Fine mapping and identification of candidate genes for a BaYMV/BaYMV-2 resistance gene located on chromosome 5H of barley

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One of the most important diseases of winter barley in Europe and East Asia is barley yellow mosaic virus disease caused by different strains of *Barley yellow mosaic virus* (BaYMV) and *Barley mild mosaic virus* (BaMMV) leading to yield losses up to 50% in susceptible winter barley varieties. Due to the transmission by the soil-borne plasmodiophorid *Polymyxa graminis*, chemical measures to prevent high yield losses are neither effective nor ecologically sound. Thus, breeding for resistance is of prime importance in order to ensure winter barley production in the growing area of infested fields. Up to now, nine different loci conferring resistance to the different strains of BaMMV and BaYMV are known. In order to get detailed information on the structure and function of a resistance gene being only effective against BaYMV and BaYMV-2 located in the centromeric region of chromosome 5H a map based cloning approach was conducted. For marker saturation of the target interval all available sequence information in barley and the synteny to rice, *Sorghum*, *Brachypodium* and sequence information included in the genome zipper was used. Phenotyping for BaYMV/BaYMV-2 resistance of respective segmental RILs derived from a high resolution mapping population comprising 5000 F_2-plants was carried out in field trials followed by DAS-ELISA. Based on marker saturation and phenotyping of 691 RILs the resistance gene was mapped in an interval of 0.22% recombination. By an additional exome capture sequencing approach of the parental lines, 249 morex contigs containing 256 genes were located in this interval. Out of these, two candidate genes were identified of which one is co-segregating with the resistance locus. Sequence analysis of this gene revealed 3 functional SNPs and a 6 bp deletion in the resistant parent.

Further analyses are in progress to get information whether this gene confers resistance to BaYMV/BaYMV-2. This shows that combination of different barley genomic resources and new generation sequencing technologies, applied in map based cloning procedures, is a powerful tool to accelerate soil-borne virus resistance gene isolation in barley.