

Abstract

Many of the traits involved in salinity 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. To map QTLs of 30 phenological, physiological and morphological traits of "Seri×Babax" derived recombinant inbred line population, an experiment was conducted at Research Farm of Agricultural and Natural Resource Center of Zabol, Iran, using alpha lattice design with two replications under normal and salinity stress, in 2012 cropping cycle. After measuring traits, statistical analysis achieved for phenotypic surveys such as analysis of variance, correlation between traits, Stepwise regression, 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. QTL analysis was performed with using of a developed map, consisting DArT, AFLP and locus specific SSR markers. The map had a reasonably good coverage. Simple correlation coefficients, a significant positive correlation between grain yield and biological yield, plant height, peduncle length and dry weight of leaf heading in terms of stress and biological yield, harvest index, plant height and dry weight awn stress conditions among all biological traits studied showed the highest correlation with grain yield in normal conditions ($r=0.680$) and salinity ($r=0.612$) respectively. The high correlation between HI and biomass yield on the results of the stepwise yield was also demonstrated. QTL analysis using genetic linkage map of 249 markers, AFLP, 74 SSR markers and marker 264 DArT marker QTL cartographer software with composite interval mapping method. For traits in total 60 QTL (35 in normal conditions and in 25 conditions of salinity) were obtained. LOD in the range of 2.17-7.75, respectively. QTL LOD for flag leaf angle in terms of salinity minimum and maximum LOD for QTL canopy temperatures were obtained in normal conditions.

Key words: Wheat, QTL, recombinant inbred lines, salinity



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The Thesis Submitted for the Degree of M.Sc (Plant Breeding)

**Identification of genomic regions controlling
agronomical traits of Seri×Babax wheat RIL under
salinity stress**

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February 2015