

QTL analysis of drought tolerance in barley double haploid lines

Abstract

Among the abiotic stresses that reduce the crop yields, drought is the most crucial factor for using in breeding programs. Morphophysiological traits which impact the drought resistance in plants inherited quantitatively and QTLs play the major role for their improving by marker assisted selection (MAS). Barley with specific genetic structure and morphology is appropriate plant model for genomics studies. In order to map the Genes/QTLs for salinity tolerance in barley, and to determine the portion of each QTL in the phenotypic variation of the related traits, 72 doubled-haploid lines derived from a cross between steptoe and morex were investigated. This experiment was carried out under hydroponic system in Botany laboratory of Zabol University in 2008. It was arranged according to completely randomized factorial design, with 3 replicates and 4 drought levels (0, 6.25, 12.5, 25 percentage). The phenotypic traits under study included: Chlorophyll Contents, Chlorophyll Fluorescence (F_o, F_v, F_m/F_v), Proline and Carbohydrate Rates, Relative Water Content (RWC), Germination Percentage, Coleoptyl Length, Stem and Radicle Length and their proportion, Dry and Wet Weight of root and shoot. After to measure traits, at first statistical analysis achieved for phenotypic surveys such as variance analysis, correlation between traits, cluster analysis, principle component analysis and factor analysis. Analysis of variance results showed that there were significant difference among the lines and different drought levels for most of the traits. The maximum correlation observed between dry and wet weight of shoot ($r=0.91^{**}$). Factor analysis extracted 7 invisible factors, when accounted for 80% of the variation and with to take into consideration characters pattern respectively are named as weight factor, length factor, germination factor and physiological sources factors. QTL analysis was carried out using genetic linkage map derived from 327 molecular marker of RFLP and QTL cartographer software with composite interval mapping method. In general we found 140 QTLs for the traits, 22 QTLs for free drought condition, 21 QTLs for first drought level, 29 QTLs for second drought level, 36 QTLs for third drought level and 32 QTLs for the mean of these four condition. Phenotypic variations that were explained by these QTLs, changed from 7.68 to 27.21. The highest and the lowest phenotypic variances were related to F_o in second drought condition and Radicle length in mean drought level, respectively. LOD was ranged in 2.51 to 7.35. The highest and the lowest LOD were attained for the QTLs of shoot dry weight in second drought condition (*Q4aDwD2*) and RWC in third drought level (*Q1RWCD3*).

Key words : QTL, Drought stress, Doubled haploid line, Barley.