

## QTL Mapping for some physiological traits of wheat under salinity stress

### Abstract

Salinity stress is genetical and physiological complex trait, controlled by quantitative trait loci (QTL). So, the identification of genes that plants can express against tolerance to salinity stress is essential for breeding programs. In order to genomic regions mapping associated with salinity tolerance and to determine the portion of each QTL in the phenotypic variation of the related trait, 167 recombinant inbred line were studied that derived from the cross of *Babax* and *Seri M82*, to gather with their two parents. In year 2012-2013 completely randomized alfa latis designed with tow replications at the Research Farm of Agriculture College of Zabol University were conducted under normal and salinity stress conditions. The studied traits includes yield of seed , left prolin content, carbohydrate content, RWC, chlorophyll a, chlorophyll b, chlorophyll c, Na and K. After measuring traits, statistical analysis including ANOVA, correlation between traits, step by step regression, cluster analysis, principle components analysis and factors analysis using version 9/0 of SAS was conducted. There was significant difference between the lines on the normal condition and stress condition for most of studied traits. There was maximum correlation between chlorophyll b traits and chlorophyll c. prolin and carbohydrate were first traits in the step by step regression on the normal condition that entered to the model and explained 60 percent of total variation. Prolin and then RWC was first trait that entered the model in the stress condition and explained 61 percent of total variation. The first Three components in principle components analysis, explained nearly 62 percent of total variation in the normal condition. And the first two components explained nearly 50 percent of total variation in the stress condition. Factors analysis extracted several invisible factors that explained over 70 percent of total variance.

QTL analysis was carried out using genetic linkage map derived 249 molecular marker of AFLP, 74 SSR marker and 264 DRT marker and using QTL cartographer software with composite interval mapping method. In general 16 QTL for studied traits were found (6 QTL for normal condition and 10 QTL for stress condition) that their explained phenotypical variance was vitiated between 6/23- 14/22 percent. The highest phenotypical variance was found for Na trait and the lowest phenotypical variance was found for carbohydrate in the stress condition. LOD ranged in 2/52-5/77. The highest and lowest LOD was attained for the Na and carbohydrate QTLs in the stress condition. In this study we found that only two QTLs were placed in the similar place and were stable (RWS 6A and Na 3D)

Key words: QTL, salinity stress, wheat



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