

MAPPING QTLs FOR GRAIN YIELD, YIELD COMPONENTS AND QUALITY IN DURUM WHEAT

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A population of 180 F_{6.7} recombinant inbred lines (RILs) developed at DISTA from the cross between the durum wheat cultivars Simeto and Levante was evaluated in four field experiments (Cadriano and Bologna in 2008; Argelato and Bologna in 2009) conducted according to a modified augmented design field layout. The following traits were considered: heading date (HD), grain yield (GY), thousand kernel weight (TKW), test weight (TW), grain yellow pigment content (GYPC), semolina color (SC), grain protein content (GPC) and gluten quality (SDS).

The population was genotyped with SSRs, DArT markers and PCR primers directly designed from known allelic variants of specific genes (UBW markers tagging *Lr14* and STS markers tagging *Psy* genes). The linkage map included 30 linkage groups, for a total length of 1.771 cM, containing 200 SSRs and 402 DArT markers. The map covers about 75-80% of the entire genome of durum wheat. HD was controlled by a major QTL (*QHD.ubo-2B*) expressed in both field experiments, with R^2 values of 24.5 and 27.2% in Cadriano and in Argelato, respectively, and by five minor QTLs with R^2 ranging from 5.3 to 15.1%, depending on the environment. The map location of the major QTL for HD is most probably coincident with that of the photoperiod-sensitivity locus *Ppd-B1*; however, further molecular analyses are needed to confirm this hypothesis. QTLs for GY were identified on chrs. 5A and 6A with R^2 values lower than 10%; the favourable alleles for GY were always contributed by Levante. A major QTL for TKW was identified on chr. 2BL (*Qtkw.ubo-2B*), distal side, with R^2 value up to 14.6% in Cadriano-2008 (between *gwm55* and *wmc546*). In this case, the favorable allele was conferred by Simeto. This QTL did not show concomitant effects on HD, GY, or other yield components and mapped ca. 40 cM proximal to *QHD.ubo-2B*. Four major QTLs controlled the grain yellow pigment content and semolina color; these QTLs, which were consistently expressed across the two locations, were located on chrs. 2BL (*QSc.ubo-2B*, R^2 ca. 8%), 5BL (*QSc.ubo-5B*, R^2 ca. 9%), 7BS (*QSc.ubo-7B.1*, R^2 ca. 13%, in the proximal region) and 7BL (*QSc.ubo-7B.2*, R^2 ca. 6%, in the distal region). For all these four QTLs the favorable alleles were always conferred by the Levante. A major QTL on chr. 6A (*Qsds.ubo-6A*, with R^2 ca. 16%), was identified for gluten quality, as estimated with the SDS assay; in this case the favorable allele was conferred by Simeto. In general, both parents contributed favorable alleles for different traits, which allowed for the identification of transgressive RILs.