HAPLOTYPE ANALYSIS OF THE *RDG2A* LOCUS IN DIFFERENT BARLEY VARIETIES

BISELLI C.*,**, MARTINI A.*, URSO S.*, FACCINI N.*, TACCONI G.*, CATTIVELLI L.*, VALÈ G.**

- *) CRA Genomics Research Centre, Via S. Protaso 302, 29017 Fiorenzuola d'Arda (Italy)
- **) CRA Unità di Ricerca per la Risicoltura, Strada Statale 11 per Torino Km 2,5, 13100 Vercelli

Resistance gene, barley, leaf stripe, haplotype analysis

Leaf stripe disease on barley is caused by the seed-transmitted hemi-biotrophic fungus Pyrenophora graminea. Race-specific resistance to leaf stripe is controlled by two known Rdg (Resistance to Drechslera graminea) genes: the H. spontaneum-derived Rdg1a, mapped to chromosome 2HL and Rdg2a, identified in H. vulgare, mapped on chromosome 7HS and cloned in the resistant cultivar (cv.) Thibaut. The Rdg2a locus contains a gene cluster of three sequencerelated Coiled-Coil, Nucleotide-Binding site, and Leucine-Rich Repeat (CC-NB-LRR) encoding genes. However, only one gene conferred resistance to isolate Dg2, against which Rdg2a is effective, when the susceptible cv. Golden Promise was transformed with the Rdg2a-candidates. The high level of sequence similarity between the three genes most likely contributed to significant rearrangements during evolution, probably derived from un-equal crossing-overs resulting in sequence exchange between paralogs and in the generation of recombinant genes, as well as in expansion/contraction of gene copy number. To examine haplotype variation at the Rdg2a locus, the sequencing of the allelic Mrdg2a (Morex rdg2a) locus of the leaf stripe susceptible barley cv. Morex was carried out and revealed large rearrangements including two deletions that generated an Rdg2a-homolog gene. This gene most likely derived from an un-equal crossing-over between the Rdg2a ancestor and its paralog Nbs2-Rdg2a. PCR analyses performed with informative markers at five loci within the Rdg2a locus identified four different haplotypes. The Thibaut haplotype was observed to be largely conserved in Dg2-resistant barley cultivars. The re-sequencing of the Rdg2agene in barley genotypes showing the same Thibaut haplotype or the same resistant phenotype revealed high sequence similarity to Thibaut Rdg2a, demonstrating the widespread conservation of the gene. Nonetheless, some sequence variation were identified in at least two barley genotypes that were verified for possible differences, with respect to Rdg2a, in the range of resistance specificities towards different leaf stripe isolates.