

## **IDENTIFICATION AND MAPPING OF RESISTANCE LOCI TO *PYRENOPHORA* SPP DERIVED FROM *HORDEUM SPONTANEUM***

G. TACCONI\*, D. RAU\*\*, V. MARTINO\*, S. GRANDO\*\*\*, E. DALL'AGLIO\*, G. TUMINO\*,  
A.M. STANCA\*, G. VALÈ\*

\*) Istituto Sperimentale per la Cerealicoltura, Consiglio per la Ricerca e sperimentazione in Agricoltura,  
Sezione di Fiorenzuola d'Arda, Via S. Protaso 302, I-29107 Fiorenzuola d'Arda (PC), Italy

\*\*) Dipartimento di Scienze Agronomiche e Genetica Vegetale Agraria, Università degli Studi di Sassari,  
Via E. de Nicola, Italy

\*\*\*) International Center for Agricultural Research (ICARDA), P. O. Box 5466, Aleppo, Syria

*barley, Pyrenophora teres, P. graminea, mapping*

Net blotch and leaf stripe caused by the fungi *Pyrenophora teres* Drechsler and *P. graminea* Ito & Kuribay respectively, represent serious threats to grain yield in barley (*Hordeum vulgare* L.). The wild progenitor of cultivated barley, *H. spontaneum* L. represents a useful source of resistance to various biotic stresses for the development of new resistant varieties. The evaluation of a *H. spontaneum* accession 41-1 to *P. graminea* and to *P. teres* demonstrated, respectively, full resistance and partial resistance to these disease. A medium-density, molecular marker map derived from a segregating population of recombinant inbred lines (RILs) obtained from the cross between *Hordeum spontaneum* 41-1 x 'Arta' (susceptible) was available. The inoculation of one hundred and ninety four RILs with the two pathogens lead to the identification and mapping of QTLs involved in the resistances. PCR-based molecular markers linked to these loci were also developed in order to improve the mapping; these marker can also represent useful tools for the introgression of these resistant loci in susceptible barley cultivars by molecular marked assisted selection.