild mosaic virus* (BaMMV) and *Barley yellow mosaic virus* (BaYMV) cannot be prevented by chemical measures. Regarding *Barley yellow mosaic virus* several loci conferring resistance to either BaMMV or BaYMV or both are known. Another important virus disease of barley is the aphid transmitted *Barley yellow dwarf virus* (BYDV).

Among others, *rym13* located on the long arm of chromosome 4H provides resistance to BaMMV/BaYMV. Regarding BYDV the locus *Ryd3* on chromosome 6HL is known. The aim of this study was to isolate the respective genes using a map based cloning approach.

For both resistance genes a high resolution population was established. Using different high density maps and genomic resources, marker saturation of the intervals of interest was conducted.

Using genotyping by sequencing (GBS) and whole genome sequencing (WGS) *rym13* was located on one BAC comprising different candidate genes.

For *Ryd3* the high resolution mapping population was extended to 7,177 F₂ plants. Due to a low recombination rate in the region of interest cosegregation of markers and phenotype could not be resolved even by analysing more than 14,000 meioses. By mapping these markers to the current physical map of barley it turned out that there are about 228 million bp between flanking markers comprising more than 2,000 annotated genes.

In a next step a mutation programme will be initiated using EMS to create genetic variation and isolate *Ryd3*.