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 Salinity risistance in wheat, and to determine the portion of each QTL in the phenotypic variation of the related traits, 167 RIL derived from greenhouse of Zabol University in 2012. The experiments was arranged as to Completely randomized block design, with two replicates and two treatments normal and saline. The studied traits were phonologic traits, morphologic traits and physiologic traits including: cloorophyll contents, clorophyll florescence, Plant height, Seed yield, SCW, RWC, Proline,.After measuring traits, statistical analysis achieved for phenotypic surveys such as analysis of variance, correlation between traits, Stepwise regression, cluster analysis, principal component analysis and factor analysis. Analysis of variance result showed significant difference among the lines and different salinity levels for most of the traits. The maximum correlation observed between Plant height and Seed yield (r= 0.84**). In stepwise regression of traits Plant height, Fm,, Days to germination, cloorophyll contents first traits that entired to model respectively and explained 66% of variation in normal condition and Plant height, Days to germination, Fm, Number of nodes, Fo and Fv/Fm were first traits that entered the model in stress condition respectively and explained 78/8% of total variation. In PCA analysis, the first tree principal components explained 51% of the total variability in normal condition and the first four principal components explained More than 50% of the total variability in stress condition. Factor analysis extracted characters taken into consideration and named as physiological factor, Phenological factor, Morphological factors respectively. Using cluster analysis grouped genotypes to salinity stress in normal conditions 4 and 5, respectively, were identified. QTL analysis was carried out using genetic linkage map drived from 249 marker of AFLP marker, 74 SSR and 264 of DArT marker and QTL cartographer software with composite interval mapping method. In total 44 QTL was found for the traits (15 QTL for free drought condition, 15 QTL for Salinity condition, 14 QTL for the mean of these two conditions). Phenotypic variation that were explained by these QTL$_s$, varied from 3.00-23.25%. The highest and lowest phenotypic variances were related to Days to tillering in normal condition and Days to germination in Salinity condition. LOD ranged between 2.51-4.44. The highest and lowest LOD were attained for the QTL$_s$ of Days to tillering in normal condition and Plant height in Salinity condition.

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

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