Map-based cloning of *Rph*$_{MBR102}$ conferring resistance to barley leaf rust

Leila Fazlikhani, Dragan Perovic and Frank Ordon
Julius Kühn Institute, Institute for Resistance Research and Stress Tolerance, Quedlinburg
E-mail of corresponding author: leila.fazlikhani@julius-kuehn.de

Leaf rust of barley is a serious disease caused by the biotrophic fungus *Puccinia hordei* Otth., which under favorable conditions may cause yield losses up to 62%. So far, twenty-five race-specific leaf rust resistance genes (*Rph1-Rph25*) have been mapped, but no one have been yet isolated. However, some of these have been overcome by new pathotypes of *P.hordei*, indicating the need for introducing new sources of resistance into barley breeding as well as the need for isolating known ones towards deciphering the structure and function offering the possibility of developing functional markers for breeding. In this respect, recent advances in the development of barley genomic resources i.e. 9K and 50K iSelect arrays, genome zipper, POPSEQ, and GBS maps, as well as the barley reference sequence, enhance the possibility of narrowing down the target region harboring respective resistance genes. The *Rph*$_{MBR1012}$ gene previously mapped in the distal region of the short arm of barley chromosome 1H is effective against the highly virulent barley leaf rust (*Puccinia hordei*) isolate I-80. In order to positionaly clone the *Rph*$_{MBR1012}$ gene, a high resolution mapping population (HRMP) was constructed based on the cross "MBR1012 (resistant) x Scarlett (susceptible)". 537 segmental homozygous recombinant inbred lines (RILs) derived from 4775 F_2-plants corresponding to a resolution of 0.010% recombination were identified by analyzing the population with two co-dominant flanking SSR markers (QBS94 and QBS113) spanning an interval of 8.0 cM. To down size the target interval, initially 37 SSRs and SNP markers derived from the 9K chip and the genome zipper were mapped at the HRMP, resulting in shortening the target interval to 0.1 cM, flanked by QBS97 and QBS98. Further marker saturation was done by employment of 19 additional SNP markers derived from currently available barley genomic resources i.e. the 50K iSelect arrays and GBS. All selected markers from 50K iSelect and GBS were converted to KASPar markers. The target interval was downsized to 0.01 cM in the window between two KASP markers QBS127 and QBS98. Using BlastN search to the barley genome reference sequence, markers were anchored to the reference barley sequence revealing a physical size of 0.44 Mb. 18 high-confidence and 11 low-confidence genes were detected of which five are related to disease resistance. Allele specific re-sequencing of all 29 candidate genes was conducted to reduce the number of putative candidate genes.