Molecular characterization of *Barley yellow dwarf virus* (BYDV) resistance gene *Ryd4^{Hb}* introgressed from *Hordeum bulbosum* into barley

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BYDV is a widespread and economically important virus disease of cereals. The disease is caused by different viruses of the family *Luteoviridae* and results in high yield losses. As a consequence of global warming, aphids which may act as virus vectors are expected to be active for a longer time during the year, thereby increasingly threatening the growing of winter barley. The primary genepool, which is represented by *Hordeum vulgare* and its subspecies *H. vulgare* subsp. *spontaneum*, contains genes for tolerance, rather than resistance, against BYDV. In contrast, the secondary genepool, with the wild species *H. bulbosum* (Hb), was shown to comprise genes which confer complete resistance. In order to supply breeders with new sources of resistance, interspecific crosses between *H. vulgare* cv. 'Igri' and *H. bulbosum* were performed to generate a segregating mapping population.

Previous studies indicate that the resistance against BYDV was introgressed to barley chromosome 3HL and is governed by a dominant gene, *Ryd4^{Hb}*.

In the present study we develop molecular markers specific for the introgressed *Hb* segment. Three strategies are applied: (I) use of anchor markers from the barley genome, (II) make use of the orthology of parts of the *Hordeum* genome and the model genome of *Oryza sativa*, and (III) perform Massive Analysis of cDNA Ends (MACE) and RNASeq.

The approaches provide approximately 200 markers for the 3HL introgression. So far, we mapped about 40 markers on cromosome 3HL. Three markers are located in the vicinity of *Ryd4^{Hb}* and are of potential use for marker-assisted breeding programs.