

Marker saturation of the *Rph*_{MBR1012} locus conferring resistance against *Puccinia hordei* in barley using the 50K iSelect chip and Genotyping by Sequencing (GBS)

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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 facilitate enhanced identification of resistance genes. The resistance gene *Rph*_{MBR1012} previously mapped on the short arm of barley chromosome 1H is effective against the highly virulent barley leaf rust (*Puccinia hordei*) isolate I-80. In order to isolate *Rph*_{MBR1012} using a map-based-cloning approach, marker saturation of the target region and construction of a high resolution mapping population were undertaken in parallel based on the cross “MBR1012 (resistant) x Scarlett (susceptible)”. 492 segmental homozygous recombinant inbred lines (RILs)

derived from 4775 F₂-plants were identified by analyzing the population with two co-dominant flanking markers, separated by 8.0 cM. For marker saturation 35 SSRs and SNP markers from the genome zipper, and 9K iSelect chip converted to PCR-based markers, were used. Using this approach the target interval was shortened to 0.15 cM. Using data from the 50k iSelect chip and genotyping by sequencing 19 additional markers were identified and the target interval was further delimited to 0.095 cM. By blasting these markers to the reference sequence, the physical size of the interval was determined at 0.4 Mb. Five disease resistance like genes were identified in the target interval and are now re-sequenced.