

## MARKER-ASSISTED SELECTION FOR *MLO*-MEDIATED POWDERY MILDEW RESISTANCE IN BARLEY

G. TACCONI\*, V. BALDASSARRE\*, D. BULGARELLI\*, N. C. COLLINS\*\*, A. M. STANCA\*, G. VALÈ\*

\*) Istituto Sperimentale per la Cerealicoltura, C.R.A., Sezione di Fiorenzuola d'Arda, Via S. Protaso 302, I-29107 Fiorenzuola d'Arda (PC), Italy

\*\*) Australian Centre for Plant Functional Genomics, University of Adelaide, Waite Campus PMB1, Glen Osmond SA 5064, Australia

*barley, powdery mildew resistance, mlo, SNPs, marker-assisted selection*

Recessive *mlo* alleles of the barley *Mlo* gene confer resistance to almost all known isolates of the barley powdery mildew fungal pathogen. We sought to generate PCR markers suitable for selection of *mlo* in breeding populations. Towards this end, a search for single nucleotide polymorphisms (SNPs) and insertion/deletions (InDels) was carried out in three chromosomal regions adjacent to the *Mlo* gene. Analysis of sequences from four *Mlo*- and from three *mlo*-containing cultivars allowed the detection of eight SNPs and one InDel. PCR-based markers were subsequently developed for typing the SNPs. Molecular markers were analyzed within 36 *Mlo* and 25 *mlo* barley cultivars. At least two molecular markers could distinguish each of 28 *Mlo* barley cultivars from all of the *mlo* barley cultivars. In progeny of crosses between these resistant and susceptible lines, the identified markers could therefore be used to select *mlo* genotypes. To verify the utility of the markers, they were used to analyse *mlo*-segregating F<sub>2</sub> families derived from two different crosses. The marker alleles correctly predicted the *Mlo* locus genotypes in both crosses, indicating that the markers could be valuable tools for selection of *mlo*-mediated powdery mildew resistance in barley.