

QTLs FOR YIELD AND RELATED TRAITS IN A DURUM WHEAT RIL POPULATION EVALUATED IN THE MEDITERRANEAN BASIN UNDER DIFFERENT WATER AVAILABILITIES

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IDuWUE (Improving Durum wheat for Water-Use Efficiency) project aims at identifying chromosome regions influencing yield and other morpho-physiological traits in Mediterranean environments with a wide range water availability. The identification of grain yield QTLs characterized by a limited QTL x E interaction would facilitate marker-assisted selection and, eventually, QTL cloning. We report the results concerning QTLs for yield and related traits identified in a RIL population tested in a broad range of water regimes in the Mediterranean basin.

During 2004, 249 RILs (Svevo x a desert durum line) were evaluated according to a modified augmented design with 3 checks in 8 trials: 5 under rainfed conditions (South Italy, Spain, Tunisia, Syria and Lebanon) and 3 with supplementary irrigation (Tunisia, Syria and Lebanon). The following traits were recorded: heading date (HD), plant height, peduncle length, chlorophyll content, leaf senescence, grain yield (GY), yield components and test weight. The linkage map (2347 cM; ca. 8 cM between markers) included 254 SSRs arranged in 23 linkage groups (Jurman et al., unpublished). The raw field data were adjusted according to the modified augmented design and the BLUPs (Best linear unbiased estimates) were subjected to ANOVA and QTL analysis.

The average GY ranged from ca. 57 q/ha to ca. 17 q/ha in the most favourable and the most severely stressed environments, respectively. Six QTLs affected GY across the environments. In particular, a QTL on chr. 2BL and one on chr. 3BS significantly influenced GY in 7 and 6 environments, respectively. Each of these 2 major QTLs accounted for ca. 17% of the variation for GY across environments and showed high LOD values (9.68 and 16.8, respectively). The

favourable allele was contributed by Svevo for the 2BL-QTL and by the desert durum for the 3BS-QTL. An additional QTL (chr. 1BL) was consistently detected in 4 rainfed and irrigated environments. A highly significant QTL effect (chr. 3BL) was detected only in the 2 environments with the highest drought stress and the lowest GY. The main GY QTLs did not coincide with QTLs for HD. Main QTLs for HD were mapped on chr. 2AS and 2BS in coincidence with the photoperiodic response genes *Ppd1* and *Ppd2* (Worland et al. 1996, *Euphytica* 89: 49-57). The 2 main GY QTLs overlapped with significant QTLs for plant height, peduncle length, kernel weight, chlorophyll content at grain milk stage and test weight. The relevance of these QTLs is further investigated by means of an association mapping approach based on a panel of unrelated elite genotypes (Maccaferri et al. 2005, *Molecular Breeding*, 15: 271-289 and 2006, *Plant Genetic Resources* 4: 79-85). The co-location of QTLs for GY with the QTLs for peduncle length, test weight and senescence rate under drought stress suggests a functional association of drought tolerance with plant vigour, photosynthesis capacity and possibly senescence. From an applicative stand point, the identification of 2 major QTLs highly effecting GY across a broad range of water availability is particularly valuable. This notwithstanding, QTLs characterized by a more specific action according to the level of water availability have been identified. As compared to QTLs for adaptation to particular target environments, QTLs more stable across water regimes play a more important role for marker-assisted selection.