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Yasser S. Moursi*, **Samar G. Thabet**, Ahmed Amro, Mona F. A. Dawood, P. Stephen Baenziger, Ahmed Sallam*

Abstract

Drought induces several challenges for plant development, growth, and production. These challenges become more severe, in particular, in arid and semiarid countries like Egypt. In terms of production, barley ranks fourth after wheat, maize, and rice. Seed germination and seedling stages are critical stages for plant establishment and growth. In the current study, 60 diverse barley genotypes were tested for drought tolerance using two different treatments: control (0-PEG) and drought (20%-PEG). Twenty-two traits were estimated for seed germination and seedling parameters. All traits were reduced under drought stress, and a significant variation was found among genotypes under control and stress conditions. The broad-sense heritability estimates were very high under both control and drought for all traits. It ranged from 0.63 to 0.97 under the control condition and from 0.89 to 0.97 under drought, respectively. These high heritabilities suggested that genetic improvement of drought tolerance in barley at both stages is feasible. The principal component analysis revealed that root-related parameters account for the largest portion of phenotypic variation in this collection. The single-marker analysis (SMA) resulted in 71 quantitative trait loci (QTLs) distributed across the seven chromosomes of barley. Thirty-three QTLs were detected for root-length-related traits. Many hotspots of QTLs were detected for various traits.

Interestingly, some markers controlled many traits in a pleiotropic manner; thus, they can be used to control multiple traits at a time. Some QTLs were constitutive, i.e., they are mapped under control and drought, and targeting these QTLs makes the selection for drought tolerance a single-step process. The results of gene annotation analysis revealed very potential candidate genes that can be targeted to select for drought tolerance.

Keywords: single-marker analysis; barley; drought tolerance index; QTL; PCA