

A COMPARATIVE MAPPING STRATEGY PROVIDES EVIDENCE ABOUT THE DERIVATION OF THE BARLEY LEAF STRIPE RESISTANCE GENE *Rdg1a*

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Leaf stripe of barley, caused by *Pyrenophora graminea*, is an important seed-borne disease in organically grown as well as in conventionally grown Nordic and Mediterranean barley districts. Two barley segregating populations represented by 103 recombinant inbred lines (RILs) of the cross 'L94' (susceptible) x 'Vada' (resistant) and 194 RILs of the cross 'Arta' (susceptible) x *Hordeum spontaneum* 41-1 (resistant), were analysed with two highly virulent leaf stripe isolates, Dg2 and Dg5, to identify QTLs for *P. graminea* resistance. A major QTL with its positive allele derived from 'Vada' and from *H. spontaneum* 41-1 was detected in both populations and for both the pathogen isolates on chromosome 2HL explaining 41.8% and 94.1% R^2 respectively for Dg2 and Dg5 in L94 x Vada and 97.8% and 96.1% R^2 respectively for Dg2 and Dg5 in Arta x *H. spontaneum* 41-1. Common markers mapped in the QTL region of the two populations allowed map comparison and highlighted an overlapping for the position of the resistance QTLs. Since the map position of the resistance QTLs identified in this report is at the same location as the leaf stripe resistance gene *Rdg1a*, mapped earlier in 'Alf' and derived from the 'botanical' barley line *H. laevigatum*, we propose that leaf stripe resistance in 'Vada' and *H. spontaneum* 41-1 is governed by the same gene, namely by *Rdg1a*, and that *Rdg1a* resistance could be traced back to *H. spontaneum*, the progenitor of cultivated barley. In the course of the mapping experiments, PCR-based molecular markers that can be used for marker-assisted selection (MAS) of *Rdg1a* were identified. An *Rdg1a* syntenic interval with the rice chromosome arm 4L was identified on the basis of rice orthologs of EST-based barley markers. Analysis of the rice genes annotated into the syntenic interval did not reveal sequences strictly belonging to the major class (nucleotide binding site plus leucine-rich repeat) of the resistance genes; nonetheless, four genes coding for domains which are present in the major disease resistance genes, namely receptor-like protein kinase and ATP/GTP binding proteins, were identified together with an homolog of the barley powdery mildew resistance gene *mlo*. Possible homologs of these genes in barley could represent candidates for *Rdg1a* or useful markers for fine mapping of the gene.