

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 one of the most important diseases of winter barley in Europe and Asia and can cause yield losses up to 50 percent. In barley 9 different loci conferring resistance to the different strains of these viruses are known. One of these loci being effective only against BaYMV and BaYMV-2 is located on chromosome 5H. Therefore, the aim of this project is to identify and isolate candidate genes for this recessive resistance gene applying a map based cloning approach. In a first step a high resolution mapping population is constructed on 5000 F2 progeny (0.01 cM resolution) derived from the

cross 'HHOR4224' x 'Igri' using co-dominant flanking markers. Up to now 5085 plants have been analysed and the interval estimated at 12.95 cM. At present marker saturation of the target region is conducted using all sequence and marker information available for this interval in barley and employing synteny to rice, Brachypodium and sorghum. First polymorphic markers located in this interval have already been identified and mapped. Respective closely linked or co-segregating markers will facilitate the identification of candidate genes by analyzing BAC contigs. In the end this project will lead to a better understanding of the molecular basis of the resistance against *Barley yellow mosaic virus*.