

Abstract

Many of the traits involved in drought resistance in plants are controlled by multiple genes, so QTL detection and its application in marker-assisted selection (MAS) to improve plants plays an important role. In order to map the Genes/QTL_s for drought resistance in wheat, and to determine the portion of each QTL in the phenotypic variation of the related traits, 168 RIL derived from Laboratory of Zabol University in 2011. The experiments was arranged as to Completely randomized block design, with two replicates and two treatments. The phenotypic traits under study included: Percentage and germination rate, SCW, RWC, shoot and root length and their proportion, root and shoot fresh and dry weight, seed vigor, counts of root and GSI .After measuring traits, statistical analysis achieved for phenotypic surveys such as analysis of variance, correlation between traits, cluster analysis, principal component analysis and factor analysis. Analysis of variance result showed significant difference among the lines and different drought levels for most of the traits. The maximum correlation observed between dry and wet weight of shoot ($r= 0.90^{**}$). Factor analysis extracted five invisible factors, accounted for 78.3% of the variation and characters taken into consideration and named as weight factor, length factor, germination factor and physiological factor respectively. QTL analysis was carried out using genetic linkage map driven from 249 marker of AFLP marker, 74 SSR and 264 of DArT marker and QTL cartographer software with composite interval mapping method. In total 34 QTL was found for the traits (11 QTL for free drought condition, 12 QTL for drought condition, 11 QTL for the mean of these two conditions). Phenotypic variation that were explained by these QTL_s, varied from 5.86-16.09%. The highest and lowest phenotypic variances were related to ratio of shoot length/root length in drought condition and GSI in mean two conditions. LOD ranged between 2.524-4.856. The highest and lowest LOD were attained for the QTL_s of shoot length in free drought condition and GSI in mean two conditions.

Key words: QTL, drought stress, recombinant inbred line, wheat



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**Mapping genomic regions associated
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