

Abstract

Common wheat (*Triticum aestivum* L.) is one of the most important seeds in the world. In addition to correcting wheat cultivars for grain yield, grain quality traits are of great importance. Also, due to the association of protein content with other qualitative and quantitative traits, awareness of overlapping of protein control genes with other traits is of great importance. The purpose of this study was to identify a genetic map of wheat for determining the QTLs related to grain quality in interaction with drought stress. For this purpose, a population of 167 lines and bacteria with their parents Babax and SeriM82 in two years of 2013 and 1393 in the form of alpha-lattice design with two replications under two normal and drought conditions at the Research Station of Yazd Agricultural and Natural Resources Research Center Genetic and phenotypic evaluation. In this experiment, 11 qualitative and quantitative qualities were measured. The QTL analysis was performed using a genetic map prepared by AFLP, DArT, and SSR markers, and the genetic locations of 11 quality and quantitative traits were identified. The genetic map made up of 29 generic linkages with a good overlay of markers. The results of analysis of variance showed that there is a significant difference between the wheat inbreds in most of the studied traits, which indicates the variation between inbred lines. Based on the results of combined analysis of variance, the effect of duration was significant for most traits in two locations. Simple correlation coefficients of trait, seed protein percentages with zeolite volume, bread volume, grain hardness, moisture content, water absorption, wet gluten, gluten elasticity, gluten index, SDS sedimentation volume and 1000 grain weight for both normal conditions and drought stress showed a positive and significant correlation. Among all studied traits, the amount of Zeleny and Gluten sediments had the highest correlation with grain protein percentage under normal and drought stress conditions. In stepwise regression, in normal conditions, traits of sediment yield, sediment volume, moisture gluten, bread volume and gluten index were measured in Zeleny sediment volume, SDS sedimentation volume, wet gluten, water absorption and bread volume. For both conditions, the high correlation between two traits of sediment volume and sediment volume of SDS with grain protein percentage was also proved in the results of stepwise regression. Factor analysis confirmed the results of correlation analysis and stepwise regression analysis. QTL analysis was performed for 3 experimental groups including normal conditions, dryness and mean of two conditions. For the studied traits, a total of 39 QTLs (13 QTLs for normal conditions, 11 QTLs for drought conditions and 15 QTLs for the mean of two conditions) were obtained. The variance of phenotypes explained by these QTLs varied from 0.5 to 13.35%. The LOD was in the range of 53.5-50 / 2. This study showed that the highest overlap among quality traits, blue whiting sedimentation volume, SDS sedimentation volume and wet gluten with protein content of grain was observed. Also, a number of wet gluten QTLs, Zeleny sedimentation volume, SDS sedimentation volume, water absorption and protein content of seeds were also in agreement.

Key words: bread wheat, inbred line, wet gluten, genetic map, QTL



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Mapping of genomic regions for quality bakery traits under drought stress

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