Towards the high-resolution mapping and isolation of virus resistance/tolerance genes derived from *H. bulbosum*

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Hordeum bulbosum is the only member in the secondary genepool of barley (*H. vulgare*) and hence owns a great genetic potential for barley breeding. This species holds resistances against many pathogens, for example against *Barley mild mosaic virus/Barley yellow mosaic virus* (BaMMV/BaYMV) or *Barley yellow dwarf virus* (BYDV). Both diseases cause high yield losses in barley. Furthermore, the control of the aphid-transmitted BYDV is becoming difficult due to governmental regulations concerning insecticides and the use of chemicals to control BaMMV/BaYMV, transferred by the soil-borne protist *Polymyxa graminis*, is not possible. Thus, breeding for resistance is the only possibility to protect barley against these diseases.

Different *H. bulbosum* introgression lines carry resistance against BaMMV/BaYMV (*Rym16*^{Hb}) and *Ryd*$_{203S11}$^{Hb} for tolerance against BYDV on chromosome 2HL. DH lines carrying an introgression containing *Rym16*^{Hb} or *Ryd*$_{203S11}$^{Hb} were identified and characterized using molecular markers. Blasting sequences of these markers against the barley reference sequence allowed anchoring the introgression to the physical map and a size of the introgression fragment of 4.2 Mb for the *Ryd*$_{203S11}$^{Hb} locus and 3 Mb for the *Rym16*^{Hb} locus was calculated. Right now, F_2 populations carrying *Ryd*$_{203S11}$^{Hb} or *Rym16*^{Hb} are genotyped by using co-dominant flanking markers to construct a high resolution mapping population. The recombination rate within the introgression was found to be approximately 0.5 %, which is lower than the intraspecific recombination rate within in the barley genome, most likely caused by the incomplete homology between the genome of *H. vulgare* and *H. bulbosum*.

As a basis for isolating the respective genes via a map-based cloning approach, recombinant plants will be selfed, phenotyped and saturated with markers using Exome capture, GBS and Illumina 50K data. A non-gridded BAC library will be utilized to construct a physical map of the target region of *Ryd*$_{203S11}$^{Hb}. This map will help to identify candidate genes located in the *H. bulbosum* introgression fragment. In addition, a genotype-specific resistance of *Rym16*^{Hb} will be examined by using resistance gene enrichment sequencing (RenSeq).

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