

# Identification of candidate genes for a BaYMV/BaYMV-2 resistance gene located on chromosome 5H of barley

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Barley yellow mosaic virus diseases caused by different strains of soil-borne *Barley yellow mosaic virus* (BaYMV) and *Barley mild mosaic virus* (BaMMV) is a serious threat for winter barley production in Europe and Asia due to yield losses up to 50 percent. Chemical measures to prevent these high yield losses are neither effective nor acceptable for ecological reasons. Thus, the only way to control barley yellow mosaic virus disease is to grow resistant cultivars. There are several loci known conferring resistance to the different strains of BaMMV and BaYMV. A new resistance gene being only effective against BaYMV and BaYMV-2 was located on chromosome 5H.

In order to identify and isolate candidate genes for this locus a map based cloning approach was started. Using co-dominant flanking markers a high resolution mapping population was constructed based on 5085 F<sub>2</sub>-plants (0.0098 cM resolution) derived

from the cross 'HHOR4224' x 'Igrí'. The interval carrying the resistance gene was estimated at 12.09% recombination according to these analyses.

Currently the marker saturation of the target interval is in progress using all available marker and sequence information in barley, and employing synteny to rice, Brachypodium and sorghum. Up to now 11 markers have been located in the interval exercising this approach. Overall 730 segmental recombinant inbred lines were identified and phenotypic analysis of 22 RILs gives first hint that the BaYMV/BaYMV-2 gene is located between markers k0xx1 and GBSxx1 comprising an interval of 2.8% recombination.

In order to integrate the BaYMV/BaYMV-2 resistance gene properly into the high resolution map all available segmental RILs are to be tested in field trials at two locations in the growing season 2012/2013.