Molecular characterization of BYDV resistance gene \( \text{Ryd4}^{\text{Hb}} \) introgressed from \( \text{Hordeum bulbosum} \) into barley

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Barley yellow dwarf virus (BYDV) causes high yield losses worldwide. Thereby aphids play an important role as virus vectors. Such yield losses caused by BYDV may be reduced using virus-tolerance genes from the primary gene pool of barley. Additionally, complete resistance to the virus has been introgressed via interspecific crosses from the secondary gene pool within the tetraploid wild species \( \text{Hordeum bulbosum} \) to barley chromosome 3HL. Previous studies indicate that this resistance is governed by a dominant gene, \( \text{Ryd4}^{\text{Hb}} \). In the present study, a \( \text{BC}_2\text{F}_4 \) mapping population consisting of 134 individuals was used to establish a molecular-marker map for \( \text{Ryd4}^{\text{Hb}} \). Using the model genome of \( \text{Oryza sativa} \), the Massive Analysis of cDNA Ends (MACE) approach was applied to develop novel markers. One of these markers cosegregated with \( \text{Ryd4}^{\text{Hb}} \). For a fine-mapping of \( \text{Ryd4}^{\text{Hb}} \) a \( \text{BC}_2\text{F}_6 \) family of 454 individuals will be used.