

Mapping genomic regions of morphological and physiological traits of wheat under salinity stress conditions in hydroponic environment.

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. 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 from Agricultural Biotechnology Research institute of Zabol University in the hydroponic environment in 2012. The experiments was arranged as to Completely randomized block design, with two replicates and two treatments normal and saline. The studied traits morphologic traits and physiologic traits including: Percentage rate, Fresh and dry weight of root and shoot and the ratio, root length and shoot and the ratio, Chlorophyll concentration, Proline, The amount of soluble sugars, Relative water content, Membrane stability index and Chlorophyll fluorescence. 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. Maximum correlation between shoot fresh weight, dry weight were ($r= 0.94^{**}$). In The PCA (principal components analysis) analysis, the first five principal components explained 66.8% of the total variability in normal condition and the first seven principal components explained 77.1% of the total variability in stress condition. Factor analysis extracted characters taken into consideration and named as germination factor, optical factor, Water-holding capacity factor and membrane stability factor respectively. Using cluster analysis grouped genotypes normal and salt stress conditions 6 and 7, 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 38 QTL was found for the traits (16 QTL for normal condition and 22 QTL for Salinity condition). Phenotypic variation that were explained by these QTLs, varied from 6.12-18.43 The highest phenotypic variances were related to F_m in Salinity conditions and lowest phenotypic variances were related to The amount of soluble sugars and shoot length in normal and Salinity conditions respectively. LOD ranged between 2.57-6.31. The highest and lowest LOD were attained for the QTLs of Chlorophyll and Root to shoot length ratio normal condition.

Key words: QTL, Salinity stress, recombinant inbredline, wheat, Hydroponic.



University of Zabol
Graduate school
Faculty of Agriculture
Department of Plant Breeding and Biotechnology

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

**Mapping genomic regions of morphological and
physiological traits of wheat under salinity
stress conditions in hydroponic environment**

Supervisor:

Dr. B. Fakheri

Advisor:

Dr. M. Heidari

By:

M. Seraji Nodej

October 2013