

High-resolution mapping of genes involved in plant stage-specific partial resistance of barley to leaf rust

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Abstract Partial resistance quantitative trait loci (QTLs) *Rphq11* and *rphq16* against *Puccinia hordei* isolate 1.2.1 were previously mapped in seedlings of the mapping populations Steptoe/Morex and Oregon Wolfe Barleys, respectively. In this study, QTL mapping was performed at adult plant stage for the two

mapping populations challenged with the same rust isolate. The results suggest that *Rphq11* and *rphq16* are effective only at seedling stage, and not at adult plant stage. The cloning of several genes responsible for partial resistance of barley to *P. hordei* will allow elucidation of the molecular basis of this type of plant defence. A map-based cloning approach requires to fine-map the QTL in a narrow genetic window. In this study, *Rphq11* and *rphq16* were fine-mapped using an approach aiming at speeding up the development of plant material and simplifying its evaluation. The plant materials for fine-mapping were identified from early plant materials developed to produce QTL-NILs. The material was first selected to carry the targeted QTL in heterozygous condition and susceptibility alleles at other resistance QTLs in homozygous condition. This strategy took four to five generations to obtain fixed QTL recombinants (i.e., homozygous resistant at the *Rphq11* or *rphq16* QTL alleles, homozygous susceptible at the non-targeted QTL alleles). In less than 2 years, *Rphq11* was fine-mapped into a 0.2-cM genetic interval and a 1.4-cM genetic interval for *rphq16*. The strongest candidate gene for *Rphq11* is a phospholipid hydroperoxide glutathione peroxidase. Thus far, no candidate gene was identified for *rphq16*.

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