High-resolution and -density mapping of *Barley mild mosaic virus* (BaMMV) resistance gene *rym15*

Yaping Wang, Antje Habekuß, Dragan Perovic and Frank Ordon
Julius Kühn-Institut, Institute for Resistance Research and Stress Tolerance, Quedlinburg
E-mail of corresponding author: yaping.wang@julius-kuehn.de

Barley is the second most important cereal crop in Europe. Besides others, *Barley mild mosaic virus* (BaMMV) which is transmitted by the soil-borne protist *Polymyxa graminis* has a serious impact on barley yield. Although a number of BaMMV resistance genes were already identified, which range from *rym1* to *rym18*, resistance of some genes has been broken by new virus isolates. For example, *rym4* is ineffective against BaYMV-2 and *rym5* has been shown to be not effective against a new BaMMV strain. Therefore, developing of closely linked molecular markers and next the isolation of up to now less used resistance genes is a genuine need for sustainable barley production.

In previous studies on double haploid (DH) lines derived from the F_1 of the cross of the resistant barley accession 'Chikurin Ibaraki 1' to the susceptible winter barley cv. 'Plaisant' *rym15* was located on the short arm of chromosome 6H. However, the study showed that the order of markers is inverted in relation of the genetic map derived from the cross from 'Lina' × *Hordeum spontaneum* 'Canada park'. Therefore, our work aims to construct high resolution mapping population of BaMMV resistance gene *rym15*, to (i) resolve the discrepancy between the two maps, (ii) narrow down the target region and saturate the map, (iii) with final aim to isolate *rym15*.

Two crosses derived from resistant barley cv. 'Chikurin Ibaraki 1' and susceptible cultivars 'Uschi' and 'Igri' comprising 2260 and 5671 F_2 grains, respectively, will be used for the construction of the high resolution mapping population of *rym15*. The reaction to BaMMV of homozygous recombinant plants concerning the target interval will be assessed by artificial inoculation and DAS-ELISA in green house tests. The Next-generation sequencing (NGS) techniques such as exome capture, and Genotyping by sequencing (GBS) based bulk segregant analysis (BSA) will be used for the detection of polymorphisms followed by the development of KASPar markers.

Until now, the resistance test of BaMMV in 365 F_2 plants originating from 'Chikurin Ibaraki 1' × 'Igri' cross showed segregation of 85 resistant : 280 susceptible. The segregation fitted a ratio 1:3 ($\chi 2=0.571$), suggesting the presence of one recessive resistance gene. We genotyped a set of 365 F_2 plants by using 6 SSR markers and 5 KASP markers developed based on the 50K Illumina array data. Genetic map was constructed and new robust co-dominant flanking markers were identified. Our plan is to screen about 5,000 F_2 plants with flanking markers, to develop a high density and resolution map of *rym15* gene in order to facilitate positional gene isolation.