

ASSOCIATION MAPPING FOR RESISTANCE TO *SEPTORIA TRITICI* BLOTCH IN DURUM WHEAT

SANGUINETI M.C. *, MACCAFERRI M. *, AMMAR K. **, MASSI A. ***, TALEBI R. ****, TABIB GHAFARY M. ***, KEMA G. ***, CORNETI S. *, TUBEROSA R. *

*) Dept. of Agroenvironmental Science and Technology (DiSTA), University of Bologna, Viale Fanin 44, 40127 Bologna (Italy)

**) CIMMYT, Int. Apdo Postal 6-641, Mexico City, 06600 (Mexico)

***) Società Produttori Sementi Bologna (PSB), Via Macero 1, 40050 Argelato (Italy)

****) Plant Research International B.V., 6700 AA Wageningen (The Netherlands)

Septoria tritici blotch (STB), Triticum durum Desf., association mapping, SSR markers, DArT markers

Durum wheat production in the Mediterranean basin is plagued by a range of biotic stresses. Among those, *Septoria tritici* blotch (*Mycosphaerella graminicola*) has become an important disease following the introduction of modern germplasm. The high genome plasticity of the pathogen and its specialization features (durum vs. bread wheat) complicate the identification of valuable resistance genes with durability and effectiveness across diverse growing areas. The genetic variation of the response to *Septoria* and the chromosomal location of resistance factors were studied using a germplasm collection of 183 durum wheat accessions of diverse origin suitable for association mapping (Maccaferri et al. 2006, Plant Genetics Resources 4: 79-85). The panel was evaluated in 2008 and 2009 in Tunisia (Beja), Mexico (Toluca) and Italy (Argelato and Ferrara). The accessions were then inoculated under controlled conditions with ten *Mycosphaerella* durum wheat isolates collected in a range of Mediterranean countries, as well as with bread wheat isolates and selected strains derived from crosses between durum and bread wheat isolates. The germplasm collection has been genotyped with ca. 300 SSRs of known map position and ca. 900 durum DArT markers. Highly diversified marker-trait association patterns have been obtained based on the field data, isolate and response-trait (% of necrotic leaf area and picnidia production). A preliminary analysis highlighted some chromosome regions consistently involved in *Septoria* resistance, particularly in chrs. 1BL, 2AL and 4AL that accounted for a sizeable portion of phenotypic variation among accessions. The detailed results will be presented and discussed.