

## Abstract

Despite the importance of drought as a global challenge, a comprehensive phenological, morphological, physiological and molecular study has not been conducted under drought stress at the beginning of the growth season in Barley. Therefore, GWAS analysis was conducted to identify molecular markers associated with thirty phenological, agricultural, morphological and physiological traits in 148 spring barley genotypes using 407 SSR and AFLP markers. The resultant data were analyzed as alpha-lattice design with two replications in two conditions (normal irrigation and drought stress from the beginning of the growth season). In the phenotypic evaluation, the results of combined analysis of variance showed that there were significant differences between all genotypes and two experimental conditions. The results of correlation between traits, heritability and stepwise regression indicate in order to have genotypes with stable performance in both environments, traits such as plant height, spike length, thousand kernel weight and flag leaf length are the most important traits. In accordance with tolerance indices, Lamba, Astoria, Adele, Senor and Evelyn genotypes were identified as the most tolerant genotypes and Christia, Chalice, Pfl 1011, Bartok and Cathrine genotypes were identified as the most susceptible genotypes for drought stress. The results of population structure analysis divided this barley population into two subgroups. Overall for all the traits we detected 222 significant associated markers in normal irrigation and 235 significant associated markers in drought conditions. The AFLP marker “E42M48-282” on 5H was detected as a common significant associated marker for grain yield and peduncle lengths in normal condition. The SSR marker “Bmag0223” on 5H was also identified as a stable QTL for internode length in drought stress. The “HVM54” and “E37M33-93” markers on 2H and 3H were stable QTLs for flag leaf length exposed to drought. The “E38M54-133” marker on 4H was identified as a stable QTL for the number of days to Spike Emergence in the normal condition. Detecting highly significant associations in the most traits in each environment and also finding common QTLs in several traits, indicating a high stability of these markers and show correlation between pleiotropic effect on agronomic traits under normal irrigation and drought stress conditions. We anticipated that the presumably pleiotropic and multiple-trait QTL identified in this study (and in fact all significant MTAs) will be useful for simultaneous improvement of different agronomic traits in Barley breeding programs and indirect selection in order to improve the traits, especially under drought stress conditions.

**Key words:** Drought Stress, Association Mapping, Linkage Disequilibrium, Mixed Linear Model



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# **Association mapping of drought tolerance in Barley**

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