Towards positional isolation of *Barley mild mosaic virus* (BaMMV) resistance gene *rym15*

Yaping Wang, Antje Habekuß, Dragan Perovic and Frank Ordon
Julius Kühn Institute, 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. *Barley mild mosaic virus* (BaMMV) and *Barley yellow mosaic virus* (BaYMV), which are transmitted by the soil-borne protist *Polymyxa graminis* have a serious impact on barley yield. Although a number of resistance genes are already known, 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* turned out 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 doubled 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 a high resolution mapping population of the gene *rym15* being effective against BaMMV, to (i) resolve the discrepancy between the two maps, (ii) narrow down the target region and saturate the map, (iii) with the final aim to isolate *rym15.*

Two crosses derived from the resistant barley cv. 'Chikurin Ibaraki 1' and susceptible cultivars 'Uschi' and 'Igri' were used for the construction of a high resolution mapping population of *rym15*. Segregation ratios in 365 and 158 F_2 plants from the 'Igri' × 'Chikurin Ibaraki 1' and 'Chikurin Ibaraki 1' × 'Uschi', i.e 85(R) : 280(S) and 30(R) : 128(S), respectively, fit to a ratio of 1r:3s ($\chi2$=0.571, $\chi2$=3.046), suggesting the presence of one recessive resistance gene. Six published SSR markers and 5 KASP markers developed based on the 50K Illumina array data were used for medium-resolution mapping. Genetic maps were constructed, new robust codominant flanking markers were identified and conflicting order of markers was solved. Furthermore, in order to construct the high resolution mapping population of *rym15*, 166 and 158 F_2 recombinants were selected by screening 2172 and 3413 F_2 plants from the crosses 'Igri' × 'Chikurin Ibaraki 1' and 'Uschi' × 'Chikurin Ibaraki 1', respectively. 86 SNPs between two flanking markers were identified by comparing the 50K Infinium Illumina array of susceptible and resistant bulks. These markers will be used for marker saturation of the target locus. Next, parental lines and bulks will be screened using Genotyping by Sequencing (GBS) for further marker saturation with the final aim to facilitate positional cloning of *rym15*.