Abstract

Drought stress is a major obstacle in the production of crops. This research is done in order to identify genes involved in drought stress by the help of gene expression data analysis extracted from the NCBI database. We considered three data from barley, tomatoes and soybeans to start data analysis of gene expression. Data analysis showed that there are 258 genes; at least two data had significant expression change in the drought stress (fold change > 2, and p-value < 0.05). We identified 18 common genes based on the regulatory factor plantfd database. We selected UGE1,EREB Two gene and unknown protein ; for validation, we tested the expression of these genes in three plants of oat, soybean, and tomato under five drought levels (10, 15, 20, 25, and 30%). This experiment was conducted in winter 2015 at the Institute of Biology and Technology, University of Zabol based on completely randomized factorial design. The first factor of drought stress was 5 levels of irrigation of 10%, 15%, 20%, 25%, and 30% of field capacity (control), and the second factor included 3 plants of barley, tomato and soybean. After applying drought stress in seedling stage (4-leaf), plants' leaf tissue was sampled. Gene expression was determined by Real Time PCR method. According to the results obtained for each UGE1 gene, highest and lowest UGE1expressions were observed in tomato and rye, respectively. In addition, the highest and lowest levels of UGE1 gene expression were observed in treatments of 25% to 10% levels, respectively. According to the results obtained for each EREB gene, highest and lowest EREB expressions were observed in tomato and rye, respectively. In addition, the highest and lowest levels of EREB gene expression were observed in treatments of 25% to 10% levels, respectively. According to the results obtained for each LOC543932 gene, highest and lowest LOC543932 expressions were observed in tomato and rye, respectively. In addition, the highest and lowest levels of EREB gene expression were observed in treatments of 15% to 20% levels, respectively.

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Identification And validation of genes associated with drought stress in crop via analysis of gene expression datasets.

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January 2017