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Poster Abstract – D.32

IDENTIFICATION OF CANDIDATES OF THE BARLEY LEAF STRIPE RESISTANCE GENE Rdg2a BY MEANS OF MAP–BASED CLONING

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The barley gene *Rdg2a* confers resistance against several isolates of the seed borne fungal pathogen *Pyrenophora graminea* (the causal agent of barley leaf stripe) and immunity against isolate *Dg2*, the most virulent isolate of a collection of monoconidial isolates. Firstly, this gene was finely mapped to the distal region of the short arm of barley chromosome 1 (7H), by using a segregating population of 2800 F1 gametes. In addition, a rice-barley syntenic relationship, and a physical contig based on cv. *Morex* barley BACs clones that overlaps the *Rdg2a* interval map were established.

In order to characterize the genetic bases of leaf stripe resistance, subsequent steps of a map-based cloning approach for the *Rdg2a* gene were carried out. For this purpose the genomic region of *Rdg2a* was saturated with molecular markers developed by using information derived from shot-gun sequencing of the Morex BACs covering the region. Because the cv. Morex does not carry a functional allele of the resistance gene, a *5X* cosmid library of barley cv. *Thibaut* (bearing a functional allele of the gene) was constructed. The screening of the cosmid library with markers co-segregating and tightly associated to *Rdg2a* allowed the identification of a cosmid contig encompassing the genomic region of the gene. Sequencing of cosmids belonging to this contig led to the identification of two sequences coding for *NBS-LRR* (Nucleotide Binding Site-Leucine Rich Repeats) proteins, the most common class of plant disease resistance proteins. The comparison of the sequences present in the candidate genomic region of cv. *Thibaut* and of two distinct susceptible cvs. (*Morex* and *Mirco*) revealed genomic rearrangements both in coding and non-coding sequences. These rearrangements suggest that the two *NBS-LRR* sequences identified could represent good candidates for *Rdg2a*.