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GENETIC ANALYSIS OF *SOIL-BORNE CEREAL MOSAIC VIRUS* (SBCMV) RESISTANCE IN A DURUM WHEAT MAPPING POPULATION

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Soil-borne cereal mosaic virus (SBCMV) is a Furovirus responsible for an important mosaic disease of wheat widespread in many wheat growing areas. Most of the durum wheat cultivars show a susceptible to medium-resistant response. Nevertheless, valuable sources of resistance have been identified (Rubies et al., 2006. Proc. 12th Congress of the Medit. Phytopat. Union, Rhodes, Greece, 10-15 June, pp. 100-102; Ratti et al., 2006. Plant Dis Protection 113: 145-149).

Recently, a main locus for disease resistance (*Sbm1*) has been identified in hexaploid wheat on chromosome 5DL (Bass et al., 2006. Genome 49: 1140-1148), but this resistance is not readily available to durum wheat breeders, due to its location on the D genome.

The objective of this study was to map a valuable source of SBCMV resistance using a durum population of recombinant inbred lines (RILs).

Genetic analysis of SBCMV resistance in durum wheat was carried out using a population of 181 RILs obtained from Meridiano (moderately resistant) x Claudio (moderately susceptible). The RILs were characterized for SBCMV response in the field under severe and uniform SBCMV infection during 2007 and 2008 and profiled with SSR and DArT markers. A wide range of disease reaction (as estimated by symptoms and DAS-ELISA) was observed. Most of the variability for SBCMV-response was explained by a major QTL (*QSbm.ubo-2BS*) located in the distal telomeric region of chromosome 2BS near *Xwmc243*, with the favourable allele contributed by Meridiano. QTLs with minor effects on SBCMV-response were also detected. Consistently with the observed transgressive segregation, both parents contributed resistance alleles. *QSbm.ubo-2BS* significantly affected grain yield and test weight of the grains.