QTLS FOR DROUGHT-RELATED TRAITS IN A DURUM WHEAT RIL POPULATION EVALUATED IN THE MEDITERRANEAN BASIN UNDER DIFFERENT WATER AVAILABILITY


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A better knowledge of the genetic basis of the developmental processes involved in tolerance to drought will allow breeders to more effectively improve yield in drought-prone environments, i.e. the vast majority of the durum wheat production area in the Mediterranean basin. Resistance to drought stress, especially in terms of yield stability under the various stress conditions, is a main objective for durum wheat improvement. In the frame of the IDuWUE (Improving Durum wheat for Water-Use Efficiency) project, a mapping population (249 RILs developed from the cross between the Italian cv. Svevo and the US cv. Kofa) was evaluated for yield (GY), its components and morpho-physiological traits in 16 field trials carried out in Mediterranean environments (Italy, Spain, Morocco, Tunisia, Syria and Lebanon) characterized by different water availabilities and yield potential. Large differences among trials were evident for the length of the cycle and water input with GY ranging from 0.5 to 5.8 ton ha$^{-1}$. A broad variation was shown by the RILs for most of the investigated traits; heritability values calculated across environments varied greatly (e.g. 0.95, 0.68 and 0.28 for heading date, GY and fertile tillers per m$^2$, respectively). Two quantitative trait loci (QTLs on chromosomes 2BL and 3BS), out of the 16 that affected GY, showed significant effects in eight and seven environments, with $R^2$ values equal to 21.5 and 13.8% (mean data of all 16 environments), respectively. In both cases, the LOD profile for GY overlapped with those for other traits such as kernel weight and plant height. Three major QTLs for heading date (chr. 2AS, 2BL, and 7BS) and the major QTL for plant height (chr. 1BS) showed limited or no effects on GY
and its components. Noticeable epistasis between the 2BL and 3BS QTL clusters was consistently detected across traits and environments. Epistasis favored the parental genotypes and negatively affected the performance of the recombinant genotypes. Trait-specific QTLs were also identified for all the considered traits. The effects of the 2BL and 3BS QTLs were fully validated in a set of 11 trials conducted in 2006. In view of the relevance and consistency of their effects on grain yield and other agronomically valuable traits, the 2BL and 3BS QTLs are being isogenized in order to proceed with their fine mapping and, on the basis of their effects on plant height and peduncle length, their positional cloning.