High resolution mapping of leaf rust resistance gene derived from barley landrace MBR1012

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

Barley production is affected by a large number of diseases that cause high economic damages. Leaf rust caused by *Puccinia hordei*, is one of the most destructive barley diseases causing high yield losses in susceptible cultivars worldwide. Therefore, durable and broad spectrum resistance to pathogens is of prime importance for sustainable barley production. Resistance gene $Rph_{MBR1012}$ identified in the landrace "MBR1012" exhibiting a hypersensitive reaction to the very virulent *P. hordei* isolate I-80 has been previously mapped on chromosome 1H. To isolate this gene via a map based cloning approach, construction of a high resolution mapping population was undertaken, i.e. extending the resolution of the mapping population, increase marker density and by this approach identify candidate genes. High-resolution mapping resulted in the identification of 433 heterozygous recombinant and 15 homozygous recombinant F_3-families derived from 2663 F_2 plants by analyzing two co-dominant flanking markers, which were originally separated by 8.0 cM. Out of these, 317 segmental homozygous recombinant inbred lines (RILs) were identified up to now. Due to this work the genetic resolution of 0.023 % recombination from previous work was increased to 0.01 % and the genetic distance between flanking markers was estimated at 6.6 cM.

Currently, 17 markers located between the two flanking markers have been genotyped in order to saturate the locus. Homozygous F_4-RILs were in parallel infected with the *P. hordei* isolate I-80 and segregated 139 resistant: 172 susceptible ($X^2_{1:1}$ = 3.525), indicating a monogenic inheritance of resistance.