

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/QTLs for Salinity resistance in wheat, and to determine the portion of each QTL in the phenotypic variation of the related traits, 167 RIL derived research center for Agriculture Zahak in 2011. The experiments was arranged as to Alpha Lattice design, with two replicates and two treatments normal and saline. The studied traits were phenologic traits, morphologic traits and physiologic traits including: Days to Emergence, days to stem elongation, Plant m^{-2} , days to heading, days to anthesis, days from emergence to stem elongation, days from stem elongation to heading, plant height (Cm), Spike m^{-2} , Grain no. spike, biological yield, thousand grain weight, harvest Index and Seed yield, chlorophyll contents, chlorophyll fluorescence (Fv/fm). After measuring traits, statistical analysis achieved for phenotypic surveys such as analysis of variance, correlation between traits, cluster analysis, principal component analysis. Analysis of variance result showed significant difference among the lines and different salinity levels for most of the traits. Results of simple correlation coefficient analysis indicated a significant positive association between grain yield with harvest index, biological yield, the number of spike m^{-2} and the number of grain m^{-2} . The maximum correlation observed between biological yield and Seed yield ($r= 0.89^{**}$). In PCA analysis, the first five principal components explained 67% of the total variability in normal condition and the first seven principal components explained more than 72% of the total variability in stress condition. Using cluster analysis grouped genotypes to salinity stress in normal conditions 5 and 6, respectively, were identified. 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 26 QTL was found for the traits (16 QTL for free drought condition, 10 QTL for Salinity condition). Phenotypic variation that were explained by these QTLs, varied from 0.16-0.05%. The highest and lowest phenotypic variances were related to days to anthesis in normal condition and days to harvest Index in salinity condition. LOD ranged between 0.63-3.66. The highest and lowest LOD were attained for the QTLs harvest Index and days to stem in normal condition.

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



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