

## **Abstract**

In order to identify quantitative trait loci (QTLs) associated with drought tolerance and determine the contribution of each QTL to the phenotypic variation of the corresponding trait, 136 double haploid lines of barley with their parents (Nure / Tremois) were cultivated in 2015-2016 in one year in two locations, respectively in Experimental Center of Agriculture and Natural Resources of Zahak, Iran and in Experimental Center of Agriculture and Natural Resources of Sararood, Kermanshah, Iran, were studied in alpha-lattice design in two replications under two normal conditions and drought stress. The studied traits include phenological, morphological and physiological traits such as chlorophyll density, chlorophyll fluorescence, leaf proline content, and leaf relative water content (RWC). Statistical analysis was performed including analysis of variance, correlation analysis between traits, stepwise regression, cluster analysis, principal component analysis using SAS software version 9.3. By analyzing farm data and molecular markers data obtained from 543 markers (396 DArT markers, 18 STS-SNP markers and 10 SSR markers) with a length of 1.114 cm Morgan and an average distance of 2.8 cm Morgan, QTLs mapping were performed. The QTL analysis was performed in two different ways by QTL Cartographer ver.2.5 and QTL Network ver.2.1 software. The results of analysis of variance in both Zahak (Zabol) and Sararood (Kermanshah) locations showed that there was a significant difference between genotypes in both normal and stress conditions for most traits. QTL analysis using QTL Network ver.2.1 software was detected 174 QTLs in total with MCMC method, 82 of which were related to additive and additive  $\times$  environmental effect at the location of the Zahak (Zabol) and 92 cases related to additive and additive  $\times$  environmental effects in Sararood (Kermanshah). Of these 174 QTLs, 161 cases only included additive effects, while 9 had both additive and additive  $\times$  environmental effects, and four had only additive  $\times$  environmental effect. 351 QTLs were detected with epistatic and epistatic  $\times$  environmental effects, of which 171 cases related to the effects of epistatic (AA) and epistatic  $\times$  environmental (AAE) in two conditions (normal and drought stress) at the location of the Zahak (Zabol) and 180 cases related to the effects of epistatic (AA) and epistatic  $\times$  environmental (AAE) in two conditions (normal and drought stress) at the location of the Sararood (Kermanshah).

**Keywords:** Drought stress, alpha lattice, barley, QTL Network



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**Mapping genomic regions of morphological and physiological  
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