

Haplotype divergence and multiple candidate genes at *Rphq2*, a partial resistance QTL of barley to *Puccinia hordei*

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Abstract

Key message *Rphq2*, a minor gene for partial resistance to *Puccinia hordei*, was physically mapped in a 188 kbp introgression with suppressed recombination between haplotypes of *rphq2* and *Rphq2* barley cultivars.

Abstract Partial and non-host resistances to rust fungi in barley (*Hordeum vulgare*) may be based on pathogen-associated molecular pattern (PAMP)-triggered immunity. Understanding partial resistance may help to understand non-host resistance, and vice versa. We constructed two non-gridded BAC libraries from cultivar Vada and line SusPtrit. Vada is immune to non-adapted *Puccinia* rust fungi, and partially resistant to *P. hordei*. SusPtrit is

susceptible to several non-adapted rust fungi, and has been used for mapping QTLs for non-host and partial resistance. The BAC libraries help to identify genes determining the natural variation for partial and non-host resistances of barley to rust fungi. A major-effect QTL, *Rphq2*, for partial resistance to *P. hordei* was mapped in a complete Vada and an incomplete SusPtrit contig. The physical distance between the markers flanking *Rphq2* was 195 Kbp in Vada and at least 226 Kbp in SusPtrit. This marker interval was predicted to contain 12 genes in either accession, of which only five genes were in common. The haplotypes represented by Vada and SusPtrit were found in 57 and 43 %, respectively, of a 194 barley accessions panel. The lack of homology between the two haplotypes probably explains the suppression of recombination in the *Rphq2* area and limit further genetic resolution in fine mapping. The possible candidate genes for *Rphq2* encode peroxidases, kinases and a member of seven-in-absentia protein family. This result suggests that *Rphq2* does not belong to the NB-LRR

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