

QTL ANALYSIS FOR YIELD COMPONENTS IN A SET OF RECOMBINANT INBRED LINES OF DURUM WHEAT GROWN IN DROUGHT ENVIRONMENTS

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Grain yield of durum wheat (*Triticum turgidum* L. var. *durum*) under Mediterranean conditions is frequently limited by both high temperature and low-erratic distribution of rainfall during grain growth. The plant's response in this stress conditions depends on its metabolic activity, morphology and stage of growth. Identifying QTLs that show consistent in expression across environments, even in different environments, would be desirable for marker assisted selection.

A set of 120 recombinant inbred lines (RIL) derived by single seed descent from the cvs Svevo and Ciccio were grown during the seasons 2004, 2005 and 2006 at Valenzano (BA, Italy), Gaudio (PZ, Italy) and Foggia (Italy). Yield components (grain yield, kernel number, 1000 kernel weight, grain yield per spike and test weight) and plant adaptive traits (plant height and heading time) were evaluated. QTLs analysis was carried out using a genetic linkage map of the RIL population obtained by genomic microsatellite and EST-derived SSR markers. QTL detection was based on Kruskal-Wallis analysis (van Ooijen, 2004) related to each RIL phenotypic mean values in single and across environments and data of polymorphic markers in the segregant population. The presence of a putative QTL was judged if a significant effect were observed in two or more trials with $P \leq 0.01$. A number of QTLs for yield were identified on group-2 chromosomes. In fact, QTLs for yield per spike, kernel weight and number kernels per spike were detected on 2BS chromosome arm. Moreover QTLs for several yield components were localized on 2AS chromosome arm that suggested that chromosome regions on 2AS and 2BS are involved in the control of grain. For yield per spike, one QTL on 2BS chromosome was detected in all environments, two QTLs, localized on 2A and 6B chromosomes, were identified in four environments and one QTL in three environments, indicating that individual QTLs seem to be sensitive to the environment. In situation with large genotype x environment interactions, such as in this study, it would be common to find a QTL significant in some trial but not in other. Three QTLs on 3BS, 3AL and 4BL chromosome arms were detected for the plant height in several experiments. Kernel weight and number of kernels per spike showed QTLs in the same regions: chromosomes 2BS, 2AS, 4BL and 6B. This result supposed that the same QTLs were involved in phenotypic expression of the two traits. Markers associated with variation in heading time were identified on 1AS and 2AS. Finally three QTLs for the test weight were detected on 2BS 7AS and 6AS.