

Analysis QTL of morphological and physiological traits of barley under aluminum stress conditions in hydroponic environment.

Abstract

Many of the traits involved in aluminum 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 genomic regions mapping associated to aluminum tolerance in barley, and to determine the portion of each QTL in the phenotypic variation of the related traits, 72 DHL derived of the cross “Steptoe/Morex” and their two parents at Agricultural Biotechnology Research institute of Zabol University in the hydroponic environment in 2013. The experiments was arranged as to Completely randomized block design, with three replicates and two treatments normal and aluminum stress. The studied traits morphologic traits and physiologic traits including: Percentage and rate of germination, 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, cluster analysis and principal component analysis. Analysis of variance result showed significant difference among the lines in both aluminum stress and normal conditions for all of the traits. Maximum correlation between percentage of germination, germination rate were ($r= 0.99^{**}$). In The PCA (principal components analysis) analysis, the first eight principal components explained 79.7% of the total variability in normal condition and the first eight principal components explained 78.2% of the total variability in stress condition. Using cluster analysis grouped genotypes in both normal and aluminum stress conditions 6 group, were identified. QTL analysis was carried out using genetic linkage map driven from 327 marker of RFLP marker, QTL cartographer software with composite interval mapping method. In total 68 QTL was found for the traits (35 QTL for normal condition and 33 QTL for aluminium stress condition). Phenotypic variation that were explained by these QTLs, varied from 1.6-27.2 The lowest phenotypic variances were related to dry weight of root/dry weight of shoot (Qwdr.wds4H.n) in normal condition and highest phenotypic variances were related to root length (Q2lrs4H.s) in stress condirion. LOD ranged between 2.50-5.98. The highest and lowest LOD were attained to the QTLs of root length (Q2lrs4H.s) in stress and germination rate (Qpijav7H.n) in normal condition.

Key words: QTL, aluminium stress, doubled haploid lines, barley, Hydroponic.



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

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June 2014